Sequence	OGE fraction	pI calculated	dCn	scan #	RT calculated	AC	half trypt.	full trypt.	m/z	Mass	dMass	ions	Xcorr.	RT & 1 pI stdev validated	RT & 2 pI stdev validated	Modification
AAFDDAIAELDTLSEESYK	1	3.38	0.443	1528	46.2	143E-DROME	TRUE	TRUE	2	2089.2	1.5	26of 36	5.6169	TRUE	TRUE	::::::::::::::::::::
YLAEFATGSDR	2	4.08	0.361	548	25.6	143E-DROME	TRUE	TRUE	2	1230.3	1.5	16of 20	3.6552	TRUE	TRUE	::::::::::::
DAAENSLIAYK	1	4.08	0.285	521	24.4	143E-DROME	TRUE	TRUE	2	1195.3	0.5	17of 20	3.7445	TRUE	TRUE	::::::::::::
DAAENSLIAYK	2	4.08	0.282	541	24.4	143E-DROME	TRUE	TRUE	2	1195.3	1.4	13of 20	2.4964	TRUE	TRUE	::::::::::::
DICSDILNVLEK	1	3.71	0.199	1556	37.2	143E-DROME	TRUE	TRUE	2	1419.6	0.5	19of 22	4.389	TRUE	TRUE	:::Cys_CAM:::::::::
DSTLIMQLLR	6	6.79	0.142	1946	37.23	143E-DROME	TRUE	TRUE	1	1190.4	2	10of 18	1.4471	TRUE	TRUE	::::::::::
NLLSVAYK	14	9.72	0.106	720	24.8	143E-DROME	TRUE	TRUE	2	908.1	0.5	10of 14	1.8843	TRUE	TRUE	::::::::
NLLSVAYK	13	9.72	0.056	850	24.8	143E-DROME	TRUE	TRUE	1	908.1	-0.3	9of 14	1.7077	TRUE	TRUE	::::::::
NLLSVAYK	15	9.72	0.025	761	24.8	143E-DROME	TRUE	TRUE	1	908.1	0.4	9of 14	1.5997	TRUE	TRUE	::::::::
SVTETGVELSNEER	1	3.8	0.4	384	21.9	143Z-DROME	TRUE	TRUE	2	1550.6	0.7	22of 26	4.2495	TRUE	TRUE	::::::::::::::
EICYEVLGLLDK	2	3.83	0.385	1249	43.9	143Z-DROME	TRUE	TRUE	2	1452.7	1.1	18of 22	3.8957	TRUE	TRUE	:::Cys_CAM:::::::::
SVTETGVELSNEER	2	3.8	0.37	420	21.9	143Z-DROME	TRUE	TRUE	2	1550.6	0.8	22of 26	4.1242	TRUE	TRUE	::::::::::::::
YLAEVATGDAR	2	4.08	0.285	372	24.7	143Z-DROME	TRUE	TRUE	2	1166.3	1.1	15of 20	3.1828	TRUE	TRUE	::::::::::
DMAQAMKSVTETGVELSNEER	1	4.01	0.208	384	35.06	143Z-DROME	TRUE	FALSE	3	2326.6	-0.1	20of 80	2.6536	TRUE	TRUE	::::::::::::::::::::
EICYEVLGLLDK	1	3.83	0.186	1328	43.9	143Z-DROME	TRUE	TRUE	1	1452.7	-0.6	12of 22	1.8914	TRUE	TRUE	:::Cys_CAM:::::::::
QAFDDAIAELDTLNEDSYK	1	3.32	0.148	1334	42.9	143Z-DROME	TRUE	TRUE	2	2159.3	1	16of 36	2.1864	TRUE	TRUE	::::::::::::::::::
DMAQAMKSVTETGVELSNEER	2	4.01	0.114	420	35.06	143Z-DROME	TRUE	FALSE	3	2326.6	0.1	17of 80	2.482	TRUE	TRUE	::::::::::::::::::::
LLLPTVLLLAADPVANVR	7	6.79	0.392	2236	73.2	2AAA-DROME	TRUE	TRUE	3	1889.3	1.8	1	4.8827	TRUE	TRUE	::::::::::::::::
LLLPTVLLLAADPVANVR	6	6.79	0.39	2447	73.2	2AAA-DROME	TRUE	TRUE	3	1889.3	0.9	34of 68	5.7879	TRUE	TRUE	::::::::::::::::
LLLPTVLLLAADPVANVR	8	6.79	0.387	2797	73.2	2AAA-DROME	TRUE	TRUE	3	1889.3	2.9	32of 68	5.1587	TRUE	TRUE	::::::::::::::::
VNQVQIILSSILPYVR	15	9.85	0.254	2219	58.3	2AAA-DROME	TRUE	TRUE	2	1843.2	0.9	18of 30	3.9503	TRUE	TRUE	::::::::::::::
VNQVQIILSSILPYVR	14	9.85	0.163	2123	58.3	2AAA-DROME	TRUE	TRUE	2	1843.2	1.4	16of 30	2.9405	TRUE	TRUE	::::::::::::::
EPCCEWVGEGGAGHFVKMVHNGIEY	3	4.68	0.049	1541	55.03	6PGD	TRUE	FALSE	3	2864.1	-2.7	20of 96	1.6789	TRUE	TRUE	:::Cys_CAM:Cys_CAM::::::::::::::::::::
DAYTSQPELSNLLLDDFFK	1	3.51	0.075	1784	56.3	6PGD-DROME	TRUE	TRUE	2	2217.4	0.5	18of 36	3.0652	TRUE	TRUE	::::::::::::::::::
ADTSQPLDACAADYEAK	1	3.51	0.039	476	27.2	6PGL-DROME	TRUE	TRUE	2	1826.9	0.8	14of 32	1.9165	TRUE	TRUE	:::::::::Cys_CAM:::::::
GTMNDEDRHVVVICRNQMYCVVLQASD	4	4.44	0.033	1861	60.66	A36526	TRUE	FALSE	3	3227.5	-2.1	7of104	0.8969	TRUE	TRUE	:::::::::::::Cys_CAM::::Oxidation_M::Cys_CAM::::::::
EAELIISYHPPIFKPLTR	11	7.75	0.31	1257	56.8	A36A-DROME	TRUE	TRUE	2	2125.5	0.4	16of 34	2.3673	TRUE	TRUE	::::::::::::::::::
AVNIISIRPLEPELGAPPGTGSGR	8	7.13	0.189	2003	55.2	A36A-DROME	TRUE	TRUE	2	2402.8	0.1	17of 46	3.1492	TRUE	TRUE	::::::::::::::::::::::
AIHRGWAEKQKWLLQCVDLQMFNR	15	9.9	0.044	1780	67.53	A37792	TRUE	FALSE	3	3029.5	1.1	9of 92	0.8954	TRUE	TRUE	:::::::::::::::::Cys_CAM:::::::::
IGIHGSILPGSHGIIECEHFDEK	4	5.16	0.133	1785	51.7	A48678	TRUE	FALSE	3	2546.8	0.8	16of 88	1.7859	TRUE	TRUE	:::::::::::::::::::Cys_CAM:::::::
LVPEGCLFDHIHNASR	5	6.02	0.003	2020	38.8	A4-DROME	TRUE	FALSE	2	1866.1	-2.9	4of 30	0.5883	TRUE	TRUE	:::::Cys_CAM:::::::::::
FNDEVSLSLR	2	4.08	0.131	730	29	A53773	TRUE	TRUE	2	1180.3	2.3	15of 18	3.071	TRUE	TRUE	::::::::::
EADDLLK	1	3.71	0.064	617	17.6	A53970	TRUE	TRUE	1	803.9	0.3	9of 12	1.4467	TRUE	TRUE	::::::::
SHDNNNASAVSMLLPQDGDASGA	1	3.6	0.067	765	32.23	A55921	TRUE	FALSE	2	2288.4	-1.5	10of 44	1.5649	TRUE	TRUE	:::::::::::Oxidation_M:::::::::::
LTQPTTVSPGIPGGAAAPNPACEK	7	6.29	0.008	1115	40.5	A56922	TRUE	FALSE	3	2335.6	0.7	30	1.917	TRUE	TRUE	:::::::::::::::::::::Cys_CAM:::
KPMTDDVTGEPLIR	3	4.31	0.331	1167	29.83	AB009996	TRUE	TRUE	2	1572.8	1.4	16of 26	2.6921	TRUE	TRUE	::::::::::::::::
FCVCHLSTGDMLR	9	7.01	0.266	1388	37.73	AB009996	TRUE	TRUE	2	1612.8	1.2	16of 24	2.426	TRUE	TRUE	::Cys_CAM::Cys_CAM::::::Oxidation_M:::
YEPENIGINAILLGPPGSGK	2	4.27	0.163	1176	48.8	AB009996	TRUE	TRUE	2	2040.3	1.4	18of 38	2.2397	TRUE	TRUE	::::::::::::::::::
GSSGVGLTAAVTTDQETGER	2	3.83	0.221	550	25.1	AB010107	TRUE	TRUE	2	1937	1.4	12of 38	2.014	TRUE	TRUE	::::::::::::::::::
CSVLAAANPVYGR	13	8.9	0.204	822	31.6	AB010107	TRUE	TRUE	2	1378.5	0.7	16of 24	2.4448	TRUE	TRUE	:Cys_CAM:::::::::::
NLYQNLISSLFPSIYGNDEVKR	6	6.89	0.382	2358	59.2	AB010108	TRUE	TRUE	2	2571.9	1.9	15of 42	3.601	TRUE	TRUE	::::::::::::::::::::
DFVEEDDPLLVVHPNYVVE	1	3.38	0.235	1349	59	AB010108	TRUE	FALSE	2	2229.4	1.4	14of 36	2.9029	TRUE	TRUE	::::::::::::::::
TGFAQMIQGLLSETFLQAHR	10	7.85	0.411	1998	56.43	AB010109	TRUE	TRUE	3	2265.6	1.3	31of 76	3.9979	TRUE	TRUE	:::::Oxidation_M:::::::::::::
MAQPGDHIVVSGVFLPLMR	10	7.85	0.177	1505	60.66	AB010109	TRUE	TRUE	2	2084.5	1.5	14of 36	2.2409	TRUE	TRUE	:::::::::::::::Oxidation_M:::
ISHIIDRSTTKGFKPDQVD	11	7.79	0.022	592	31.6	AB010109	TRUE	FALSE	3	2158.4	1.9	25of 72	2.6058	TRUE	TRUE	::::::::::::::::::
HLLFEADADHDDKLTK	3	4.53	0.34	1164	30.5	AB011261	TRUE	TRUE	2	1869	1.4	20of 30	2.7506	TRUE	TRUE	::::::::::::::
DLDKDGYLNEEEVK	1	3.76	0.335	504	24.6	AB011261	TRUE	TRUE	2	1667.8	1.5	18of 26	3.7576	TRUE	TRUE	::::::::::::::
LTYTLAVNHLADKTEEELK	4	4.63	0.274	1609	44.3	AB011376	TRUE	TRUE	3	2189.5	2.5	25of 72	2.5272	TRUE	TRUE	::::::::::::::::::
FQFTHLSAGDLLR	9	7.85	0.417	1860	40.2	AB025924	TRUE	TRUE	2	1505.7	2.6	21of 24	4.1633	TRUE	TRUE	::::::::::::::
KFLLKIVYDAS	13	9.63	0.016	939	39	AB026979	TRUE	FALSE	3	1297.6	-2.6	11of 40	1.3411	TRUE	TRUE	::::::::::::
AILRFLTDLANTYCK	13	8.88	0.019	1527	49	AB031048	TRUE	FALSE	2	1800.1	3	5of 28	0.8358	TRUE	TRUE	:::::::::::Cys_CAM::
CKDEPGQQPKSVLKYNDYEAMSVNMEYDV	1	4.07	0.026	1910	52.06	AB031086	TRUE	FALSE	3	3471.8	1.7	13of112	1.2223	TRUE	TRUE	:Cys_CAM::::::::::::::::Oxidation_M:::Oxidation_M:::::
STIGVEFATR	6	6.98	0.136	1146	23.8	AB035354	TRUE	TRUE	2	1081.2	1.7	14of 18	2.282	TRUE	TRUE	::::::::::
DIPMPEDLK	1	3.71	0.052	633	24.43	AB035419	TRUE	FALSE	1	1074.2	0	7of 16	1.498	TRUE	TRUE	:::Oxidation_M:::::
VSRLPPSVQARPSYKSNGYVSEPEPNYDSD	3	4.56	0.022	2012	45.3	AB053478	TRUE	FALSE	3	3340.6	-1.8	17of116	1.6068	TRUE	TRUE	::::::::::::::::::::::::
VQPFNNLDEPIAEGYFPKM	1	3.83	0.067	1358	53.63	AB055857	TRUE	FALSE	2	2210.5	2.3	14of 36	1.8755	TRUE	TRUE	::::::::::::::::::
LHNVALYKAHI	15	9.72	0.276	963	30.2	AB069961	TRUE	FALSE	1	1279.5	-0.5	11of 20	1.7204	TRUE	TRUE	::::::::::::
PLGTCSSNGTGEQSTGLYRK	13	8.88	0.174	780	23.5	AB069961	TRUE	FALSE	3	2114.2	2.5	19of 76	2.0993	TRUE	TRUE	:::::Cys_CAM:::::::::::::
LHNVALYKAHI	14	9.72	0.097	878	30.2	AB069961	TRUE	FALSE	1	1279.5	-0.3	12of 20	1.5837	TRUE	TRUE	::::::::::::
AYYRGAMGIMLVYDITQEK	6	6.84	0.105	2287	55.26	AB112933	TRUE	FALSE	2	2239.6	-2.5	10of 36	1.249	TRUE	TRUE	:::::::::Oxidation_M:::::::::
PEEHPVLLTEAPLNPK	3	4.54	0.46	1335	38.4	ACT1-DROME	TRUE	FALSE	2	1785.1	0.4	21of 30	4.1871	TRUE	TRUE	::::::::::::::::
VAPEEHPVLLTEAPLNPK	3	4.54	0.451	1331	45.4	ACT1-DROME	TRUE	TRUE	2	1955.3	2.5	20of 34	4.4175	TRUE	TRUE	::::::::::::::::
SYELPDGQVITIGNER	1	3.83	0.427	1022	35.6	ACT1-DROME	TRUE	TRUE	2	1792	2.3	22of 30	3.8154	TRUE	TRUE	::::::::::::::::
RVAPEEHPVLLTEAPLNPK	6	5.4	0.423	1263	44.8	ACT1-DROME	TRUE	FALSE	2	2111.4	0.5	18of 36	3.8677	TRUE	TRUE	::::::::::::::::::
SYELPDGQVITIGNER	2	3.83	0.422	994	35.6	ACT1-DROME	TRUE	TRUE	2	1792	2	23of 30	4.2999	TRUE	TRUE	::::::::::::::::
VLDSGDGVSHTVPIYEGYALPHAILR	5	5.12	0.367	1882	67.4	ACT1-DROME	TRUE	FALSE	3	2781.1	2.7	32of100	4.4665	TRUE	TRUE	::::::::::::::::::::::::
KDLYANTVLSGGTTMYPGIADR	6	6.77	0.367	1534	47.23	ACT1-DROME	TRUE	TRUE	2	2344.6	-0.2	23of 42	4.2718	TRUE	TRUE	::::::::::::::::::::
KDLYANTVLSGGTTMYPGIADR	7	6.77	0.331	1341	47.23	ACT1-DROME	TRUE	TRUE	2	2344.6	-0.4	1	3.5578	TRUE	TRUE	::::::::::::::::::::
IWHHTFYNELR	11	7.92	0.305	773	33.2	ACT1-DROME	TRUE	TRUE	1	1516.7	0.1	12of 20	2.7596	TRUE	TRUE	::::::::::::
IWHHTFYNELR	10	7.92	0.26	986	33.2	ACT1-DROME	TRUE	TRUE	3	1516.7	0.8	19of 40	2.3078	TRUE	TRUE	::::::::::::
DLYANTVLSGGTTMYPGIADR	2	3.89	0.236	1014	49.33	ACT1-DROME	TRUE	TRUE	2	2232.5	1.2	16of 40	2.8498	TRUE	TRUE	:::::::::::::Oxidation_M:::::::::
APEEHPVLLTEAPLNPK	3	4.54	0.221	1340	40.4	ACT1-DROME	TRUE	FALSE	2	1856.1	0.9	14of 32	2.4095	TRUE	TRUE	::::::::::::::::
DLYANTVLSGGTTMYPGIADR	1	3.89	0.186	1133	49.33	ACT1-DROME	TRUE	TRUE	2	2216.5	1.4	12of 40	1.9453	TRUE	TRUE	::::::::::::::::::::
DLTDYLMK	1	3.89	0.168	712	25.13	ACT1-DROME	TRUE	TRUE	2	1015.2	1.7	11of 14	2.3811	TRUE	TRUE	::::::Oxidation_M:::
AGFAGDDAPR	2	3.89	0.133	121	15.5	ACT1-DROME	TRUE	TRUE	2	977	2.4	15of 18	2.2434	TRUE	TRUE	::::::::::
MLYQNIVLSGGSTLFK	14	9.72	0.18	1434	51.93	ACTZ-DROME	TRUE	TRUE	2	1772.1	0.1	17of 30	2.2557	TRUE	TRUE	::::::::::::::::
KFGFTDFVNPK	14	9.89	0.374	980	27.1	ADHX-DROME	TRUE	TRUE	2	1300.5	1.3	14of 20	2.6327	TRUE	TRUE	::::::::::::
KPLVIEDIEVAPPK	3	4.45	0.322	1399	39.1	ADHX-DROME	TRUE	TRUE	2	1548.9	-0.5	21of 26	4.408	TRUE	TRUE	::::::::::::::
FGFTDFVNPK	6	6.76	0.12	1630	29.2	ADHX-DROME	TRUE	TRUE	1	1172.3	-0.2	13of 18	2.0129	TRUE	TRUE	::::::::::
YFISR	14	9.85	0.005	258	19.2	ADRL-DROME	TRUE	FALSE	1	685.8	0	6of 8	0.9265	TRUE	TRUE	:::::::
IHVNYEFAHDQLVNSFVGKPK	11	7.88	0.44	1076	46.5	AE003122	TRUE	TRUE	2	2443.8	1.7	24of 40	5.5544	TRUE	TRUE	::::::::::::::::::::::

NETASNEDDDNAQVKHIGTITKIFSIAQRMKEK	4	5.49	0.024	2462	46.43	AE003411	TRUE	FALSE	3	3750.1	0.3	20of128	1.6724	TRUE		TRUE	::::::::::::::::::::::::::::::Oxidation_M::::
QYQLGPNGGIVTALNMFTTK	14	9.72	0.223	1589	48.63	AE003419	TRUE	TRUE	2	2154.5	2.2	12of 38	2.2612	TRUE		TRUE	::::::::::::::::::
DYEAMRRPVESLRMVKQKEVLVDR	13	9.63	0.179	1483	52.66	AE003420	TRUE	FALSE	3	2949.5	0.3	12of 92	1.3971	TRUE		TRUE	::::::::::::::::::::
IANLAPAAPAGGSSAAASASAAAK	15	10.1	0.343	503	39.6	AE003422	TRUE	TRUE	2	1997.2	0	24of 46	3.0801	TRUE		TRUE	::::::::::::::::::::
IEGLLAAFPK	7	6.95	0.219	1400	36.5	AE003422	TRUE	TRUE	2	1059.3	1.4	1	2.0897	TRUE		TRUE	::::::::::
NLGKPFPLNTDVGVLK	13	9.89	0.16	1198	41.4	AE003422	TRUE	TRUE	2	1713	0.1	16of 30	2.0764	TRUE		TRUE	::::::::::::::::
YDFEKELIHRSNRHIR	14	9.72	0.085	1442	29	AE003422	TRUE	FALSE	2	2114.4	-0.8	10of 30	1.4253	TRUE		TRUE	::::::::::::::::
LSPNHTQGLQLQTHPNVDKELFK	11	7.95	0.021	850	42	AE003422	TRUE	TRUE	3	2646	1.4	21of 88	1.8278	TRUE		TRUE	::::::::::::::::::::
KSSVVEGFGIANNLARLTSMAL	15	10.09	0.005	1524	58.13	AE003422	TRUE	FALSE	2	2295.7	1.9	12of 42	1.8202	TRUE		TRUE	::::::::::::::::::Oxidation_M:::
SLVHQAVLGVDK	9	7.82	0.369	1288	28.8	AE003423	TRUE	TRUE	2	1266.5	0.8	18of 22	3.2725	TRUE		TRUE	::::::::::::
ATKPLEEALASSHLSLDVINQVILFGGGTR	6	5.35	0.25	2284	78.4	AE003423	TRUE	TRUE	3	3138.6	2.6	26of116	3.2836	TRUE		TRUE	::::::::::::::::::::::::::::::
ALFALMNPYPQK	15	9.72	0.178	1320	39.63	AE003423	TRUE	TRUE	2	1393.7	0.9	16of 22	2.9942	TRUE		TRUE	::::::::::::
LESAFNALEAHIIEVQQK	3	4.54	0.14	1699	48.4	AE003423	TRUE	TRUE	2	2041.3	1.6	15of 34	2.0623	TRUE		TRUE	::::::::::::::::::
TSAAVVSYQLVK	14	9.72	0.086	675	29.7	AE003423	TRUE	TRUE	1	1266.5	-0.5	12of 22	1.7773	TRUE		TRUE	::::::::::::
VYIHIVEQQGR	10	7.77	0.027	657	27.5	AE003423	TRUE	TRUE	2	1342.5	0.4	12of 20	1.5587	TRUE		TRUE	::::::::::::
KPPYSVEGIPTLIR	15	9.72	0.343	1119	37	AE003426	TRUE	TRUE	2	1570.9	2.7	16of 26	2.6752	TRUE		TRUE	::::::::::::::
KDNMFRKPPYSVEGIPTLIR	15	10.18	0.238	1119	47.53	AE003426	TRUE	FALSE	3	2362.8	-3	20of 76	2.6727	TRUE		TRUE	::::::::::::::::::
AIELSPGNALFHAK	11	7.82	0.271	940	35.6	AE003429	TRUE	TRUE	1	1468.7	0.4	17of 26	2.6695	TRUE		TRUE	::::::::::::::
TQQSIFEGITAFNQNNLK	6	6.95	0.476	1766	39.1	AE003430	TRUE	TRUE	2	2054.3	0.3	22of 34	4.9798	TRUE		TRUE	::::::::::::::::::
TQQSIFEGITAFNQNNLK	7	6.95	0.429	1571	39.1	AE003430	TRUE	TRUE	2	2054.3	0.2	1	4.0105	TRUE		TRUE	::::::::::::::::::
NQFIAGIENFDAK	2	4.08	0.345	978	32.8	AE003430	TRUE	TRUE	2	1467.6	1.9	18of 24	3.6311	TRUE		TRUE	::::::::::::::
NQFIAGIENFDAKK	6	6.99	0.274	1450	30.7	AE003430	TRUE	TRUE	2	1595.8	1.8	18of 26	3.5533	TRUE		TRUE	::::::::::::::
TQQSIFEGITAFNQNNLK	9	6.95	0.233	1957	39.1	AE003430	TRUE	TRUE	2	2054.3	0.5	14of 34	2.104	TRUE		TRUE	::::::::::::::::::
YVHYVDFNKRLDEWVNEEDLYTR	4	4.37	0.096	2515	59.5	AE003430	TRUE	FALSE	3	3005.3	-2.7	21of 88	1.5724	TRUE		TRUE	::::::::::::::::::::
CTVYTTLVGLLNAK	13	8.88	0.017	1666	42.3	AE003431	TRUE	TRUE	1	1553.8	1.3	10of 26	1.5171	TRUE		TRUE	:Cys_CAM::::::::::::
TVLLANNISLLSK	15	10.1	0.225	1256	43.7	AE003434	TRUE	TRUE	2	1386.7	1.5	21of 24	3.5648	TRUE		TRUE	::::::::::::::
GYQVATGGTDVHLVLVDVR	5	5.1	0.583	1638	46	AE003435	TRUE	TRUE	2	2000.3	2.1	28of 36	5.8926	TRUE		TRUE	::::::::::::::::::
INQAVFPSLQGGPHNNAVAGIATAFK	15	10.1	0.484	1400	56.9	AE003435	TRUE	TRUE	2	2624	-0.1	22of 50	4.2368	TRUE		TRUE	::::::::::::::::::::::
IMGLDLPDGGHLTHGFFTPTKK	11	7.94	0.301	1248	50.43	AE003435	TRUE	TRUE	2	2383.8	2.1	19of 42	3.0103	TRUE		TRUE	::::::::::::::::::::
TLAENVELK	2	4.27	0.138	430	23.3	AE003435	TRUE	TRUE	2	1017.2	1.4	14of 16	1.7762	TRUE		TRUE	::::::::::
YGNFQPNTYTFTKSL	13	9.53	0.051	816	33.4	AE003435	TRUE	FALSE	2	1782	-1.3	10of 28	1.2837	TRUE		TRUE	::::::::::::::
SELQAARRDRGEALQMQRSLRDEL	12	7.26	0.001	1613	44.03	AE003435	TRUE	FALSE	3	2830.2	-3	17of 92	1.7761	TRUE		TRUE	::::::::::::::::::::
GETLKRTSIM	15	10.09	0.036	501	20.23	AE003436	TRUE	FALSE	2	1152.4	-2.9	9of 18	1.2792	TRUE		TRUE	:::::::::Oxidation_M:
VTNYPATFDIHSYCLGHR	11	7.31	0.381	924	39.8	AE003437	TRUE	TRUE	2	2152.3	0.8	19of 34	3.1392	TRUE		TRUE	::::::::::::Cys_CAM::::::
EVIELPLLNPELFLR	1	3.97	0.159	1893	67.1	AE003437	TRUE	TRUE	2	1796.2	2.4	13of 28	2.0756	TRUE		TRUE	::::::::::::::
IAELTSLPFVTAPNKFEALAAR	8	7.1	0.252	2277	66.8	AE003438	TRUE	TRUE	2	2360.8	1.3	17of 42	2.5866	TRUE		TRUE	::::::::::::::::::
APKSLDYPVNTPDTDESLLSVHEKVSRFTHSAEK	4	5.32	0.055	1773	54.9	AE003438	TRUE	FALSE	3	3800.2	-1.1	22of132	2.4663	TRUE		TRUE	::::::::::::::::::::::::::::::
ILSQSNGVLGVLAK	15	10.1	0.258	1140	40.2	AE003439	TRUE	TRUE	2	1399.7	1	13of 26	1.953	TRUE		TRUE	::::::::::::::
NLSGSQDAQLIEQR	2	4.08	0.174	530	25.1	AE003439	TRUE	TRUE	2	1559.7	2.8	14of 26	2.2128	TRUE		TRUE	::::::::::::::
ERMSHAPDFKPNRPEILLER	9	7.83	0.046	2234	41.93	AE003440	TRUE	FALSE	2	2436.8	-2.3	9of 38	1.1618	TRUE		TRUE	::::::::::::::::::
VNVHGGAVSIGHP	11	8	0.043	426	20.8	AE003442	TRUE	FALSE	2	1244.4	0.6	7of 24	1.1355	TRUE		TRUE	::::::::::::::
ALETTNHVFNYK	11	7.74	0.495	592	24.6	AE003444	TRUE	TRUE	2	1437.6	3	15of 22	3.8454	TRUE		TRUE	::::::::::::::
AAGSLEETYYGEHTR	3	4.54	0.249	1000	22.3	AE003444	TRUE	TRUE	3	1684.8	0.9	23of 56	1.9939	TRUE		TRUE	::::::::::::::
CNYFLNNVVK	13	8.88	0.238	1044	29.4	AE003444	TRUE	TRUE	1	1271.4	1.8	10of 18	2.3569	TRUE		TRUE	:Cys_CAM:::::::::
FHGVALAFNALDSK	9	7.82	0.199	1769	38.4	AE003444	TRUE	TRUE	1	1490.7	-0.8	14of 26	2.1565	TRUE		TRUE	::::::::::::::
NAGHVEVTNDGATILR	5	5.22	0.455	1245	27.7	AE003446	TRUE	TRUE	2	1667.8	0.3	20of 30	4.5778	TRUE		TRUE	::::::::::::::::
LSSFIGAIAIGDLVK	7	6.76	0.44	1855	52.8	AE003446	TRUE	TRUE	2	1504.8	0.3	1	4.9934	TRUE		TRUE	::::::::::::::
SLHDALCVLAATVK	9	7.16	0.418	1988	39.3	AE003446	TRUE	TRUE	2	1498.7	0.6	22of 26	4.2258	TRUE		TRUE	::::::Cys_CAM::::::::
IIFGGGCSEALMATAVLK	7	6.29	0.136	1660	57.03	AE003446	TRUE	TRUE	2	1839.2	0.5	1	2.4674	TRUE		TRUE	::::::Cys_CAM::::::::::
FLYRIGNEK	14	9.72	0.056	500	25.7	AE003446	TRUE	FALSE	2	1140.3	1.1	6of 16	1.0529	TRUE		TRUE	::::::::::
SATATTNATTATATTTNLTTHSPQQIALLSAAEK	9	7.82	0.456	1648	51.4	AE003447	TRUE	TRUE	3	3389.7	1.3	37of132	5.1265	TRUE		TRUE	::::::::::::::::::::::::::::::
AAHLVSAGIATLINK	15	10.1	0.417	1108	39.4	AE003447	TRUE	TRUE	2	1479.8	1.8	21of 28	4.4577	TRUE		TRUE	::::::::::::::::
FLALDLGGTNFR	6	6.79	0.207	1736	41.7	AE003447	TRUE	TRUE	2	1324.5	0.7	18of 22	3.1016	TRUE		TRUE	::::::::::::
GDIIGVVGHPGK	11	7.82	0.204	566	22	AE003447	TRUE	TRUE	2	1149.3	2.4	12of 22	1.6641	TRUE		TRUE	::::::::::::
EGDILTLLESER	1	3.69	0.181	1302	34.8	AE003447	TRUE	TRUE	2	1375.5	0.4	16of 22	2.5843	TRUE		TRUE	::::::::::::
FHNLMVEK	9	7.82	0.113	1173	23.03	AE003447	TRUE	TRUE	1	1018.2	-0.3	10of 14	1.8133	TRUE		TRUE	::::::::::
IAPELYHK	11	7.74	0.047	340	20.9	AE003447	TRUE	TRUE	1	971.1	-0.3	11of 14	1.7015	TRUE		TRUE	::::::::::
STFFNVLTQSAAPAENFPFCTIKPNESR	6	6.44	0.177	2048	66.4	AE003448	TRUE	TRUE	3	3175.5	2.8	20of108	2.3938	TRUE		TRUE	::::::::::::::::::Cys_CAM:::::::::
SPPPLADAAVGKGFHPWK	15	9.89	0.127	2007	37.3	AE003448	TRUE	TRUE	2	1876.2	-0.9	9of 34	1.2475	TRUE		TRUE	::::::::::::::::
SLNDPQSLPPTLTIDK	1	3.89	0.105	882	36.2	AE003449	TRUE	FALSE	2	1740	2.9	5of 30	0.8809	TRUE		TRUE	::::::::::::::
QQLMEIFGRYGPLASIKIMWPR	15	10.39	0.004	2919	74.06	AE003452	TRUE	FALSE	3	2668.2	-0.6	6of 84	0.8857	TRUE		TRUE	::::Oxidation_M::::::::::::::Oxidation_M::::
LRLAKTLEATTF	14	10.09	0.114	762	36.6	AE003453	TRUE	FALSE	3	1364.6	2.9	11of 44	1.4261	TRUE		TRUE	::::::::::::
YSPGDEDILRGLNFESQPMEKI	2	3.93	0.061	1821	52.73	AE003453	TRUE	FALSE	2	2539.8	0.3	5of 42	0.7855	TRUE		TRUE	::::::::::::::::::::
HHGPDGGFLTGLDSLNRLLNEIVAEER	4	4.68	0.111	1805	61.7	AE003454	TRUE	FALSE	3	2961.3	1.4	8of104	1.0721	TRUE		TRUE	::::::::::::::::::::::
LKPTISEDSQVNNIPPKEGAFQGDNTNKD	3	4.21	0.018	1719	38.5	AE003455	TRUE	FALSE	3	3158.4	-1	23of112	2.4563	TRUE		TRUE	::::::::::::::::::::::::
LILPGILEQVVSCR	7	6.29	0.302	1907	53.8	AE003456	TRUE	TRUE	2	1597.9	1.3	1	2.3517	TRUE		TRUE	::::::::::Cys_CAM::
DVVIANSGTLPVSEAFSVAK	1	4.08	0.403	1142	50	AE003458	TRUE	TRUE	2	2005.3	0.7	20of 38	3.5968	TRUE		TRUE	::::::::::::::::::
FNMSVAIVAFTNANSSNPNYP	6	5.93	0.095	2168	50.63	AE003458	TRUE	FALSE	2	2275.5	-2.4	15of 40	1.861	TRUE		TRUE	::::Oxidation_M:::::::::::::::::
IVFAMALAEGMTSISNLSSK	6	6.95	0.018	1392	59.16	AE003458	TRUE	FALSE	2	2103.5	-0.4	10of 38	1.3311	TRUE		TRUE	:::::Oxidation_M::::::Oxidation_M:::::::::
PDAISQTSTGSVERKSGIGQQLFK	15	9.89	0.017	857	36.3	AE003459	TRUE	FALSE	3	2407.7	-1	20of 88	1.8744	TRUE		TRUE	::::::::::::::::::::
ILGIGSGSTVVYAVQR	15	9.85	0.506	1168	43.4	AE003460	TRUE	TRUE	2	1620.9	0.4	19of 30	4.2638	TRUE		TRUE	::::::::::::::::
PGVLETGLFVNMAHK	11	7.82	0.061	1631	40.33	AE003460	TRUE	FALSE	2	1613.9	0.5	8of 28	1.1357	TRUE		TRUE	::::::::::::::
STVDPNDPFAFEGPEIYK	1	3.59	0.144	1112	41.2	AE003462	TRUE	TRUE	2	2027.2	1.8	14of 34	1.7135	TRUE		TRUE	::::::::::::::::
PKMDVGMGFDK	6	6.88	0.17	1031	21.96	AE003463	TRUE	FALSE	2	1225.5	2.2	11of 20	1.4302	TRUE		TRUE	::::::::::
KAVIRSRSYDGDAFVNL	15	9.72	0.006	1411	38	AE003464	TRUE	FALSE	3	1912.2	0.9	21of 64	1.9543	TRUE		TRUE	::::::::::::::::
EAGLTPSWRCCSMGNTVLR	12	8.3	0.005	892	44.43	AE003464	TRUE	FALSE	3	2196.4	0.9	20of 72	1.7578	TRUE		TRUE	:::::::::Cys_CAM:Cys_CAM:::::::::
LAELPYYQEVNGDGADELK	1	3.51	0.366	964	44.9	AE003465	TRUE	TRUE	2	2125.3	0.8	19of 36	4.0387	TRUE		TRUE	::::::::::::::::::
LHLDSGHLFAR	11	8	0.296	766	29.4	AE003465	TRUE	TRUE	2	1266.4	1.8	16of 20	2.8856	TRUE		TRUE	::::::::::::
LHADFQSNPPIAGSYTPK	10	7.74	0.255	896	33.5	AE003467	TRUE	TRUE	2	1944.2	0.7	18of 34	2.6066	TRUE		TRUE	::::::::::::::::::
CSMGIKPDCVLCPNKGGAMKSNKSGK	13	9.67	0.162	1400	32.46	AE003467	TRUE	FALSE	3	2826.2	-0.8	13of100	1.2493	TRUE		TRUE	:Cys_CAM:::::::Cys_CAM:::Cys_CAM::::::::::::::
LSSFIFLSS	6	6.02	0.103	1343	39	AE003467	TRUE	FALSE	1	1001.2	0.9	8of 16	1.4958	TRUE		TRUE	::::::::::
TVIRTAESSAMGAGSGSIPTTPTARTTPTTPCK	13	10.11	0.075	1623	45.73	AE003467	TRUE	FALSE	3	3307.7	1.3	21of128	1.7786	TRUE		TRUE	::::::::::::::::::::::::::::::Cys_CAM::
LESVNNSNFIGTILYPK	7	6.87	0.017	1609	47.8	AE003467	TRUE	TRUE	2	1910.2	0	1	1.703	TRUE		TRUE	::::::::::::::::::

IGMVETDKNDRPVDPLR	3	4.46	0.107	1143	33.23	AE003468	TRUE	TRUE	3	1956.2	1.4	19of 64	1.6823	TRUE		TRUE	::::::::::::::::
GFYTLHPEFEEVPLHIFCESYGGK	4	4.68	0.406	2005	66.4	AE003469	TRUE	TRUE	3	2858.1	2.6	34of 92	5.047	TRUE		TRUE	:::::::::::::::::Cys_CAM::::::
TDFMKPVIHIIVNELLEK	6	5.35	0.405	2230	52.73	AE003469	TRUE	TRUE	3	2027.4	2.4	32of 64	4.7725	TRUE		TRUE	::::::::::::::::
VLVTLLYALER	7	6.89	0.394	1793	50	AE003471	TRUE	TRUE	2	1290.6	0.9	1	3.6691	TRUE		TRUE	::::::::::
INPGTVGYYR	15	9.59	0.325	235	22.4	AE003471	TRUE	TRUE	2	1140.3	0.6	11of 18	2.0009	TRUE		TRUE	::::::::::
VMGLGPVTAVEALLQK	7	6.95	0.318	1949	50.03	AE003471	TRUE	TRUE	2	1627	0	2	2.2883	TRUE		TRUE	::::::::::::::::
IFNEMLDLYR	2	4.08	0.288	1132	41.83	AE003471	TRUE	TRUE	2	1314.5	0.3	16of 18	3.0228	TRUE		TRUE	::::::::::
FAGVTQFEATDAR	2	4.08	0.258	648	28.9	AE003471	TRUE	TRUE	2	1413.5	1.3	20of 24	3.9889	TRUE		TRUE	::::::::::::
YQGGFLLSR	14	9.85	0.244	812	27.6	AE003471	TRUE	TRUE	2	1041.2	0.3	16of 16	2.2843	TRUE		TRUE	::::::::::
ATFDITLVVPK	7	6.76	0.225	1489	36.9	AE003471	TRUE	TRUE	2	1204.5	1.5	2	2.6888	TRUE		TRUE	::::::::::::
TVALGYQAIR	14	9.85	0.206	599	28.8	AE003471	TRUE	TRUE	2	1092.3	2	16of 18	2.7064	TRUE		TRUE	::::::::::
SSIPEELPHNPLEHDPLHPR	5	5.16	0.188	1427	37.3	AE003471	TRUE	FALSE	2	2315.6	0.2	15of 38	2.6224	TRUE		TRUE	::::::::::::::::::::
TPIGSFNGTLSK	15	10.1	0.176	611	23.3	AE003471	TRUE	TRUE	2	1222.4	0.5	12of 22	2.3159	TRUE		TRUE	::::::::::::
HYELLLQPNLK	9	7.74	0.16	1632	35.2	AE003471	TRUE	TRUE	2	1368.6	1.8	15of 20	2.8862	TRUE		TRUE	::::::::::
DYFNIAYPLPK	6	6.62	0.152	1706	36.1	AE003471	TRUE	TRUE	1	1341.5	-0.7	12of 20	2.3794	TRUE		TRUE	::::::::::
VALSNMPVIK	15	10.1	0.13	832	32.13	AE003471	TRUE	TRUE	2	1072.4	1.5	15of 18	2.1548	TRUE		TRUE	::::::::::
YLIENFASEER	2	3.97	0.108	804	32	AE003471	TRUE	TRUE	2	1371.5	2.4	15of 20	2.8349	TRUE		TRUE	::::::::::
GVAFHQQMPLFVSGGDDYK	5	5.1	0.429	1592	43.73	AE003472	TRUE	TRUE	2	2097.4	1.7	21of 36	4.6145	TRUE		TRUE	::::::::::::::::::::
LVGQSIIAYLQQK	15	9.72	0.344	1490	40	AE003472	TRUE	TRUE	2	1461.7	1.7	16of 24	2.7822	TRUE		TRUE	::::::::::::
FHSILISIPLLVVDTK	9	7.82	0.331	2290	62.8	AE003472	TRUE	TRUE	1	1796.2	-1.3	13of 30	2.1783	TRUE		TRUE	::::::::::::::
LLHDQLGVVNFQPFK	10	7.82	0.265	1484	47.7	AE003472	TRUE	TRUE	2	1756.1	0.9	16of 28	2.6337	TRUE		TRUE	::::::::::::::
YAITNGDHGIIR	10	7.76	0.26	648	25.8	AE003472	TRUE	TRUE	2	1330.5	0.3	16of 22	2.1341	TRUE		TRUE	::::::::::::
KVDANVLLPIN	6	6.76	0.181	1194	34.5	AE003472	TRUE	FALSE	2	1196.4	-0.6	9of 20	1.3651	TRUE		TRUE	::::::::::
LLHDQLGVVNFQPFK	11	7.82	0.154	1241	47.7	AE003472	TRUE	TRUE	2	1756.1	0.3	13of 28	2.2379	TRUE		TRUE	::::::::::::::
LQAGYQLTTSGK	15	9.72	0.147	196	21.2	AE003472	TRUE	TRUE	2	1267.4	2.2	11of 22	1.8034	TRUE		TRUE	::::::::::::
LSFLYLITGNLEK	7	6.87	0.125	1967	51	AE003472	TRUE	TRUE	2	1511.8	1.7	1	2.0101	TRUE		TRUE	::::::::::::
LLELAPRPDVAQQVR	7	7.05	0.113	1103	42.4	AE003472	TRUE	TRUE	2	1706	0.3	192	2.0615	TRUE		TRUE	::::::::::::::
FHTMAALGLLLLVGVHGAT	12	8	0.028	1867	66.53	AE003472	TRUE	FALSE	2	1922.3	1.8	9of 36	1.3517	TRUE		TRUE	::::::::::::::::::
PYHLNGSKSSGAMDFP	10	7.74	0.068	817	26.63	AE003474	TRUE	FALSE	3	1724.9	1	14of 60	1.5904	TRUE		TRUE	::::::::::::Oxidation_M::::
LLGDAFFLQCYLK	6	6.09	0.008	1566	55.6	AE003474	TRUE	FALSE	1	1588.9	0.2	8of 24	1.2182	TRUE		TRUE	:::::::::Cys_CAM::::
ELFIAPEGMHTGQFVYCGR	5	5.3	0.471	1690	52.83	AE003475	TRUE	TRUE	2	2213.5	0.4	22of 36	4.2892	TRUE		TRUE	::::::::::::::::Cys_CAM:::
TSGNYATVIAHNQDTK	9	7.74	0.413	984	17.1	AE003475	TRUE	TRUE	2	1720.8	1.7	19of 30	4.0719	TRUE		TRUE	::::::::::::::::
KATLQIGNVMPLSQMPEGTIICNLEEK	4	4.56	0.368	2011	69.66	AE003475	TRUE	TRUE	2	3016.5	0.7	18of 52	3.5463	TRUE		TRUE	::::::::::::::::::::::Cys_CAM::::::
HKTNIDLSMMLTFSVT	12	7.82	0.083	1151	44.56	AE003475	TRUE	FALSE	2	1871.2	0.7	7of 30	1.3672	TRUE		TRUE	:::::::::Oxidation_M:Oxidation_M:::::::
QVVVCGYGDVGK	6	6.09	0.353	950	24.6	AE003476	TRUE	TRUE	2	1281.4	1.9	16of 22	2.6708	TRUE		TRUE	:::::Cys_CAM::::::::
IPLLSDLTHK	12	7.82	0.154	1352	30.1	AE003476	TRUE	TRUE	2	1137.4	1.7	15of 18	2.3226	TRUE		TRUE	::::::::::
IPLLSDLTHK	11	7.82	0.138	996	30.1	AE003476	TRUE	TRUE	1	1137.4	-0.3	11of 18	1.9005	TRUE		TRUE	::::::::::
AVISKPAPQFEGTAVVNK	15	9.89	0.12	525	37	AE003476	TRUE	TRUE	2	1857.2	0.9	13of 34	1.8157	TRUE		TRUE	::::::::::::::::::
GLFIIDQTGVLR	7	6.79	0.086	1575	43.9	AE003476	TRUE	TRUE	2	1332.6	1	6	2.6356	TRUE		TRUE	::::::::::::
VDVNGDNAAPLYK	1	3.89	0.412	438	25.5	AE003477	TRUE	TRUE	2	1376.5	1.6	18of 24	3.2419	TRUE		TRUE	::::::::::::::
DTYSIVVAPHLDKK	10	7.72	0.386	857	28.5	AE003477	TRUE	TRUE	2	1586.8	0.9	16of 26	3.0959	TRUE		TRUE	::::::::::::::
VVLVVNIASK	15	10.1	0.213	927	34.6	AE003477	TRUE	TRUE	1	1042.3	-0.4	11of 18	1.7674	TRUE		TRUE	::::::::::
ALLGGANEIHVFNR	11	7.85	0.192	977	37.5	AE003477	TRUE	TRUE	2	1511.7	1.4	16of 26	2.083	TRUE		TRUE	::::::::::::::
YNTLHEPLGIR	10	7.77	0.169	788	28.3	AE003477	TRUE	TRUE	2	1313.5	0.3	11of 20	2.3742	TRUE		TRUE	::::::::::::
LTQSHQLQEFLR	10	7.85	0.16	1061	31.2	AE003477	TRUE	TRUE	2	1500.7	1.9	13of 22	2.0524	TRUE		TRUE	::::::::::::
CAAMLDERQKLHAAWNKKKIML	13	10.17	0.095	1648	51.76	AE003477	TRUE	FALSE	3	2673.2	2.9	11of 84	1.5865	TRUE		TRUE	:Cys_CAM:::Oxidation_M::::::::::::::::::
LHCSVSSSAERLV	12	7.16	0.062	1255	28.4	AE003477	TRUE	FALSE	2	1445.6	-1.3	10of 24	1.4482	TRUE		TRUE	:::Cys_CAM:::::::::::
SIGVSNFNSEQLTR	6	6.98	0.422	1254	27.7	AE003479	TRUE	TRUE	2	1552.7	0.8	20of 26	3.8091	TRUE		TRUE	::::::::::::::
LIVPNQIGYLILK	15	9.72	0.183	1627	55.1	AE003479	TRUE	TRUE	2	1484.9	2.8	18of 24	2.3916	TRUE		TRUE	::::::::::::::
YLIEIGTIPLPK	7	6.87	0.151	1661	46.3	AE003479	TRUE	TRUE	2	1357.7	2.1	2	2.0908	TRUE		TRUE	::::::::::::::
ATLHAIDVGYR	11	7.76	0.049	617	26.9	AE003479	TRUE	TRUE	2	1216.4	0.7	12of 20	1.3589	TRUE		TRUE	::::::::::::
YLIEIGTIPLPK	6	6.87	0.008	1862	46.3	AE003479	TRUE	TRUE	2	1357.7	0.5	9of 22	1.5963	TRUE		TRUE	::::::::::::::
HAIDVGYR	9	7.76	0	912	16.2	AE003479	TRUE	FALSE	1	931	-0.3	11of 14	1.878	TRUE		TRUE	::::::::
CMENISAFLACAK	5	6.14	0.328	1747	38.53	AE003480	TRUE	TRUE	2	1515.7	1.8	17of 24	2.7381	TRUE		TRUE	:Cys_CAM::::::::Cys_CAM:::
AVTEEPINTSGDTDNFFEVLK	1	3.51	0.215	1242	47.5	AE003480	TRUE	TRUE	2	2327.5	0.1	13of 40	2.1118	TRUE		TRUE	::::::::::::::::::::
AGANVISLQYGSNK	15	9.72	0.052	599	24.9	AE003480	TRUE	TRUE	2	1422.6	0	14of 26	2.0737	TRUE		TRUE	::::::::::::::
VQALAYGTR	13	9.85	0.033	902	21.4	AE003480	TRUE	FALSE	2	979.1	2.1	9of 16	1.5149	TRUE		TRUE	::::::::::
YEYKGEVAMAETKSIN	3	4.56	0.003	1535	29.63	AE003480	TRUE	FALSE	2	1834.1	-1.2	8of 30	1.3794	TRUE		TRUE	::::::::::::::::
ITVSSINDINSFNLER	2	4.08	0.096	1038	42.3	AE003484	TRUE	TRUE	2	1823	1.2	13of 30	1.9462	TRUE		TRUE	::::::::::::::::
RQMPLLVVTGTSSEIGGITTESATA	2	4.27	0.041	2268	55.93	AE003484	TRUE	FALSE	2	2520.9	0.4	12of 48	1.9873	TRUE		TRUE	::::::::::::::::::::::
LANSLPMNPEQELKDVDEPLGQQR	1	3.93	0.021	1282	50.33	AE003484	TRUE	FALSE	3	2739	-0.3	12of 92	1.1348	TRUE		TRUE	::::::Oxidation_M::::::::::::::::
KLVGDPNLEFVAMPALLPPEVK	3	4.45	0.4	1875	70.43	AE003485	TRUE	TRUE	2	2378.9	0.7	24of 42	5.3543	TRUE		TRUE	::::::::::::::::::
SNYNFEKPFLWLAR	14	9.72	0.372	1396	46.7	AE003485	TRUE	TRUE	2	1786	2.8	15of 26	3.247	TRUE		TRUE	::::::::::::::
LTPATPGAEGVLANFFNSLLHK	11	7.82	0.233	1882	59.9	AE003485	TRUE	TRUE	2	2298.6	1.9	16of 42	2.5816	TRUE		TRUE	::::::::::::::::::
DLYPALDHAASFIR	5	5.1	0.214	1796	41.7	AE003485	TRUE	TRUE	2	1589.8	1.6	15of 26	2.0098	TRUE		TRUE	::::::::::::::
KGFLRKGPGICHGVAGNGYV	14	10.19	0.017	1683	36	AE003485	TRUE	FALSE	3	2088.4	-1.4	12of 76	1.4437	TRUE		TRUE	:::::::::Cys_CAM:::::::::
TIMHASIIKAAAGVASSATLP	15	10.1	0.008	1223	51.03	AE003485	TRUE	FALSE	2	2027.4	-0.6	10of 40	1.2643	TRUE		TRUE	:::Oxidation_M:::::::::::::::::
AKEVIEFGGENIDFDKDGYNGLSHLINNVK	3	4.37	0.434	1748	63.2	AE003486	TRUE	TRUE	3	3337.7	2.5	29of116	4.4334	TRUE		TRUE	::::::::::::::::::::::::::::
FHAQRPAFDNVQELVLNLK	9	7.82	0.197	1954	51.8	AE003487	TRUE	TRUE	2	2240.6	1.4	18of 36	3.6383	TRUE		TRUE	::::::::::::::::::
HLDSSLDYFTALMK	4	5.1	0.022	1914	40.83	AE003487	TRUE	TRUE	2	1641.9	1.6	12of 26	1.5287	TRUE		TRUE	::::::::::::
CGGKSAVCVGP	12	8.3	0.156	869	16.3	AE003488	TRUE	FALSE	2	1092.2	2.8	10of 20	1.529	TRUE		TRUE	:Cys_CAM::::::Cys_CAM::::
SNGLGPVVSGSTNYPVINCPPVK	13	8.88	0.379	1096	46.1	AE003490	TRUE	TRUE	2	2357.6	1.7	11of 44	2.4569	TRUE		TRUE	::::::::::::::::Cys_CAM:::::
YSSLHDIVIK	10	7.74	0.176	820	28	AE003491	TRUE	TRUE	2	1175.4	0.6	13of 18	2.8227	TRUE		TRUE	::::::::::
NKPVEEMPEANPDWRRHLK	10	7.8	0.106	438	30.23	AE003492	TRUE	FALSE	2	2347.7	2.9	5of 36	0.699	TRUE		TRUE	::::::::::::::::::
TNFEATHPPILIDNGLAILENEKIER	3	4.36	0.514	1847	69	AE003493	TRUE	TRUE	3	2949.3	1.7	36of100	4.2428	TRUE		TRUE	::::::::::::::::::::::::
YMYHMYQLDAFTQSCPADQDIINHYK	5	5.03	0.441	1811	62.76	AE003493	TRUE	TRUE	3	3254.6	1.4	38of100	6.8655	TRUE		TRUE	::::::::::::::Cys_CAM:::::::::::
QQITQHSRTLVSPPPDAIGSTSGDGSGGSISHKLRT	13	10.09	0.091	1461	44.3	AE003495	TRUE	FALSE	3	3675	-1.3	25of140	2.4709	TRUE		TRUE	::::::::::::::::::::::::::::::::
ANVPFIQRYQFNKDRDGSQRYGK	15	10.33	0.097	1336	34.2	AE003496	TRUE	FALSE	3	2789.1	1	20of 88	2.0828	TRUE		TRUE	::::::::::::::::::::
SDKYAVGVHVLPK	14	9.63	0.219	259	25.1	AE003499	TRUE	TRUE	3	1413.7	2.8	24of 48	2.8406	TRUE		TRUE	::::::::::::::
YAVGVHVLPK	15	9.72	0.206	244	27.2	AE003499	TRUE	TRUE	2	1083.3	0.7	9of 18	1.6537	TRUE		TRUE	::::::::::
LNELIGDFDELLSR	1	3.59	0.198	1768	48.9	AE003499	TRUE	FALSE	3	1634.8	0.8	9of 52	1.2102	TRUE		TRUE	::::::::::::::
SDKYAVGVHVLPK	13	9.63	0.047	674	25.1	AE003499	TRUE	TRUE	2	1413.7	1.1	13of 24	1.7984	TRUE		TRUE	::::::::::::::
VPVNPMKPVNSMEAMNLTAQMNATGKT	15	9.89	0.036	1590	53.12	AE003499	TRUE	FALSE	3	2892.4	0.9	13of104	1.4439	TRUE		TRUE	::::::::::::::::::::::Oxidation_M::::::::

TLAVNSGYDAQDTIVK	2	3.89	0.44	629	32.5	AE003500	TRUE	TRUE	2	1695.9	0	19of 30	3.8393	TRUE		TRUE	::::::::::::::::
YTFVEDCKNPLSVTILIK	7	6.36	0.432	1607	55.7	AE003500	TRUE	TRUE	2	2141.5	0	1	4.7762	TRUE		TRUE	::::::Cys_CAM::::::::::::
LPNAYIVLPSLLPR	15	9.85	0.379	1667	55.9	AE003500	TRUE	TRUE	2	1566.9	0.2	17of 26	3.3297	TRUE		TRUE	::::::::::::::::
ASTAQDDSTGDGTTTTTVMLIGELLK	1	3.51	0.378	1638	48.43	AE003500	TRUE	TRUE	2	2526.8	1	17of 48	3.0873	TRUE		TRUE	::::::::::::::::::::::::
LAVQAFADALLVIPK	7	6.76	0.287	1985	57.9	AE003500	TRUE	TRUE	2	1569.9	0.6	1	3.2492	TRUE		TRUE	::::::::::::::::
LAVQAFADALLVIPK	8	6.76	0.203	2587	57.9	AE003500	TRUE	TRUE	2	1569.9	0.9	15of 28	2.2793	TRUE		TRUE	::::::::::::::::
GLVMDHGAR	11	7.85	0.187	281	17.73	AE003500	TRUE	TRUE	2	956.1	0.5	10of 16	1.8591	TRUE		TRUE	::::::::::
MLVSGAGDIK	6	6.76	0.147	945	25.53	AE003500	TRUE	TRUE	2	991.2	1.7	15of 18	3.0132	TRUE		TRUE	::::::::::
FVDVTLACEGQQVHCHRLVLAACS	5	6.01	0.051	2494	62.9	AE003500	TRUE	FALSE	3	2772	-0.9	21of 92	2.0854	TRUE		TRUE	:::::::Cys_CAM:::::::Cys_CAM:::::::Cys_CAM::
TFVLINQK	14	10.1	0.006	635	26.5	AE003500	TRUE	TRUE	1	963.2	1	10of 14	2.2164	TRUE		TRUE	::::::::
SSTGALAVLHLPPPTATALVQA	9	7.85	0	2109	57.5	AE003500	TRUE	FALSE	2	2116.5	-1.5	12of 42	1.5428	TRUE		TRUE	::::::::::::::::::::
GAVLRPSLDDPVTIEYVK	3	4.31	0.213	1491	48.1	AE003501	TRUE	TRUE	2	1973.3	1.5	17of 34	2.2698	TRUE		TRUE	::::::::::::::::::
IKLDDLSAPLR	7	6.9	0.2	1148	33.2	AE003502	TRUE	TRUE	2	1241.5	2.2	11	2.438	TRUE		TRUE	::::::::::::
LLTSEGPGGGVHGISTK	10	7.82	0.376	632	27.3	AE003503	TRUE	TRUE	2	1610.8	0.7	19of 32	2.9341	TRUE		TRUE	::::::::::::::::
QEAAKPQLNNGLEILRR	14	10.09	0.1	1216	35.2	AE003503	TRUE	FALSE	2	1951.2	-2.6	10of 32	1.1386	TRUE		TRUE	::::::::::::::::
AHPNTRYELIDWTPEKGYAR	9	7.69	0.092	1978	38.7	AE003503	TRUE	FALSE	2	2418.7	-2.4	8of 38	1.1274	TRUE		TRUE	::::::::::::::::::
ANDTFTRLLTSEGPGGGVHGISTK	10	7.82	0.056	632	37.6	AE003503	TRUE	FALSE	3	2416.7	0.1	21of 92	2.2477	TRUE		TRUE	::::::::::::::::::::::
QMPNVEERIEKTTKVEKKTMDIEE	3	4.61	0.022	1731	36.86	AE003503	TRUE	FALSE	3	2939.3	-2.7	21of 92	2.5865	TRUE		TRUE	::Oxidation_M::::::::::::::::Oxidation_M::::::
VPKEEMICPPKKGHVYRLA	15	9.59	0	612	39.13	AE003503	TRUE	FALSE	3	2253.7	-2.1	19of 72	1.6066	TRUE		TRUE	:::::::Cys_CAM::::::::::::
WGVMLVGPTGGGKSVVLHA	13	10.1	0.043	1167	49.73	AE003507	TRUE	FALSE	2	1866.2	-0.7	13of 36	1.6131	TRUE		TRUE	::::::::::::::::::
TFLIVPELVR	6	6.98	0.193	1844	44.8	AE003508	TRUE	TRUE	1	1187.5	-0.2	11of 18	2.3304	TRUE		TRUE	::::::::::
KPLFFDEGTVLR	7	7.02	0.093	1273	38.4	AE003508	TRUE	TRUE	2	1422.7	2.4	1	1.9493	TRUE		TRUE	::::::::::::
AVPCVGVSIGVER	8	6.29	0.095	1664	33.9	AE003509	TRUE	TRUE	1	1343.5	-0.7	14of 24	1.9837	TRUE		TRUE	::::Cys_CAM:::::::::
FDGAQIIVHAR	10	7.85	0.288	838	29.2	AE003510	TRUE	TRUE	2	1227.4	1.3	15of 20	2.3882	TRUE		TRUE	::::::::::::
SQNLLIQALCDILK	6	6.1	0.203	2545	49.1	AE003510	TRUE	TRUE	2	1629.9	2.2	11of 26	1.8542	TRUE		TRUE	:::::::::Cys_CAM:::::
DVSEPVSRPAAPMSTLSIPGPAL	3	4.08	0.15	2587	55.43	AE003510	TRUE	FALSE	2	2293.6	2.1	14of 44	1.5312	TRUE		TRUE	::::::::::::::::::::::
NPEISHMLNNPDLLR	5	5.22	0.398	1558	37.83	AE003512	TRUE	TRUE	2	1764	1.4	19of 28	4.1687	TRUE		TRUE	::::::::::::::
LLSSSPLMSNNPALQEQVR	7	6.98	0.383	1272	47.43	AE003512	TRUE	TRUE	2	2085.4	1.8	1	3.2261	TRUE		TRUE	::::::::::::::::::
HNASILHLYEGAR	10	7.92	0.359	849	27.4	AE003512	TRUE	TRUE	2	1481.7	-0.1	17of 24	3.0559	TRUE		TRUE	::::::::::::
AVDASHPVIHSCIIR	12	7.32	0.087	923	35.8	AE003512	TRUE	TRUE	2	1675.9	0.3	12of 28	1.4381	TRUE		TRUE	::::::::::Cys_CAM::::
CFRHRKTDPAVPF	13	10.11	0.019	999	25.2	AE003512	TRUE	FALSE	2	1631.8	1.2	8of 24	1.2235	TRUE		TRUE	:Cys_CAM::::::::::::
TITGFQTHTTPVLLAIGER	9	7.85	0.411	1865	49.1	AE003515	TRUE	TRUE	2	2056.4	2.1	20of 36	3.3679	TRUE		TRUE	::::::::::::::::::
KEIQFYLTPAEEAPSGTFSR	3	4.56	0.346	1487	45.4	AE003515	TRUE	TRUE	2	2272.5	0.8	17of 38	3.5882	TRUE		TRUE	::::::::::::::::::
GTLSLSPYHSDR	11	7.76	0.205	534	20	AE003515	TRUE	TRUE	2	1333.4	0.6	12of 22	2.0228	TRUE		TRUE	::::::::::::
EIVHGLK	11	7.82	0.117	296	17.2	AE003515	TRUE	TRUE	1	796	0.3	8of 12	1.4753	TRUE		TRUE	::::::::
EIQFYLTPAEEAPSGTFSR	2	3.97	0.069	1082	47.5	AE003515	TRUE	TRUE	2	2144.3	0.8	13of 36	2.1419	TRUE		TRUE	::::::::::::::::::
SHYLLYTLVPAMQAR	14	9.59	0.037	1339	47.53	AE003515	TRUE	TRUE	2	1764.1	1.3	8of 28	1.514	TRUE		TRUE	::::::::::::::
EIGKLFTKKFSIDVAAAGHVK	15	10.16	0.012	657	45.9	AE003515	TRUE	TRUE	3	2260.7	3	24of 80	1.7856	TRUE		TRUE	::::::::::::::::::
QLGSFGISGPLALQSIASLSGGQK	14	10.1	0.357	1605	57.2	AE003516	TRUE	TRUE	2	2317.6	0.3	19of 46	3.8514	TRUE		TRUE	::::::::::::::::::::
GRPDEEYRRQLGSFGISGPLALQSIASLSGGQK	14	9.72	0.316	1605	64.1	AE003516	TRUE	FALSE	3	3476.9	-0.5	20of128	3.2854	TRUE		TRUE	::::::::::::::::::::::::::::::
VLLQNANLLLSYGR	15	9.85	0.305	1416	49.8	AE003516	TRUE	TRUE	2	1574.9	1.6	19of 26	3.0353	TRUE		TRUE	::::::::::::::
LLLDEPTNMLDIK	1	3.71	0.01	1672	46.73	AE003516	TRUE	FALSE	2	1531.8	2.6	13of 24	1.9989	TRUE		TRUE	::::::::Oxidation_M:::::
EVVHTVTLHEIDVINSR	5	5.18	0.397	1439	40.9	AE003517	TRUE	TRUE	2	1962.2	2	16of 32	3.4724	TRUE		TRUE	::::::::::::::::
THGFLALFSGDTGEIK	5	5.22	0.299	1831	39.3	AE003517	TRUE	TRUE	2	1693.9	0.4	15of 30	2.0847	TRUE		TRUE	::::::::::::::::
ISPLAFFQINTEGANVLYQK	7	6.87	0.108	1940	60.7	AE003518	TRUE	TRUE	2	2254.6	0.2	1	2.0236	TRUE		TRUE	::::::::::::::::::
SSKDYKNYGNLIY	12	9.36	0.081	1313	23.2	AE003518	TRUE	FALSE	2	1565.7	2.7	10of 24	1.3939	TRUE		TRUE	::::::::::::::
IDPAVAAFVDIHNTLVNSLMIK	5	5.1	0.301	2566	70.43	AE003519	TRUE	TRUE	3	2398.8	1.5	32of 84	2.3581	TRUE		TRUE	:::::::::::::::::Oxidation_M:::
MCIVKY	13	8.88	0.012	842	22.93	AE003522	TRUE	FALSE	1	814	0.6	6of 10	1.1093	TRUE		TRUE	::Cys_CAM::::::
GQKESPWEGGIRSAGALWSPL	9	7.1	0.002	1286	47.3	AE003522	TRUE	FALSE	3	2227.5	-2.9	18of 80	1.633	TRUE		TRUE	::::::::::::::::::
VAIYAKVEDNFR	9	6.94	0.084	1808	32	AE003525	TRUE	FALSE	1	1425.6	0.4	9of 22	1.49	TRUE		TRUE	::::::::::::
HQAVHVQISHLTPEVHHK	11	8.17	0.596	496	23.4	AE003526	TRUE	TRUE	2	2098.4	0.5	24of 34	5.3526	TRUE		TRUE	::::::::::::::::
HQAVHVQISHLTPEVHHK	12	8.17	0.369	871	23.4	AE003526	TRUE	TRUE	3	2098.4	1	24of 68	3.3244	TRUE		TRUE	::::::::::::::::
EFATHTGAAFAPYLQSAFENVYK	5	5.3	0.223	2054	56.6	AE003526	TRUE	TRUE	2	2563.8	1.4	17of 44	3.8255	TRUE		TRUE	::::::::::::::::::::
PQPNASTKVNH	15	10.1	0.208	79	6	AE003526	TRUE	FALSE	1	1193.3	-2.1	3of 20	0.5275	TRUE		TRUE	::::::::::::
TAAFFALGQFSEFLQPTICK	7	6.29	0.176	2103	66.4	AE003526	TRUE	TRUE	2	2277.6	1.8	6	2.0757	TRUE		TRUE	::::::::::::::::::Cys_CAM::
SIYNLMSSLSSVVNESMASVFPK	6	6.87	0.13	2733	62.66	AE003526	TRUE	TRUE	2	2491.9	-0.8	13of 44	1.7973	TRUE		TRUE	::::::::::::::::::::
KATAIADTPELK	9	6.99	0.023	1117	21.8	AE003526	TRUE	FALSE	2	1258.5	-0.6	10of 22	1.396	TRUE		TRUE	::::::::::::
LLGLNLLYLLSGNR	14	9.85	0.248	2024	58.8	AE003527	TRUE	TRUE	2	1559.9	2.4	15of 26	2.1884	TRUE		TRUE	::::::::::::::
RLNLPDLMASSAMLK	14	10.09	0.013	1768	45.96	AE003528	TRUE	FALSE	2	1677	-2.3	4of 28	0.7649	TRUE		TRUE	::::::::::::Oxidation_M:::
NAYPDHIIYYR	9	7.65	0.046	1404	29.2	AE003530	TRUE	TRUE	2	1425.6	0.6	12of 20	1.3349	TRUE		TRUE	::::::::::::
GTIGKPGQVGINYLDLDLSK	8	6.81	0.013	1960	45.8	AE003530	TRUE	TRUE	2	2089.4	0.4	13of 38	1.5199	TRUE		TRUE	::::::::::::::::::
LVLYIK	15	9.72	0	679	31	AE003530	TRUE	FALSE	1	749	0.8	8of 10	1.7728	TRUE		TRUE	::::::
SAYDLGQHTAATGVR	10	7.76	0.463	392	21.7	AE003532	TRUE	TRUE	2	1547.7	0.4	21of 28	4.0422	TRUE		TRUE	::::::::::::::::
LPYATMGSGSLAAMTVFESR	8	6.89	0.451	2256	53.56	AE003532	TRUE	TRUE	2	2090.4	1.7	19of 38	3.4764	TRUE		TRUE	::::::::::::::::::
YQGHISAALVLGGVDK	9	7.74	0.431	1625	37.3	AE003532	TRUE	TRUE	2	1628.9	0.7	25of 30	3.7218	TRUE		TRUE	::::::::::::::
SAAQVQIGEAVASK	6	6.95	0.403	948	23.8	AE003532	TRUE	TRUE	2	1359.5	1.3	22of 26	4.2773	TRUE		TRUE	::::::::::::::
TVHVEEFIPSVVEPSFGIGR	3	4.54	0.402	1784	55.4	AE003532	TRUE	TRUE	2	2200.5	1.6	21of 38	3.7729	TRUE		TRUE	::::::::::::::::::
LPYATMGSGSLAAMTVFESR	7	6.89	0.324	1716	53.56	AE003532	TRUE	TRUE	2	2090.4	0.7	1	2.8459	TRUE		TRUE	::::::::::::::::::
LDGLNKQELAGVLAK	7	6.99	0.307	1189	37.5	AE003532	TRUE	TRUE	2	1569.8	1.4	1	3.714	TRUE		TRUE	::::::::::::::
CYFTLPPLVAPIK	12	8.88	0.293	1744	50.3	AE003532	TRUE	TRUE	2	1519.8	-0.9	14of 24	2.6971	TRUE		TRUE	:Cys_CAM::::::::::::
CYFTLPPLVAPIK	13	8.88	0.291	1537	50.3	AE003532	TRUE	TRUE	2	1519.8	1.6	19of 24	2.7182	TRUE		TRUE	:Cys_CAM::::::::::::
YDLGQHTAATGVR	10	7.76	0.249	398	19.9	AE003532	TRUE	FALSE	2	1389.5	1.3	15of 24	2.1615	TRUE		TRUE	::::::::::::
LVANETLGYYMAR	7	6.83	0.167	1061	40.03	AE003532	TRUE	TRUE	2	1517.7	1.8	1	1.8635	TRUE		TRUE	:::::::::::Oxidation_M:::
PGKVHVVQE	12	7.82	0.039	703	13.7	AE003535	TRUE	FALSE	2	993.2	-1.2	9of 16	1.0656	TRUE		TRUE	::::::::::
NVIFVDFGHSSLQASACAFTK	9	7.16	0.561	1940	53.6	AE003536	TRUE	TRUE	2	2300.5	2.3	29of 40	6.2521	TRUE		TRUE	::::::::::::::::Cys_CAM:::::
YDHLTETEFINISETADK	2	3.92	0.41	921	38	AE003536	TRUE	TRUE	2	2127.3	0.8	21of 34	3.3623	TRUE		TRUE	::::::::::::::::::
ALLDAAQIAGLNVLR	7	6.79	0.369	1699	51.6	AE003536	TRUE	TRUE	2	1538.8	1.9	1	4.5717	TRUE		TRUE	::::::::::::::::
LPLNIECFLDDIDVSSSMQR	1	3.51	0.355	1793	62.23	AE003536	TRUE	TRUE	2	2353.6	1.4	23of 38	4.0995	TRUE		TRUE	::::::Cys_CAM:::::::::::::
QEVQTLNSCVSSVINR	6	6.29	0.343	1383	32.4	AE003536	TRUE	TRUE	2	1835	0.3	17of 30	3.1438	TRUE		TRUE	::::::::Cys_CAM:::::::::
ALLDAAQIAGLNVLR	8	6.79	0.328	2251	51.6	AE003536	TRUE	TRUE	2	1538.8	1.8	19of 28	3.3765	TRUE		TRUE	::::::::::::::::
KALLDAAQIAGLNVLR	15	10.09	0.326	1365	49.5	AE003536	TRUE	TRUE	2	1667	2.1	21of 30	3.0562	TRUE		TRUE	::::::::::::::::
DIDLALGDYFAK	1	3.6	0.319	1269	38.5	AE003536	TRUE	TRUE	1	1341.5	0.5	15of 22	3.0576	TRUE		TRUE	::::::::::::
ATPSFVAFDGKK	15	9.89	0.315	403	23.4	AE003536	TRUE	TRUE	2	1268.5	1.9	10of 22	1.4583	TRUE		TRUE	::::::::::::

ASDYEQGPAAFDELK	1	3.59	0.263	760	28.8	AE003536	TRUE	TRUE	2	1641.7	2.9	17of 28	2.6409	TRUE	TRUE	::::::::::::::::
LMNETTATALAYGFYK	7	6.81	0.247	1495	44.83	AE003536	TRUE	TRUE	2	1795.1	1.6	1	2.669	TRUE	TRUE	::::::::::::::::
INNNGIVLISSATLVEK	7	6.95	0.142	1428	47.6	AE003536	TRUE	TRUE	2	1786.1	1.6	30	2.0751	TRUE	TRUE	::::::::::::::::
INNNGIVLISSATLVEK	8	6.95	0.05	1976	47.6	AE003536	TRUE	TRUE	2	1786.1	1.6	12of 32	1.4818	TRUE	TRUE	::::::::::::::::
DYGLQINPLVPEPHKRK	14	9.63	0.116	1524	32.7	AE003540	TRUE	TRUE	2	2005.3	3	12of 32	1.9627	TRUE	TRUE	::::::::::::::::
HIDTAYFYQNEAEVGK	3	4.43	0.537	1259	31.5	AE003541	TRUE	TRUE	2	1886	2.1	24of 30	5.3709	TRUE	TRUE	::::::::::::::::
NDLSICGTLHSVDQYLNIK	5	5.1	0.482	2074	46.2	AE003541	TRUE	TRUE	2	2191.4	2.4	21of 36	4.5261	TRUE	TRUE	::::::Cys_CAM::::::::::::
VLANCEIKPVTNQVECSPALNQK	7	6.29	0.443	1071	48.4	AE003541	TRUE	TRUE	3	2613.9	2.8	1	6.2197	TRUE	TRUE	:::::Cys_CAM::::::::::Cys_CAM::::::::
NEDDVLQLSDVDYLDTYK	1	3.27	0.405	1244	43.1	AE003541	TRUE	TRUE	2	2146.3	1	21of 34	4.8959	TRUE	TRUE	::::::::::::::::::
SIGVSNFNSEQLAR	6	6.98	0.38	1234	29.1	AE003541	TRUE	TRUE	2	1522.7	0.1	21of 26	3.9082	TRUE	TRUE	::::::::::::::
YLVGLGVIPIPK	13	9.72	0.34	1501	47	AE003541	TRUE	TRUE	2	1269.6	1.1	15of 22	2.6248	TRUE	TRUE	::::::::::::
YLVGLGVIPIPK	14	9.72	0.336	1395	47	AE003541	TRUE	TRUE	2	1269.6	0.7	19of 22	4.0099	TRUE	TRUE	::::::::::::
YLVGLGVIPIPK	15	9.72	0.31	1506	47	AE003541	TRUE	TRUE	2	1269.6	-0.4	17of 22	3.8129	TRUE	TRUE	::::::::::::
PKPDIQKPDFIYSPEVAVIAK	9	6.96	0.278	1720	51.8	AE003541	TRUE	TRUE	3	2356.8	0.7	26of 80	3.2347	TRUE	TRUE	::::::::::::::::::::
LNNGYEMPILGLGTYNSK	7	6.81	0.243	1535	45.23	AE003541	TRUE	TRUE	2	1985.3	-0.3	1	2.1864	TRUE	TRUE	::::::::::::::::::
KNDVTLTGYTPLGK	14	9.63	0.185	674	24.5	AE003541	TRUE	TRUE	1	1507.7	0.1	13of 26	1.946	TRUE	TRUE	::::::::::::::
KNDVTLTGYTPLGK	15	9.63	0.161	681	24.5	AE003541	TRUE	TRUE	1	1507.7	-0.8	14of 26	1.9506	TRUE	TRUE	::::::::::::::
LNNGYEMPILGLGTYNSK	8	6.81	0.117	2099	45.23	AE003541	TRUE	TRUE	2	1985.3	0.5	15of 34	1.7248	TRUE	TRUE	::::::::::::::::::
MLFYSFFK	14	9.72	0.059	1490	40.13	AE003541	TRUE	FALSE	1	1083.3	0.2	9of 14	1.5295	TRUE	TRUE	::::::::
PKPDIQKPDFIYSPEVAVIAK	8	6.96	0.021	1864	51.8	AE003541	TRUE	TRUE	2	2356.8	-0.1	12of 40	1.5366	TRUE	TRUE	::::::::::::::::::::
MLGYFSLVGLLR	14	9.85	0.321	1797	54.33	AE003542	TRUE	TRUE	2	1369.7	0.6	17of 22	2.9087	TRUE	TRUE	::::::::::::
LFEEQLNLLRPK	8	7.1	0.138	1943	41.4	AE003542	TRUE	TRUE	2	1500.8	1.4	18of 22	3.7782	TRUE	TRUE	::::::::::::
LASFIDPNASEDDVSK	1	3.51	0.118	729	33	AE003542	TRUE	TRUE	2	1708.8	0.6	14of 30	2.0271	TRUE	TRUE	::::::::::::::
NPVVLALPK	14	10.1	0.113	814	29.5	AE003542	TRUE	TRUE	2	951.2	0.7	12of 16	1.849	TRUE	TRUE	::::::::::
TIFEHSFK	10	7.82	0.112	692	20.9	AE003542	TRUE	TRUE	2	1009.1	1.2	12of 14	1.7494	TRUE	TRUE	::::::::
HLAVYMR	15	9.85	0.08	229	22.43	AE003542	TRUE	FALSE	2	906.1	0.9	12of 12	2.6334	TRUE	TRUE	::::::Oxidation_M::
VHSLLGDYYQAIK	10	7.68	0.034	1288	35.2	AE003542	TRUE	TRUE	2	1507.7	0.7	18of 24	2.6043	TRUE	TRUE	::::::::::::
LYTTLPLTK	15	9.72	0.032	803	30.5	AE003542	TRUE	TRUE	1	1050.3	-0.3	8of 16	1.2722	TRUE	TRUE	::::::::::
NPVVLALPK	15	10.1	0.029	856	29.5	AE003542	TRUE	TRUE	1	951.2	0	8of 16	1.5949	TRUE	TRUE	::::::::::
VHMRHYLAACKIASELKLVDQQLGVRR	14	10.18	0.007	2843	64.13	AE003542	TRUE	FALSE	3	3193.8	-2.4	9of104	1.1265	TRUE	TRUE	::::::::::Cys_CAM::::::::::::::::
NLPTIFIYHEGALR	9	7.77	0.131	1868	45.8	AE003543	TRUE	TRUE	2	1644.9	1.9	11of 26	1.7117	TRUE	TRUE	::::::::::::::
ESLSPELPKPVLAIAK	7	7.07	0.071	1785	44.3	AE003543	TRUE	FALSE	2	1693	0.2	129	1.2673	TRUE	TRUE	::::::::::::::::
NVIIVAK	13	10.1	0.003	1248	24.1	AE003543	TRUE	FALSE	1	757	-0.5	9of 12	1.5535	TRUE	TRUE	::::::::
HIDCAYVYQNEDEVGDGVEAK	1	3.76	0.241	629	36.7	AE003544	TRUE	TRUE	2	2412.5	1.5	21of 40	2.7508	TRUE	TRUE	::::Cys_CAM::::::::::::::::
AKAGDPVILEEAK	3	4.45	0.183	1248	26.5	AE003544	TRUE	FALSE	2	1341.5	0.4	12of 24	1.7082	TRUE	TRUE	::::::::::::
TLDIGGPEDEPGIQSAR	1	3.59	0.159	664	30.7	AE003544	TRUE	TRUE	2	1755.9	0.5	17of 32	2.2449	TRUE	TRUE	::::::::::::::::
NAGIFMYASNLR	13	9.85	0.441	1234	35.43	AE003545	TRUE	TRUE	2	1357.6	0.9	18of 22	3.3865	TRUE	TRUE	::::::::::::
NAGIFMYASNLR	14	9.85	0.367	1131	35.43	AE003545	TRUE	TRUE	2	1357.6	2.1	18of 22	3.142	TRUE	TRUE	::::::::::::
ALLVDPIEDTADDQLYFTK	1	3.37	0.295	1296	56.3	AE003545	TRUE	FALSE	2	2168.4	0.3	17of 36	3.0638	TRUE	TRUE	::::::::::::::::::
ELIGMFNVPHVTSIYLVK	10	7.74	0.288	1636	62.63	AE003545	TRUE	TRUE	2	2077.5	-0.5	20of 34	2.9109	TRUE	TRUE	:::::Oxidation_M::::::::::::
YRPDEQPSLRPHHDSSTYTINIAMNR	10	7.85	0.218	996	40.33	AE003545	TRUE	TRUE	3	3100.4	-0.2	26of100	3.0063	TRUE	TRUE	::::::::::::::::::::::::
AFTGYFHNPPR	15	9.85	0.18	417	23.8	AE003545	TRUE	TRUE	2	1307.5	0.6	11of 20	1.861	TRUE	TRUE	::::::::::::
FALSTDELDER	1	3.59	0.139	750	28.7	AE003545	TRUE	TRUE	1	1296.4	-0.2	11of 20	1.6934	TRUE	TRUE	::::::::::::
VDLNAYGNYLAR	6	6.64	0.099	1419	32.4	AE003545	TRUE	TRUE	2	1369.5	0.9	13of 22	1.6707	TRUE	TRUE	::::::::::::
TAFDAISFK	6	6.76	0.045	1378	26.1	AE003545	TRUE	TRUE	1	1000.1	0.7	11of 16	1.5794	TRUE	TRUE	::::::::::
HAKEYATAKFAL	13	9.63	0.011	599	24.1	AE003545	TRUE	FALSE	2	1350.6	-2.3	11of 22	1.3261	TRUE	TRUE	::::::::::::
NVNFVDDTGMSCLAHASFK	5	5.1	0.283	1691	41.43	AE003547	TRUE	TRUE	2	2114.3	1.9	13of 36	2.9511	TRUE	TRUE	::::::::::Cys_CAM::::::::
SHDLNELLAFK	5	5.22	0.251	1586	30.7	AE003547	TRUE	TRUE	2	1287.5	1.3	14of 20	2.6273	TRUE	TRUE	::::::::::::
AEAQNLARRLCDAPANCMTPTI	7	6.22	0.01	1708	48.43	AE003548	TRUE	FALSE	3	2490.7	-2.5	75	1.2792	TRUE	TRUE	::::::::::Cys_CAM:::::Cys_CAM:Oxidation_M::::::
GIMITPPPPAMPPTPTSSPNTH	9	7.85	0.055	1502	42.96	AE003550	TRUE	FALSE	3	2274.6	-1.3	21of 84	2.2174	TRUE	TRUE	:::Oxidation_M::::::::Oxidation_M::::::::::::
LAICVQEVVQNFCSK	7	6.14	0.018	1700	44	AE003550	TRUE	TRUE	2	1796	1.4	7	1.4155	TRUE	TRUE	::::Cys_CAM::::::::Cys_CAM:::
HLPIAPNDDTQSLASVAGGTGAAGTVK	4	5.1	0.476	1477	43.8	AE003551	TRUE	TRUE	2	2549.8	-0.6	21of 52	4.342	TRUE	TRUE	::::::::::::::::::::::::::
VYAILTHGIFSGPAISR	15	9.85	0.424	1323	51	AE003551	TRUE	TRUE	2	1803.1	0.7	26of 32	4.4574	TRUE	TRUE	::::::::::::::::::
VYAILTHGIFSGPAISR	14	9.85	0.319	1248	51	AE003551	TRUE	TRUE	2	1803.1	0.2	17of 32	3.1589	TRUE	TRUE	::::::::::::::::::
VMDGFGSYR	9	6.7	0.073	501	22.13	AE003551	TRUE	FALSE	2	1032.2	1.2	8of 16	1.2339	TRUE	TRUE	::::::::::
TPDIVLIPKK	14	9.89	0.01	586	28.5	AE003551	TRUE	FALSE	2	1124.4	2.9	9of 18	1.4264	TRUE	TRUE	::::::::::
NLEPIHGLIFLFK	9	7.82	0.376	2184	53.4	AE003552	TRUE	TRUE	2	1541.9	2.1	19of 24	3.5946	TRUE	TRUE	::::::::::::::
LPENAVMNYSNLK	7	6.87	0.273	1111	32.23	AE003552	TRUE	TRUE	2	1493.7	1.2	1	2.6528	TRUE	TRUE	::::::::::::::
VATYPLQLLGFDVDPLNSVQFSNHTGYK	5	5.1	0.136	2330	74	AE003552	TRUE	TRUE	3	3125.5	2.2	26of108	2.8427	TRUE	TRUE	::::::::::::::::::::::::::
GLSDYVGLPGHLNILLLR	11	7.76	0.104	1548	63.6	AE003552	TRUE	TRUE	3	1951.3	0.6	22of 68	2.4181	TRUE	TRUE	::::::::::::::::
TVHNSFARPTLFELDTK	9	7.82	0.06	1652	38.9	AE003552	TRUE	TRUE	2	1977.2	0.6	15of 32	2.274	TRUE	TRUE	::::::::::::::::
SGLPAGSLAVSILPVTLDTPMNR	6	6.79	0.49	2082	64.53	AE003553	TRUE	TRUE	2	2310.7	0.7	23of 44	4.5743	TRUE	TRUE	::::::::::::::::::::
QSVLTSAISAAVAAQHLK	15	10.1	0.415	1449	39.4	AE003553	TRUE	TRUE	2	1796.1	1.5	15of 34	3.2605	TRUE	TRUE	::::::::::::::::
NADLMWKQSVLTSAISAAVAAQHLK	15	9.89	0.314	1665	61.33	AE003553	TRUE	TRUE	3	2671.1	-0.7	25of 96	3.8529	TRUE	TRUE	:::::Oxidation_M::::::::::::::::::
PALEGTPGMIGYGMAK	9	6.87	0.279	1284	37.86	AE003553	TRUE	TRUE	2	1625.9	1.3	13of 30	2.054	TRUE	TRUE	::::::::Oxidation_M::::Oxidation_M:::
NADLMWKQSVLTSAISAAVAAQHLK	14	9.89	0.235	1559	61.33	AE003553	TRUE	TRUE	3	2671.1	-2.6	20of 96	3.5137	TRUE	TRUE	:::::Oxidation_M:::::::::::::::::
IVDRIAASNLFQYATELP	3	4.08	0.131	2299	57.1	AE003553	TRUE	FALSE	2	2022.3	-2.2	10of 34	1.3888	TRUE	TRUE	::::::::::::::::::
SGLPAGSLAVSILPVTLDTPMNRK	15	10.09	0.107	1564	62.43	AE003553	TRUE	TRUE	2	2438.9	1.7	18of 46	2.1806	TRUE	TRUE	::::::::::::::::::::
REDFASALRFLMGGCAREPEM	3	4.65	0.02	1532	55.16	AE003554	TRUE	FALSE	3	2460.8	-1.2	12of 80	1.2707	TRUE	TRUE	::::::::::::Cys_CAM:::::Oxidation_M:
DKTEDQVTIDCAEAIKK	2	4.21	0.384	441	24.1	AE003555	TRUE	TRUE	2	1965.1	0.3	22of 32	4.86	TRUE	TRUE	::::::::Cys_CAM::::::
AGPVVDVLGDEMTR	1	3.71	0.366	936	33.73	AE003555	TRUE	TRUE	2	1459.7	2.5	21of 26	4.1867	TRUE	TRUE	::::::::::::::
LSPAVSAIYPVLFTK	15	9.72	0.335	1527	52.3	AE003555	TRUE	TRUE	1	1606.9	1.1	15of 28	3.894	TRUE	TRUE	::::::::::::::
FKDIFEDLYNK	3	4.31	0.275	1583	32.9	AE003555	TRUE	TRUE	2	1432.6	0	18of 20	4.6811	TRUE	TRUE	::::::::::::
RDYQETFEFINTLAK	3	4.45	0.252	1663	38.5	AE003555	TRUE	TRUE	2	1876.1	2.2	18of 28	2.959	TRUE	TRUE	::::::::::::::::
LSPAVSAIYPVLFTK	14	9.72	0.209	1419	52.3	AE003555	TRUE	TRUE	2	1606.9	2.1	11of 28	2.1592	TRUE	TRUE	::::::::::::::::
LIDDMVAYAMK	2	3.89	0.192	1018	38.36	AE003555	TRUE	TRUE	1	1270.5	1.6	12of 20	1.6288	TRUE	TRUE	::::::::::::
DYQETFEFINTLAK	1	3.83	0.159	1405	39.1	AE003555	TRUE	TRUE	2	1719.9	1.4	14of 26	1.9034	TRUE	TRUE	::::::::::::::
GSPKPEIPEDGVLR	3	4.45	0.121	1123	25.6	AE003555	TRUE	TRUE	2	1494.7	1.9	14of 26	1.8942	TRUE	TRUE	::::::::::::::
DIFEDLYNK	1	3.71	0.07	1042	26.9	AE003555	TRUE	TRUE	1	1157.3	1.3	11of 16	2.0348	TRUE	TRUE	::::::::::
DGALHMIGTLADVLLK	5	5.1	0.419	2398	50.73	AE003556	TRUE	TRUE	2	1668	1.6	19of 30	3.8153	TRUE	TRUE	::::::::::::::::
DGALHMIGTLADVLLKK	11	7.79	0.363	1610	48.63	AE003556	TRUE	TRUE	3	1796.2	1.5	27of 64	2.7956	TRUE	TRUE	::::::::::::::::
ALQEVVVTADQR	2	4.08	0.299	472	28.4	AE003556	TRUE	TRUE	2	1329.5	0.7	15of 22	2.4643	TRUE	TRUE	::::::::::::
ISADTLLFLQTHK	11	7.82	0.257	1082	38.8	AE003556	TRUE	TRUE	2	1487.7	2.7	14of 24	2.2786	TRUE	TRUE	::::::::::::

IVPALILLFDGLK	7	6.76	0.249	2380	62.2	AE003556	TRUE	TRUE	2	1412.8	-0.3	1	3.6091	TRUE		TRUE		::::::::::::::
IVPALILLFDGLKR	15	10.09	0.239	1946	61.6	AE003556	TRUE	TRUE	2	1569	2.2	20of 26	2.8642	TRUE		TRUE		::::::::::::::
KFDLVLSALDNR	6	6.9	0.198	1616	36.3	AE003556	TRUE	TRUE	2	1391.6	-0.2	16of 22	3.0093	TRUE		TRUE		::::::::::::
PALILLFDGLKR	15	10.09	0.151	1948	49.2	AE003556	TRUE	FALSE	2	1356.7	1.5	15of 22	2.6625	TRUE		TRUE		::::::::::::
ITAYHDSVTSTDYGVNFFK	5	5.1	0.149	1627	41.4	AE003556	TRUE	TRUE	2	2166.4	0.6	16of 36	2.2052	TRUE		TRUE		::::::::::::::::::
NLEDLQTMAVPKKYLDMCS	4	4.31	0.101	1675	48.56	AE003556	TRUE	FALSE	3	2273.6	2.8	19of 72	1.7392	TRUE		TRUE		:::::::Oxidation_M:::::::::Cys_CAM::
AMEDDPQRRKPDITRARQLLHWE	11	7.83	0.055	1789	42.73	AE003556	TRUE	FALSE	3	2879.2	-0.7	13of 88	1.255	TRUE		TRUE		::Oxidation_M::::::::::::::::::
PALILLFDGLK	7	6.76	0.049	2390	49.8	AE003556	TRUE	FALSE	2	1200.5	-1.9	6	2.52	TRUE		TRUE		::::::::::::
QQMGPQLTEVEFEEVMSRNR	2	4.26	0.018	1029	42.06	AE003556	TRUE	FALSE	3	2425.7	1.5	9of 76	1.0692	TRUE		TRUE		::::::::::::::::Oxidation_M:::::
ELGNAEPAPSVSSTTVSSPPAGVK	2	4.27	0.317	586	36.4	AE003557	TRUE	TRUE	2	2283.5	0.5	16of 46	1.997	TRUE		TRUE		::::::::::::::::::::::::
AQLALIEEK	3	4.27	0.096	1160	27.7	AE003557	TRUE	TRUE	2	1015.2	0.4	13of 16	2.6082	TRUE		TRUE		::::::::::
AGGEVLTFDQLALR	2	4.08	0.217	1073	42.3	AE003559	TRUE	TRUE	2	1490.7	2.4	18of 26	3.3778	TRUE		TRUE		::::::::::::::
IYASWVQLELQNQTAQPSNVKTT	9	6.87	0.112	1809	52.1	AE003562	TRUE	FALSE	3	2620.9	2.9	13of 88	1.3393	TRUE		TRUE		::::::::::::::::::::::
DELEMCKMRILLTDDPEEQSNYR	3	3.96	0.046	2398	53.36	AE003563	TRUE	FALSE	3	2903.2	-0.5	9of 88	1.2545	TRUE		TRUE		:::::Oxidation_M:Cys_CAM::::::::::::::::
FQLHGGFVGFDK	9	7.82	0.087	1676	32.8	AE003564	TRUE	TRUE	2	1352.5	0.7	15of 22	2.0006	TRUE		TRUE		::::::::::::
IAPIFETFPTKYPK	15	9.63	0.274	1193	41.6	AE003565	TRUE	TRUE	2	1653	2.3	14of 26	2.403	TRUE		TRUE		::::::::::::::
TLLAQPLGPVK	15	10.1	0.246	879	33.6	AE003565	TRUE	TRUE	1	1137.4	-0.2	15of 20	2.2393	TRUE		TRUE		::::::::::::
FQNVQNIQIFVK	14	10.1	0.225	1074	37.7	AE003565	TRUE	TRUE	2	1478.7	2.1	16of 22	2.3714	TRUE		TRUE		::::::::::::
TLLAQPLGPVK	14	10.1	0.225	818	33.6	AE003565	TRUE	TRUE	1	1137.4	-0.3	15of 20	2.1329	TRUE		TRUE		::::::::::::
MIEPFQVLYEKPSEIVAQFK	3	4.56	0.187	2056	64.03	AE003565	TRUE	TRUE	3	2397.8	1.5	25of 76	3.2909	TRUE		TRUE		::::::::::::::::::::
ICTFDIMIHTLQNTELPAK	5	5.22	0.147	1614	56.93	AE003565	TRUE	FALSE	2	2246.6	0.6	12of 36	2.0402	TRUE		TRUE		::Cys_CAM:::::::::::::::::
KSQRYGNAVSPDSSSNL	13	9.72	0.043	946	16.7	AE003565	TRUE	FALSE	3	1810.9	-1.4	15of 64	1.2405	TRUE		TRUE		::::::::::::::::
TQFSSDTLWTRATAPAMATK	13	10.09	0.048	1371	40.63	AE003567	TRUE	FALSE	2	2201.5	1.4	10of 38	1.6997	TRUE		TRUE		::::::::::::::::Oxidation_M::::
ANAGTFFVAHDIFR	10	7.85	0.525	1456	40	AE003569	TRUE	TRUE	2	1566.8	0.7	17of 26	3.5933	TRUE		TRUE		::::::::::::::
ANAGTFFVAHDIFR	11	7.85	0.227	1213	40	AE003569	TRUE	TRUE	3	1566.8	2.1	15of 52	2.4074	TRUE		TRUE		::::::::::::::
TMLVVYAK	13	9.72	0.182	716	28.63	AE003569	TRUE	FALSE	1	925.2	0.7	8of 14	1.3613	TRUE		TRUE		::::::::
NRFWFPGPADSMVI	8	6.79	0.035	2137	47.53	AE003569	TRUE	FALSE	2	1653.9	0.8	6of 26	0.8787	TRUE		TRUE		::::::::::Oxidation_M:::
TGWYPMYSCVPDANCNRVKFMFNVG	12	8.27	0.067	1843	66.96	AE003572	TRUE	FALSE	3	3031.4	0.4	25of 96	2.2492	TRUE		TRUE		:::::::Cys_CAM::::::Cys_CAM::::::Oxidation_M:::::
VNGMVLEAKLILAA	7	6.95	0.007	1707	51.43	AE003575	TRUE	FALSE	2	1442.8	-0.6	35	1.4928	TRUE		TRUE		::::::::::::
CRDPCPGVCGSNAECYVINHTPMCTCLA	5	5.21	0.101	1934	59.13	AE003576	TRUE	FALSE	3	3317.4	-2.7	17of108	1.7518	TRUE		TRUE		:Cys_CAM:::Cys_CAM:::Cys_CAM:::::Cys_CAM:::::::Oxidation_M:Cys_CAM::Cys_CAM:::
FGDPYVECRPECVINSDCPRSRACVNQK	5	6.22	0.038	2168	50.3	AE003576	TRUE	FALSE	3	3415.6	2.4	21of108	1.814	TRUE		TRUE		:::::::Cys_CAM::::Cys_CAM:::::Cys_CAM:::::Cys_CAM:::::
LYSADGHALIDLLQK	5	5.1	0.416	1783	44.1	AE003577	TRUE	TRUE	2	1657.9	2.4	22of 28	4.8529	TRUE		TRUE		::::::::::::::::
RAYVIPSHVESLYK	14	9.53	0.153	751	34.4	AE003577	TRUE	TRUE	2	1662.9	1	13of 26	1.7978	TRUE		TRUE		::::::::::::::
AYVIPSHVESLYK	10	7.69	0.09	1082	35	AE003577	TRUE	TRUE	2	1506.7	0.8	15of 24	1.9385	TRUE		TRUE		::::::::::::::
PIASAMMCHQQTSSSCAHLMY	8	7.16	0.015	2449	45.39	AE003578	TRUE	FALSE	2	2428.7	2.8	5of 40	0.7962	TRUE		TRUE		::::::Oxidation_M::Cys_CAM::::::::Cys_CAM::::::
FSDFLGIHDLLVGK	5	5.1	0.259	2030	48.5	AE003579	TRUE	TRUE	2	1561.8	2.1	20of 26	3.1831	TRUE		TRUE		::::::::::::::
LLNLPIIGLSTCALMP	6	5.33	0.158	2386	69.03	AE003579	TRUE	FALSE	2	1727.1	0	11of 30	2.0981	TRUE		TRUE		::::::::::Cys_CAM:::::
FFVTFPFPY	5	5.93	0.022	2507	46.5	AE003579	TRUE	FALSE	1	1165.4	0.4	10of 16	1.6331	TRUE		TRUE		::::::::::
VDKYK	13	9.63	0.002	194	5.5	AE003579	TRUE	FALSE	1	652.8	-0.2	5of 8	1.0353	TRUE		TRUE		::::::
YLIATSEQPIAAYHR	10	7.7	0.497	1006	38.7	AE003581	TRUE	TRUE	2	1734	1.8	24of 28	5.128	TRUE		TRUE		::::::::::::::
ELVSCSNCLDYQAR	2	4.08	0.416	561	32.6	AE003581	TRUE	TRUE	2	1715.8	1.3	15of 26	2.6619	TRUE		TRUE		:::::Cys_CAM:::Cys_CAM::::::
KKEPVGAMSEDLPADVTK	3	4.56	0.393	1105	28.13	AE003581	TRUE	TRUE	2	1916.2	0.4	22of 34	4.2157	TRUE		TRUE		::::::::::::::::
FKDVALVETVIAK	6	6.99	0.344	1503	40.3	AE003581	TRUE	TRUE	2	1433.7	2.2	20of 24	4.3088	TRUE		TRUE		::::::::::::::
FKDVALVETVIAK	7	6.99	0.235	1283	40.3	AE003581	TRUE	TRUE	2	1433.7	1.8	1	3.3126	TRUE		TRUE		::::::::::::::
EPVGAMSEDLPADVTK	1	3.59	0.22	714	32.33	AE003581	TRUE	TRUE	2	1659.8	1.6	14of 30	2.126	TRUE		TRUE		::::::::::::::::
VLDLDLFR	2	3.89	0.106	1137	37.2	AE003581	TRUE	FALSE	1	991.2	0.3	9of 14	1.6769	TRUE		TRUE		::::::::
MLVAIDWHAL	5	4.94	0.034	1654	45.03	AE003581	TRUE	FALSE	2	1185.4	0.8	12of 18	2.5255	TRUE		TRUE		:Oxidation_M:::::::::
SQTAAASEDTIFGK	2	4.08	0.304	497	21.3	AE003582	TRUE	TRUE	2	1426.5	0.3	15of 26	3.0615	TRUE		TRUE		::::::::::::::
NLENATSHLR	9	7.85	0.115	985	15.8	AE003582	TRUE	TRUE	2	1155.3	0.9	11of 18	2.0114	TRUE		TRUE		::::::::::
YLLNSLK	15	9.72	0.064	224	25.9	AE003582	TRUE	FALSE	2	851	-0.4	11of 12	1.7206	TRUE		TRUE		::::::::
SVEALLSALQNAPLR	6	6.98	0.049	2042	44.9	AE003582	TRUE	TRUE	2	1582.8	0	17of 28	2.3074	TRUE		TRUE		::::::::::::::
DHALNITLR	10	7.85	0.017	770	23.1	AE003582	TRUE	TRUE	2	1053.2	1.5	11of 16	2.0519	TRUE		TRUE		::::::::::
VAIGLLK	15	10.1	0.01	791	28.3	AE003582	TRUE	FALSE	1	713.9	1.5	8of 12	1.6513	TRUE		TRUE		::::::::
EKSFATK	14	9.89	0.082	167	7.4	AE003583	TRUE	FALSE	2	810.9	1.2	9of 12	1.5712	TRUE		TRUE		::::::::
LSGGPFVTNQPGLLPPLVTTK	15	10.1	0.051	1494	56.8	AE003583	TRUE	TRUE	2	2137.5	1.3	16of 40	2.1506	TRUE		TRUE		::::::::::::::::::::
CNWKVEREK	13	8.93	0.074	768	13.2	AE003585	TRUE	FALSE	2	1249.4	2.9	10of 16	1.1912	TRUE		TRUE		:Cys_CAM:::::::::
DEFPHSTSAWTKGASGVPMVKCTPR	13	8.94	0.025	968	40.23	AE003585	TRUE	TRUE	3	2764.1	-0.6	10of 96	1.1849	TRUE		TRUE		::::::::::::::::Oxidation_M:::Cys_CAM::::
HIVSLNEK	9	7.82	0.024	376	16.6	AE003585	TRUE	TRUE	2	940.1	2.5	10of 14	2.6932	TRUE		TRUE		::::::::
LANLYQEFIK	8	6.87	0	2013	36.6	AE003585	TRUE	TRUE	2	1239.5	1.1	16of 18	3.4001	TRUE		TRUE		::::::::::
KAFNIPMAIASGCCR	13	9.15	0.192	876	37.93	AE003586	TRUE	FALSE	2	1712.9	-1.4	8of 28	1.0488	TRUE		TRUE		::::::Oxidation_M:::::Cys_CAM:Cys_CAM::
HVVCGDDPALGPGRGKPYPDIYLLAASR	8	7.15	0.033	2208	61.5	AE003586	TRUE	FALSE	3	2996.4	-1	21of108	1.9529	TRUE		TRUE		:::::Cys_CAM::::::::::::::::::::::
CTLVFDGTPKGVQAATDARLPVVMLAEK	8	6.42	0.015	3257	70.63	AE003586	TRUE	FALSE	2	3005.5	-1.2	7of 54	1.215	TRUE		TRUE		:Cys_CAM::::::::::::::::::::Oxidation_M:::::
DQLEAMVGLVGPFHALGYATK	5	5.22	0.535	2146	57.53	AE003587	TRUE	TRUE	2	2218.6	2.8	24of 40	5.0794	TRUE		TRUE		::::::::::::::::::::
SAFGSQLQYVTLATQIAQPAQPK	14	9.72	0.408	1403	51.7	AE003587	TRUE	TRUE	2	2448.8	1.9	24of 44	5.6987	TRUE		TRUE		::::::::::::::::::::::
SALFAQINQGADITK	6	6.76	0.388	1418	34.7	AE003587	TRUE	TRUE	2	1577.8	2	23of 28	5.2545	TRUE		TRUE		::::::::::::::
DSLGVEIVNSK	2	4.08	0.332	585	23.5	AE003587	TRUE	TRUE	2	1161.3	0.7	15of 20	3.0558	TRUE		TRUE		::::::::::
SAFGSQLQYVTLATQIAQPAQPK	13	9.72	0.255	1461	51.7	AE003587	TRUE	TRUE	2	2448.8	0.7	20of 44	3.2455	TRUE		TRUE		::::::::::::::::::::
DSLGVEIVNSK	1	4.08	0.215	589	23.5	AE003587	TRUE	TRUE	1	1161.3	0	12of 20	2.3461	TRUE		TRUE		::::::::::
EMNDAGQFYTNR	2	4.08	0.142	432	20.03	AE003587	TRUE	TRUE	2	1446.5	0.9	13of 22	2.1967	TRUE		TRUE		::::::::::::
SLANDVHIVR	10	7.85	0.109	701	24.2	AE003587	TRUE	TRUE	2	1124.3	0	14of 18	1.6321	TRUE		TRUE		::::::::::
SHLSLSTEELQESALKR	6	5.4	0.173	1223	32.7	AE003589	TRUE	TRUE	3	1929.1	1.5	19of 64	2.0006	TRUE		TRUE		::::::::::::::::
SLIDAVMPEVKPLK	9	6.99	0.137	488	42.03	AE003589	TRUE	FALSE	3	1540.9	2.1	17of 52	1.7752	TRUE		TRUE		::::::::::::::
GGAEVPSNKDVTSLDWNCDGSLLA	1	3.51	0.051	2080	49.5	AE003589	TRUE	FALSE	2	2506.7	1.4	5of 46	0.8804	TRUE		TRUE		::::::::::::::::::Cys_CAM:::::::
HYHAAIEHDPTDITFYNNIAAVHFER	6	5.6	0.5	1567	56	AE003590	TRUE	TRUE	3	3083.3	1	42of100	5.6899	TRUE		TRUE		::::::::::::::::::::::::
YDPTNAILLQGR	6	6.7	0.342	1335	31.5	AE003590	TRUE	TRUE	2	1361.5	1.5	17of 22	4.0033	TRUE		TRUE		::::::::::::
ALELDPNNAEAIEGYR	1	3.69	0.335	853	37.6	AE003590	TRUE	TRUE	2	1775.9	1.8	20of 30	3.3592	TRUE		TRUE		::::::::::::::::
KGAAAAGLNDFMK	15	9.89	0.318	425	24.73	AE003590	TRUE	TRUE	2	1294.5	0.7	18of 24	3.3883	TRUE		TRUE		::::::::::::::
MAYINPEKAEEEKEQGNLFFK	3	4.43	0.129	1428	45.53	AE003590	TRUE	TRUE	3	2516.8	1.2	26of 80	2.5864	TRUE		TRUE		::::::::::::::::::::
NSSKDVLATMETGNARNFSVSDAILSTFSPQRPA	8	7.07	0.093	2416	64.13	AE003590	TRUE	FALSE	3	3614	1.7	23of132	1.7772	TRUE		TRUE		::::::::::::::::::::::::::::::::
RLENLATMQNML	6	6.98	0.061	1134	37.26	AE003590	TRUE	FALSE	2	1434.7	2.9	9of 22	1.3665	TRUE		TRUE		::::::::::::
QLETQLTPIHADLCLLSLK	5	5.22	0.295	1948	60.7	AE003592	TRUE	TRUE	2	2194.5	2.3	15of 36	3.0495	TRUE		TRUE		::::::::::::Cys_CAM:::::::
YFLTFK	14	9.72	0.066	867	27.3	AE003593	TRUE	FALSE	1	819	0.6	6of 10	1.8704	TRUE		TRUE		::::::
LAKIVLPPAY	13	9.72	0.064	1686	39	AE003593	TRUE	FALSE	2	1085.4	-0.6	7of 18	1.2301	TRUE		TRUE		::::::::::

YFLTFK	15	9.72	0	952	27.3	AE003593	TRUE	FALSE	1	819	0	6of 10	1.2896	TRUE	TRUE	::::::
SNDIDLVTQTDKDVEQLLMDGIR	1	3.64	0.343	1840	54.23	AE003594	TRUE	TRUE	2	2619.9	1.3	16of 44	3.7417	TRUE	TRUE	::::::::::::::::::::
RVLAAATPELAQEISK	7	7.1	0.322	1101	38.5	AE003594	TRUE	TRUE	2	1698	1.3	1	4.0645	TRUE	TRUE	::::::::::::::
VLAAATPELAQEISK	3	4.27	0.233	1359	39.1	AE003594	TRUE	TRUE	2	1541.8	2.5	17of 28	1.981	TRUE	TRUE	::::::::::::::
FIGEEESSGAEGVK	2	3.8	0.176	400	23.8	AE003594	TRUE	TRUE	2	1439.5	1.3	16of 26	2.5519	TRUE	TRUE	::::::::::::::
EAGGVVIDPAGGEFDIMSR	1	3.59	0.144	1141	45.43	AE003594	TRUE	TRUE	2	1921.1	1.9	14of 36	2.3321	TRUE	TRUE	::::::::::::::::::
ASESFSPIVGDLHGILPQQPSELVKSYR	6	5.35	0.114	1656	65.9	AE003594	TRUE	FALSE	3	3056.4	0.6	11of108	1.0369	TRUE	TRUE	::::::::::::::::::::::::::
YQFDQSQQGRFAHVKDTPVLD	5	5.2	0.027	1300	38.8	AE003594	TRUE	FALSE	3	2480.7	2.4	8of 80	0.9912	TRUE	TRUE	::::::::::::::::::::
LKDFPIANEPILGYLK	7	6.92	0.093	1664	54	AE003595	TRUE	TRUE	2	1832.2	0.1	23	2.6689	TRUE	TRUE	::::::::::::::::
SPSGDETVVIGSIK	2	4.08	0.39	616	25.6	AE003597	TRUE	TRUE	2	1389.5	1.3	18of 26	3.5366	TRUE	TRUE	::::::::::::::
DLHYKPLFPYFAK	15	9.47	0.259	1271	41.3	AE003597	TRUE	TRUE	3	1639.9	2.2	30of 48	3.153	TRUE	TRUE	::::::::::::::
TLPVKYPVSEIIAIHK	14	9.63	0.22	1050	46	AE003597	TRUE	TRUE	2	1809.2	1.7	16of 30	2.5242	TRUE	TRUE	::::::::::::::::
DLHYKPLFPYFAK	14	9.47	0.181	1188	41.3	AE003597	TRUE	TRUE	2	1639.9	1.5	16of 24	2.4805	TRUE	TRUE	::::::::::::::
LYLINSPVVR	15	9.85	0.178	1065	38.7	AE003597	TRUE	TRUE	2	1174.4	1.8	12of 18	2.67	TRUE	TRUE	::::::::::
SCVFGNEPVCGNLRG	5	6.14	0.056	1470	31.9	AE003600	TRUE	FALSE	2	1666.8	-1.7	6of 28	0.9574	TRUE	TRUE	::Cys_CAM::::::::Cys_CAM::::::
LGLATQLVESIYR	8	6.89	0.349	2255	43.9	AE003601	TRUE	TRUE	2	1463.7	1.6	19of 24	3.0884	TRUE	TRUE	::::::::::::
IDRPAGIIYFTQK	15	9.72	0.257	965	36.7	AE003601	TRUE	TRUE	2	1522.8	2	16of 24	3.7351	TRUE	TRUE	::::::::::::::
LPLDATAAQPVIKVLKAAGVA	14	9.89	0.114	2000	59.1	AE003601	TRUE	FALSE	2	2047.5	-1.3	10of 40	1.3222	TRUE	TRUE	::::::::::::::::::::
KSVDVFVTDESGGYISAEHIK	3	4.54	0.023	2016	40.3	AE003601	TRUE	FALSE	2	2282.5	-2.2	6of 40	0.9808	TRUE	TRUE	::::::::::::::::::::
SFPGVLAYNVSK	14	9.72	0.333	967	31.4	AE003602	TRUE	TRUE	2	1282.5	0.8	15of 22	2.4439	TRUE	TRUE	::::::::::::
SLYQLTHLVTPELIK	9	7.74	0.28	2016	49.2	AE003602	TRUE	TRUE	3	1756.1	1.4	26of 56	2.6737	TRUE	TRUE	::::::::::::::::
SLYQLTMLATPELVK	6	6.87	0.259	1960	51.43	AE003602	TRUE	TRUE	1	1708.1	1.1	14of 28	2.9653	TRUE	TRUE	::::::::::::::::
QVFLDKELNEIVK	3	4.45	0.17	1551	39.3	AE003602	TRUE	TRUE	2	1575.8	1.9	19of 24	3.1533	TRUE	TRUE	::::::::::::::
EAEVQQIVGATLAK	2	4.27	0.12	918	32	AE003602	TRUE	TRUE	2	1457.7	2.8	14of 26	1.3647	TRUE	TRUE	::::::::::::::
VGSTPLNPLDRVGHIK	14	10.09	0.041	686	32.4	AE003602	TRUE	FALSE	3	1704	1.2	15of 60	1.4819	TRUE	TRUE	::::::::::::::::
LYTGPGVVGNVLVDPTAK	6	6.68	0.499	1571	44.8	AE003605	TRUE	TRUE	2	1801.1	1.5	23of 34	5.1215	TRUE	TRUE	::::::::::::::::
IVDITHALFQTNK	11	7.82	0.39	1060	34.6	AE003605	TRUE	TRUE	2	1500.7	-0.2	17of 24	3.4717	TRUE	TRUE	::::::::::::
INAGIYIFNPSVLDR	7	6.7	0.378	1688	49.9	AE003605	TRUE	TRUE	2	1693	1.4	1	3.2178	TRUE	TRUE	::::::::::::::
ECNNPVHLTVDTSLQGGR	5	5.22	0.377	1339	28.8	AE003605	TRUE	TRUE	2	1998.1	1.2	19of 34	3.2886	TRUE	TRUE	::Cys_CAM:::::::::::::::
IVDITHALFQTNK	10	7.82	0.348	1308	34.6	AE003605	TRUE	TRUE	2	1500.7	2.3	17of 24	3.8577	TRUE	TRUE	::::::::::::::
AQFLPAFEQVAPHFVK	10	7.82	0.346	1572	49.3	AE003605	TRUE	TRUE	2	1830.1	1.6	18of 30	3.2594	TRUE	TRUE	::::::::::::::
LYTGPGVVGNVLVDPTAK	7	6.68	0.328	1360	44.8	AE003605	TRUE	TRUE	2	1801.1	-0.2	1	3.1058	TRUE	TRUE	::::::::::::::::
AQFLPAFEQVAPHFVK	11	7.82	0.325	1326	49.3	AE003605	TRUE	TRUE	2	1830.1	0.7	19of 30	3.2432	TRUE	TRUE	::::::::::::::
FHSQVIPGLLSLLDDVENPR	3	4.3	0.319	2136	59.5	AE003605	TRUE	TRUE	2	2250.6	-1	18of 38	2.935	TRUE	TRUE	::::::::::::::::
VIVTEPEPDVQSELLNSLAK	1	3.69	0.258	1236	53.7	AE003605	TRUE	TRUE	2	2182.5	1.1	21of 38	3.3493	TRUE	TRUE	::::::::::::::::
FIIQNANSDDLR	2	3.89	0.254	624	31.4	AE003605	TRUE	TRUE	2	1406.5	2.3	19of 22	3.6239	TRUE	TRUE	::::::::::::
LGVELIFSHETEPLGTAGPLALAK	3	4.54	0.23	1881	70.5	AE003605	TRUE	TRUE	2	2464.9	1.8	14of 46	2.34	TRUE	TRUE	::::::::::::::::::::
YIVALIPLILH	10	7.76	0.222	2000	57.9	AE003605	TRUE	FALSE	1	1265.6	-0.6	12of 20	1.9419	TRUE	TRUE	::::::::::::
FYFHDGVR	9	7.76	0.192	1296	23	AE003605	TRUE	TRUE	2	1041.2	0.2	10of 14	1.8721	TRUE	TRUE	::::::::
IVSIIAESFCTK	7	6.29	0.182	1324	39.1	AE003605	TRUE	TRUE	2	1368.6	2.9	146	1.5047	TRUE	TRUE	:::::::::Cys_CAM:::
YIVALIPLILH	11	7.76	0.152	1691	57.9	AE003605	TRUE	FALSE	2	1265.6	0.8	13of 20	2.7329	TRUE	TRUE	::::::::::
ICEVVAEVAR	2	4.27	0.078	493	30.6	AE003605	TRUE	TRUE	2	1146.3	0.7	11of 18	1.5658	TRUE	TRUE	::Cys_CAM:::::::::
VHPVVLFQVVDAFER	5	5.22	0.02	2082	51.9	AE003605	TRUE	TRUE	2	1756.1	1.4	9of 28	1.6025	TRUE	TRUE	::::::::::::::
AFFVFGSLVAFY	6	5.93	0.006	1304	58.6	AE003605	TRUE	FALSE	2	1368.6	-1.4	10of 22	1.1424	TRUE	TRUE	::::::::::::
FYFHDGVR	10	7.76	0.004	708	23	AE003605	TRUE	TRUE	2	1041.2	0.6	8of 14	1.4269	TRUE	TRUE	::::::::
YDTPVDIIATPTEIIR	1	3.71	0.432	1256	47.8	AE003606	TRUE	TRUE	2	1818.1	2.4	20of 30	3.9295	TRUE	TRUE	::::::::::::::::
SASSTGANAGAGEDGKADAQNGGEAVTVAGGDVGGAR	2	3.85	0.407	428	30.5	AE003606	TRUE	TRUE	3	3234.3	1.5	46of144	5.6014	TRUE	TRUE	::::::::::::::::::::::::::::::::::::
AAALFANEEEFKK	3	4.56	0.393	1203	30.8	AE003606	TRUE	TRUE	2	1468.6	1.2	17of 24	2.9123	TRUE	TRUE	::::::::::::::
TIIVTIVHDMQVVDSLPPNLFQK	5	5.1	0.299	2465	72.63	AE003606	TRUE	TRUE	2	2609.1	-0.7	16of 44	3.4613	TRUE	TRUE	::::::::::::::::::::
RLEEIPLFEK	3	4.56	0.279	1437	34.3	AE003606	TRUE	TRUE	2	1274.5	0.5	13of 18	2.5038	TRUE	TRUE	::::::::::
LLQLASFCNIFELEK	3	4.27	0.104	2072	59.9	AE003606	TRUE	TRUE	2	1826.1	1.7	10of 28	1.9982	TRUE	TRUE	::::::::Cys_CAM:::::::::
SASSTGANAGAGEDGKADAQNGGEAVTVAGGDVGGAR	1	3.85	0.103	393	30.5	AE003606	TRUE	TRUE	3	3234.3	0.8	29of144	2.7047	TRUE	TRUE	::::::::::::::::::::::::::::::::::::
FIEADKSPLEK	3	4.45	0.096	1010	25.6	AE003606	TRUE	TRUE	2	1277.5	1	16of 20	2.5194	TRUE	TRUE	::::::::::::
VLHEFK	10	7.82	0.086	276	18.1	AE003606	TRUE	TRUE	1	772.9	0.1	7of 10	1.4446	TRUE	TRUE	::::::
ILPVLQQLK	15	10.1	0.084	1156	36.6	AE003606	TRUE	TRUE	2	1052.3	2.1	9of 16	1.2913	TRUE	TRUE	::::::::::
TVLAHGVHLEDDEVALLK	4	4.53	0.523	1573	48.1	AE003607	TRUE	TRUE	2	1960.2	0.2	23of 34	5.2896	TRUE	TRUE	::::::::::::::::::
FSNHQYAQQVYQGVVEATLR	9	7.7	0.519	1876	42.2	AE003607	TRUE	TRUE	2	2339.6	-0.1	26of 38	6.4635	TRUE	TRUE	::::::::::::::::::::
NIVEVFVAGK	6	6.95	0.235	1512	30.7	AE003607	TRUE	TRUE	1	1076.3	-0.4	11of 18	2.4453	TRUE	TRUE	::::::::::
GHNFLDLGTATVLENQMR	5	5.22	0.337	1823	43.13	AE003608	TRUE	TRUE	2	2017.3	1.4	23of 34	4.1528	TRUE	TRUE	::::::::::::::::
LINPNMLVLGQEPR	7	6.98	0.279	1409	45.33	AE003608	TRUE	TRUE	2	1594.9	2.6	1	2.5797	TRUE	TRUE	::::::::::::::
KLEELVAILGPSFPR	7	7.1	0.257	1676	49.9	AE003608	TRUE	TRUE	2	1670	0.7	1	2.2449	TRUE	TRUE	::::::::::::::::
DLPKDTKINGRIVNGYP	15	9.63	0.022	1506	31	AE003608	TRUE	FALSE	3	1901.2	2.2	24of 64	2.8447	TRUE	TRUE	::::::::::::::::
IVRQGAQEPITK	14	10.09	0	638	22.6	AE003608	TRUE	FALSE	2	1340.6	1.2	10of 22	1.73	TRUE	TRUE	::::::::::::
PPQKQFIINPHTG	15	10.1	0.082	356	24.5	AE003609	TRUE	FALSE	3	1477.7	2.3	13of 48	1.3115	TRUE	TRUE	::::::::::::
DAFSAALEEVNAINPALKLDAIK	1	4.07	0.156	1990	63.2	AE003610	TRUE	FALSE	2	2414.8	1.7	7of 44	1.2167	TRUE	TRUE	::::::::::::::::::::
EYSGLLHLHK	11	7.89	0.039	630	23.2	AE003610	TRUE	TRUE	2	1197.4	2	13of 18	1.6216	TRUE	TRUE	::::::::::
YFVLGLPTGSTPLGMYK	14	9.53	0.03	1510	54.23	AE003610	TRUE	TRUE	2	1845.2	2.6	13of 32	1.8508	TRUE	TRUE	::::::::::::::::
MGNVMDRKVSCSEAR	12	8.97	0.004	888	22.46	AE003610	TRUE	FALSE	3	1757	0.8	14of 56	1.3516	TRUE	TRUE	:Oxidation_M::::::::Cys_CAM:::::
YEKRGVSITESQLA	7	7.02	0.167	1481	26.5	AE003611	TRUE	FALSE	2	1581.8	0.2	11	1.8211	TRUE	TRUE	::::::::::::::
HSLTAAMCLQDFPSQVVER	4	5.22	0.396	1681	47.23	AE003612	TRUE	TRUE	2	2190.4	0.4	20of 36	3.4247	TRUE	TRUE	::::::::Cys_CAM:::::::::::
YGYHGHYVQVEVR	10	7.8	0.113	749	24.4	AE003613	TRUE	TRUE	2	1607.8	0.2	13of 24	2.2278	TRUE	TRUE	::::::::::::
MPGVDPHDIERRR	11	7.86	0.007	845	19.33	AE003613	TRUE	FALSE	2	1578.8	2.7	12of 24	2.0153	TRUE	TRUE	::::::::::::
NMFITAK	13	10.1	0.028	695	20.93	AE003614	TRUE	FALSE	1	825	0.1	7of 12	1.2868	TRUE	TRUE	::::::::
IPTHYKDPILILGTDGVGTK	10	7.72	0.282	1312	47.2	AE003615	TRUE	TRUE	2	2139.5	1.2	17of 38	2.3481	TRUE	TRUE	::::::::::::::::::
NSSNNGSLIRKSLSLDHSIQRDQNI	14	10.09	0.031	1446	37.7	AE003615	TRUE	FALSE	3	2798	-2.3	17of 96	1.8933	TRUE	TRUE	::::::::::::::::::::::
MMMHMPSGGMSSSTMGGSVYA	11	7.76	0.044	890	43.38	AE003616	TRUE	FALSE	3	2186.5	-2.3	20of 80	1.8912	TRUE	TRUE	:Oxidation_M:Oxidation_M::::::::::::Oxidation_M:::::::
PILPALCDAPQNSHYR	12	7.16	0.016	1109	37.4	AE003617	TRUE	FALSE	3	1853.1	0.8	20of 60	1.8108	TRUE	TRUE	::::::Cys_CAM:::::::::::
VFYVSKSYQVNVNM	13	9.53	0.041	371	38.93	AE003619	TRUE	FALSE	2	1678.9	1	6of 26	0.9396	TRUE	TRUE	::::::::::::::
IKYSLKQTILGVEAFNSQMNGNGTPR	15	10.18	0.001	1129	52.83	AE003619	TRUE	FALSE	3	2884.3	0.3	19of100	2.0753	TRUE	TRUE	::::::::::::::::::Oxidation_M:::::::
REYNVSVMDAPALKMSDAYVQVGSVAR	7	6.94	0.032	1953	59.96	AE003620	TRUE	FALSE	3	2958.4	1.5	153	1.194	TRUE	TRUE	::::::::::::::::::::::::::
TNFYAESGGQIYDQGALVK	2	4.08	0.5	864	40	AE003621	TRUE	TRUE	2	2062.2	2.4	21of 36	3.798	TRUE	TRUE	::::::::::::::::::
EIVELTEQISHATIPYVK	3	4.54	0.335	1704	48.9	AE003621	TRUE	TRUE	3	2071.4	2.4	25of 68	3.2958	TRUE	TRUE	::::::::::::::::::
GGYILHIGVVEGTLK	10	7.74	0.331	1364	42.2	AE003621	TRUE	TRUE	2	1556.8	1.4	20of 28	3.0233	TRUE	TRUE	::::::::::::::::

KSEAFEQEIVR	3	4.56	0.316	1056	22.9	AE003621	TRUE	TRUE	2	1336.5	0.9	16of 20	3.2345	TRUE	TRUE	::::::::::
GGYILHIGVVEGTLK	11	7.74	0.274	1113	42.2	AE003621	TRUE	TRUE	1	1556.8	-0.8	16of 28	2.8606	TRUE	TRUE	::::::::::::::
SAFTHLSDNQVK	9	7.82	0.273	1076	18.8	AE003621	TRUE	TRUE	2	1347.5	0.1	14of 22	2.196	TRUE	TRUE	::::::::::::
AAPAPSTVEEAAKPK	9	7.07	0.268	894	19.4	AE003621	TRUE	TRUE	2	1467.7	0.1	16of 28	2.1188	TRUE	TRUE	::::::::::::::
SGHIMDFVISSEEAIAK	3	4.43	0.261	1773	42.23	AE003621	TRUE	TRUE	2	1835.1	0	14of 32	2.0697	TRUE	TRUE	::::::::::::::::
RIVALTGPEALK	15	10.09	0.2	635	33.4	AE003621	TRUE	TRUE	2	1268.5	1.3	14of 22	2.0633	TRUE	TRUE	::::::::::::
EAAAGEDITPLADESIK	1	3.51	0.193	704	34.7	AE003621	TRUE	TRUE	2	1730.9	0.8	15of 32	2.468	TRUE	TRUE	::::::::::::::::
LYVTYFGGDAASGLEPDLECK	1	3.59	0.188	1193	55.3	AE003621	TRUE	TRUE	2	2306.5	0.9	17of 40	2.248	TRUE	TRUE	::::::::::::::::::Cys_CAM:::
FYAPILSK	14	9.72	0.165	838	29.8	AE003621	TRUE	TRUE	1	939.1	0.2	8of 14	1.627	TRUE	TRUE	::::::::
RIVALTGPEALK	14	10.09	0.138	676	33.4	AE003621	TRUE	TRUE	2	1268.5	-0.3	16of 22	2.5612	TRUE	TRUE	::::::::::::
VGADDVDGIDMAYR	1	3.43	0.134	730	31.23	AE003621	TRUE	TRUE	2	1497.6	1.6	11of 26	1.936	TRUE	TRUE	::::::::::::::
MRTMRSASEFDEAMR	9	7.17	0.049	866	29.49	AE003622	TRUE	FALSE	3	1851.1	-2.9	19of 56	1.8069	TRUE	TRUE	:Oxidation_M::::::::::::Oxidation_M:::
IDGDFYCVMGLPLHR	5	5.1	0.114	1819	48.63	AE003623	TRUE	TRUE	2	1794	2.4	10of 28	1.6364	TRUE	TRUE	::::::Cys_CAM::::::::
SNGQTNGLDDKSGNGIQHSPSRISMVLGNFAG	11	7.82	0.026	1542	45.23	AE003623	TRUE	FALSE	3	3276.5	1.9	23of124	2.0832	TRUE	TRUE	::::::::::::::::::::::::Oxidation_M::::::::
HSVQPMLPTGGGSNIGLAKT	13	10.1	0.021	1055	35.33	AE003623	TRUE	FALSE	3	1982.3	-0.9	21of 76	2.4251	TRUE	TRUE	::::::Oxidation_M::::::::::::::
AGTVWVNTYNVLAAQAPFGGYK	15	9.53	0.466	1637	56.3	AE003624	TRUE	TRUE	2	2328.6	-0.1	21of 42	4.6172	TRUE	TRUE	::::::::::::::::::::::
ANNSEYGLAAAVFTK	7	6.87	0.429	1309	31.7	AE003624	TRUE	TRUE	2	1556.7	1.9	1	2.6536	TRUE	TRUE	::::::::::::::::
LIQLASGNTNLK	15	10.1	0.124	589	30.6	AE003624	TRUE	TRUE	2	1272.5	0.4	14of 22	2.0357	TRUE	TRUE	::::::::::::
CICILDHPVASTK	9	7	0.476	1412	33.5	AE003625	TRUE	TRUE	2	1514.7	0.9	20of 24	4.0718	TRUE	TRUE	:Cys_CAM::Cys_CAM:::::::::::
DKADLDGQLTK	2	4.18	0.125	146	15	AE003625	TRUE	TRUE	2	1204.3	1.8	15of 20	2.9958	TRUE	TRUE	::::::::::
RLDIYLDTNGNRSLDLGMEL	3	3.97	0.093	2803	57.23	AE003625	TRUE	FALSE	3	2325.6	2.6	13of 76	1.5517	TRUE	TRUE	::::::::::::::::Oxidation_M:::
LKECILSGMLSVSGKKVLHIDRNK	13	10.17	0.067	1507	53.93	AE003625	TRUE	FALSE	3	2743.2	2.3	6of 92	0.7532	TRUE	TRUE	::::Cys_CAM::::Oxidation_M:::::::::::::::
GYEKGGLVAHFSLSDQRVVSGA	9	7.75	0.062	1588	42.9	AE003625	TRUE	FALSE	3	2278.5	2	23of 84	2.9267	TRUE	TRUE	::::::::::::::::::::
LVDGTEFDSSLSR	1	3.71	0.434	660	30	AE003626	TRUE	TRUE	2	1426.5	1.7	18of 24	3.6182	TRUE	TRUE	::::::::::::
YIKPGMTMIQICEELENTAR	4	4.56	0.383	1922	53.46	AE003626	TRUE	TRUE	2	2398.8	-0.8	18of 38	3.2694	TRUE	TRUE	::::::::::Cys_CAM:::::::::
VFEDRDVEFDYGEGK	1	3.76	0.266	692	31.5	AE003626	TRUE	TRUE	2	1805.9	0.4	16of 28	2.6367	TRUE	TRUE	::::::::::::::
NILPTTVHTNEEVKK	9	7.8	0.197	1096	24	AE003626	TRUE	TRUE	2	1724	0.6	17of 28	2.6869	TRUE	TRUE	::::::::::::::
YAFVGDHAGQITMLR	10	7.76	0.405	1240	40.33	AE003628	TRUE	TRUE	2	1679.9	2.3	17of 28	2.3135	TRUE	TRUE	::::::::::::::
IDLTPILHDVLPALGTFLR	5	5.1	0.392	2724	73.1	AE003628	TRUE	TRUE	2	2105.5	0	18of 36	3.0486	TRUE	TRUE	::::::::::::::::::
HSSFIDQFFGGTFEVK	4	5.22	0.327	2013	41.7	AE003628	TRUE	TRUE	2	1847	0.2	18of 30	3.0911	TRUE	TRUE	::::::::::::::::
KDESVAEDFHGTQIK	3	4.54	0.245	987	19	AE003628	TRUE	TRUE	3	1704.8	0.8	25of 56	3.335	TRUE	TRUE	::::::::::::::
RIEEATDILTFLSK	3	4.45	0.223	1804	41.8	AE003628	TRUE	TRUE	2	1636.9	1.3	15of 26	1.9887	TRUE	TRUE	::::::::::::::
VFLDPNTLSEDGTIALTQK	1	3.71	0.222	1210	49	AE003628	TRUE	TRUE	2	2063.3	-0.1	17of 36	2.6207	TRUE	TRUE	::::::::::::::::::
IVSGLTLSDFAK	7	6.76	0.187	1347	36.8	AE003628	TRUE	TRUE	2	1251.5	2.8	4	2.2372	TRUE	TRUE	::::::::::::
YSEIFYNFSSFLNPGSIYR	6	6.78	0.186	2299	61	AE003628	TRUE	TRUE	2	2305.6	1.2	15of 36	2.7399	TRUE	TRUE	::::::::::::::::
SDIFHAYVALLK	10	7.74	0.145	1656	41	AE003628	TRUE	TRUE	2	1377.6	0.7	13of 22	2.0999	TRUE	TRUE	::::::::::::
ELQEEKDEALSVLDSNVSNL	1	3.44	0.102	1265	45.3	AE003628	TRUE	FALSE	2	2233.4	2.1	14of 38	2.3836	TRUE	TRUE	::::::::::::::::::
YSEIFYNFSSFLNPGSIYR	7	6.78	0.089	2054	61	AE003628	TRUE	TRUE	2	2305.6	2.9	1	1.978	TRUE	TRUE	::::::::::::::::
AQLFALTGVQPDR	7	6.79	0.074	1267	35.3	AE003628	TRUE	TRUE	2	1416.6	0.4	107	1.5588	TRUE	TRUE	::::::::::::
DSEALREAIESGGIDVNCMDDVGQT	1	3.28	0.062	1788	47.53	AE003628	TRUE	FALSE	3	2682.8	2.9	19of 96	1.758	TRUE	TRUE	::::::::::::::::Cys_CAM:::::::::
FGEFLVPFHSTILK	10	7.82	0.038	1688	52	AE003628	TRUE	TRUE	2	1635.9	1.9	13of 26	2.3213	TRUE	TRUE	::::::::::::::
ATAGAPSEVVQLHK	11	7.82	0.037	438	23.2	AE003628	TRUE	TRUE	2	1408.6	0.8	14of 26	1.8341	TRUE	TRUE	::::::::::::::
LLTLAKGDMR	15	10.09	0.013	1291	29.73	AE003628	TRUE	FALSE	2	1134.4	0.8	12of 18	2.4145	TRUE	TRUE	::::::::Oxidation_M::
PQSISTTISLLSTLCRGSPSITHDILR	13	9.02	0.002	1745	66.5	AE003628	TRUE	FALSE	3	2955.3	-1.7	23of104	1.906	TRUE	TRUE	::::::::::::::Cys_CAM::::::::::::
SPIAFQITMK	15	10.1	0.149	1076	30.73	AE003630	TRUE	TRUE	1	1136.4	0.9	10of 18	2.0242	TRUE	TRUE	::::::::::
HILTISGHTAPIK	15	10.1	0.14	183	28.8	AE003630	TRUE	TRUE	3	1388.7	1.7	19of 48	1.9271	TRUE	TRUE	::::::::::::
MLVGVYR	14	9.85	0.15	731	27.33	AE003631	TRUE	FALSE	1	854.1	0.2	8of 12	1.6915	TRUE	TRUE	:Oxidation_M:::::::
MLVGVYR	13	9.85	0.065	874	27.33	AE003631	TRUE	FALSE	1	854.1	-0.3	8of 12	1.6224	TRUE	TRUE	:Oxidation_M:::::::
MLVGVYR	15	9.85	0.045	796	27.33	AE003631	TRUE	FALSE	1	854.1	1	9of 12	2.0542	TRUE	TRUE	:Oxidation_M:::::::
EISRLEVMRNTIAELHKTNSDREVELE	3	4.6	0.023	1432	57.03	AE003631	TRUE	FALSE	3	3229.6	-1.7	12of104	1.1242	TRUE	TRUE	::::::::Oxidation_M:::::::::::::::::
PYMGVGGGVSGVGGAIYEGGTFPR	8	6.83	0.087	2395	50.13	AE003632	TRUE	FALSE	2	2302.6	0.6	12of 46	2.0105	TRUE	TRUE	:::Oxidation_M:::::::::::::::::::
KQKDVSGEIVLITGTGHGIG	12	7.8	0.025	919	35.3	AE003634	TRUE	FALSE	3	2010.3	-0.2	20of 76	1.7134	TRUE	TRUE	::::::::::::::::::::
VHGEVSVAELITK	5	5.3	0.467	1407	30.7	AE003635	TRUE	TRUE	2	1382.6	0.4	21of 24	3.8447	TRUE	TRUE	::::::::::::::
VLEGNCTLQLLK	7	6.29	0.415	1212	38.8	AE003635	TRUE	TRUE	2	1388.6	1.3	1	3.5646	TRUE	TRUE	::::::Cys_CAM::::::
EQELFFFHELSPGSCFFQPR	3	4.54	0.345	1964	63.3	AE003635	TRUE	TRUE	2	2503.7	1.1	19of 38	3.7361	TRUE	TRUE	::::::::::::::Cys_CAM::::::
GAHIYNTLMGFIK	15	9.72	0.307	1420	38.43	AE003635	TRUE	TRUE	1	1465.8	-0.8	11of 24	2.2276	TRUE	TRUE	::::::::::::
GIEEEDVSPGFVLCDAANPIK	1	3.51	0.189	1145	52	AE003636	TRUE	TRUE	2	2261.5	0.9	18of 40	2.5195	TRUE	TRUE	::::::::::::::Cys_CAM:::::::::
GPAFIPFIDELPSLNRK	8	7.02	0.009	2359	52.8	AE003636	TRUE	TRUE	2	1915.2	0.4	14of 32	2.5841	TRUE	TRUE	::::::::::::::
TLHCRPIASLDHFTAENLSSADLVEEVASGTNK	4	4.68	0.472	1817	66.9	AE003637	TRUE	TRUE	3	3584.9	2.8	40of128	7.5085	TRUE	TRUE	::::Cys_CAM::::::::::::::::::::::::::::
APAQTAVVEYPGDIVVKPGQVLTPTQVK	8	6.92	0.388	1923	62.5	AE003637	TRUE	TRUE	3	2907.4	1.6	41of108	6.5417	TRUE	TRUE	::::::::::::::::::::::::::
GLHPTAISDSFQR	10	7.85	0.354	781	25.1	AE003637	TRUE	TRUE	2	1429.6	1.7	15of 24	2.6846	TRUE	TRUE	::::::::::::
GLHPTAISDSFQR	11	7.85	0.326	640	25.1	AE003637	TRUE	TRUE	2	1429.6	1.5	18of 24	2.3585	TRUE	TRUE	::::::::::::
VVSQQSSLLAPIAVDAVLK	6	6.76	0.279	1851	57.2	AE003637	TRUE	TRUE	2	1939.3	1.9	18of 36	3.3013	TRUE	TRUE	::::::::::::::::::
APAQTAVVEYPGDIVVKPGQVLTPTQVK	9	6.92	0.267	1752	62.5	AE003637	TRUE	TRUE	3	2907.4	1.3	36of108	5.6712	TRUE	TRUE	::::::::::::::::::::::::::
SKVVSQQSSLLAPIAVDAVLK	14	9.89	0.183	1254	54.9	AE003637	TRUE	FALSE	2	2154.6	2.6	16of 40	2.2163	TRUE	TRUE	::::::::::::::::::
SLHDALCVVR	9	7.16	0.161	1224	28.1	AE003637	TRUE	TRUE	1	1170.3	-0.4	12of 18	2.21	TRUE	TRUE	::::::Cys_CAM::::
YVFLIYEQR	7	6.83	0.127	1351	38.1	AE003637	TRUE	TRUE	2	1231.4	1.8	2	2.4411	TRUE	TRUE	::::::::
GEVLSAYVGSGPPPDTGLHR	5	5.22	0.064	1398	36.7	AE003637	TRUE	TRUE	2	2010.2	1.4	9of 38	1.3698	TRUE	TRUE	::::::::::::::::::
KLAENASSAAATGQTLEER	3	4.56	0.482	952	26.8	AE003639	TRUE	TRUE	2	1948.1	1.7	26of 36	5.5666	TRUE	TRUE	::::::::::::::::::
GSAVDRVDGVDIAAISAK	2	4.18	0.265	720	34.9	AE003639	TRUE	TRUE	2	1744.9	1.4	16of 34	3.166	TRUE	TRUE	::::::::::::::::
PVVNVSAAEEYQK	3	4.27	0.236	1078	24.8	AE003639	TRUE	FALSE	2	1434.6	0.9	15of 24	2.4882	TRUE	TRUE	::::::::::::::
HQIEAVPTVIFFAK	9	7.82	0.186	1894	44.5	AE003639	TRUE	TRUE	2	1600.9	2	18of 26	3.0278	TRUE	TRUE	::::::::::::::
GELIGGLDIIK	2	4.08	0.167	1032	37	AE003639	TRUE	TRUE	1	1128.4	0.9	11of 20	2.5141	TRUE	TRUE	::::::::::::
GYPTILYFSYLK	15	9.4	0.069	1612	45.3	AE003639	TRUE	TRUE	2	1465.7	0.6	12of 22	1.4287	TRUE	TRUE	::::::::::::
QLVDQNKIPVVQMGKHQLD	9	7.79	0.015	1058	39.43	AE003639	TRUE	FALSE	3	2207.6	-1.8	18of 72	1.8554	TRUE	TRUE	::::::::::::Oxidation_M:::::::
AIVGASLAEILAK	8	6.95	0.265	2136	42.6	AE003640	TRUE	TRUE	2	1256.5	1.1	21of 24	4.2694	TRUE	TRUE	::::::::::::::
AIVGASLAEILAK	7	6.95	0.263	1559	42.6	AE003640	TRUE	TRUE	2	1256.5	1.4	1	3.4453	TRUE	TRUE	::::::::::::::
SFTFLDKK	14	9.89	0.138	584	20.7	AE003640	TRUE	TRUE	2	986.2	0.8	10of 14	1.6503	TRUE	TRUE	::::::::
SLEAVSFALDTIHSSLLSLGDLHR	5	5.12	0.35	2581	69.2	AE003641	TRUE	TRUE	3	2582.9	1.3	26of 92	2.8171	TRUE	TRUE	::::::::::::::::::::::
KPLGQLMAEFR	15	10.09	0.263	1112	32.03	AE003641	TRUE	TRUE	2	1290.6	1.7	14of 20	2.4616	TRUE	TRUE	::::::::::::
HPISADRTSSPGRPPCMS	13	9.02	0.018	788	22.03	AE003641	TRUE	FALSE	3	1954.1	0.3	18of 68	1.6738	TRUE	TRUE	::::::::::::::Cys_CAM:::
YLTVLLSLK	15	9.72	0.056	809	40.2	AE003642	TRUE	TRUE	1	1050.3	1.9	9of 16	1.6505	TRUE	TRUE	::::::::::
YLEMVIGQFSSR	9	6.89	0.021	1102	38.53	AE003645	TRUE	FALSE	2	1446.7	1.4	9of 22	1.6361	TRUE	TRUE	::::Oxidation_M:::::::::

LHLVSYIGPAASLLQEIK	10	7.74	0.329	1785	59	AE003646	TRUE	TRUE	3	1953.3	1.1	28of 68	3.6586	TRUE		TRUE	::::::::::::::::::
VLASVHTISNATER	10	7.85	0.179	560	28.1	AE003648	TRUE	TRUE	2	1498.7	1.1	17of 26	2.4976	TRUE		TRUE	::::::::::::::
VGSVNADADSTLSGQFGVR	2	3.89	0.418	750	33.8	AE003650	TRUE	TRUE	2	1881	1.9	17of 36	2.9928	TRUE		TRUE	::::::::::::::::::
FYSPSDGVVELTPSNFDR	1	3.71	0.402	1072	42.9	AE003650	TRUE	FALSE	2	2031.2	1.8	19of 34	4.0785	TRUE		TRUE	::::::::::::::::::
LGALDATAHQSK	11	7.82	0.311	300	18.4	AE003650	TRUE	TRUE	2	1212.3	2.1	19of 22	3.1878	TRUE		TRUE	::::::::::::
LGALDATAHQSK	10	7.82	0.31	284	18.4	AE003650	TRUE	TRUE	2	1212.3	1.1	20of 22	3.4821	TRUE		TRUE	::::::::::::
AIAEAALAEVK	2	4.27	0.298	637	30.6	AE003650	TRUE	TRUE	2	1086.3	2	17of 20	3.9133	TRUE		TRUE	::::::::::::
VQVDEIVDDDVTKENFDR	1	3.58	0.275	856	36	AE003650	TRUE	TRUE	2	2137.3	2.5	17of 34	2.3312	TRUE		TRUE	::::::::::::::::::
IIVPDSVHQASVK	10	7.82	0.191	597	29.4	AE003650	TRUE	TRUE	2	1393.6	0.6	16of 24	2.508	TRUE		TRUE	::::::::::::::
TLASGGGTADR	9	6.79	0.063	592	12.1	AE003650	TRUE	FALSE	2	1006.1	0	11of 20	1.2034	TRUE		TRUE	::::::::::::
MAKPLTDLLQATMQLTK	14	9.89	0.384	1607	47.26	AE003652	TRUE	TRUE	2	1904.3	0.2	20of 32	5.1215	TRUE		TRUE	::::::::::::::::::
NIALYK	13	9.72	0.021	531	19.3	AE003652	TRUE	TRUE	1	721.9	0	8of 10	1.7428	TRUE		TRUE	::::::
GEMIEMTGTMSGGGSRPIRGKMG	14	10.09	0.012	1427	37.22	AE003652	TRUE	FALSE	2	2341.7	-1.9	6of 44	0.9399	TRUE		TRUE	::::::::::::::::::::::
NPESLALAESIKNEGNR	3	4.56	0.429	1247	27.8	AE003655	TRUE	TRUE	2	1843	1.2	20of 32	4.0922	TRUE		TRUE	::::::::::::::::
LREDLINMLSQPMVR	7	7.05	0.357	1583	49.06	AE003655	TRUE	TRUE	2	1816.2	1.9	1	4.1959	TRUE		TRUE	::::::::::::::::
NPESLALAESIK	2	4.27	0.306	696	28.7	AE003655	TRUE	TRUE	2	1272.4	0.9	15of 22	2.1545	TRUE		TRUE	::::::::::::
SALVYNNNYSK	14	9.53	0.257	172	19.8	AE003655	TRUE	TRUE	2	1273.4	1.7	15of 20	2.5634	TRUE		TRUE	::::::::::::
INAVYNVLLEYMPLPK	7	6.81	0.181	2057	60.03	AE003655	TRUE	TRUE	2	1878.3	0.4	5	1.713	TRUE		TRUE	::::::::::::::::
EIQQEVNEIDDQNNK	1	3.51	0.169	452	19.6	AE003655	TRUE	TRUE	2	1816.9	1.3	14of 28	2.2717	TRUE		TRUE	::::::::::::::::
SEVPRPLGVPLAK	15	10.09	0.121	669	32.2	AE003655	TRUE	FALSE	2	1363.6	0.5	14of 24	2.7274	TRUE		TRUE	::::::::::::::
PELGRAASQITLAYLTD	2	4.08	0.001	2284	45.7	AE003655	TRUE	FALSE	2	1820.1	-2.8	7of 32	0.8227	TRUE		TRUE	::::::::::::::::::
DVFKERRLHWQQLQEK	15	9.88	0.075	1247	33	AE003657	TRUE	FALSE	2	2141.4	2.1	12of 30	1.4231	TRUE		TRUE	::::::::::::::::
ILLAQKVNTLDLR	15	10.09	0.041	1031	44.3	AE003658	TRUE	FALSE	2	1497.8	1.4	12of 24	1.6112	TRUE		TRUE	::::::::::::::
CVLDKAKESVIPSDLE	3	4.07	0.025	1809	38.2	AE003659	TRUE	FALSE	2	1804	-2.9	9of 30	0.9352	TRUE		TRUE	:Cys_CAM::::::::::::::::
TISIHQLIDFLGK	9	7.82	0.436	2172	42.7	AE003660	TRUE	FALSE	2	1485.8	3	19of 24	4.2536	TRUE		TRUE	::::::::::::
YLEDLFGGPTVFEPFLR	2	3.83	0.371	1669	64.1	AE003660	TRUE	TRUE	2	2001.3	1.7	20of 32	3.2415	TRUE		TRUE	::::::::::::::::
RLDEILEFANSNFR	3	4.45	0.275	1723	41.6	AE003660	TRUE	TRUE	2	1724.9	1.8	22of 26	3.8987	TRUE		TRUE	::::::::::::
TTISIHQLIDFLGK	9	7.82	0.246	2164	43.3	AE003660	TRUE	TRUE	2	1586.9	0.6	18of 26	3.1191	TRUE		TRUE	::::::::::::::
VESKIVGRMQGAKELDFK	14	9.76	0.079	1522	36.03	AE003660	TRUE	FALSE	3	2036.4	2.1	18of 68	2.3368	TRUE		TRUE	::::::::::::::::::
HAGKEPFPTIYVDTKDPNAAEPYEPAAK	4	4.7	0.471	1437	45.2	AE003661	TRUE	TRUE	3	3058.4	2.1	38of108	5.2307	TRUE		TRUE	::::::::::::::::::::::::::
VYGTMPHGGYGLGLER	10	7.7	0.455	1028	35.73	AE003661	TRUE	TRUE	2	1707.9	1.7	23of 30	3.7652	TRUE		TRUE	::::::::::::::::
HAGKEPFPTIYVDTKDPNAAEPYEPAAK	3	4.7	0.334	1315	45.2	AE003661	TRUE	TRUE	3	3058.4	1.2	32of108	4.1008	TRUE		TRUE	::::::::::::::::::::::::::
DDGTFYEFGEDIPEAPER	1	3.33	0.276	1073	38.7	AE003661	TRUE	TRUE	2	2088.1	2	17of 34	2.8507	TRUE		TRUE	::::::::::::::::::
GYNEVTPPTLVQTQVEGGSTLFK	2	4.27	0.231	1124	48.9	AE003661	TRUE	TRUE	2	2466.8	0.7	17of 44	2.4176	TRUE		TRUE	::::::::::::::::::::
DYNVAVAVHQTK	10	7.74	0.43	416	19.5	AE003663	TRUE	TRUE	2	1345.5	0.9	19of 22	3.7927	TRUE		TRUE	::::::::::::
AISPLAGDAIHKPLK	15	9.89	0.309	252	34.5	AE003663	TRUE	TRUE	2	1531.8	0.9	18of 28	2.7789	TRUE		TRUE	::::::::::::::::
TFVFESHLNASGVAPFK	9	7.82	0.257	1810	44.7	AE003663	TRUE	TRUE	2	1852.1	-0.4	16of 32	2.4409	TRUE		TRUE	::::::::::::::::
APAEVKPGADVALEIK	3	4.45	0.13	1195	35.5	AE003663	TRUE	TRUE	2	1608.9	1	14of 30	2.6032	TRUE		TRUE	::::::::::::::::
RGEVINVPALVFNYLPK	14	9.72	0.101	1675	54.2	AE003663	TRUE	TRUE	2	1930.3	0.5	12of 32	1.5031	TRUE		TRUE	::::::::::::::::
DFASYLPHK	11	7.74	0.026	801	20.5	AE003663	TRUE	TRUE	2	1078.2	1.4	9of 16	1.6056	TRUE		TRUE	::::::::::
YGRVDAK	15	9.72	0.021	327	8.8	AE003663	TRUE	FALSE	2	808.9	1.8	9of 12	1.5391	TRUE		TRUE	::::::::
KLDVLSNELFINMLK	7	6.99	0.394	1808	54.13	AE003664	TRUE	TRUE	2	1778.2	1.9	1	3.6856	TRUE		TRUE	::::::::::::::::
YGGIFIYPATK	14	9.53	0.229	990	34	AE003664	TRUE	TRUE	1	1230.4	-0.5	12of 20	2.3361	TRUE		TRUE	::::::::::::
LLLISQLLALSYAQLSLDEAKK	6	6.92	0.137	2340	79.2	AE003664	TRUE	TRUE	2	2431.9	2.3	11of 42	2.0991	TRUE		TRUE	::::::::::::::::::::
RIRICCISTCGQIGSSQVR	13	9.3	0.04	1806	40.2	AE003664	TRUE	FALSE	2	2252.5	-1	9of 36	1.2003	TRUE		TRUE	:::::Cys_CAM:Cys_CAM:::::Cys_CAM::::::::::
QPLLKGMGQEWALTK	13	9.89	0.013	1155	39.73	AE003664	TRUE	FALSE	2	1717	-1.7	4of 28	0.595	TRUE		TRUE	:::::::Oxidation_M:::::::::
SSHTDKLTGLATPAASVDK	9	7.79	0.488	1172	24.3	AE003665	TRUE	TRUE	2	1900.1	0.8	27of 36	5.8544	TRUE		TRUE	::::::::::::::::::
ALVIFAEHR	12	7.85	0.25	1141	31	AE003666	TRUE	TRUE	2	1056.3	2.2	12of 16	2.0971	TRUE		TRUE	::::::::::
ALVIFAEHR	11	7.85	0.202	777	31	AE003666	TRUE	TRUE	2	1056.3	0.9	12of 16	2.3736	TRUE		TRUE	::::::::::
WVGATEEGLCAASAMLLYPQMR	4	4.27	0.253	2629	67.86	AE003667	TRUE	FALSE	2	2455.8	-2.4	13of 42	1.9787	TRUE		TRUE	:::::::::Cys_CAM::::::::::::
DRYPQLPVVLFASFLPR	15	9.85	0.394	2031	61.8	AE003668	TRUE	TRUE	2	2019.4	2	21of 32	3.1722	TRUE		TRUE	::::::::::::::::
LLPVLDPNEVCTHLLEVLNAR	3	4.43	0.338	2163	71.3	AE003668	TRUE	TRUE	2	2416.8	2.1	20of 40	3.1738	TRUE		TRUE	:::::::::::Cys_CAM:::::::::::
SLQVLLGSFPISQLAVPYR	14	9.85	0.177	1799	67	AE003668	TRUE	TRUE	2	2089.5	1.1	13of 36	2.4092	TRUE		TRUE	::::::::::::::::::
SLQVLLGSFPISQLAVPYR	15	9.85	0.177	1898	67	AE003668	TRUE	TRUE	2	2089.5	1.2	14of 36	2.1053	TRUE		TRUE	::::::::::::::::::
IVSCQLRFSRNGVFRETPYCVSLEAR	13	9.08	0.119	1727	67.5	AE003669	TRUE	FALSE	3	3146.5	1.4	23of100	2.4606	TRUE		TRUE	::::Cys_CAM:::::::::::::::Cys_CAM::::::
LSNFLYEICELTPNFTMGSR	2	4.27	0.053	2112	63.53	AE003669	TRUE	FALSE	2	2409.7	1.6	6of 38	0.8553	TRUE		TRUE	:::::::Cys_CAM::::::::Oxidation_M::::
RDLGNDLGLPQELVERQPFPGPGLAIR	3	4.56	0.046	2553	70.4	AE003669	TRUE	FALSE	3	2959.4	-0.1	14of104	1.2918	TRUE		TRUE	::::::::::::::::::::::::
GGNSFEGLFSYQLVR	9	6.89	0.241	789	40.8	AE003671	TRUE	FALSE	3	1674.9	0.3	16of 56	2.0956	TRUE		TRUE	::::::::::::::
FMKSVSSSIVDFTEIKCSNGEK	7	6.48	0.084	1545	44.03	AE003672	TRUE	FALSE	3	2510.8	0.2	340	1.7229	TRUE		TRUE	::Oxidation_M:::::::::::::Cys_CAM::::::
EQGAGDYIPIEEPKEPAKLSNRLP	4	4.36	0.053	1907	46.1	AE003673	TRUE	FALSE	3	2653	2.1	10of 92	1.2699	TRUE		TRUE	::::::::::::::::::::::
KNQFYQIYLVLFNVA	15	9.53	0.04	1888	57.5	AE003674	TRUE	FALSE	2	1861.2	2.4	9of 28	1.277	TRUE		TRUE	::::::::::::::::
GKSVEGTVEALLNHLREGHMR	11	7.98	0.109	726	36.83	AE003675	TRUE	FALSE	3	2334.7	-0.6	22of 80	2.3456	TRUE		TRUE	::::::::::::::::::
ELHKIVFDPRYLLLT	11	7.75	0.014	2600	56.5	AE003675	TRUE	FALSE	3	1858.2	1.1	9of 56	0.3751	TRUE		TRUE	::::::::::::::::
QNLGHGSQPSFSLSFLA	10	7.85	0.069	1585	40.6	AE003676	TRUE	FALSE	2	1791	-0.2	10of 32	1.1987	TRUE		TRUE	::::::::::::::::
SENITVTAYSPLGSK	6	6.87	0.347	1299	27.8	AE003677	TRUE	TRUE	1	1567.7	-1	16of 28	1.9053	TRUE		TRUE	::::::::::::::
MLVLDEADEMLNK	1	3.59	0.075	1421	42.26	AE003678	TRUE	TRUE	1	1537.8	0.5	8of 24	1.2369	TRUE		TRUE	:Oxidation_M::::::::::::
STQVVVQSRLGEKMQTQCNPLAGSDWFN	5	6.36	0.015	1906	57.83	AE003678	TRUE	FALSE	3	3198.5	1.3	20of108	2.8727	TRUE		TRUE	:::::::::::::Oxidation_M::::Cys_CAM:::::::::::
TAAFLVPILNQMYELGHVPPPQSTR	10	7.77	0.294	1990	70.43	AE003679	TRUE	TRUE	2	2781.2	-0.1	13of 48	1.9827	TRUE		TRUE	::::::::::::::::::::::
VVNAVLTQLDSLK	7	6.76	0.185	1443	39.2	AE003679	TRUE	TRUE	2	1400.7	0.9	17	2.0557	TRUE		TRUE	::::::::::::::
GAAAASSSTISSSSAKPTDITHLIK	15	9.89	0.506	817	36.4	AE003680	TRUE	TRUE	2	2402.7	1.8	19of 48	4.5543	TRUE		TRUE	::::::::::::::::::::::
AALDSYIKPMSSGDAAAASSSSSSSSANGAASSSSSSSK	7	6.81	0.495	1055	37.33	AE003680	TRUE	TRUE	3	3471.6	1.2	1	6.0812	TRUE		TRUE	::::::::::::::::::::::::::::::::
TVAVEPVAADTTPDNAPAVSTEGSGK	1	3.59	0.38	537	37.5	AE003680	TRUE	TRUE	2	2485.7	-0.2	14of 50	2.8441	TRUE		TRUE	::::::::::::::::::::::
SQDAEVGDGTTSVVLLAGEFLK	1	3.59	0.377	1613	52.1	AE003680	TRUE	TRUE	2	2237.5	1.2	22of 42	3.2394	TRUE		TRUE	::::::::::::::::::::
LGQSEATSLQHK	11	7.82	0.369	284	15.1	AE003680	TRUE	TRUE	2	1299.4	2	15of 22	2.4767	TRUE		TRUE	::::::::::::
VTGGSLEESQLVSGVAFK	2	4.27	0.363	937	40.8	AE003680	TRUE	TRUE	2	1809	1.7	18of 34	3.1654	TRUE		TRUE	::::::::::::::::::
VIDPFTVKPLDAELIIEHGK	3	4.54	0.339	1771	59.2	AE003680	TRUE	TRUE	3	2235.6	0.2	29of 76	4.0442	TRUE		TRUE	::::::::::::::::::::
INEMAVQIVEQSK	2	4.27	0.331	729	31.63	AE003680	TRUE	TRUE	2	1489.7	2.7	20of 24	4.6381	TRUE		TRUE	::::::::::::::
IHESGANVVLSK	10	7.82	0.326	301	23.2	AE003680	TRUE	TRUE	2	1254.4	1.4	16of 22	3.0273	TRUE		TRUE	::::::::::::::
TSRPNTCVIYDNEEPFTIGR	4	4.45	0.276	1518	40.4	AE003680	TRUE	TRUE	3	2370.5	0.6	33of 76	4.9874	TRUE		TRUE	::::::Cys_CAM::::::::::::::
LLEIIHPAAK	11	7.82	0.267	692	33.9	AE003680	TRUE	TRUE	1	1105.4	0	13of 18	2.5987	TRUE		TRUE	::::::::::::
LLEIIHPAAK	10	7.82	0.229	861	33.9	AE003680	TRUE	TRUE	2	1105.4	2.6	15of 18	2.9967	TRUE		TRUE	::::::::::::
ALAELHYK	11	7.74	0.203	444	21.6	AE003680	TRUE	TRUE	2	945.1	2.3	11of 14	1.6962	TRUE		TRUE	::::::::::
SLHDAIMIVR	10	7.85	0.197	1038	32.73	AE003680	TRUE	TRUE	1	1155.4	0.6	11of 18	2.0642	TRUE		TRUE	::::::::::::

VIDPFTVKPLDAELIIEHGK	4	4.54	0.164	1897	59.2	AE003680	TRUE	TRUE	3	2235.6	2.8	22of 76	2.9247	TRUE		TRUE	::::::::::::::::::::
PPSVLIDMFGISAR	6	6.79	0.141	2080	46.53	AE003680	TRUE	FALSE	2	1503.8	1.3	12of 26	2.1959	TRUE		TRUE	::::::::::::::
HLEGLIVNK	9	7.82	0.14	1236	24.7	AE003680	TRUE	TRUE	2	1023.2	1.2	13of 16	2.5472	TRUE		TRUE	:::::::::
IHESGANVVLSK	11	7.82	0.138	353	23.2	AE003680	TRUE	TRUE	2	1254.4	0.8	12of 22	1.8508	TRUE		TRUE	::::::::::::
SLHDAIMIVR	9	7.85	0.119	1538	32.73	AE003680	TRUE	TRUE	2	1155.4	0.9	11of 18	1.8445	TRUE		TRUE	::::::::::
ACGGAVMTTANDIKPNVLGLCEHFEER	4	4.63	0.085	1709	58.53	AE003680	TRUE	TRUE	3	2991.3	0.1	33of104	3.3393	TRUE		TRUE	::Cys_CAM::::::::::::::::::Cys_CAM::::::
HLYVPTVPR	14	9.85	0.083	614	24.5	AE003680	TRUE	TRUE	2	1082.3	2.7	10of 16	1.9472	TRUE		TRUE	:::::::::
IIPRQLCDNAGFDATNILNKLRQK	14	9.9	0.04	1608	56.8	AE003680	TRUE	FALSE	3	2800.2	-2.9	21of 92	1.8355	TRUE		TRUE	::::::Cys_CAM::::::::::::::::
SGPPSVLIDMFGISAR	6	6.79	0.032	1728	46.13	AE003680	TRUE	TRUE	2	1663.9	1.5	11of 30	1.5207	TRUE		TRUE	:::::::::Oxidation_M:::::::
VFWLIPPTDR	9	6.79	0.039	1222	41.6	AE003681	TRUE	TRUE	2	1244.5	-0.2	8of 18	1.1386	TRUE		TRUE	::::::::::
LSGLLGKEK	13	9.89	0.004	530	20.6	AE003681	TRUE	FALSE	1	945.1	-0.5	9of 16	1.4073	TRUE		TRUE	:::::::::
VHCLIPCAIDQDPYFR	5	5.1	0.277	1686	49.4	AE003682	TRUE	TRUE	2	2005.2	2.6	20of 30	4.4049	TRUE		TRUE	:::Cys_CAM::::Cys_CAM:::::::::
MSASDQNSAVYLTDTPK	2	3.89	0.266	568	27.43	AE003682	TRUE	TRUE	2	1829	0.2	14of 32	2.6701	TRUE		TRUE	::::::::::::::::
TFIFNNLEFVGK	6	6.95	0.265	1842	43	AE003682	TRUE	TRUE	2	1429.7	1.2	19of 22	3.4713	TRUE		TRUE	::::::::::::
CPAMYQNIIR	13	8.9	0.082	882	30.23	AE003682	TRUE	TRUE	2	1266.5	1.4	13of 18	1.7565	TRUE		TRUE	:Cys_CAM:::::::::
DLHTILTLR	10	7.85	0.016	1290	30.4	AE003682	TRUE	TRUE	1	1082.3	0.5	12of 16	1.4787	TRUE		TRUE	:::::::::
YYSSEVHSAAFALPR	10	7.7	0.404	1073	36	AE003683	TRUE	TRUE	2	1698.9	0.7	19of 28	3.9824	TRUE		TRUE	::::::::::::::::
FGITPPAVANTATAVAVAINK	15	10.1	0.302	1556	52.2	AE003683	TRUE	TRUE	2	2027.4	0.1	19of 40	2.4447	TRUE		TRUE	::::::::::::::::::::
AHFGLPSVESEDNTEGKPPIQVR	4	4.63	0.273	1469	39.5	AE003683	TRUE	TRUE	3	2508.8	1.9	23of 88	2.4363	TRUE		TRUE	::::::::::::::::::::
SRTHYTPAPILNPDR	15	9.85	0.014	119	25.3	AE003683	TRUE	FALSE	2	1738.9	2.8	5of 28	0.8381	TRUE		TRUE	::::::::::::::
AIELHPNSAIYYANR	11	7.7	0.248	754	36.9	AE003684	TRUE	TRUE	2	1732.9	1.7	18of 28	2.9029	TRUE		TRUE	::::::::::::::
GLGLDEVGAAVHSAAGLVGQK	5	5.22	0.486	1942	43.2	AE003686	TRUE	TRUE	2	1950.2	2.5	22of 40	3.7337	TRUE		TRUE	::::::::::::::::
EAAGIVVDLIK	2	4.08	0.118	996	35.9	AE003686	TRUE	TRUE	1	1128.4	0.7	12of 20	1.4783	TRUE		TRUE	::::::::::::
CLLFLGDSVTTDHISPAGSIAR	5	5.1	0.477	1814	58.7	AE003687	TRUE	TRUE	2	2331.6	0.7	23of 42	5.54	TRUE		TRUE	:Cys_CAM:::::::::::::::::::
ANYLASPLLVIAYAIAGR	14	9.59	0.327	2447	63.5	AE003687	TRUE	TRUE	2	1877.2	0.3	22of 34	3.689	TRUE		TRUE	::::::::::::::::
TSLSPGSGVVTYYLK	14	9.53	0.199	1058	35.3	AE003687	TRUE	TRUE	1	1572.8	-0.1	15of 28	2.2462	TRUE		TRUE	::::::::::::::
GLSILPYIK	15	9.72	0.028	1301	35	AE003687	TRUE	TRUE	1	1004.3	0.4	9of 16	1.7012	TRUE		TRUE	:::::::::
TVLDVGCGTGILSMFAAK	6	6.1	0.538	2079	52.33	AE003688	TRUE	TRUE	2	1841.1	1.6	23of 34	4.6294	TRUE		TRUE	::::::Cys_CAM:::::::::::
ISGTAGHGSLLLPNTAGEK	10	7.82	0.424	784	34	AE003688	TRUE	FALSE	2	1824	1	23of 36	3.4664	TRUE		TRUE	::::::::::::::::
LQPFATDEHVNEALR	3	4.43	0.257	1255	35	AE003688	TRUE	TRUE	2	1740.9	-0.2	15of 28	2.1132	TRUE		TRUE	::::::::::::::
GTLYITAIEDR	2	4.08	0.135	796	31.1	AE003688	TRUE	TRUE	2	1252.4	0.9	12of 20	2.0896	TRUE		TRUE	::::::::::
VLIQGIYSIR	15	9.85	0.106	1117	38.8	AE003688	TRUE	TRUE	2	1162.4	2.5	9of 18	1.9958	TRUE		TRUE	::::::::::
FLTTFTQNEHFPTFYEHLTEGER	4	4.68	0.415	1839	56.9	AE003691	TRUE	TRUE	3	2846.1	2.4	31of 88	4.1003	TRUE		TRUE	::::::::::::::::::::
NLLVHQESPPLVGR	9	7.85	0.305	1460	35.7	AE003691	TRUE	TRUE	2	1559.8	0	18of 26	3.635	TRUE		TRUE	::::::::::::::
LPGFLDGIMALVPGSK	7	6.76	0.221	2116	53.63	AE003691	TRUE	TRUE	2	1616	2.3	2	2.8269	TRUE		TRUE	::::::::::::::
ITPLAIAVFLK	15	10.1	0.209	1728	48.6	AE003691	TRUE	TRUE	2	1186.5	1.3	13of 20	2.1044	TRUE		TRUE	::::::::::
NIYVAYADHLR	9	7.7	0.289	1513	30.4	AE003692	TRUE	TRUE	2	1335.5	1.9	15of 20	2.3776	TRUE		TRUE	::::::::::
LFGLNATTTTPFAFGGAAAGAADK	7	6.76	0.202	1701	55.6	AE003692	TRUE	FALSE	2	2271.5	-2.5	8	0.9765	TRUE		TRUE	::::::::::::::::::::
SENFDEYMK	1	3.83	0.124	545	17.63	AE003692	TRUE	TRUE	1	1163.2	-0.4	10of 16	1.6694	TRUE		TRUE	::::::::::
TLIVTHSNQALNQLFEK	9	7.82	0.092	1773	43.5	AE003693	TRUE	TRUE	2	1957.2	1.7	15of 32	1.9828	TRUE		TRUE	::::::::::::::::
MIILNTPHNPIGK	15	10.1	0.067	889	34.83	AE003693	TRUE	TRUE	2	1448.8	2.1	14of 24	1.8937	TRUE		TRUE	::::::::::::::
AEKSAQLSAEELKARIR	15	9.88	0.005	884	29.1	AE003693	TRUE	FALSE	3	1901.2	-1	14of 64	1.481	TRUE		TRUE	::::::::::::::::
FIGVSAYPISVLK	15	9.72	0.283	1391	46.8	AE003694	TRUE	TRUE	2	1394.7	-0.3	20of 24	3.2102	TRUE		TRUE	::::::::::::::
FIGVSAYPISVLK	14	9.72	0.207	1298	46.8	AE003694	TRUE	TRUE	2	1394.7	0.5	19of 24	3.3007	TRUE		TRUE	::::::::::::::
SEEVLGLALK	2	4.27	0.167	828	31	AE003694	TRUE	TRUE	1	1059.2	0.9	12of 18	1.9683	TRUE		TRUE	::::::::::
YTLLDNTLLR	6	6.7	0.04	1646	37.1	AE003694	TRUE	TRUE	2	1222.4	1.3	13of 18	2.0136	TRUE		TRUE	::::::::::
SLIINNSLDHGTQLPYVR	10	7.76	0.429	1324	46.9	AE003695	TRUE	TRUE	2	2041.3	1.1	20of 34	4.5836	TRUE		TRUE	::::::::::::::::::
IDDAFAMFNTLLK	1	3.89	0.425	1610	47.63	AE003695	TRUE	TRUE	2	1499.8	1.7	21of 24	4.4384	TRUE		TRUE	::::::::::::::
QVDLDAGEHLKPEFVK	3	4.54	0.149	1283	34.4	AE003695	TRUE	TRUE	2	1826.1	1.3	14of 30	2.8082	TRUE		TRUE	::::::::::::::::
LYLGAILNKQ	15	9.72	0.084	1137	35.3	AE003695	TRUE	FALSE	2	1133.4	2	15of 18	3.0119	TRUE		TRUE	::::::::::
EENAHHSSIKVLIR	11	7.97	0.015	1021	24.2	AE003695	TRUE	FALSE	3	1633.8	0.2	14of 52	1.2548	TRUE		TRUE	::::::::::::::
ILIAGLCGLGAEITK	7	6.29	0.478	1619	52.1	AE003696	TRUE	TRUE	2	1529.8	0.2	1	5.2215	TRUE		TRUE	::::::Cys_CAM:::::::::
ILIAGLCGLGAEITK	8	6.29	0.44	2175	52.1	AE003696	TRUE	TRUE	2	1529.8	2.3	24of 28	3.8882	TRUE		TRUE	::::::Cys_CAM:::::::::
NGPGVLLLSVLQK	14	10.1	0.389	1466	41.1	AE003696	TRUE	TRUE	2	1338.6	0.3	19of 24	3.0316	TRUE		TRUE	::::::::::::
NIILSGVNSVK	14	10.1	0.189	782	29	AE003696	TRUE	TRUE	1	1144.4	-0.3	15of 20	2.5296	TRUE		TRUE	::::::::::::
ATGDLYDEFIDEFMHACVR	2	3.84	0.425	1581	53.83	AE003697	TRUE	TRUE	2	2290.5	2.1	21of 36	4.021	TRUE		TRUE	:::::::::::::::Cys_CAM:::
LHFAQLHEPIDTLAEAVR	5	5.18	0.424	1738	51	AE003697	TRUE	TRUE	2	2061.3	1.3	23of 34	5.7158	TRUE		TRUE	::::::::::::::::
AECTAEEAYTYTK	2	3.97	0.332	386	20.6	AE003697	TRUE	TRUE	2	1537.6	-1.1	16of 24	2.7746	TRUE		TRUE	:::Cys_CAM:::::::::
CIFASGSPFAPVTYNNK	13	8.88	0.323	1227	40.4	AE003697	TRUE	TRUE	2	1874.1	-0.7	20of 32	3.333	TRUE		TRUE	:Cys_CAM:::::::::::::::
NGLATVRPEPVNK	13	10.09	0.246	484	21.7	AE003697	TRUE	TRUE	2	1395.6	0.4	14of 24	2.9812	TRUE		TRUE	::::::::::::
ILGLGDLGANGMGIPVGK	7	6.76	0.124	1651	49.93	AE003697	TRUE	TRUE	2	1683	0.9	5	1.7618	TRUE		TRUE	::::::::::::::::
DKGHIYDVLK	10	7.72	0.085	668	18.9	AE003697	TRUE	TRUE	2	1188.4	0.2	13of 18	2.1442	TRUE		TRUE	::::::::::
GSLYPPLSSIVSCSMAIAER	7	6.28	0.009	1948	55.93	AE003697	TRUE	TRUE	2	2139.4	2.7	80	1.7747	TRUE		TRUE	:::::::::::Cys_CAM:::::::::
GHIYDVLK	10	7.74	0	764	20.8	AE003697	TRUE	TRUE	1	945.1	-0.1	8of 14	1.8555	TRUE		TRUE	::::::::
EVNHMCSLNAQAYPDSLALANK	5	5.22	0.423	1452	46.83	AE003698	TRUE	TRUE	2	2447.7	0.9	19of 42	3.612	TRUE		TRUE	:::::Cys_CAM:::::::::::::::
FNESLGCSDPQTHPVLIIGQLR	5	5.22	0.34	1702	56.6	AE003698	TRUE	TRUE	2	2482.8	1.7	20of 42	4.9574	TRUE		TRUE	:::::::Cys_CAM:::::::::::::::
NNQVEIDLVTPEGLRPLK	3	4.45	0.301	1571	44.6	AE003698	TRUE	TRUE	2	2036.3	1.9	19of 34	2.9387	TRUE		TRUE	::::::::::::::::
DCGGAAAILGTFYAAVQCGFR	5	5.95	0.282	2605	55.8	AE003698	TRUE	TRUE	2	2206.4	0.6	17of 40	2.4185	TRUE		TRUE	::Cys_CAM::::::::::::::Cys_CAM::::
VTEETFLNAVACLHPAPTDK	3	4.43	0.251	1659	46.3	AE003698	TRUE	TRUE	3	2214.4	0.3	24of 76	2.6278	TRUE		TRUE	:::::::::::Cys_CAM:::::::::
IAYQESSQTFAVSTLR	7	6.89	0.054	1167	38.2	AE003698	TRUE	TRUE	2	1802	0.4	2	1.9124	TRUE		TRUE	::::::::::::::
ENAALTKESMELQCLIDKLQVK	3	4.65	0.028	1464	53.93	AE003698	TRUE	TRUE	3	2578.9	2.2	17of 84	1.7989	TRUE		TRUE	:::::::::Oxidation_M::::Cys_CAM:::::::::
LIGLGCYGAFR	12	8.9	0.009	2155	39.6	AE003698	TRUE	FALSE	2	1227.4	-1.1	5of 20	0.9355	TRUE		TRUE	::::::Cys_CAM::::::
LHLRPDLER	10	7.85	0.108	540	24.3	AE003699	TRUE	TRUE	2	1149.3	0.8	10of 16	1.5938	TRUE		TRUE	:::::::::
AISQAYEVLSDADKR	3	4.31	0.173	1300	29.4	AE003700	TRUE	TRUE	2	1666.8	0.2	14of 28	2.2707	TRUE		TRUE	::::::::::::::::
VPNVDQPVVYAPVSELTDYDDVR	1	3.37	0.488	1212	56.2	AE003701	TRUE	TRUE	2	2591.8	0.8	26of 44	4.5858	TRUE		TRUE	::::::::::::::::::::::
HGLDSMLPIK	9	7.82	0.242	1265	26.73	AE003701	TRUE	TRUE	2	1127.3	1.5	15of 18	2.4691	TRUE		TRUE	::::::Oxidation_M:::::
CNLFAPVVDAFIR	5	6.1	0.091	2274	49.3	AE003701	TRUE	TRUE	2	1522.8	2.3	12of 24	2.1375	TRUE		TRUE	:Cys_CAM:::::::::::
GLRPVLPPSERNCDAEKQALYL	7	6.47	0.064	1616	52.6	AE003701	TRUE	FALSE	3	2527.8	-2	13	1.2787	TRUE		TRUE	:::::::::::Cys_CAM:::::::::
MQALQVAVK	15	10.1	0.003	983	25.53	AE003701	TRUE	FALSE	1	1004.2	0.9	10of 16	1.6794	TRUE		TRUE	:Oxidation_M:::::::::
RIDLEEEQIHVSR	3	4.63	0.162	1291	27.9	AE003703	TRUE	FALSE	2	1624.8	1.1	12of 24	1.8523	TRUE		TRUE	::::::::::::::
SMMHGHGGCSGKQSKSLDSVAAMTPEEENRK	10	7.32	0.157	1166	28.89	AE003704	TRUE	FALSE	3	3364.7	0.8	15of120	1.4342	TRUE		TRUE	:::Oxidation_M::::::Cys_CAM:::::::::::::::::::::
RIPLHELEQR	9	7.86	0.031	1138	24.5	AE003706	TRUE	TRUE	3	1291.5	2	15of 36	1.9743	TRUE		TRUE	::::::::::::
QVRIAASPVMQPQE	9	6.98	0.022	612	31.23	AE003707	TRUE	FALSE	3	1554.8	1.8	16of 52	1.399	TRUE		TRUE	::::::::::::::

TILTEVLLRRNPKFCDRYFVHVPMQK	13	10.18	0.133	2395	73.33	AE003708	TRUE	FALSE	2	3278.9	0.5	6of 50	1.0009	TRUE	TRUE	:::::::::::::Cys_CAM::::::::Oxidation_M:::
VLEEARQRLNKLIAVNFRAVALELRDQDV	8	7.23	0.09	3255	82	AE003708	TRUE	FALSE	2	3380.9	0.8	6of 56	1.1887	TRUE	TRUE	::::::::::::::::::::::::::
YFFVEDIYVRPEHR	6	5.35	0.086	1554	43.7	AE003708	TRUE	TRUE	2	1871.1	0.5	12of 26	2.4967	TRUE	TRUE	::::::::::::::
FYGQPVGIILANSNSLANR	14	9.85	0.249	1294	51.4	AE003709	TRUE	TRUE	2	2035.3	0.1	14of 36	2.4306	TRUE	TRUE	::::::::::::::::
SPNPVGFMRSKATGE	15	10.09	0.032	520	22.23	AE003709	TRUE	FALSE	3	1594.8	0.6	13of 56	1.2114	TRUE	TRUE	:::::::Oxidation_M:::::::
SLVAYK	14	9.72	0	727	17.3	AE003709	TRUE	FALSE	1	680.8	-0.2	5of 10	1.0654	TRUE	TRUE	::::::
IQQMTPQSTTSSNNFLK	15	10.1	0.083	540	29.03	AE003710	TRUE	FALSE	3	1942.2	-2.6	17of 64	2.0986	TRUE	TRUE	::::Oxidation_M::::::::::::
LDRLFILLETGSTAATRQAAAKQIGE	12	7.14	0.141	1899	65.6	AE003711	TRUE	FALSE	3	2775.2	-1	20of100	1.6829	TRUE	TRUE	::::::::::::::::::::::::::
SPTGGFGGGPGQYAHLAPTYAAVNSLCIIGSEQAYR	9	7.15	0.303	2012	73.2	AE003713	TRUE	TRUE	3	3670	1.5	27of140	3.627	TRUE	TRUE	:::::::::::::::::::::::::::Cys_CAM:::::::::
STIELIHGLMAQIVK	9	7.82	0.05	2249	48.03	AE003713	TRUE	TRUE	2	1654	0.9	9of 28	1.2073	TRUE	TRUE	::::::::::::::::
ENEIKHKLWIEQPENIPTCIALK	4	5.47	0.007	2447	58.6	AE003714	TRUE	TRUE	2	2805.2	-1.7	4of 44	0.8783	TRUE	TRUE	:::::::::::::::::::Cys_CAM:::::
KVDVEIVAALASLGTTIHK	11	7.8	0.175	1440	47.8	AE003715	TRUE	TRUE	2	1966.3	2	16of 36	1.9599	TRUE	TRUE	::::::::::::::::::
YILQVLPQLK	15	9.72	0.115	1159	41.1	AE003715	TRUE	FALSE	1	1215.5	-0.3	11of 18	2.3852	TRUE	TRUE	::::::::::
LPLPTTGGNVTAEVR	7	6.98	0.314	1093	33.5	AE003716	TRUE	TRUE	2	1525.7	0.9	1	2.5807	TRUE	TRUE	::::::::::::::
YTPLLPGEHYITVK	10	7.69	0.23	1200	39.5	AE003716	TRUE	TRUE	2	1631.9	1.3	15of 26	2.515	TRUE	TRUE	::::::::::::::
NLTYTVSYIPK	13	9.53	0.209	979	29.8	AE003716	TRUE	TRUE	2	1299.5	1.3	13of 20	2.461	TRUE	TRUE	::::::::::
ALQTIYLEYNPLAK	8	6.81	0.094	2096	45.7	AE003717	TRUE	TRUE	1	1637.9	0.2	13of 26	2.1926	TRUE	TRUE	::::::::::::::
GLGLLGIGAFLLAQSK	15	10.1	0.149	2138	56.9	AE003718	TRUE	FALSE	2	1558.9	1.9	11of 30	1.2118	TRUE	TRUE	::::::::::::::::
QAKPLENFTMKGL	13	9.89	0.139	1151	30.53	AE003718	TRUE	FALSE	3	1493.8	2.6	17of 48	1.9021	TRUE	TRUE	:::::::::Oxidation_M::::
AGAGSATLSMAYAGAR	15	9.85	0.419	608	29.13	AE003721	TRUE	TRUE	2	1455.6	1.5	16of 30	2.4586	TRUE	TRUE	::::::::::::::::
EAHAAQLGNEELIK	3	4.54	0.204	1066	27.9	AE003721	TRUE	TRUE	2	1523.7	0.3	18of 26	2.5074	TRUE	TRUE	::::::::::::::
QQTGSRFRFSSVEELK	15	10.09	0.12	353	28	AE003721	TRUE	FALSE	3	1900.1	2.3	13of 60	1.4757	TRUE	TRUE	::::::::::::::::
AFDEQKVPVMLLFR	8	7.02	0.039	2201	50.53	AE003721	TRUE	TRUE	2	1694	1.4	14of 26	1.8079	TRUE	TRUE	::::::::::::::
FVYVSGKPPTGQNPELPLRE	7	7.02	0.002	1453	45.7	AE003722	TRUE	FALSE	3	2229.5	-0.1	146	1.8067	TRUE	TRUE	::::::::::::::::::
TNLYEHGIR	9	7.77	0.198	968	18.2	AE003724	TRUE	TRUE	2	1103.2	0.7	11of 16	1.928	TRUE	TRUE	::::::::::
FRRVDIGPADGLITWDEYHR	5	5.33	0.146	1843	51.3	AE003725	TRUE	FALSE	3	2417.7	-1.3	12of 76	1.2699	TRUE	TRUE	::::::::::::::::::
ASASNFPQEIGYFSGNPIVEVTK	4	4.27	0	2482	52	AE003725	TRUE	FALSE	2	2456.7	-1.4	10of 44	1.4363	TRUE	TRUE	::::::::::::::::::::
GVSVEHVCHAIHR	12	7.42	0.346	719	20.8	AE003727	TRUE	TRUE	2	1501.7	0.2	15of 24	2.4394	TRUE	TRUE	:::::::Cys_CAM::::::
GVAIGNGLSDPLHQLK	11	7.82	0.358	946	35.3	AE003728	TRUE	TRUE	2	1619.9	1.7	15of 30	2.732	TRUE	TRUE	::::::::::::::
MYSYVTQELVDVVNANLPVVPGKR	7	6.89	0.182	1971	64.33	AE003728	TRUE	TRUE	3	2693.1	2	7	2.2041	TRUE	TRUE	::::::::::::::::::::::::
PFGISTAAGASGSSSSSSSSSRLLLVDEQLMMK	8	7.02	0.03	2821	68.36	AE003729	TRUE	FALSE	3	3322.7	1.8	15of128	1.332	TRUE	TRUE	::::::::::::::::::::::::::::Oxidation_M:Oxidation_M::
CHMQFRQQSTLTNHLK	13	10.11	0.05	1240	25.93	AE003730	TRUE	FALSE	3	2046.3	-2.9	18of 60	1.5572	TRUE	TRUE	:Cys_CAM::Oxidation_M:::::::::::::
PNPEIPVRIQVQLNQVSDLQK	8	7.02	0.234	2575	49.2	AE003731	TRUE	FALSE	3	2416.8	-2.4	20of 80	1.6295	TRUE	TRUE	::::::::::::::::::
FLESELSVPVR	2	4.27	0.096	854	37.5	AE003732	TRUE	TRUE	2	1276.5	0.9	11of 20	1.9083	TRUE	TRUE	::::::::::
SGSFMSSSINPAAAGHHSKSYRKSSAEAA	14	10.18	0.166	67	28.83	AE003733	TRUE	FALSE	3	2941.2	2.3	13of112	1.334	TRUE	TRUE	:::::Oxidation_M:::::::::::::::::::
VEIRECRVRCKV	12	9.15	0.068	1277	25.9	AE003733	TRUE	FALSE	2	1604.8	-1	7of 22	1.147	TRUE	TRUE	::::::Cys_CAM::::Cys_CAM:::
HHCEAVLHLR	10	7.42	0.008	824	20	AE003733	TRUE	FALSE	2	1272.4	2.8	9of 18	1.6092	TRUE	TRUE	:::Cys_CAM::::::::
KVVDHTTAAEYAAQLGIPFLETSAK	6	5.35	0.332	1812	55.7	AE003734	TRUE	TRUE	2	2662	0.5	20of 48	3.5279	TRUE	TRUE	::::::::::::::::::::::
TYWICSKKGSTKCNARVVTNV	13	10.06	0.064	1376	36	AE003734	TRUE	FALSE	3	2473.8	-1.4	10of 80	1.1538	TRUE	TRUE	:::::Cys_CAM:::::::Cys_CAM::::::::
MSEDASDLRPEISKTIA	3	4.07	0.005	1100	34.33	AE003734	TRUE	FALSE	2	1864.1	-0.8	12of 32	1.8483	TRUE	TRUE	::::::::::::::::::
FNNALVGPQDNVIAHAASSK	10	7.82	0.147	1089	37.2	AE003737	TRUE	TRUE	2	2054.3	2	16of 38	2.3464	TRUE	TRUE	::::::::::::::::::
LSQTITLLPGDIIVTGTPK	7	6.76	0.058	1631	55.4	AE003737	TRUE	TRUE	2	1968.3	0.1	448	2.0213	TRUE	TRUE	::::::::::::::::::
NVFGLYQLTTGK	13	9.72	0.438	1295	31.9	AE003738	TRUE	TRUE	2	1341.5	2.2	18of 22	3.3908	TRUE	TRUE	::::::::::::
FTTFDLGGHTQAR	10	7.85	0.4	860	25.2	AE003738	TRUE	TRUE	2	1451.6	0.8	17of 24	3.1827	TRUE	TRUE	::::::::::::::
NVFGLYQLTTGK	14	9.72	0.392	1194	31.9	AE003738	TRUE	TRUE	2	1341.5	1.9	17of 22	3.5735	TRUE	TRUE	::::::::::::
ADLPGRPLELFMCSVLK	8	6.36	0.144	2455	57.83	AE003738	TRUE	TRUE	2	1947.3	2.3	13of 32	2.3973	TRUE	TRUE	:::::::::::Cys_CAM:::::
SLLLLNYLVR	14	9.85	0.129	1617	48.6	AE003738	TRUE	TRUE	2	1204.5	1.4	12of 18	2.1953	TRUE	TRUE	::::::::::
MDDTYMYDEALRTGGGMGIAGLGM	1	3.51	0.096	2034	59.82	AE003738	TRUE	FALSE	2	2542.9	-1.5	7of 46	1.1343	TRUE	TRUE	:::::Oxidation_M:::::::::::::::::
NPYRPMSSPSMGGYGGSQQSFGLASMPVPQQDSK	14	9.53	0.078	1620	53.29	AE003738	TRUE	FALSE	3	3608	2.3	26of132	2.4687	TRUE	TRUE	:::::Oxidation_M::::::::::::::::::Oxidation_M:::::::::
SVVAEHLVAQDSAIK	5	5.22	0.346	1298	33.2	AE003739	TRUE	TRUE	2	1567.8	0.7	17of 28	3.1099	TRUE	TRUE	::::::::::::::::
EEQMQITSQVTGQIGWRREG	4	4.56	0.013	1441	36.63	AE003739	TRUE	FALSE	3	2350.6	-0.6	21of 76	2.1216	TRUE	TRUE	::::Oxidation_M:::::::::::::::
YIFLLYR	15	9.59	0.009	1377	40.1	AE003739	TRUE	TRUE	1	988.2	0.5	8of 12	1.3872	TRUE	TRUE	::::::::
TKSIDVQQPSQILAGKEVVIERR	15	9.88	0.007	1957	46.3	AE003739	TRUE	FALSE	3	2596	0	13of 88	1.3807	TRUE	TRUE	::::::::::::::::::::::
YIFLLYR	14	9.59	0	1286	40.1	AE003739	TRUE	TRUE	2	988.2	1.7	10of 12	1.9621	TRUE	TRUE	::::::::
TSLSPGSGVVTYYLR	14	9.59	0.387	1094	36.8	AE003740	TRUE	TRUE	2	1600.8	0.3	18of 28	2.856	TRUE	TRUE	::::::::::::::::
CLLLLGDSVTTDHISPAGSIAR	5	5.1	0.385	1762	58.7	AE003740	TRUE	TRUE	2	2297.6	1.2	21of 42	4.3165	TRUE	TRUE	:Cys_CAM:::::::::::::::::::
TSLSPGSGVVTYYLRE	8	6.83	0.097	1843	37.9	AE003740	TRUE	FALSE	3	1729.9	0.3	19of 60	2.4744	TRUE	TRUE	::::::::::::::::
PFFEGMTRALPK	15	10.09	0.031	549	34.63	AE003740	TRUE	FALSE	2	1410.7	0.6	9of 22	1.1941	TRUE	TRUE	:::::Oxidation_M::::::
MVKSQKDCVTILCWNSECDKD	4	4.46	0.046	1909	42.63	AE003741	TRUE	FALSE	3	2617.8	3	8of 80	1.0669	TRUE	TRUE	::::::::Cys_CAM::::::Cys_CAM::::::Cys_CAM::::
ISALELKPNFK	15	9.89	0.043	880	31.8	AE003741	TRUE	TRUE	2	1260.5	0.9	12of 20	1.6605	TRUE	TRUE	::::::::::
NLAIEATFINHNFSQQVLK	9	7.82	0.415	1946	51.7	AE003744	TRUE	TRUE	2	2188.5	0.7	21of 36	4.0213	TRUE	TRUE	::::::::::::::::::
TVGNVFATDAILATIMCSTR	6	6.1	0.412	2318	56.13	AE003744	TRUE	TRUE	2	2142.4	2.2	16of 38	2.9433	TRUE	TRUE	::::::::::::::::Cys_CAM::::
TVGNVFATDAILATIMCSTR	5	6.1	0.258	2418	56.13	AE003744	TRUE	TRUE	2	2142.4	-0.3	16of 38	2.5596	TRUE	TRUE	::::::::::::::::Cys_CAM::::
ISLLCLMEMTFK	7	6.29	0.179	2207	52.86	AE003744	TRUE	TRUE	2	1486.8	0.6	4	2.3654	TRUE	TRUE	:::::Cys_CAM::::::::
ISLLCLMEMTFK	8	6.29	0.141	2784	52.86	AE003744	TRUE	TRUE	2	1486.8	-0.5	10of 22	1.7076	TRUE	TRUE	:::::Cys_CAM::::::::
AISFTDIAQETK	2	4.08	0.14	806	27.1	AE003744	TRUE	TRUE	2	1324.5	1.1	13of 22	1.6191	TRUE	TRUE	::::::::::::
SIAPVTYLVANK	14	9.72	0.333	943	33.7	AE003745	TRUE	TRUE	2	1276.5	0.5	17of 22	2.8252	TRUE	TRUE	::::::::::::
DFGYVLQHPK	10	7.74	0.325	862	23.5	AE003745	TRUE	TRUE	2	1204.4	2	13of 18	2.5872	TRUE	TRUE	::::::::::
VDVAYAPPSGYTNVPSPIVLFSIPDGHTK	5	5.1	0.298	2102	69.8	AE003745	TRUE	TRUE	2	3043.4	0.5	14of 56	2.5221	TRUE	TRUE	::::::::::::::::::::::::::::
KDLALNTPQLN	9	6.76	0.018	1084	25.8	AE003746	TRUE	FALSE	3	1227.4	2.6	16of 40	1.6982	TRUE	TRUE	::::::::::
MAQYAGRASVALNTHL	15	9.85	0.003	1277	36.13	AE003747	TRUE	FALSE	2	1720	-1.3	12of 30	1.4199	TRUE	TRUE	:Oxidation_M:::::::::::::::
ATQIIGMLFASVTK	15	10.1	0.022	789	44.23	AE003748	TRUE	FALSE	2	1480.8	-0.6	9of 26	1.2934	TRUE	TRUE	::::::::::::::
YVQINPLGGVYVQFPNSGR	14	9.59	0.427	1374	49	AE003749	TRUE	TRUE	2	2109.4	1.9	20of 36	3.8496	TRUE	TRUE	::::::::::::::::::
HVSPAGAAVGVPLNPAQAK	15	10.1	0.287	517	33.7	AE003749	TRUE	TRUE	2	1785.1	2.1	15of 36	2.0638	TRUE	TRUE	::::::::::::::::::
QLSGVALGSDAFFPFR	6	6.79	0.281	1984	50.3	AE003749	TRUE	TRUE	2	1712.9	2.5	11of 30	1.6776	TRUE	TRUE	::::::::::::::
IIMYDLIQSNLDKRR	15	9.72	0.04	1332	44.73	AE003750	TRUE	FALSE	2	1895.2	0.6	4of 28	0.6082	TRUE	TRUE	:::Oxidation_M::::::::::::
SNNADLARSKTTD	9	6.9	0.029	667	9.4	AE003750	TRUE	FALSE	3	1393.5	1.6	12of 48	1.016	TRUE	TRUE	::::::::::::
NAMFTNPKYVQVMTEV	9	6.87	0.128	898	41.66	AE003751	TRUE	FALSE	3	1889.2	-0.3	14of 60	1.4405	TRUE	TRUE	:::Oxidation_M::::::::::::
KEVTILLAR	15	10.09	0.029	853	29.6	AE003751	TRUE	FALSE	1	1043.3	2.8	10of 16	1.1786	TRUE	TRUE	::::::::::
LETEPATSKGDNYASVMTRINLEYST	3	4.17	0.004	2578	50.33	AE003751	TRUE	FALSE	2	2892.2	-2.2	6of 50	0.9765	TRUE	TRUE	::::::::::::::::::::::::::
IQDWPTKSQLPTPQGNEFRKLLGSSS	15	9.89	0.132	1887	50.5	AE003752	TRUE	FALSE	2	2916.3	-1.9	8of 50	1.1413	TRUE	TRUE	::::::::::::::::::::::::::
TLGKVLHYFNS	13	9.72	0.035	1646	29.2	AE003754	TRUE	FALSE	2	1279.5	0.7	6of 20	0.8355	TRUE	TRUE	::::::::::::
AVALTHVLGLTGSSEGK	10	7.82	0.232	1178	35.4	AE003755	TRUE	TRUE	2	1640.9	2.7	12of 32	2.013	TRUE	TRUE	::::::::::::::::::

DGGSPLIYGR	9	6.7	0.002	870	20.8	AE003755	TRUE	FALSE	2	1035.1	1.1	10of 18	1.1664	TRUE	TRUE	::::::::::
VAFTGSVEIGR	7	6.98	0.352	1045	28	AE003758	TRUE	TRUE	2	1136.3	1.8	1	3.1548	TRUE	TRUE	::::::::::
YGPKEILGK	15	9.63	0.183	1047	18.5	AE003759	TRUE	FALSE	1	1005.2	-0.1	12of 16	2.5897	TRUE	TRUE	::::::::::
IEEVMVYR	2	4.27	0.056	498	29.03	AE003759	TRUE	TRUE	2	1039.2	1.6	9of 14	1.4678	TRUE	TRUE	::::::::
NYIEELNRHLNATVGNLQAKVESLTTT	5	5.4	0.044	1618	56.4	AE003759	TRUE	FALSE	3	3030.4	-1.6	19of104	2.2362	TRUE	TRUE	::::::::::::::::::::::::
AQGFLAPASGGRPLLEPVGFGQSQG	8	6.98	0.017	1736	56.4	AE003759	TRUE	FALSE	3	2442.7	-1.2	13of 96	1.2003	TRUE	TRUE	::::::::::::::::::::::
VEGEGLEASIGVPPSKATPKPK	12	7.13	0.087	1368	34.1	AE003760	TRUE	TRUE	3	2192.5	-2.8	22of 84	2.0905	TRUE	TRUE	::::::::::::::::::::
ISLTHTSLLYEK	10	7.74	0.216	1044	33.9	AE003762	TRUE	TRUE	2	1405.6	2.1	14of 22	2.3599	TRUE	TRUE	::::::::::::
YREVITNAIEADK	3	4.45	0.081	1121	28	AE003762	TRUE	TRUE	2	1522.7	2.6	14of 24	2.2746	TRUE	TRUE	::::::::::::::
EIMADAAYAILTREPR	3	4.45	0.023	1740	44.73	AE003762	TRUE	FALSE	2	1821.1	-1.7	9of 30	1.1115	TRUE	TRUE	::::::::::::::::
MSATFIGNSTAIQEIFK	6	6.95	0.448	1910	46.93	AE003763	TRUE	TRUE	2	1875.1	1.1	22of 32	3.8198	TRUE	TRUE	:Oxidation_M::::::::::::::::
GVVDSDDLPLNVSR	1	3.6	0.366	777	32	AE003763	TRUE	TRUE	2	1486.6	1.5	22of 26	4.6803	TRUE	TRUE	::::::::::::::
QEHIYYIAGANR	10	7.7	0.292	580	25.4	AE003763	TRUE	TRUE	2	1435.6	0.4	12of 22	2.2415	TRUE	TRUE	::::::::::::::
YSQFINFPIR	14	9.85	0.283	1204	36.1	AE003763	TRUE	TRUE	2	1285.5	1.1	12of 18	2.9933	TRUE	TRUE	::::::::::
ELISNASDAIDK	1	3.71	0.281	550	25.3	AE003763	TRUE	TRUE	1	1276.4	-0.5	13of 22	2.8898	TRUE	TRUE	::::::::::::::
KPAEVTEDEYTSFYK	2	4.17	0.236	610	26.4	AE003763	TRUE	TRUE	2	1808	-0.2	15of 28	2.6259	TRUE	TRUE	::::::::::::::::
ELETNPELHIR	3	4.54	0.195	1088	26.2	AE003763	TRUE	TRUE	2	1351.5	0.8	13of 20	2.3971	TRUE	TRUE	::::::::::::
IDVYYNEASSGK	2	4.08	0.181	421	21.4	AE003763	TRUE	TRUE	2	1346.4	1	13of 22	2.2019	TRUE	TRUE	::::::::::::::
FTFQTEVNR	6	6.98	0.17	1136	22.3	AE003763	TRUE	TRUE	2	1142.3	0.7	10of 16	1.9334	TRUE	TRUE	::::::::::
YSQFINFPIR	15	9.85	0.137	1284	36.1	AE003763	TRUE	TRUE	2	1285.5	0.8	13of 18	2.1597	TRUE	TRUE	::::::::::
SLLYVPK	14	9.72	0.086	640	25.4	AE003763	TRUE	TRUE	1	820	-0.1	8of 12	1.715	TRUE	TRUE	::::::::
SSTIAALNSVNAISALTQQVEGGAAELAGHLSGLAESVKPK	6	5.4	0.223	2698	83.3	AE003764	TRUE	TRUE	3	3992.5	0.8	29of160	3.4921	TRUE	TRUE	::
CGIFAYLNYLTPK	13	8.81	0.377	1690	45	AE003765	TRUE	FALSE	2	1560.8	1.2	18of 24	4.3842	TRUE	TRUE	:Cys_CAM:::::::::::
NNYPTEHACNYNCR	9	7	0.252	413	14.8	AE003765	TRUE	TRUE	2	1813.8	0.1	17of 26	2.4354	TRUE	TRUE	::::::::Cys_CAM:::Cys_CAM::
LAKENSDYLGTIIDYLEKV	1	4.07	0.092	1541	53.1	AE003765	TRUE	FALSE	2	2185.5	1.3	9of 36	1.3086	TRUE	TRUE	::::::::::::::::::
LATDHIPILYAK	11	7.74	0.023	904	38.1	AE003765	TRUE	TRUE	2	1355.6	1.9	14of 22	1.906	TRUE	TRUE	::::::::::::
VSICHTATVIANAFMHSGTTSDQFLR	11	7.32	0.381	1492	59.63	AE003768	TRUE	TRUE	3	2866.2	2.5	32of100	4.1908	TRUE	TRUE	:::Cys_CAM::::::::::::::::::::
LLHVAVSDVNDDVR	3	4.17	0.269	1199	35.3	AE003768	TRUE	TRUE	2	1552.7	0.9	17of 26	3.2954	TRUE	TRUE	::::::::::::::
SNHADLQVLR	9	7.85	0.258	1100	19.9	AE003768	TRUE	TRUE	2	1153.3	2.4	16of 18	2.6265	TRUE	TRUE	::::::::::
LAYAYNVTMSLIQNR	15	9.59	0.167	1364	45.73	AE003768	TRUE	FALSE	2	1774	2.3	4of 28	0.75	TRUE	TRUE	::::::::Oxidation_M::::::
CLVSLYR	13	8.9	0.121	835	27.5	AE003768	TRUE	TRUE	2	911.1	1.3	10of 12	1.6887	TRUE	TRUE	:Cys_CAM::::::
LEEADPLVTSLSSDKDPVLR	1	3.85	0.075	1018	48.5	AE003768	TRUE	TRUE	2	2185.4	2.4	13of 38	1.6851	TRUE	TRUE	::::::::::::::::::
QNKILIMDEATANVDPETDN	1	3.43	0.012	1750	39.53	AE003768	TRUE	FALSE	2	2248.4	1.2	6of 38	0.7938	TRUE	TRUE	::::::Oxidation_M::::::::::::
DKASGALATPTEAPAVP	2	4.08	0.083	1396	29.1	AE003769	TRUE	FALSE	2	1596.8	2.1	11of 32	1.4164	TRUE	TRUE	::::::::::::::::
IFFPISDKDNFTACK	8	6.24	0.125	1721	41.7	AE003770	TRUE	FALSE	2	1804	2.7	7of 28	1.0678	TRUE	TRUE	:::::::::::::Cys_CAM::
QGVLASLGQDHAALVEKIPAEV	3	4.43	0.089	1780	54.3	AE003771	TRUE	FALSE	3	2246.6	-2.6	22of 84	1.8444	TRUE	TRUE	::::::::::::::::::::
FMNTPYEV	1	3.3	0.029	924	26.23	AE003771	TRUE	FALSE	1	1001.1	0.2	8of 14	2.2309	TRUE	TRUE	::::::::
SLRPNVEFPNGSVTFK	14	10.09	0.375	947	35.5	AE003772	TRUE	TRUE	2	1793	0.5	19of 30	3.8703	TRUE	TRUE	::::::::::::::::
AHVHYVVTEHGIASLFGK	11	7.98	0.265	1061	39.8	AE003772	TRUE	TRUE	2	1966.2	1.1	18of 34	3.1244	TRUE	TRUE	::::::::::::::::
WPSMNTDSGISMFSADTVTKYKDAST	2	4.18	0.097	1236	47.86	AE003772	TRUE	FALSE	3	2858.1	0	7of100	0.9973	TRUE	TRUE	:::Oxidation_M::::::::::::::::::::
NEMLMVYMPTAKCLGIVINYKKPESFESAA	5	6.51	0.027	2822	83.09	AE003772	TRUE	FALSE	3	3469	-0.6	24of116	1.8837	TRUE	TRUE	:::Oxidation_M::Oxidation_M::::::::Cys_CAM::::::::::::::::
SYDYLLLATHFNSYQK	9	7.64	0.336	1916	43.5	AE003773	TRUE	TRUE	2	1964.2	0.1	17of 30	2.9811	TRUE	TRUE	::::::::::::::::
HVVVIAER	9	7.85	0.208	921	22.8	AE003773	TRUE	TRUE	2	923.1	0.6	10of 14	2.1197	TRUE	TRUE	::::::::
ANDLAKLMK	15	9.89	0.021	624	21.13	AE003773	TRUE	FALSE	2	1004.2	1.8	9of 16	1.1512	TRUE	TRUE	::::::::::
EHSDASHDITAYVSNPINAYLLTK	5	5.12	0.382	1850	47.6	AE003774	TRUE	TRUE	2	2660.9	0.8	18of 46	4.4145	TRUE	TRUE	::::::::::::::::::::::
LQDTYQLDTSSVAR	2	3.89	0.32	581	28.3	AE003774	TRUE	TRUE	2	1597.7	1.6	16of 26	3.0258	TRUE	TRUE	::::::::::::::::
ATVQNSVTGALETANYR	7	6.89	0.194	1157	29.3	AE003774	TRUE	TRUE	2	1795.9	2.2	4	2.1047	TRUE	TRUE	::::::::::::::::
SIVGVIPYLPYSK	14	9.53	0.182	1328	43.2	AE003774	TRUE	TRUE	2	1436.7	2.1	12of 24	1.9515	TRUE	TRUE	::::::::::::::
TTSVSVGVPEHIVK	9	7.82	0.073	1289	26.9	AE003774	TRUE	TRUE	2	1453.7	0.1	15of 26	2.1416	TRUE	TRUE	::::::::::::::
FPSDEDLNGAAVALLR	1	3.71	0.02	1209	45.3	AE003774	TRUE	TRUE	2	1688.9	0.5	15of 30	1.9463	TRUE	TRUE	::::::::::::::::
SSTSSATTSSATTVATGLTSSSVSK	15	10.1	0.405	620	24	AE003775	TRUE	TRUE	2	2307.4	-0.5	17of 48	3.3686	TRUE	TRUE	::::::::::::::::::::::
GFKDECLSIVDQYYHVIYETLVSK	3	4.54	0.374	2213	66.5	AE003775	TRUE	TRUE	3	2908.2	2.1	34of 92	4.6085	TRUE	TRUE	:::::Cys_CAM::::::::::::::::::
LVASLGWAK	14	10.1	0.054	343	31.5	AE003775	TRUE	FALSE	1	945.1	-0.5	8of 16	1.3236	TRUE	TRUE	::::::::::
ATYYLSILNSERPELYK	8	6.92	0.425	2023	48.3	AE003778	TRUE	TRUE	2	2061.3	0	19of 32	4.3924	TRUE	TRUE	::::::::::::::::
ILYLINQGEQLVAR	7	6.89	0.354	1547	50.3	AE003778	TRUE	TRUE	2	1630.9	1.4	1	4.0442	TRUE	TRUE	::::::::::::::
MLSPAFSILQLFCSSPK	13	8.97	0.305	1874	59.13	AE003778	TRUE	TRUE	2	1943.3	0.9	14of 32	2.2252	TRUE	TRUE	:Oxidation_M::::::::::::Cys_CAM::::::
FPATLVLDSMVAALLR	6	6.79	0.123	2715	64.03	AE003778	TRUE	TRUE	2	1718.1	0.8	11of 30	1.9118	TRUE	TRUE	::::::::::::::::
YLQNMFALHSSQYPHR	14	9.59	0.432	894	37.03	AE003779	TRUE	TRUE	2	1993.2	2.1	19of 30	4.2535	TRUE	TRUE	::::::::::::::::
NMITGTSQADCAVLIVAAGTGEFEAGISK	2	3.83	0.229	2245	66.83	AE003779	TRUE	TRUE	3	2913.2	2.2	25of112	2.4808	TRUE	TRUE	:::::::::Cys_CAM::::::::::::::::::
AAVMAFQSSGDSKNGS	9	6.76	0.05	521	20.93	AE003780	TRUE	FALSE	3	1557.7	1.5	18of 60	1.721	TRUE	TRUE	::::::::::::::::
ASITENGGAEEESVAK	2	3.8	0.449	183	19.9	AE003781	TRUE	TRUE	2	1592.7	0.2	18of 30	4.0774	TRUE	TRUE	::::::::::::::::
ASITENGGAEEESVAK	1	3.8	0.416	190	19.9	AE003781	TRUE	TRUE	2	1592.7	0.2	18of 30	3.5705	TRUE	TRUE	::::::::::::::::
DAVAAEEVAAEK	1	3.69	0.407	218	21.4	AE003781	TRUE	TRUE	2	1203.3	1.1	19of 22	4.4506	TRUE	TRUE	::::::::::::
AKLDEASTKDEVQNGAEASEVAA	2	3.82	0.357	510	30.1	AE003781	TRUE	FALSE	2	2334.5	-0.5	19of 44	3.9372	TRUE	TRUE	::::::::::::::::::::::
ASEPTVSFAADKDEK	2	4.07	0.316	376	19.7	AE003781	TRUE	TRUE	2	1595.7	0.6	16of 28	2.5097	TRUE	TRUE	::::::::::::::::
LDEASTKDEVQNGAEASEVAA	1	3.44	0.297	490	30.2	AE003781	TRUE	FALSE	2	2135.2	1.8	21of 40	4.2884	TRUE	TRUE	::::::::::::::::::
GGEFILYGGNVLGK	7	6.87	0.263	1423	38.6	AE003781	TRUE	TRUE	2	1424.6	0.4	1	2.8272	TRUE	TRUE	::::::::::::::
LHQLFQDFK	10	7.82	0.255	1106	28.4	AE003781	TRUE	TRUE	1	1176.4	-0.2	11of 16	2.0779	TRUE	TRUE	::::::::::
IGQSDIECAVDSVDK	1	3.51	0.254	814	28.4	AE003781	TRUE	TRUE	2	1636.7	0.6	13of 28	2.2573	TRUE	TRUE	:::::::Cys_CAM::::::::
SQTTQFIHLIWGPETSK	9	7.82	0.221	1968	39.9	AE003781	TRUE	TRUE	2	1974.2	0.4	13of 32	2.6199	TRUE	TRUE	::::::::::::::::
ASITENGGAEEESVAKENGAADSSATEPTDAVDGEK	1	3.53	0.083	553	36.5	AE003781	TRUE	TRUE	3	3538.6	2.4	27of140	2.5909	TRUE	TRUE	::::::::::::::::::::::::::::::::
TLTYKAAKMITNLDASNELVTIR	15	9.63	0.121	1360	57.63	AE003782	TRUE	FALSE	3	2568	-0.8	18of 88	1.9771	TRUE	TRUE	::::::::::::::::::::
KLEEPIALAPIPYEFIA	1	3.97	0.002	1596	64.2	AE003783	TRUE	FALSE	2	1915.3	1.7	12of 32	1.8057	TRUE	TRUE	::::::::::::::::
YLFKEHLGLLESEGSSRSDLDINDPVCEKF	3	4.22	0.024	2204	74.5	AE003784	TRUE	FALSE	3	3499.8	0.7	21of116	1.9955	TRUE	TRUE	:::::::::::::::::::::::::Cys_CAM::::
LLGAYLHEVGKL	10	7.74	0.333	1424	40.4	AE003785	TRUE	FALSE	2	1313.6	1.9	19of 22	3.5931	TRUE	TRUE	::::::::::::
FFAFVDGK	6	6.76	0.166	1431	29.2	AE003785	TRUE	TRUE	1	931.1	0.8	11of 14	1.8063	TRUE	TRUE	::::::::
LNIALPVNVK	15	10.1	0.128	1105	34.3	AE003785	TRUE	TRUE	1	1081.3	2	11of 18	2.0131	TRUE	TRUE	::::::::::
TFNPHLIFK	13	10.1	0.002	634	29.5	AE003785	TRUE	FALSE	2	1117.3	0.8	10of 16	1.6489	TRUE	TRUE	::::::::::
GVVDSEDIPLNLSR	1	3.71	0.366	877	35.3	AE003789	TRUE	TRUE	2	1514.7	1.8	21of 26	4.8114	TRUE	TRUE	::::::::::::::
SLHCCGSSSALDYIGK	9	7	0.476	1362	30.1	AE003790	TRUE	TRUE	2	1755.9	0.9	20of 30	3.7949	TRUE	TRUE	::::Cys_CAM:Cys_CAM::::::::::
YLVQLGVVPLPK	14	9.72	0.376	1308	45.5	AE003790	TRUE	TRUE	2	1326.7	1.8	18of 22	3.5296	TRUE	TRUE	::::::::::::
SLPGTAASGVSSSYR	14	9.85	0.326	350	22.2	AE003790	TRUE	TRUE	2	1440.6	-0.1	21of 28	2.7538	TRUE	TRUE	::::::::::::::::
HALDVGYR	9	7.76	0.002	892	16.9	AE003790	TRUE	TRUE	2	931	1	10of 14	1.7664	TRUE	TRUE	::::::::

FLKVFSNVAPQSTDRVV	14	10.09	0.012	1802	45.4	AE003791	TRUE	FALSE	2	1908.2	0.5	8of 32	0.9344	TRUE		TRUE	::::::::::::::::
RHFGDGGEEMSD	2	4.06	0.031	445	12.73	AE003796	TRUE	FALSE	1	1353.4	0.3	5of 22	0.8481	TRUE		TRUE	:::::::::Oxidation_M:::
MAATPPMPPGSNTHQLNGK	13	10.1	0.01	1016	26.36	AE003796	TRUE	FALSE	2	1950.2	1.6	5of 36	0.6507	TRUE		TRUE	::::::::::::::::::
GVATHLCAKLASLRER	13	10.11	0.027	680	33.8	AE003797	TRUE	FALSE	3	1783.1	-2.2	17of 60	1.8799	TRUE		TRUE	::::::Cys_CAM::::::::::
DNVPFHSVVWPSVLLAINK	10	7.82	0.277	1838	60.9	AE003798	TRUE	TRUE	2	2136.5	0.1	14of 36	2.3766	TRUE		TRUE	::::::::::::::::::
LLVDTTPTVADTVTNEEISAAK	1	3.59	0.22	993	49.3	AE003798	TRUE	TRUE	2	2289.5	0.3	15of 42	2.5637	TRUE		TRUE	::::::::::::::::::::
YFELHNAIYR	10	7.7	0.212	1064	32.4	AE003798	TRUE	TRUE	2	1326.5	1.1	14of 18	2.0939	TRUE		TRUE	::::::::::
KAKDLPLAEDGSKLNDTHFK	11	7.75	0.012	185	29.2	AE003798	TRUE	FALSE	2	2228.5	-1.5	7of 38	0.8764	TRUE		TRUE	::::::::::::::::::::
EVNLQAGEHLSEEYVK	2	4.25	0.429	726	31.9	AE003799	TRUE	TRUE	2	1846	0.1	18of 30	3.3809	TRUE		TRUE	::::::::::::::::
SAAVIPPISLSTTFK	15	10.1	0.417	1312	42.5	AE003799	TRUE	TRUE	1	1532.8	1.4	15of 28	3.0239	TRUE		TRUE	::::::::::::::::
LHFESGVVFANGIR	10	7.85	0.408	1292	40.9	AE003799	TRUE	TRUE	2	1546.8	1.3	21of 26	4.1155	TRUE		TRUE	::::::::::::::::
LHFESGVIFANALR	10	7.85	0.37	1500	46.2	AE003799	TRUE	TRUE	1	1574.8	0.2	14of 26	2.8488	TRUE		TRUE	::::::::::::::::
LILYGLEASPPVR	7	6.89	0.359	1389	47.3	AE003799	TRUE	TRUE	2	1428.7	2.1	2	3.365	TRUE		TRUE	::::::::::::::
SAAVIPPISLSTTFK	14	10.1	0.345	1235	42.5	AE003799	TRUE	TRUE	1	1532.8	1.7	15of 28	2.7053	TRUE		TRUE	::::::::::::::::
KLEQLPYYEEANGK	3	4.56	0.333	1139	27.5	AE003799	TRUE	TRUE	2	1682.9	1.4	23of 26	4.9111	TRUE		TRUE	::::::::::::::::
LHFESGVVFANGIR	11	7.85	0.291	1050	40.9	AE003799	TRUE	TRUE	1	1546.8	0.7	12of 26	1.8717	TRUE		TRUE	::::::::::::::
NVLETCFAALDNAK	2	4.08	0.29	1037	36.5	AE003799	TRUE	TRUE	2	1566.7	2	17of 26	3.3243	TRUE		TRUE	::::::Cys_CAM:::::::::
LGISATFVDPTKLDLIK	7	6.88	0.287	1679	53.2	AE003799	TRUE	TRUE	3	1832.2	1.6	1	2.9331	TRUE		TRUE	::::::::::::::::
LTLYGLDPSPPVR	7	6.7	0.287	1327	39.6	AE003799	TRUE	TRUE	2	1428.7	1.3	1	2.9195	TRUE		TRUE	::::::::::::::
LVWIESPTNPLVK	7	6.95	0.261	1479	45.2	AE003799	TRUE	TRUE	2	1496.8	1.4	1	3.8619	TRUE		TRUE	::::::::::::::
FLQNAVGIVPSPFDCYQVNR	6	6.09	0.223	1840	57.8	AE003799	TRUE	TRUE	2	2325.6	2.6	19of 38	3.2568	TRUE		TRUE	::::::::::::::Cys_CAM::::::
LSVGLEDADDLIKDLEQALEIASK	1	3.63	0.209	2185	65.6	AE003799	TRUE	TRUE	2	2586.9	1.6	17of 46	3.3623	TRUE		TRUE	::::::::::::::::::::::
LVNLLAGEHK	11	7.82	0.188	661	27.4	AE003799	TRUE	TRUE	2	1094.3	0.2	14of 18	2.2041	TRUE		TRUE	::::::::::
LTLYGLDPSPPVR	6	6.7	0.184	1547	39.6	AE003799	TRUE	TRUE	2	1428.7	-0.7	12of 24	1.8151	TRUE		TRUE	::::::::::::::
LVWIESPTNPLVK	8	6.95	0.166	2029	45.2	AE003799	TRUE	TRUE	2	1496.8	1.2	15of 24	2.8805	TRUE		TRUE	::::::::::::::
LTLYGLDPSPPVR	8	6.7	0.157	1892	39.6	AE003799	TRUE	TRUE	2	1428.7	1.6	13of 24	2.8349	TRUE		TRUE	::::::::::::::
LDAVHQGLK	10	7.82	0.157	280	19	AE003799	TRUE	TRUE	1	981.1	-0.1	9of 16	1.931	TRUE		TRUE	::::::::::
LDAVHQGLK	11	7.82	0.156	292	19	AE003799	TRUE	TRUE	2	981.1	0.7	14of 16	2.6372	TRUE		TRUE	::::::::::
LGISATFVDPTKLDLIK	8	6.88	0.145	2216	53.2	AE003799	TRUE	TRUE	3	1832.2	1.6	20of 64	2.951	TRUE		TRUE	::::::::::::::::
FLQNAVGIVPSPFDCYQVNR	5	6.09	0.129	1931	57.8	AE003799	TRUE	TRUE	2	2325.6	0.6	13of 38	3.1857	TRUE		TRUE	::::::::::::::Cys_CAM::::::
AQLSPEYLEK	3	4.27	0.101	1106	24.6	AE003799	TRUE	TRUE	1	1178.3	-0.6	10of 18	1.7372	TRUE		TRUE	::::::::::
YLETNPFVEK	3	4.27	0.021	1279	27.8	AE003799	TRUE	TRUE	2	1240.4	0.4	13of 18	2.6877	TRUE		TRUE	::::::::::
SLEAINSLTHK	10	7.82	0.232	740	22.1	AE003800	TRUE	TRUE	2	1213.4	2.3	13of 20	1.8688	TRUE		TRUE	::::::::::
SSSIGQVINSYLTNSK	14	9.72	0.201	1338	28.5	AE003800	TRUE	TRUE	2	1698.9	0	12of 30	1.7009	TRUE		TRUE	::::::::::::::::
LQCCKCR	12	8.58	0.038	725	13.2	AE003800	TRUE	FALSE	2	1025.1	-1.4	6of 12	1.2846	TRUE		TRUE	:::Cys_CAM:Cys_CAM::Cys_CAM::
FLQRNSEQLDEFYGRAHSWMQE	3	4.63	0.071	1412	52.23	AE003801	TRUE	FALSE	3	2789	-2.1	19of 84	1.9345	TRUE		TRUE	::::::::::::::::::Oxidation_M:::
DAHHCLVDLMVTGKPK	11	7.32	0.166	590	30.73	AE003802	TRUE	TRUE	3	1838.1	1.2	30of 60	2.9168	TRUE		TRUE	:::::Cys_CAM:::::Oxidation_M::::::
AILAHIYHH	12	8	0.111	880	25.1	AE003802	TRUE	FALSE	2	1075.3	2.7	10of 16	1.9341	TRUE		TRUE	::::::::::
AIYEMYSEVILVTSAVRNSLHANPS	5	5.3	0.08	2312	66.63	AE003802	TRUE	FALSE	3	2782.1	1.4	11of 96	1.1951	TRUE		TRUE	:::::Oxidation_M:::::::::::::::::::
HSLNALLGGGAPLSLLQTN	11	7.85	0.069	1100	50.9	AE003802	TRUE	FALSE	2	1877.2	-2.7	13of 36	1.5551	TRUE		TRUE	::::::::::::::::::
RYENLTSIIK	14	9.72	0.069	767	25.6	AE003802	TRUE	TRUE	2	1237.4	0.7	13of 18	2.4368	TRUE		TRUE	::::::::::
TVPSTLDGFAVK	6	6.76	0.007	1334	29.1	AE003802	TRUE	TRUE	1	1235.4	-0.2	12of 22	1.5771	TRUE		TRUE	::::::::::::
KLEDVNKVCVRSPLIPAR	15	9.9	0.006	1288	42.3	AE003802	TRUE	TRUE	2	2095.5	-2.1	11of 34	1.4842	TRUE		TRUE	::::::::Cys_CAM:::::::::
NLFHVADCK	9	7.16	0.229	1274	21.2	AE003803	TRUE	TRUE	2	1104.2	0.7	14of 16	2.3591	TRUE		TRUE	:::::::Cys_CAM::
PKPYEVIKKIPYEVKVPVDKPYEVK	13	9.61	0.204	2007	54.2	AE003803	TRUE	FALSE	3	2987.6	1.1	16of 96	1.7028	TRUE		TRUE	::::::::::::::::::::::
PRPPTLLSEEK	9	7.1	0.119	1168	22.1	AE003803	TRUE	TRUE	2	1267.5	1.3	12of 20	2.1922	TRUE		TRUE	::::::::::
GHAEMAVTKPKG	15	9.89	0	535	11.53	AE003804	TRUE	FALSE	1	1242.4	1.3	3of 22	0.512	TRUE		TRUE	:::::Oxidation_M:::::::
KPITIYPK	13	10.18	0.022	775	19.7	AE003806	TRUE	FALSE	1	960.2	-0.2	4of 14	0.5693	TRUE		TRUE	::::::::
NNHAAPYTPTGSISALFPGTYYLK	13	9.4	0.466	1489	52.8	AE003807	TRUE	TRUE	2	2584.9	2.3	16of 46	3.5121	TRUE		TRUE	::::::::::::::::::::::
VVIELNDADRPSK	3	4.31	0.332	1050	27.5	AE003807	TRUE	TRUE	2	1456.6	1.6	18of 24	3.1315	TRUE		TRUE	::::::::::::::
LHENLMANNTELPQYLTR	5	5.3	0.305	1550	45.33	AE003807	TRUE	TRUE	2	2158.4	0	15of 34	2.9025	TRUE		TRUE	::::::::::::::::
GPAIEVFALTQAFK	9	6.95	0.461	2173	44.1	AE003808	TRUE	TRUE	2	1492.8	0.6	22of 26	5.0333	TRUE		TRUE	::::::::::::::
GPAIEVFALTQAFK	8	6.95	0.436	2368	44.1	AE003808	TRUE	TRUE	2	1492.8	2.4	22of 26	4.8194	TRUE		TRUE	::::::::::::::
VLIDQYHIYLLK	11	7.68	0.328	1216	49.1	AE003808	TRUE	TRUE	2	1518.8	2.4	15of 22	3.2619	TRUE		TRUE	::::::::::::
SIGFIGHYMDQK	9	7.74	0.31	1608	28.33	AE003808	TRUE	TRUE	2	1396.6	2.1	16of 22	3.0516	TRUE		TRUE	::::::::::::
LVEHNVSIFVR	10	7.85	0.305	1000	36.2	AE003808	TRUE	TRUE	2	1313.5	1.6	13of 20	1.9418	TRUE		TRUE	::::::::::::
AHPYVISGSVDQTVK	10	7.74	0.28	640	26.9	AE003808	TRUE	TRUE	2	1601.8	0.6	17of 28	3.0029	TRUE		TRUE	::::::::::::::
ESCTIGGSGSSFIYGFVR	7	6.28	0.274	1557	42.6	AE003808	TRUE	TRUE	2	1925.1	0.9	1	2.524	TRUE		TRUE	:::Cys_CAM:::::::::::::::
AVQHAIYHDGSSGGVVR	11	7.91	0.273	313	25.3	AE003808	TRUE	TRUE	2	1753.9	0.8	20of 32	4.3257	TRUE		TRUE	::::::::::::::::
TILNLMTSSPK	15	10.1	0.248	1079	29.23	AE003808	TRUE	TRUE	2	1205.5	0.3	14of 20	2.2432	TRUE		TRUE	::::::::::
EHYRPNMALEDCVTFVK	5	5.35	0.243	1435	40.43	AE003808	TRUE	TRUE	2	2110.4	1.1	16of 32	2.9166	TRUE		TRUE	::::::::::Cys_CAM::::::
VAADFLHTQLNR	11	7.85	0.176	764	30.8	AE003808	TRUE	TRUE	2	1385.6	0.8	18of 22	2.1203	TRUE		TRUE	::::::::::::
NYCYSYR	13	8.77	0.168	299	14.7	AE003808	TRUE	TRUE	2	1026.1	0.7	11of 12	2.2933	TRUE		TRUE	:::Cys_CAM:::::
VNLSVGAYR	15	9.85	0.161	405	23	AE003808	TRUE	TRUE	2	979.1	0	10of 16	1.9711	TRUE		TRUE	::::::::::
SYISFDILR	6	6.7	0.133	1734	34.7	AE003808	TRUE	TRUE	1	1114.3	1.1	8of 16	1.2839	TRUE		TRUE	::::::::::
NFVTIQEALKK	14	9.89	0.109	824	27.5	AE003808	TRUE	TRUE	2	1291.5	2.2	14of 20	2.1955	TRUE		TRUE	::::::::::
GGQVYSIPLGGMLTR	15	9.85	0.087	1308	39.63	AE003808	TRUE	TRUE	2	1549.8	1.8	20of 28	2.8563	TRUE		TRUE	::::::::::::::
YSAFDENGLPTHDKEGK	3	4.54	0.07	1021	20.4	AE003808	TRUE	TRUE	3	1909	1.6	23of 64	1.8236	TRUE		TRUE	::::::::::::::::
HSTQLRPRSLADLGC	12	9.02	0.067	1185	27.8	AE003808	TRUE	FALSE	2	1711.9	-1.8	7of 28	0.998	TRUE		TRUE	::::::::::::Cys_CAM:
MAEHTIDAAIKACNLKPER	7	7.17	0.056	1153	36.53	AE003809	TRUE	FALSE	3	2169.5	-1.3	109	2.3442	TRUE		TRUE	::::::::::Cys_CAM:::::::
DLIGIHAATQR	10	7.85	0.218	700	24.8	AE003810	TRUE	TRUE	2	1195.4	0.7	11of 20	1.6194	TRUE		TRUE	::::::::::
LELLNGTTSYAYVFDHSHSMDMR	4	5.12	0.053	1583	55.96	AE003814	TRUE	FALSE	3	2705	-0.5	8of 88	1.131	TRUE		TRUE	::::::::::::::::::::Oxidation_M::
YPVHTPHIDQMISTGQQQSTLRTQR	13	9.85	0.102	387	38.53	AE003815	TRUE	FALSE	2	2940.3	0.2	5of 48	0.7631	TRUE		TRUE	::::::::::Oxidation_M:::::::::::::
HIIPAVASTNAAIAAACALEVFK	8	7.16	0.334	2435	65.7	AE003816	TRUE	TRUE	2	2339.7	2.1	17of 44	2.8448	TRUE		TRUE	::::::::::::::::Cys_CAM:::::::
VSGGYTAAGSEDTTIK	2	4.08	0.306	210	20.9	AE003816	TRUE	TRUE	2	1557.7	2.2	15of 30	2.6287	TRUE		TRUE	::::::::::::::::
TLIVHLPESEDVDDDRKQQIK	3	4.3	0.201	1237	39.5	AE003816	TRUE	TRUE	3	2479.7	2.2	25of 80	2.796	TRUE		TRUE	::::::::::::::::::::
SPMPEIPSSSKH	9	7.82	0.049	534	15.03	AE003816	TRUE	FALSE	2	1313.5	2.8	8of 22	1.1111	TRUE		TRUE	:::Oxidation_M:::::::::::
DTSGLEMKAVADLFDR	3	3.97	0.022	2001	38.03	AE003816	TRUE	FALSE	2	1769	2.4	11of 30	1.2491	TRUE		TRUE	::::::::::::::::
MKTNCMINQAIDQSEPQ	2	4.08	0.057	1745	30.86	AE003817	TRUE	FALSE	2	2025.2	-0.3	7of 32	1.2817	TRUE		TRUE	:Oxidation_M::::Cys_CAM::::::::::::
LLQEVDSFIPTPVR	3	4.08	0.077	1407	46.8	AE003818	TRUE	TRUE	2	1614.9	3	11of 26	1.3626	TRUE		TRUE	::::::::::::::
RLPIVCDEFVDMAFGTGAVK	3	4.31	0.455	1837	59.83	AE003819	TRUE	TRUE	2	2226.6	2	22of 38	4.2298	TRUE		TRUE	::::::Cys_CAM:::::::::::::::
GITLEGLHAQLVGSNLDPR	5	5.22	0.379	1764	46.6	AE003819	TRUE	TRUE	2	1991.3	0.8	18of 36	3.4605	TRUE		TRUE	::::::::::::::::::
SAISDIEVDKVEIPGR	2	4.07	0.212	856	35.5	AE003819	TRUE	TRUE	2	1728.9	1.5	12of 30	2.5347	TRUE		TRUE	::::::::::::::::

NPASSQSLSSTILGGHGQTDSSVLAAK	9	7.82	0.432	1592	39.3	AE003820	TRUE	TRUE	2	2614.8	2	19of 52	4.1168	TRUE		TRUE	::::::::::::::::::::::::::
YHYHEVLHTIGNTFTSIFK	11	7.93	0.389	1364	46.6	AE003820	TRUE	TRUE	2	2308.6	1.3	19of 36	5.0833	TRUE		TRUE	::::::::::::::::
YGCPPHAGGGIGMER	9	7.16	0.351	1017	23.43	AE003820	TRUE	TRUE	2	1559.7	-0.1	16of 28	2.5542	TRUE		TRUE	:::Cys_CAM::::::::::::
EAGVETGDEEDLSTPNEK	1	3.38	0.304	337	20.9	AE003820	TRUE	TRUE	2	1920.9	1	19of 34	2.4703	TRUE		TRUE	::::::::::::::::
IISAASEGGANVFTVSYFK	7	6.87	0.229	1516	49.5	AE003820	TRUE	TRUE	2	1962.2	0.4	1	2.7832	TRUE		TRUE	::::::::::::::::::
IHDPEYLIER	3	4.43	0.196	1171	29.1	AE003820	TRUE	TRUE	2	1285.4	0.2	14of 18	2.4504	TRUE		TRUE	::::::::::
IISAASEGGANVFTVSYFK	8	6.87	0.177	2067	49.5	AE003820	TRUE	TRUE	2	1962.2	1.1	19of 36	2.4834	TRUE		TRUE	::::::::::::::::::
VYTVGAVFR	15	9.85	0.061	860	29.4	AE003820	TRUE	TRUE	2	1012.2	2.5	13of 16	1.6552	TRUE		TRUE	::::::::::
FSAVIVSPAFSGK	15	10.1	0.331	1067	36.7	AE003821	TRUE	TRUE	1	1310.5	-0.4	16of 24	2.8338	TRUE		TRUE	::::::::::::::
RHYSMRPHREQEQRNAEDVLFDMFASEETGL	3	4.88	0.011	2405	57.66	AE003821	TRUE	FALSE	3	3781.1	-0.3	20of120	1.9286	TRUE		TRUE	::::::::::::::::::::::::::::::
SSDVLDILIPILYHLNYSR	5	5.1	0.116	2665	67.1	AE003822	TRUE	TRUE	3	2232.6	0.7	23of 72	2.4716	TRUE		TRUE	::::::::::::::::::
EADQLSTLEQYAFR	1	3.83	0.355	1190	35	AE003823	TRUE	TRUE	2	1671.8	1.2	19of 26	3.8335	TRUE		TRUE	::::::::::::::
IMVSPDGDVTVTNDGATIMK	1	3.6	0.335	860	43.96	AE003823	TRUE	TRUE	2	2065.4	1.4	21of 38	3.2735	TRUE		TRUE	::::::::::::::::::::
LDVTSAEDYR	1	3.71	0.285	456	20.9	AE003823	TRUE	TRUE	2	1169.2	2.8	14of 18	3.5875	TRUE		TRUE	::::::::::
NKEPLIQIAMTTLGSK	13	9.89	0.181	1465	37.63	AE003823	TRUE	TRUE	2	1745.1	1.7	18of 30	2.9443	TRUE		TRUE	::::::::::::::::
NKEPLIQIAMTTLGSK	14	9.89	0.165	1102	37.63	AE003823	TRUE	TRUE	2	1761.1	1.9	16of 30	2.1294	TRUE		TRUE	:::::::::Oxidation_M::::::::
VHLVVYDSYEVPFEMASLRD	3	4.06	0.147	1520	62.33	AE003823	TRUE	FALSE	3	2370.7	1.8	25of 76	2.8863	TRUE		TRUE	::::::::::::::::::::
IVYGGGAAEISCSLAVAK	8	6.28	0.13	1779	46	AE003823	TRUE	TRUE	2	1767	2.8	15of 34	3.1501	TRUE		TRUE	:::::::::::Cys_CAM::::::::
GGQGPGLGQIPTPKPDILTEEKLQEKALK	7	7.14	0.124	1573	52.5	AE003823	TRUE	FALSE	3	3044.5	2.7	284	1.3966	TRUE		TRUE	::::::::::::::::::::::::::
IADGFELAAQCAIK	2	4.08	0.055	917	40.6	AE003823	TRUE	TRUE	2	1507.7	0.8	12of 26	1.887	TRUE		TRUE	:::::::::::Cys_CAM::::
DLWHDVSPGDAGIRLNLNV	3	4.17	0.031	1529	50.6	AE003823	TRUE	FALSE	2	2092.3	2.3	10of 36	1.4002	TRUE		TRUE	::::::::::::::::::
TGYTYILPKNILK	13	9.94	0.012	1450	38.2	AE003823	TRUE	FALSE	2	1524.8	0.5	11of 24	1.7261	TRUE		TRUE	::::::::::::::
AEQDVLELGDDDFATTLK	1	3.32	0.369	1152	43.3	AE003824	TRUE	FALSE	2	1981.1	2.5	25of 34	4.8749	TRUE		TRUE	::::::::::::::::::
TLIDALDAILPPARPTDK	2	4.18	0.333	1356	50.2	AE003824	TRUE	TRUE	3	1921.2	2.7	25of 68	3.1613	TRUE		TRUE	::::::::::::::::::
TLIDALDAILPPARPTDK	1	4.18	0.177	1512	50.2	AE003824	TRUE	TRUE	2	1921.2	2.3	20of 34	3.0218	TRUE		TRUE	::::::::::::::::::
TLIDALDAILPPARPTDKA	2	4.18	0.058	1358	52.2	AE003824	TRUE	FALSE	2	1992.3	2.9	13of 36	2.07	TRUE		TRUE	::::::::::::::::::
LATLAGLGTGAAIVK	15	10.1	0.126	1032	43.2	AE003826	TRUE	FALSE	2	1356.6	-0.3	11of 28	1.2121	TRUE		TRUE	::::::::::::::
AGSSYWSSGGVVAKVSSFKNHEGY	12	9.47	0.094	1103	37.1	AE003826	TRUE	FALSE	3	2505.7	-0.9	10of 92	1.2315	TRUE		TRUE	::::::::::::::::::::::
VLEDQAVEAIVHR	3	4.43	0.011	1377	34.2	AE003828	TRUE	FALSE	2	1479.7	0.4	12of 24	1.5174	TRUE		TRUE	::::::::::::::
INASELQAALVNGR	7	6.98	0.423	1291	33.5	AE003829	TRUE	TRUE	2	1456.6	1.9	1	4.474	TRUE		TRUE	::::::::::::::
FSPEFINFLVK	7	6.95	0.312	1803	45	AE003829	TRUE	TRUE	2	1341.6	-0.9	48	2.4828	TRUE		TRUE	::::::::::
FSPEFINFLVK	6	6.95	0.267	2019	45	AE003829	TRUE	TRUE	2	1341.6	0.2	16of 20	2.4129	TRUE		TRUE	::::::::::
SYCLDIPGDFPYPIIADPTR	1	3.6	0.182	1472	60.2	AE003829	TRUE	TRUE	2	2311.6	2.3	14of 38	2.2302	TRUE		TRUE	:::Cys_CAM:::::::::::::::
ALFIISPDHK	12	7.82	0.139	1205	30.8	AE003829	TRUE	TRUE	1	1141.4	0	13of 18	2.3167	TRUE		TRUE	::::::::::
ALFIISPDHK	11	7.82	0.119	829	30.8	AE003829	TRUE	TRUE	1	1141.4	0.5	12of 18	2.4574	TRUE		TRUE	::::::::::
SGCGSVSGSRIITHGLTGRSTSISSQLEK	13	10.11	0.064	1509	40.9	AE003829	TRUE	FALSE	3	2964.2	-1.9	14of112	1.2274	TRUE		TRUE	:::Cys_CAM:::::::::::::::::::::::
NFMGKNAIAVPD	9	6.76	0.053	1281	28.73	AE003829	TRUE	FALSE	3	1293.5	2	17of 44	1.6377	TRUE		TRUE	:::Oxidation_M:::::::::
AVANETGAFFFLINGPEIMSK	3	4.27	0.437	2126	64.63	AE003831	TRUE	TRUE	2	2257.6	2.9	13of 40	3.2348	TRUE		TRUE	::::::::::::::::::
KYEMFAQTLQQSR	15	9.72	0.407	743	27.03	AE003831	TRUE	TRUE	2	1630.9	0.7	18of 24	3.2608	TRUE		TRUE	::::::::::::
GILMYGPPGTGK	15	9.72	0.398	827	27.23	AE003831	TRUE	TRUE	1	1191.4	0.2	12of 22	2.0438	TRUE		TRUE	::::::::::::
IVSQLLTLMDGMK	6	6.76	0.394	2026	46.06	AE003831	TRUE	TRUE	2	1449.8	2.4	18of 24	3.4018	TRUE		TRUE	::::::::::::
VTQGFSGADLTEICQR	2	4.08	0.378	780	34.5	AE003831	TRUE	TRUE	2	1782.9	1.2	20of 30	3.5895	TRUE		TRUE	:::::::::::::Cys_CAM:::
NNLCVHLSDVVSVQSCPDVK	5	5.1	0.371	1491	42.8	AE003831	TRUE	TRUE	2	2271.5	0.4	24of 38	4.1886	TRUE		TRUE	:::::Cys_CAM::::::::::::Cys_CAM:::::
LDQLIYIPLPDDK	1	3.6	0.348	1241	46.1	AE003831	TRUE	TRUE	2	1543.8	1.2	19of 24	4.0845	TRUE		TRUE	::::::::::::::
IVSQLLTLMDGMK	7	6.76	0.32	1799	46.06	AE003831	TRUE	TRUE	2	1449.8	0	1	4.0969	TRUE		TRUE	::::::::::::::
LIVEEAQNDDNSVVSLSQAK	1	3.59	0.289	798	41.3	AE003831	TRUE	TRUE	2	2160.3	0.1	16of 38	2.1407	TRUE		TRUE	::::::::::::::::::
KYEMFAQTLQQSR	14	9.72	0.284	722	27.03	AE003831	TRUE	TRUE	2	1630.9	2.1	17of 24	3.4099	TRUE		TRUE	::::::::::::::
GITNLVVIGGDGSLTGANLFR	7	6.79	0.243	1813	57.6	AE003831	TRUE	TRUE	2	2075.4	2.4	1	3.1636	TRUE		TRUE	::::::::::::::::::
FLEAYRPIHMGDNFIVR	9	7.77	0.183	1821	55.33	AE003831	TRUE	FALSE	2	2079.4	0.5	13of 32	2.4496	TRUE		TRUE	::::::::::::::::
EVDLTYIAK	1	4.08	0.108	652	26.8	AE003831	TRUE	TRUE	1	1052.2	-0.2	11of 16	1.7637	TRUE		TRUE	::::::::::
EVDLTYIAK	2	4.08	0.088	628	26.8	AE003831	TRUE	TRUE	1	1052.2	-0.3	10of 16	1.6395	TRUE		TRUE	::::::::::
ELQELVQYPVEHPDKFLK	3	4.63	0.061	1521	48.1	AE003831	TRUE	TRUE	3	2213.5	2.4	22of 68	2.0535	TRUE		TRUE	::::::::::::::::::
IRVHTVCLPVTASLPEVMHSA	10	7.32	0.049	1780	56.83	AE003831	TRUE	FALSE	2	2318.7	0.1	9of 40	1.0963	TRUE		TRUE	:::::::Cys_CAM:::::::::::::
SITLHDTATCGLHDLSSQFYLTEADIGK	3	4.43	0.554	1787	63.2	AE003832	TRUE	TRUE	3	3095.4	1.7	39of108	5.9464	TRUE		TRUE	:::::::::Cys_CAM:::::::::::::::::
VVVLTNSDGEEQQR	2	3.83	0.42	205	24.5	AE003832	TRUE	TRUE	2	1574.7	1.1	20of 26	3.6219	TRUE		TRUE	::::::::::::::
TISFKPLAQATEEPEFLISDFAK	3	4.17	0.369	1999	65.4	AE003832	TRUE	TRUE	2	2583.9	1.3	19of 44	4.3479	TRUE		TRUE	::::::::::::::::::::::
IIPAIATTTSVLSGLAVLEVIK	7	6.95	0.362	2594	77.1	AE003832	TRUE	TRUE	3	2210.7	-2.4	1	4.3848	TRUE		TRUE	::::::::::::::::::
LPGIQPLEILDSIKK	8	6.99	0.301	2279	47.2	AE003832	TRUE	TRUE	3	1665	2.5	23of 56	3.9518	TRUE		TRUE	::::::::::::::
FAHENGIALIIAETR	5	5.3	0.25	1716	43.7	AE003832	TRUE	TRUE	1	1655.9	-0.8	13of 28	2.0939	TRUE		TRUE	::::::::::::::
LDGVANALDNVDAR	1	3.6	0.244	733	30.8	AE003832	TRUE	TRUE	2	1443.6	2.2	20of 26	3.6207	TRUE		TRUE	::::::::::::::
AHNGALPRPWNEEDANSFLEVVR	4	4.63	0.242	1741	51.1	AE003832	TRUE	TRUE	2	2622.9	1.8	14of 44	2.3571	TRUE		TRUE	::::::::::::::::::::
QLYVLGHDAMR	10	7.76	0.239	897	30.53	AE003832	TRUE	TRUE	2	1303.5	2.1	11of 20	1.804	TRUE		TRUE	::::::::::
AEVYGIEQVR	2	4.27	0.174	492	25.3	AE003832	TRUE	TRUE	2	1164.3	1.1	11of 18	2.309	TRUE		TRUE	::::::::::
IIPAIATTTSVLSGLAVLEVIK	8	6.95	0.16	2963	77.1	AE003832	TRUE	TRUE	3	2210.7	1.9	27of 84	3.0825	TRUE		TRUE	::::::::::::::::::::
SFAHCVEWAR	9	7.16	0.129	1348	26.7	AE003832	TRUE	TRUE	2	1263.4	0.1	12of 18	1.3417	TRUE		TRUE	:::::Cys_CAM::::::
NVILGGVK	14	10.1	0.128	246	22.4	AE003832	TRUE	TRUE	1	800	-0.1	10of 14	2.126	TRUE		TRUE	::::::::
YDSQIAIFGK	6	6.68	0.069	1331	27.1	AE003832	TRUE	TRUE	1	1142.3	0.2	10of 18	1.4478	TRUE		TRUE	::::::::::
NGFANLALPFMAFSEPLPAAK	6	6.95	0.058	2323	67.53	AE003832	TRUE	TRUE	2	2207.6	0.4	14of 40	1.7302	TRUE		TRUE	::::::::::::::::::::
ITMLSQGVSMLYSFFMPK	14	9.72	0.052	1913	65.59	AE003832	TRUE	TRUE	2	2113.6	-0.2	13of 34	2.086	TRUE		TRUE	:::Oxidation_M::::::::::::Oxidation_M:::
EDFFGKLDGVANALDNVDAR	1	3.77	0.028	733	46	AE003832	TRUE	FALSE	3	2167.3	0.7	22of 76	2.2612	TRUE		TRUE	::::::::::::::::::
MNAFLEHGIPANLVATHIVNASR	10	8	0.473	1516	59.33	AE003833	TRUE	TRUE	3	2476.9	1.9	37of 88	5.6201	TRUE		TRUE	::::::::::::::::::::
DLFKYLAPFLR	14	9.72	0.143	1192	46.5	AE003833	TRUE	FALSE	1	1383.7	0.4	12of 20	1.5283	TRUE		TRUE	::::::::::::
ELLHIHSTVASLR	11	8	0.058	813	35.2	AE003833	TRUE	TRUE	2	1476.7	1.6	12of 24	1.9575	TRUE		TRUE	::::::::::::::
DTQDDDSEAAQICLKEWMEERDQLRNK	2	3.94	0.056	1122	44.33	AE003833	TRUE	FALSE	3	3325.5	0.4	17of104	1.6932	TRUE		TRUE	:::::::::::Cys_CAM:::::::::::::
PSTSAAAAAAAAGGHGLQ	9	7.85	0.024	1156	23.6	AE003833	TRUE	FALSE	3	1509.6	-2.9	22of 68	1.8498	TRUE		TRUE	::::::::::::::::::
YVATPMVPFAILR	15	9.85	0.233	1594	51.63	AE003834	TRUE	TRUE	2	1478.8	0.5	15of 24	2.6675	TRUE		TRUE	::::::::::::::
LGITTAEISDGYEK	2	3.83	0.444	700	30.3	AE003835	TRUE	TRUE	2	1497.6	1.9	23of 26	4.202	TRUE		TRUE	::::::::::::::
IVEVGRHPDADSLYLEK	3	4.54	0.393	1183	39.5	AE003835	TRUE	TRUE	2	1942.2	1.8	18of 32	3.5566	TRUE		TRUE	::::::::::::::::
FVEGDVTYAEK	2	3.83	0.307	425	25.3	AE003835	TRUE	TRUE	2	1258.4	1.2	17of 20	3.184	TRUE		TRUE	::::::::::::
KFANALEVFPK	15	9.89	0.283	980	31.6	AE003835	TRUE	TRUE	2	1264.5	1.9	16of 20	2.9835	TRUE		TRUE	::::::::::::
VGDMALHFLNK	10	7.82	0.272	1176	32.03	AE003835	TRUE	TRUE	2	1245.5	1.8	16of 20	3.2856	TRUE		TRUE	::::::::::::
VGDMALHFLNK	11	7.82	0.236	934	32.03	AE003835	TRUE	TRUE	2	1245.5	1.6	16of 20	2.512	TRUE		TRUE	::::::::::::
KFANALEVFPK	14	9.89	0.233	907	31.6	AE003835	TRUE	TRUE	2	1264.5	2.8	17of 20	3.5156	TRUE		TRUE	::::::::::::

TIGFDIEAEK	2	3.83	0.182	702	25.6	AE003835	TRUE	TRUE	2	1123.2	1.4	9of 18	1.7268	TRUE	TRUE	:::::::::::
YAVGAAATILK	15	9.72	0.18	821	31.3	AE003835	TRUE	TRUE	2	1078.3	1.8	17of 20	2.4579	TRUE	TRUE	:::::::::::
YAVGAAATILKVDQIIMAK	14	9.63	0.169	1535	56.73	AE003835	TRUE	TRUE	2	1977.4	1.4	19of 36	3.5164	TRUE	TRUE	::::::::::::::::::
INNAVNLDYTQPQAAVAAAPHGYQPTR	10	7.7	0.153	1080	49.2	AE003835	TRUE	TRUE	3	2882.2	1.3	25of104	3.0955	TRUE	TRUE	::::::::::::::::::::::::
YAVGAAATILK	14	9.72	0.148	780	31.3	AE003835	TRUE	TRUE	1	1078.3	1.8	11of 20	2.3926	TRUE	TRUE	:::::::::::
ACVSILPDEGTFNVDNIR	1	3.71	0.128	1162	47.5	AE003835	TRUE	TRUE	2	2021.2	1	15of 34	2.3955	TRUE	TRUE	::Cys_CAM:::::::::::::
NAMLCYICAGSIDK	5	5.95	0.105	1383	39.23	AE003835	TRUE	TRUE	2	1632.8	0.6	12of 26	1.5697	TRUE	TRUE	:::Oxidation_M::Cys_CAM:::Cys_CAM::::::
ALEILPNLVSHK	11	7.82	0.061	1048	36.8	AE003835	TRUE	TRUE	2	1334.6	0.6	14of 22	2.8972	TRUE	TRUE	::::::::::::
LTAATNTTNVLEAVR	7	6.98	0.033	1128	33.9	AE003835	TRUE	TRUE	2	1574.8	0.7	14	1.8949	TRUE	TRUE	::::::::::::::
HGYGKMAFGAIIGGSV	13	9.72	0.002	1147	36.53	AE003836	TRUE	FALSE	3	1581.8	-0.9	21of 60	1.7968	TRUE	TRUE	::::::Oxidation_M:::::::::::
WVECPPIKIKPK	13	9.79	0.06	862	32	AE003837	TRUE	FALSE	2	1495.8	2.5	11of 22	1.3847	TRUE	TRUE	::::Cys_CAM:::::::::
TLSHNLLITELFNQLTFPVKPADLK	9	7.8	0.345	2339	78.6	AE003838	TRUE	TRUE	3	2854.4	1.8	28of 96	3.6077	TRUE	TRUE	::::::::::::::::::::::::
WCRAAKSLEMLMTGR	13	10.11	0.088	1092	40.66	AE003838	TRUE	FALSE	2	1811.1	1.3	6of 28	0.9978	TRUE	TRUE	::Cys_CAM:::::::::::::
RHFADVGTELQQLR	9	7.85	0.456	1533	29.7	AE003839	TRUE	TRUE	2	1670.9	2.1	19of 26	3.4158	TRUE	TRUE	::::::::::::::
HFADVGTELQQLR	4	5.22	0.399	1493	30.3	AE003839	TRUE	TRUE	2	1514.7	0.9	22of 24	3.7094	TRUE	TRUE	::::::::::::::
FDGILGLGYNSISVDK	2	3.89	0.187	1192	45.3	AE003839	TRUE	TRUE	2	1698.9	0.2	13of 30	2.1591	TRUE	TRUE	::::::::::::::::
IGPSILNADLSNLAAESQK	2	4.08	0.294	1160	44.3	AE003840	TRUE	TRUE	2	1942.2	1.9	14of 36	2.456	TRUE	TRUE	::::::::::::::::::
DVVHSYLK	10	7.74	0.217	536	18.4	AE003840	TRUE	TRUE	2	961.1	0.3	9of 14	1.6569	TRUE	TRUE	::::::::
GKEIPPSFKQFFTST	13	9.89	0.089	1734	33.2	AE003840	TRUE	FALSE	2	1715	-0.1	5of 28	0.7649	TRUE	TRUE	::::::::::::::::
GYNPKLMEAPLLPSLSAK	15	9.63	0.033	1967	48.13	AE003840	TRUE	FALSE	2	1930.3	-1.9	9of 34	1.1971	TRUE	TRUE	::::::::::::::::::
LAAQFNLSHTVSDIR	10	7.85	0.063	1164	37.8	AE003841	TRUE	TRUE	2	1672.9	1.1	17of 28	2.269	TRUE	TRUE	::::::::::::::
FNPLLQSPVK	15	10.1	0.035	891	30.4	AE003841	TRUE	FALSE	1	1143.4	0.5	10of 18	1.5851	TRUE	TRUE	::::::::::
PVVTAVRTSTTTAVSIATSTSDP	9	6.79	0.077	2186	40.4	AE003844	TRUE	FALSE	2	2263.5	1.3	7of 44	1.077	TRUE	TRUE	::::::::::::::::::::::
LLQAATSDTTALALKELIER	3	4.45	0.028	2282	57.2	AE003844	TRUE	FALSE	2	2158.5	-0.1	13of 38	1.3681	TRUE	TRUE	::::::::::::::::::::
DTEAFKKLLQQLGSQARQ	13	9.89	0.12	404	33.1	AE003846	TRUE	FALSE	2	2062.3	-2.8	6of 34	1.0046	TRUE	TRUE	::::::::::::::::::
PFCGASGMLLDKMLNAINLDR	5	6.24	0.22	1876	63.46	AE017256	TRUE	FALSE	3	2353.7	-2.2	8of 80	1.1903	TRUE	TRUE	:::Cys_CAM::::::::::Oxidation_M:::::::::
FENLYVYSGSEHKHQGQQPEKIDFA	5	5.26	0.032	1402	43.4	AE017256	TRUE	FALSE	3	2953.2	-1.6	13of 96	1.1553	TRUE	TRUE	::::::::::::::::::::::::
EFHYYGPFTSAAAVK	9	7.69	0.025	1101	35.3	AE017256	TRUE	FALSE	3	1688.9	1.3	17of 56	1.4254	TRUE	TRUE	::::::::::::::::
FEYDDQEIERRLIKSVMKKVQGKLSQSDIP	9	7.13	0.084	2310	62.03	AE017257	TRUE	FALSE	3	3582.1	-1.5	9of116	0.8052	TRUE	TRUE	::::::::::::::::::::::::::::::
PVNEIFREALKLVAN	9	7.1	0.078	1318	46	AE017257	TRUE	FALSE	3	1714	2.9	17of 56	2.035	TRUE	TRUE	::::::::::::::::
MYFGMMGFGR	15	9.85	0.061	1421	36.09	AE017257	TRUE	FALSE	2	1197.5	-2.9	7of 18	0.9108	TRUE	TRUE	::::::::::
TKSKIGRGMNVTYNYYATLAIAICKGK	15	10.22	0.005	1121	53.73	AE017257	TRUE	FALSE	3	3039.5	0.9	16of104	1.6137	TRUE	TRUE	::::::::Oxidation_M::::::::::::::Cys_CAM::::
LSAKLERSIAELYSPACRAQFCDDK	5	6.36	0.045	1942	56.1	AE017258	TRUE	FALSE	3	2930.2	-1.7	23of 96	2.2816	TRUE	TRUE	:::::::::::::::::Cys_CAM::::Cys_CAM::::
LKEKLLLLAKEFPEMILEVR	9	7.19	0.033	2218	76.13	AE017258	TRUE	FALSE	2	2414	-0.7	7of 38	0.932	TRUE	TRUE	::::::::::::::::::::
TGEGKTLVATLAAYLNSLE	4	4.27	0.014	1851	48.6	AE017258	TRUE	FALSE	2	1952.2	1.6	9of 36	1.1405	TRUE	TRUE	::::::::::::::::::::
KECQNLATKIMCQVNEM	8	6.29	0.014	1653	36.16	AE017258	TRUE	FALSE	2	2130.4	2.4	10of 32	1.4287	TRUE	TRUE	:::Cys_CAM::::::::Oxidation_M:Cys_CAM::::Oxidation_M:
RFLARIFTPEKIEIISNPIYDNME	4	4.65	0.075	2744	76.73	AE017259	TRUE	FALSE	3	2927.4	2.1	9of 92	1.3196	TRUE	TRUE	:::::::::::::::::::::Oxidation_M::
YLPIYNK	15	9.53	0.04	1027	23.8	AE017259	TRUE	FALSE	1	911.1	0.3	10of 12	2.1806	TRUE	TRUE	::::::::
AVVAMSGGVDSSVAAALLHNLG	3	4.94	0.054	1391	56.13	AE017260	TRUE	FALSE	2	2056.3	-1.2	9of 42	1.3054	TRUE	TRUE	:::::Oxidation_M:::::::::::::::
GDPYASQVERSVELIVEKL	2	4.17	0.023	1473	47.3	AE017260	TRUE	FALSE	3	2133.4	-2.5	19of 72	2.5869	TRUE	TRUE	::::::::::::::::::::
VECVPGGHGPPHPPPKLRINSPEKLNSTAVAAAASVR	13	9.91	0.005	2374	61	AF099184	TRUE	FALSE	3	3813.3	2.1	19of144	1.6142	TRUE	TRUE	:::Cys_CAM:::::::::::::::::::::::::::::::::
AASDASEALGSGSALSPTAAKPIK	9	6.99	0.389	1334	37.9	AF132166	TRUE	TRUE	2	2201.4	-0.3	27of 46	5.2386	TRUE	TRUE	::::::::::::::::::::::::
EDLKVEVISTPEVCEQK	2	4.01	0.315	682	35.9	AF132555	TRUE	FALSE	2	2004.2	0.3	18of 32	3.1722	TRUE	TRUE	:::::::::::::Cys_CAM::::
RLDNYAFIGLGQMGYQMA	9	6.64	0.018	1892	54.16	AF309689	TRUE	FALSE	2	2049.4	-2.2	10of 34	1.3652	TRUE	TRUE	::::::::::::::::::
VGMCMGGAPAGPAGTGK	13	8.97	0.002	1078	25.96	AF313480	TRUE	FALSE	3	1519.7	-1.9	19of 64	1.6394	TRUE	TRUE	::::Cys_CAM:::::::::::::
LAPLCLIYQI	4	5.33	0.002	2015	50.2	AF353202	TRUE	FALSE	1	1204.5	0.2	3of 18	0.6424	TRUE	TRUE	:::::Cys_CAM::::::
QILYPIHFQGFK	14	9.72	0.096	1575	41.2	AF365402	TRUE	FALSE	2	1491.8	2.1	6of 22	1.0132	TRUE	TRUE	::::::::::::
YNQLIR	14	9.85	0	146	18.8	AF541948	TRUE	FALSE	1	806.9	0.1	7of 10	1.4049	TRUE	TRUE	::::::
FRMKCHLCVNYIEMQTDPANC	9	6.92	0.06	994	51.86	AK015911	TRUE	FALSE	3	2689	1.4	17of 80	1.562	TRUE	TRUE	:::::Cys_CAM:::Cys_CAM::::::::::::Cys_CAM:
MEIKPGISLATVSAVLHTK	14	9.89	0.051	1875	47.93	AK077634	TRUE	FALSE	2	2012.4	0	11of 36	2.0624	TRUE	TRUE	:Oxidation_M:::::::::::::::::
MAERLEDSVLKGMQAASSK	12	7.11	0.003	772	35.06	AK078485	TRUE	FALSE	3	2084.4	-2.6	18of 72	1.5168	TRUE	TRUE	:Oxidation_M::::::::::Oxidation_M:::::::
SVTIIDTPGVLSGIKQISRGYDFEKV	8	6.98	0.028	1981	64	AL034558	TRUE	FALSE	3	2824.2	0.4	23of100	2.6312	TRUE	TRUE	::::::::::::::::::::::::::
ADYLVVKR	15	9.72	0.011	452	22.1	AL390075	TRUE	FALSE	2	964.2	0.2	7of 14	1.3404	TRUE	TRUE	::::::::
FGALRCLYLMSDGATSDAFASTIFR	5	6.24	0.023	2392	76.03	AL451020	TRUE	FALSE	3	2788.1	-0.6	17of 96	1.4976	TRUE	TRUE	:::::Cys_CAM:::Oxidation_M:::::::::::::::
MFASLYALVYECK	8	6.28	0.042	1815	49.23	AL929352	TRUE	FALSE	2	1595.9	1	11of 24	1.7424	TRUE	TRUE	::::::::::::Cys_CAM:::
GVVPLFGSEDEVTTQGLDDLAAR	1	3.43	0.453	1342	56	ALF-DROME	TRUE	TRUE	2	2390.6	1.4	25of 44	5.7467	TRUE	TRUE	::::::::::::::::::::::
NTPSYQSILENANVLAR	6	6.89	0.42	1750	38	ALF-DROME	TRUE	TRUE	2	1891.1	0.5	18of 32	3.4725	TRUE	TRUE	::::::::::::::::::
YVAGSAGAGSGSLFVANHAY	11	7.7	0.416	900	41.1	ALF-DROME	TRUE	FALSE	2	1900.1	0.4	25of 38	4.1367	TRUE	TRUE	::::::::::::::::::::
VTETVLAAVYK	8	6.87	0.415	1697	31.8	ALF-DROME	TRUE	TRUE	2	1194.4	0.3	17of 20	3.4624	TRUE	TRUE	::::::::::::
ALSDHHVYLEGTLLKPNMVTAGQSAK	12	7.88	0.409	1341	53.13	ALF-DROME	TRUE	TRUE	2	2782.2	-0.1	23of 50	4.5148	TRUE	TRUE	::::::::::::::::::::::::
GILAADESGPTMGK	2	4.08	0.393	528	26.03	ALF-DROME	TRUE	TRUE	2	1347.5	1.7	15of 26	2.5473	TRUE	TRUE	::::::::::::::
KNTPEEIALATVQALR	7	7.1	0.375	1628	36.7	ALF-DROME	TRUE	TRUE	2	1755	2.6	1	4.3501	TRUE	TRUE	::::::::::::::
VTETVLAAVYK	7	6.87	0.366	1107	31.8	ALF-DROME	TRUE	TRUE	2	1194.4	2.4	1	4.1136	TRUE	TRUE	::::::::::::
YVAGSAGAGSGSLFVANHAY	10	7.7	0.322	1140	41.1	ALF-DROME	TRUE	FALSE	2	1900.1	1.6	25of 38	4.4698	TRUE	TRUE	::::::::::::::::::::
GILAADESGPTMGKR	9	7.02	0.288	972	25.43	ALF-DROME	TRUE	TRUE	2	1519.7	1.2	15of 28	2.6064	TRUE	TRUE	::::::::::Oxidation_M::::
ADDGTPFAEILK	1	3.71	0.267	1029	29.4	ALF-DROME	TRUE	TRUE	2	1277.4	0.4	17of 22	2.6254	TRUE	TRUE	::::::::::::
ENIAAGQNELLK	2	4.27	0.176	496	26.3	ALF-DROME	TRUE	TRUE	2	1300.5	1	17of 22	1.9843	TRUE	TRUE	::::::::::::
CTPTVYPADPFDPVEDAAILR	1	3.51	0.098	1386	57	ANX9-DROME	TRUE	TRUE	2	2348.6	1	10of 40	1.552	TRUE	TRUE	:Cys_CAM:::::::::::::::::
RQIFLEYENLSGNDIEKAIKREFSGSVEK	4	4.91	0.048	2282	62.1	ANX9-DROME	TRUE	FALSE	3	3401.8	0.6	21of112	2.344	TRUE	TRUE	::::::::::::::::::::::::::
TLHSAVVAETSGDYKR	9	7.75	0.272	1026	23.7	ANXX-DROME	TRUE	TRUE	2	1734.9	0.3	20of 30	2.8672	TRUE	TRUE	::::::::::::::
DNTINLIHMFR	10	7.85	0.366	1486	33.43	AR34-DROME	TRUE	TRUE	2	1374.6	1.7	15of 20	2.3809	TRUE	TRUE	::::::::::::
DYLHYHIK	11	7.84	0.114	558	18.4	AR34-DROME	TRUE	TRUE	2	1089.2	1.8	11of 14	1.8223	TRUE	TRUE	::::::::
HYFQNTQGLIFVVDSNDRER	5	5.28	0.398	1579	43.4	ARF1-DROME	TRUE	TRUE	3	2439.6	2.2	33of 76	3.105	TRUE	TRUE	::::::::::::::::::
HYFQNTQGLIFVVDSNDRER	4	5.28	0.246	1597	43.4	ARF1-DROME	TRUE	TRUE	3	2439.6	1.8	33of 76	2.7479	TRUE	TRUE	::::::::::::::::::
YAALDLQSPHK	9	7.74	0.004	812	22.5	AY028966	TRUE	FALSE	3	1243.4	-2.1	17of 40	1.5595	TRUE	TRUE	::::::::::::
IHHKPKPPKSDYPVSGEFNPAA	14	9.56	0.07	1546	28.6	AY051438	TRUE	FALSE	2	2417.7	2.8	7of 42	0.9324	TRUE	TRUE	::::::::::::::::::::
ANSPNLSAVLLEAKKDADQMEQSLQQLQLK	3	4.56	0.034	2425	63.63	AY052123	TRUE	FALSE	3	3328.8	2.8	19of116	1.7451	TRUE	TRUE	:::::::::::::::::::Oxidation_M:::::::::::
ANPQGQVVYWSACQSSRFNTSPSPVCGING	12	8.29	0.003	1732	55.6	AY052138	TRUE	FALSE	3	3270.5	2.7	13of116	1.2091	TRUE	TRUE	::::::::::::Cys_CAM::::::::::::Cys_CAM:::::
FPYHIKGVVSN	14	9.72	0.155	470	26.8	AY052143	TRUE	FALSE	2	1261.5	-0.8	9of 20	1.3499	TRUE	TRUE	::::::::::::
LSDHLIDVLLR	5	5.1	0.281	1818	42.3	AY071327	TRUE	TRUE	2	1294.5	0.8	15of 20	3.1437	TRUE	TRUE	::::::::::::
YMKIGQGPKS	14	10.18	0.033	472	14.63	AY113346	TRUE	FALSE	2	1109.3	1.6	9of 18	1.3386	TRUE	TRUE	::::::::::::
GNCISSYSAFVK	13	8.88	0.119	812	26.1	AY118651	TRUE	FALSE	3	1333.4	0.7	13of 44	1.4692	TRUE	TRUE	:::Cys_CAM:::::::::
FFYLFNSSFK	13	9.72	0.006	1195	41.9	AY118929	TRUE	FALSE	1	1300.5	1.4	5of 18	0.7307	TRUE	TRUE	::::::::::::

AIPVVPITLFAK	15	10.1	0.181	1546	47.5	AY119238	TRUE	TRUE	1	1269.6	-0.5	13of 22	2.5838	TRUE	TRUE	::::::::::::
NIPGIETINVDKLNLLK	6	6.99	0.342	1811	49.2	AY231643	TRUE	TRUE	2	1895.2	2.9	19of 32	2.5947	TRUE	TRUE	::::::::::::::::
GTALNVAEYLTPVLK	8	6.87	0.129	2260	44.2	AY231658	TRUE	TRUE	2	1589.9	1.3	13of 28	1.6245	TRUE	TRUE	::::::::::::::
KSAEFLLQLLR	15	10.09	0.104	1486	40.7	AY231666	TRUE	TRUE	2	1318.6	1.1	17of 20	3.4014	TRUE	TRUE	::::::::::
LVHEAFEQPSRTEELLEK	3	4.42	0.183	1263	42.5	AY231684	TRUE	TRUE	3	2156.4	2.1	23of 68	2.3218	TRUE	TRUE	::::::::::::::::
VCTLSITDPGDSDIIR	1	3.6	0.169	904	40.5	AY231694	TRUE	TRUE	2	1762.9	2.3	17of 30	2.7403	TRUE	TRUE	::Cys_CAM::::::::::::::
KSEIEYYAMLAK	7	6.95	0.069	1153	31.83	AY231694	TRUE	TRUE	2	1446.7	-0.9	1	2.226	TRUE	TRUE	::::::::::::
SYLHLPPEIVPSTLK	9	7.74	0.056	1840	44.3	AY231709	TRUE	TRUE	2	1695	2.4	14of 28	1.7948	TRUE	TRUE	::::::::::::::
KPDIDGFLVGGASLKPEFVDIINAR	3	4.46	0.354	1896	68.1	AY231717	TRUE	TRUE	2	2673.1	0.7	22of 48	3.513	TRUE	TRUE	::::::::::::::::::::::
GWDEGVAQLSVGQR	2	4.08	0.032	784	28.8	AY231765	TRUE	TRUE	2	1502.6	1.9	18of 26	1.8839	TRUE	TRUE	::::::::::::
TYAICGEIR	6	6.28	0.302	1030	24.8	AY231767	TRUE	TRUE	2	1083.2	2.1	13of 16	2.669	TRUE	TRUE	:::::Cys_CAM:::::
FPALLSHQESMIGK	10	7.82	0.361	1065	37.53	AY231773	TRUE	TRUE	2	1574.8	0	22of 26	3.349	TRUE	TRUE	::::::::::Oxidation_M::::
SYDAFLASESLIK	2	4.08	0.133	1066	38.8	AY231773	TRUE	TRUE	2	1444.6	1.9	14of 24	1.631	TRUE	TRUE	::::::::::::
ENANGTNVYVGIHPSK	10	7.74	0.422	421	21	AY231776	TRUE	TRUE	2	1700.8	0.3	16of 30	2.5407	TRUE	TRUE	::::::::::::::::
NHEQVFVK	9	7.82	0.175	406	14.4	AY231783	TRUE	TRUE	2	1001.1	0.9	12of 14	1.9764	TRUE	TRUE	::::::::
DVEHGDIVTIGECRPLSK	3	4.54	0.424	1221	35.3	AY231785	TRUE	TRUE	2	2026.2	-0.3	22of 34	4.5899	TRUE	TRUE	::::::::::::Cys_CAM::::::
DYLHFVR	10	7.76	0.112	940	23.2	AY231785	TRUE	TRUE	2	950.1	0.8	11of 12	2.1859	TRUE	TRUE	::::::::
VTPDVVFAFGFR	7	6.79	0.392	1713	43.3	AY231786	TRUE	TRUE	2	1355.6	1.6	1	2.6513	TRUE	TRUE	::::::::::::
CVYVYK	13	8.81	0.031	283	19.5	AY231792	TRUE	TRUE	2	832	0.7	10of 10	2.2937	TRUE	TRUE	:Cys_CAM::::::
EHGSFYVGK	10	7.74	0.007	297	13.9	AY231792	TRUE	TRUE	1	1024.1	-0.1	9of 16	0.9575	TRUE	TRUE	::::::::::
IEDFLER	1	3.83	0.131	665	25.4	AY231798	TRUE	TRUE	1	922	0.1	7of 12	1.4178	TRUE	TRUE	::::::::
VSGGGHVAQIYAIR	15	9.85	0.412	232	29.8	AY231801	TRUE	TRUE	2	1428.6	2.3	19of 26	3.7748	TRUE	TRUE	::::::::::::::
ALVAFYQK	15	9.72	0.236	644	27.6	AY231801	TRUE	TRUE	1	940.1	-0.2	11of 14	2.5992	TRUE	TRUE	::::::::::
LQEPLLLLGK	7	6.95	0.079	1408	41.3	AY231801	TRUE	TRUE	2	1124.4	1.4	20	2.6089	TRUE	TRUE	::::::::::
FLYTLVVQDK	6	6.68	0.146	1531	37.5	AY231803	TRUE	TRUE	2	1226.5	1.7	13of 18	2.1876	TRUE	TRUE	::::::::::
ESLPLLIFLR	7	6.98	0.165	1968	50.2	AY231807	TRUE	TRUE	2	1201.5	1.7	1	2.1184	TRUE	TRUE	::::::::::
HSGNIGFEDILAIAR	4	5.22	0.411	1845	39.8	AY231811	TRUE	TRUE	2	1613.8	2	23of 28	4.621	TRUE	TRUE	::::::::::::::
CVGGEVGATSSLAPK	5	6.29	0.335	1050	25.3	AY231811	TRUE	TRUE	2	1433.6	0.8	23of 28	4.1373	TRUE	TRUE	:Cys_CAM::::::::::::
EVLGTAQSVGCTVDGK	2	4.08	0.295	532	27.3	AY231811	TRUE	TRUE	2	1621.8	2	15of 30	3.0266	TRUE	TRUE	::::::::::Cys_CAM::::::
EVLGTAQSVGCTVDGK	1	4.08	0.117	509	27.3	AY231811	TRUE	TRUE	2	1621.8	0.8	13of 30	1.4451	TRUE	TRUE	::::::::::Cys_CAM::::::
CVGGEVGATSSLAPK	6	6.29	0.077	938	25.3	AY231811	TRUE	TRUE	2	1433.6	0.7	17of 28	2.0258	TRUE	TRUE	:Cys_CAM::::::::::::
DLLHPLPAEEK	3	4.43	0.33	1227	28.5	AY231814	TRUE	TRUE	2	1262.4	2.4	15of 20	3.3582	TRUE	TRUE	::::::::::
LVQHPNSYFMDVK	10	7.74	0.287	722	33.43	AY231814	TRUE	TRUE	2	1594.8	0.2	18of 24	2.7367	TRUE	TRUE	::::::::Oxidation_M::::
VEQALEDQFTSGR	1	3.83	0.356	570	25.2	AY231815	TRUE	TRUE	2	1480.6	0	18of 24	3.8487	TRUE	TRUE	::::::::::::
VEQALEDQFTSGR	2	3.83	0.083	574	25.2	AY231815	TRUE	TRUE	2	1480.6	0.7	13of 24	1.9733	TRUE	TRUE	::::::::::::
VANVSLLALYK	15	9.72	0.281	1204	39.9	AY231818	TRUE	TRUE	2	1191.5	0.2	17of 20	4.0041	TRUE	TRUE	::::::::::
YHVYYHLVQVAK	14	9.4	0.397	680	32.3	AY231825	TRUE	TRUE	2	1520.8	0.9	17of 22	2.9323	TRUE	TRUE	::::::::::
AAAADAAGDAADNGTSKDGEDAADAAAAAPAK	1	3.53	0.457	352	31.3	AY231858	TRUE	TRUE	2	2802.8	0.2	29of 62	4.6943	TRUE	TRUE	::::::::::::::::::::::::::::
AAAEDKAAAADAAGDAADNGTSKDGEDAADAAAAAPAK	1	3.65	0.355	408	36.5	AY231858	TRUE	TRUE	3	3388.5	0.2	39of148	5.1317	TRUE	TRUE	::::::::::::::::::::::::::::::::::
VAADDVSAVKDDLK	1	3.88	0.334	496	25.5	AY231858	TRUE	TRUE	2	1446.6	0.6	20of 26	4.0976	TRUE	TRUE	::::::::::::::
DFGQVEVKPEMIGHYLGEFALTYKPVK	6	5.44	0.43	2034	70.43	AY231867	TRUE	TRUE	3	3097.6	2.2	29of104	5.0756	TRUE	TRUE	::::::::::::::::::::::::
HVINFDLPSDVEEYVHR	3	4.53	0.378	1651	42.1	AY231903	TRUE	TRUE	3	2070.3	2.1	30of 64	3.8583	TRUE	TRUE	::::::::::::::::
AIGLDLELRPINLLK	8	7.02	0.31	2271	57.1	AY231906	TRUE	TRUE	2	1679.1	2.5	17of 28	4.9047	TRUE	TRUE	::::::::::::::
SIAQALVELEANSDLKPYLR	3	4.45	0.486	1963	56	AY231915	TRUE	TRUE	2	2231.6	3	22of 38	4.1799	TRUE	TRUE	::::::::::::::::::
SIAQALVELEANSDLKPYLR	4	4.45	0.313	2085	56	AY231915	TRUE	TRUE	3	2231.6	0.2	23of 76	3.0996	TRUE	TRUE	::::::::::::::::::
AVIIYVPIPQQK	15	9.72	0.068	1157	40.6	AY231915	TRUE	TRUE	2	1369.7	0.3	10of 22	1.9894	TRUE	TRUE	::::::::::::
MADFGVLHR	10	7.85	0.33	604	26.03	AY231919	TRUE	TRUE	2	1062.2	1.8	13of 16	2.8842	TRUE	TRUE	:Oxidation_M::::::::
IDITIMDALKR	7	6.9	0.117	1407	36.13	AY231919	TRUE	TRUE	2	1289.6	1.3	36	2.0169	TRUE	TRUE	::::::::::::
MIAILTENFAGK	6	6.95	0.087	1626	39.33	AY231919	TRUE	TRUE	1	1308.6	-0.5	14of 22	2.2471	TRUE	TRUE	::::::::::::
IFVFFAVPETKGKSLNEIQQELAGNR	8	7.16	0.13	2309	68.6	AY231934	TRUE	FALSE	3	2937.4	0.4	19of100	2.1288	TRUE	TRUE	::::::::::::::::::::::::
NFVPVSELSGQVGK	6	6.95	0.232	1379	30.8	AY231969	TRUE	TRUE	2	1461.7	2.3	21of 26	3.0214	TRUE	TRUE	::::::::::::::
AQLPLQIEDASRPENADDAEGLNIR	1	3.76	0.049	978	52.2	AY231969	TRUE	TRUE	2	2737	0.6	11of 48	1.5871	TRUE	TRUE	::::::::::::::::::::::::
SLNYNHLMPTR	14	9.85	0.232	620	24.73	AY232028	TRUE	TRUE	2	1346.5	1.8	12of 20	2.9644	TRUE	TRUE	::::::::::::
SLNYNHLMPTR	15	9.85	0.088	592	24.73	AY232028	TRUE	TRUE	2	1346.5	1.4	12of 20	2.1125	TRUE	TRUE	::::::::::::
IEDLSQQAQVAAAEK	1	3.83	0.409	473	28.6	AY232038	TRUE	TRUE	2	1601.8	2.9	25of 28	5.5072	TRUE	TRUE	::::::::::::::
IEDLSQQAQVAAAEK	2	3.83	0.386	520	28.6	AY232038	TRUE	TRUE	2	1601.8	0.5	25of 28	5.6575	TRUE	TRUE	::::::::::::::
NPHSDTYIVFGEAK	5	5.22	0.223	1338	25.7	AY232038	TRUE	TRUE	2	1578.7	1.7	16of 26	1.9723	TRUE	TRUE	::::::::::::::
NILFVINNPDVYKNPHSDTYIVFGEAK	5	5.28	0.158	1940	69.5	AY232038	TRUE	TRUE	2	3109.5	1.4	13of 52	2.0664	TRUE	TRUE	::::::::::::::::::::::::
DTVNRPGFAEHFFK	10	7.82	0.116	1110	29.6	AY232043	TRUE	TRUE	2	1665.8	1.3	9of 26	2.0634	TRUE	TRUE	::::::::::::::
AQASLPTNTFAITGHGENK	11	7.82	0.315	704	28.5	AY232049	TRUE	TRUE	2	1958.1	0.2	14of 36	2.8768	TRUE	TRUE	::::::::::::::::
KLSVNTIPGIEEVNIIK	7	7.07	0.3	1480	46.7	AY232049	TRUE	TRUE	2	1868.2	1.6	1	3.4665	TRUE	TRUE	::::::::::::::::
KLSVNTIPGIEEVNIIK	8	7.07	0.294	2005	46.7	AY232049	TRUE	TRUE	2	1868.2	2.5	17of 32	3.0343	TRUE	TRUE	::::::::::::::::
HGVIPLSTYMR	14	9.85	0.245	844	30.03	AY232061	TRUE	TRUE	2	1274.5	1.4	17of 20	2.6548	TRUE	TRUE	::::::::::
HGVIPLSTYMR	15	9.85	0.184	916	30.03	AY232061	TRUE	TRUE	2	1274.5	2.2	13of 20	2.3527	TRUE	TRUE	::::::::::
YLDLYLIHWPMGYK	10	7.64	0.335	1786	57.33	AY232095	TRUE	TRUE	2	1813.2	2.8	15of 26	3.1356	TRUE	TRUE	::::::::::::
SALENTLSSLK	6	6.95	0.203	1371	24.7	AY232095	TRUE	TRUE	2	1163.3	1.2	15of 20	2.8577	TRUE	TRUE	::::::::::
VQDEEVGDGTTSVTVLASELLR	1	3.51	0.333	1517	50.4	AY232123	TRUE	TRUE	2	2319.5	1.4	16of 42	2.7161	TRUE	TRUE	::::::::::::::::::
SGGTLGDSFLDEGFLLDK	1	3.51	0.226	1414	47.6	AY232123	TRUE	TRUE	2	1872	1.6	17of 34	2.5305	TRUE	TRUE	::::::::::::::::
IIEELRDVLEEAGNVTPVHGK	3	4.36	0.33	1759	49.4	AY232135	TRUE	TRUE	3	2319.6	2.4	31of 80	4.6701	TRUE	TRUE	::::::::::::::::::
YVATLGVEVHPLIFHTNR	11	7.92	0.447	1140	51.9	AY232185	TRUE	TRUE	2	2067.4	0.5	19of 34	3.332	TRUE	TRUE	::::::::::::::::
HMTGEFEKKYVATLGVEVHPLIFHTNR	9	7.97	0.358	2037	61.83	AY232185	TRUE	TRUE	3	3171.6	-2.5	25of104	3.5872	TRUE	TRUE	::Oxidation_M:::::::::::::::::::::::
VCENIPIVLCGNK	7	6.14	0.256	1133	37.7	AY232185	TRUE	TRUE	2	1516.7	2.8	1	3.6601	TRUE	TRUE	::Cys_CAM::::::Cys_CAM::::
KDPNTHLIFLPTLLR	15	10.09	0.051	1437	47.9	AY232193	TRUE	TRUE	2	1779.1	0	13of 28	2.4072	TRUE	TRUE	::::::::::::::
NGVKVEEFAGANAQ	2	4.27	0.18	457	22.6	AY232202	TRUE	FALSE	2	1434.5	1.3	16of 26	3.1375	TRUE	TRUE	::::::::::::::
YLVPSDLTVGQFYFLIR	6	6.64	0.164	2308	68.7	AY232215	TRUE	TRUE	2	2032.4	-0.9	14of 32	1.6931	TRUE	TRUE	::::::::::::::::
VLLGTLGK	15	10.1	0.158	457	27.4	AY232222	TRUE	TRUE	1	801	-0.2	8of 14	1.281	TRUE	TRUE	::::::::
IEDNNTLVFLTHLR	5	5.22	0.413	1798	43.4	AY232233	TRUE	TRUE	2	1685.9	2	19of 26	3.4169	TRUE	TRUE	::::::::::::::
KIEDNNTLVFLTHLR	10	7.82	0.404	1421	41.3	AY232233	TRUE	TRUE	2	1814.1	2.7	19of 28	3.9492	TRUE	TRUE	::::::::::::::
DYDALDIANK	1	3.6	0.231	602	21.9	AY232233	TRUE	TRUE	2	1138.2	2.4	16of 18	3.416	TRUE	TRUE	::::::::::
EIKSSGGKAFGYV	14	9.63	0.122	728	22.9	AY232234	TRUE	FALSE	2	1343.5	-1.8	9of 24	1.2295	TRUE	TRUE	::::::::::::
VGDSLPAVDLFEDSPANK	1	3.51	0.313	1148	40.7	AY232240	TRUE	TRUE	2	1875	2.4	12of 34	2.5853	TRUE	TRUE	::::::::::::::::
LKDAGFDMAYTVLGQYLVLK	7	6.75	0.181	2024	65.43	BAFL-DROME	TRUE	TRUE	2	2246.7	1.8	1	2.7679	TRUE	TRUE	::::::::::::::::::
TDAYSHQGLVWR	12	7.76	0.114	1479	26.1	BT001400	TRUE	FALSE	2	1433.6	0.1	9of 22	1.7404	TRUE	TRUE	::::::::::::

TSREMQVPLSD	3	4.08	0.063	1185	21.53	BT001533	TRUE	FALSE	2	1279.4	0.8	9of 20	1.1876	TRUE	TRUE	:::::Oxidation_M::::::
VKEAGSTISRVVRLTEEKLGTTER	15	9.88	0.036	1544	40.6	BT001605	TRUE	FALSE	3	2661	0.3	12of 92	1.4211	TRUE	TRUE	::::::::::::::::::::::
KMGNSLSPTVEVTLEGDTYTLTTTSTFK	3	4.45	0.406	1711	55.83	BT012432	TRUE	TRUE	2	3023.4	-0.4	19of 54	2.7419	TRUE	TRUE	::::::::::::::::::::::::::
LGVEFDEETLDGR	1	3.51	0.394	848	32.6	BT012432	TRUE	TRUE	2	1480.6	1.9	19of 24	3.7122	TRUE	TRUE	::::::::::::
EFTDNELITTLTIGNVK	1	3.83	0.362	1357	45.4	BT012432	TRUE	TRUE	2	1909.1	2.6	20of 32	3.4347	TRUE	TRUE	::::::::::::::::
TSAISFK	14	10.1	0.153	163	15.6	BT012432	TRUE	TRUE	1	753.9	-0.1	9of 12	1.5414	TRUE	TRUE	::::::::
VYDRMVGGVEALGKQLQ	9	6.94	0.122	878	41.23	BT012434	TRUE	FALSE	3	1880.2	-1.2	18of 64	1.8319	TRUE	TRUE	:::::Oxidation_M::::::::::::
DIEEFVK	1	3.83	0.098	625	20.8	BT012447	TRUE	TRUE	1	880	1.4	8of 12	1.7001	TRUE	TRUE	::::::::
NLYENVHSK	9	7.74	0.059	433	13.1	BT012447	TRUE	TRUE	1	1104.2	-0.6	8of 16	1.4613	TRUE	TRUE	::::::::::
AHIFGQHVADYMR	11	7.91	0.469	540	29.73	BT012458	TRUE	TRUE	2	1561.8	1.5	20of 24	3.9083	TRUE	TRUE	::::::::::Oxidation_M::
SLEEEDEESFKR	2	3.89	0.247	219	18.8	BT012458	TRUE	TRUE	2	1498.5	1.9	14of 22	2.3334	TRUE	TRUE	::::::::::::
GAVDGGLNIPHSVK	12	7.82	0.189	963	24.1	BT012458	TRUE	TRUE	2	1364.5	0.7	15of 26	3.6531	TRUE	TRUE	::::::::::::::
ASIKDLEFIHHTGFIGGAK	11	7.95	0.421	1033	43.2	BT012460	TRUE	TRUE	2	2042.3	2	16of 36	3.8223	TRUE	TRUE	::::::::::::::::::
ASIKDLEFIHHTGFIGGAK	12	7.95	0.322	1380	43.2	BT012460	TRUE	TRUE	2	2042.3	0.8	15of 36	2.719	TRUE	TRUE	::::::::::::::::::
NVHPTGEILVLK	9	7.82	0.142	1500	32.3	BT012460	TRUE	TRUE	1	1320.6	-0.2	11of 22	1.6996	TRUE	TRUE	::::::::::::
NGDSLTMHYTGTLQADGK	5	5.1	0.31	1302	24.83	BT012468	TRUE	TRUE	2	1910.1	1.3	15of 34	2.6214	TRUE	TRUE	::::::::::::::::
ISSGLNYLTTSPK	15	9.72	0.274	784	27.8	BT012474	TRUE	TRUE	2	1381.6	0.4	15of 24	2.8154	TRUE	TRUE	::::::::::::::
FVKEEYVDQLTSEEGAHYAVQK	3	4.36	0.041	1319	42.7	BT012497	TRUE	TRUE	3	2571.8	-1.4	24of 84	2.2634	TRUE	TRUE	::::::::::::::::::::::
TQLAEYQKVIDEMDDAASVK	2	3.85	0.039	1892	40.53	C190-DROME	TRUE	FALSE	2	2255.5	-0.5	11of 38	1.6127	TRUE	TRUE	::::::::::::::::::::
WSLECIGRVALDTRLGCLESNLKP	6	6.33	0.109	2054	69.2	C301-DROME	TRUE	FALSE	3	2789.1	1.5	13of 92	1.2733	TRUE	TRUE	:::::Cys_CAM::::::::::Cys_CAM::::::::
AAFEQGTRGSLAQCELKAAALEREREQNGG	3	4.86	0.034	2348	47.6	C4GF-DROME	TRUE	FALSE	3	3249.5	-1	19of116	1.5613	TRUE	TRUE	:::::::::::::Cys_CAM:::::::::::::::
IKQMSKVIVDVGLRLGDAM	15	9.89	0.04	1696	54.06	C6AE-DROME	TRUE	FALSE	3	2090.5	-1.6	23of 72	2.0736	TRUE	TRUE	:::::::::::::::::::Oxidation_M:
FYMKIVQDTIDYRM	8	6.77	0.072	1999	46.26	C6AJ-DROME	TRUE	FALSE	2	1840.2	1.3	12of 26	1.5981	TRUE	TRUE	:::::::::::::Oxidation_M:
YGLFDFEYMHQCQGTSESSK	3	4.43	0.523	1619	39.23	CADF-DROME	TRUE	TRUE	2	2415.6	2.4	20of 38	4.1478	TRUE	TRUE	::::::::::Cys_CAM:::::::::
YGLFDFEYMHQCQGTSESSKK	6	5.35	0.453	1543	37.13	CADF-DROME	TRUE	TRUE	2	2543.7	0.1	18of 40	3.6995	TRUE	TRUE	::::::::::Cys_CAM:::::::::
MLYSSSFDALKK	15	9.63	0.317	836	31.73	CADF-DROME	TRUE	TRUE	2	1390.6	2	18of 22	3.3635	TRUE	TRUE	::::::::::::
MLYSSSFDALKK	14	9.63	0.305	643	31.73	CADF-DROME	TRUE	TRUE	2	1406.6	1	16of 22	2.5038	TRUE	TRUE	:Oxidation_M:::::::::::
YIQATDLSEASR	2	4.08	0.297	508	24.9	CADF-DROME	TRUE	TRUE	2	1354.5	0.4	19of 22	3.499	TRUE	TRUE	::::::::::::
MLYSSSFDALKK	13	9.63	0.283	766	31.73	CADF-DROME	TRUE	TRUE	2	1406.6	0.3	14of 22	2.6584	TRUE	TRUE	:Oxidation_M:::::::::::
QIDVETVADR	1	3.71	0.254	436	20.9	CADF-DROME	TRUE	TRUE	2	1146.2	0.3	13of 18	2.024	TRUE	TRUE	::::::::::
YVIFYIR	14	9.59	0.18	1147	36.3	CADF-DROME	TRUE	TRUE	2	974.2	1.3	11of 12	2.2734	TRUE	TRUE	::::::::
YVIFYIRDEK	7	6.89	0.147	1156	35.5	CADF-DROME	TRUE	TRUE	2	1346.6	1.1	4	2.9934	TRUE	TRUE	::::::::::
MLYSSSFDALK	6	6.68	0.045	1430	33.83	CADF-DROME	TRUE	TRUE	1	1262.5	-0.7	9of 20	1.901	TRUE	TRUE	::::::::::
LTDEEVDEMIR	1	3.51	0.362	768	29.73	CALM-DROME	TRUE	TRUE	2	1350.5	0.8	18of 20	3.921	TRUE	TRUE	::::::::::
HVMTNLGEK	9	7.82	0.207	396	15.33	CALM-DROME	TRUE	TRUE	2	1029.2	-0.2	13of 16	1.756	TRUE	TRUE	::::::::
QQEQDANVSESSPHIANIGK	3	4.43	0.229	996	22	CAPB-DROME	TRUE	TRUE	3	2153.3	2.9	23of 76	2.9445	TRUE	TRUE	::::::::::::::::::
LVQNIAGHLSNASQFLQER	10	7.85	0.513	1376	45.4	CATA-DROME	TRUE	TRUE	2	2126.4	1.8	24of 36	5.3147	TRUE	TRUE	::::::::::::::::::
LFSYSDTHR	11	7.76	0.295	414	18.4	CATA-DROME	TRUE	TRUE	2	1126.2	2.1	12of 16	2.5092	TRUE	TRUE	::::::::::
DPILFPSFIHTQK	10	7.82	0.075	1492	39.5	CATA-DROME	TRUE	TRUE	2	1543.8	2.5	15of 24	2.3562	TRUE	TRUE	::::::::::::
NSQTVSPGAITTGNGAPIGIK	14	10.1	0.04	766	32.5	CATA-DROME	TRUE	TRUE	2	1984.2	0.1	13of 40	1.8249	TRUE	TRUE	::::::::::::::::::::
LGPGGLDPADVFESLPDELK	1	3.43	0.439	1576	53.4	CC37-DROME	TRUE	TRUE	2	2070.3	0.5	22of 38	3.5815	TRUE	TRUE	::::::::::::::::::::
NIEISDDEDDTHPNIDTPSLFR	1	3.58	0.239	1017	42.5	CC37-DROME	TRUE	TRUE	2	2544.6	0.1	16of 42	2.6664	TRUE	TRUE	::::::::::::::::::::
IHRPDVFKGVGGLASDQGQEW	5	5.28	0.01	1319	42.1	CCB2-DROME	TRUE	FALSE	3	2297.5	3	18of 80	1.71	TRUE	TRUE	::::::::::::::::::::
VGGSSEVEVNEK	2	3.97	0.361	86	14.8	CH60-DROME	TRUE	TRUE	2	1234.3	1.1	17of 22	3.0271	TRUE	TRUE	::::::::::::
KISSVQSIIPALELANAQR	15	10.09	0.333	1368	48.6	CH60-DROME	TRUE	TRUE	2	2039.4	0.5	20of 36	3.5221	TRUE	TRUE	::::::::::::::::::
VSDLGQVGEVVITK	2	4.08	0.332	760	34.7	CH60-DROME	TRUE	TRUE	2	1444.7	1.3	16of 26	2.7267	TRUE	TRUE	::::::::::::::
LVQDVANNTNEEAGDGTTTATVLAR	1	3.59	0.306	637	42	CH60-DROME	TRUE	TRUE	2	2561.7	-0.6	15of 48	2.2873	TRUE	TRUE	::::::::::::::::::::::::
GYISPYFINSSK	15	9.53	0.282	996	30.4	CH60-DROME	TRUE	TRUE	2	1376.6	2.2	17of 22	3.1281	TRUE	TRUE	::::::::::::
IGLQVAAVK	15	10.1	0.263	392	27.2	CH60-DROME	TRUE	TRUE	2	899.1	1.7	15of 16	2.9951	TRUE	TRUE	::::::::::
GVMLAVETVKDNLK	8	6.99	0.261	1873	35.63	CH60-DROME	TRUE	TRUE	2	1517.8	1.1	18of 26	3.5761	TRUE	TRUE	::::::::::::::
ISADTIFVTAPHEASGGIIGVNR	5	5.22	0.476	1706	53.9	CLH-DROME	TRUE	TRUE	2	2326.6	2	23of 44	3.9885	TRUE	TRUE	::::::::::::::::::::::
ADDPSAYVDVVDVASK	1	3.43	0.352	861	30.8	CLH-DROME	TRUE	TRUE	2	1651.8	1.8	21of 30	3.4632	TRUE	TRUE	::::::::::::::::
VSQAIEGHAASFATFK	10	7.82	0.304	924	33.5	CLH-DROME	TRUE	TRUE	2	1664.9	1.3	22of 30	4.4202	TRUE	TRUE	::::::::::::::::
FDFVHDLVLYLYR	5	5.1	0.256	2453	57.2	CLH-DROME	TRUE	TRUE	2	1701	1	17of 24	2.5484	TRUE	TRUE	::::::::::::::
NLQNLLILTAIK	14	10.1	0.256	1519	46.5	CLH-DROME	TRUE	TRUE	2	1354.7	-0.2	19of 22	4.4468	TRUE	TRUE	::::::::::::
KVNYTPDYVFLLR	14	9.53	0.235	1203	42.8	CLH-DROME	TRUE	TRUE	2	1628.9	2.1	18of 24	2.9344	TRUE	TRUE	::::::::::::
LLYNNVSNFAR	15	9.85	0.235	931	33.2	CLH-DROME	TRUE	TRUE	2	1311.5	0.1	16of 20	3.248	TRUE	TRUE	::::::::::::
NLQNLLILTAIK	15	10.1	0.189	1625	46.5	CLH-DROME	TRUE	TRUE	2	1354.7	0.2	14of 22	2.588	TRUE	TRUE	::::::::::::
IDANKEPTTLFCFAVR	8	6.36	0.188	1981	44.5	CLH-DROME	TRUE	TRUE	2	1883.1	0.3	17of 30	2.8882	TRUE	TRUE	::::::::::Cys_CAM:::::
LHIIEVGAPPNGNQPFAK	10	7.82	0.167	1181	41.3	CLH-DROME	TRUE	TRUE	2	1903.2	-0.4	17of 34	3.0292	TRUE	TRUE	::::::::::::::::
NSIDGFDNFDNIALAQK	1	3.6	0.14	1101	39.4	CLH-DROME	TRUE	TRUE	2	1883	0.7	15of 32	2.0789	TRUE	TRUE	::::::::::::::::
YDTIYLITK	6	6.62	0.053	1387	31.2	CLH-DROME	TRUE	TRUE	1	1130.3	0.5	12of 16	2.309	TRUE	TRUE	::::::::::
TLQIFNIEMK	6	6.95	0.03	1722	35.53	CLH-DROME	TRUE	TRUE	1	1237.5	0.5	12of 18	2.3908	TRUE	TRUE	::::::::::
NLILVVK	14	10.1	0.026	802	30.9	CLH-DROME	TRUE	TRUE	1	799	0	10of 12	1.9124	TRUE	TRUE	::::::::
SVVAYDCAMKESAPIMVSIKVRRVCETK	13	9	0.001	1891	63.46	CLS1-DROME	TRUE	FALSE	2	3245.8	0.6	8of 54	1.015	TRUE	TRUE	::::::Cys_CAM::::::::Oxidation_M::::::::Cys_CAM::::
VTSDGTYATQSAYSLAPVAK	6	6.62	0.447	1250	36.2	COPB-DROME	TRUE	TRUE	2	2031.2	0	19of 38	3.9666	TRUE	TRUE	::::::::::::::::::
CIYNLLNSSSNAVR	13	8.9	0.181	1082	34.7	COPB-DROME	TRUE	TRUE	2	1611.8	-0.1	13of 26	1.7491	TRUE	TRUE	:Cys_CAM:::::::::::::
VTSDGTYATQSAYSLAPVAK	7	6.62	0.137	1084	36.2	COPB-DROME	TRUE	TRUE	2	2031.2	0.4	1	2.055	TRUE	TRUE	::::::::::::::::::
CIAVHPTQPLVLTSSDDMLIK	5	5.1	0.459	1724	60.23	COPP-DROME	TRUE	TRUE	2	2339.7	1.4	25of 40	4.5461	TRUE	TRUE	:Cys_CAM:::::::::::::::::::
TMYLLGYVPK	14	9.53	0.001	1198	36.03	COPP-DROME	TRUE	TRUE	1	1185.5	-0.6	11of 18	1.5478	TRUE	TRUE	::::::::::
KFDGFSNEDKPLVVQFSVK	7	7.02	0.448	1344	43.4	CRTC-DROME	TRUE	TRUE	3	2185.5	-2.7	1	4.5401	TRUE	TRUE	::::::::::::::::::
KFDGFSNEDKPLVVQFSVK	8	7.02	0.435	1872	43.4	CRTC-DROME	TRUE	TRUE	2	2185.5	1.2	24of 36	5.1515	TRUE	TRUE	::::::::::::::::::
SGTIFDNVLITDDVELAAK	1	3.51	0.258	2149	52.9	CRTC-DROME	TRUE	TRUE	2	2022.3	0.7	18of 36	2.7841	TRUE	TRUE	::::::::::::::::::
AQVCENICLYAK	7	6.14	0.444	1017	32.6	CSE1-DROME	TRUE	TRUE	2	1469.6	2.6	1	3.972	TRUE	TRUE	:::Cys_CAM:::Cys_CAM:::::
FASGDFNVINGVLQTAHSLFK	10	7.82	0.427	2115	56.5	CSE1-DROME	TRUE	TRUE	2	2266.6	1.7	18of 40	4.2334	TRUE	TRUE	::::::::::::::::::::
IFGIFGQYLER	7	6.89	0.325	1757	43.7	CSE1-DROME	TRUE	TRUE	2	1343.6	1.9	1	3.0445	TRUE	TRUE	::::::::::::
AQVCENICLYAK	8	6.14	0.316	1596	32.6	CSE1-DROME	TRUE	TRUE	2	1469.6	1.4	15of 22	3.2102	TRUE	TRUE	:::Cys_CAM:::Cys_CAM:::::
YDSLVSHALQFLSVVADR	5	5.1	0.29	2535	53	CSE1-DROME	TRUE	TRUE	2	2021.3	-1.2	23of 34	3.1662	TRUE	TRUE	::::::::::::::::::
LLHSLIDLFERPPEK	6	5.35	0.275	1802	49.3	CSE1-DROME	TRUE	TRUE	3	1808.1	1.6	29of 56	3.5322	TRUE	TRUE	::::::::::::::::
LSGILGIFQK	15	10.1	0.246	1482	36.4	CSE1-DROME	TRUE	TRUE	1	1076.3	-0.3	11of 18	2.1558	TRUE	TRUE	::::::::::::
FASGDFNVINGVLQTAHSLFK	11	7.82	0.197	1807	56.5	CSE1-DROME	TRUE	TRUE	2	2266.6	1.3	15of 40	3.0002	TRUE	TRUE	::::::::::::::::::::
FASGDFNVINGVLQTAHSLFK	9	7.82	0.142	2560	56.5	CSE1-DROME	TRUE	TRUE	3	2266.6	2	21of 80	1.9168	TRUE	TRUE	::::::::::::::::::::
VIYGSLVLVNK	15	9.72	0.042	1060	40	CSE1-DROME	TRUE	TRUE	1	1205.5	0.2	11of 20	1.8712	TRUE	TRUE	::::::::::::

ALYEQSLHIK	11	7.74	0.225	626	26.8	CSN2-DROME	TRUE	TRUE	2	1202.4	1.8	12of 18	1.6773	TRUE		TRUE	::::::::::
KTGQAAGFAYTDANK	14	9.63	0.46	122	16.8	CYC2-DROME	TRUE	TRUE	2	1543.7	1.6	20of 28	4.3362	TRUE		TRUE	::::::::::::::
MIFAGLK	14	10.1	0.104	846	28.83	CYC2-DROME	TRUE	TRUE	1	780	1	9of 12	1.8634	TRUE		TRUE	::::::::
MIFAGLK	15	10.1	0.101	911	28.83	CYC2-DROME	TRUE	TRUE	1	780	-0.2	9of 12	1.8993	TRUE		TRUE	::::::::
VTLGGLPLAIEDVNK	1	4.08	0.079	1417	44.5	CYGE-DROME	TRUE	TRUE	2	1539.8	2.9	16of 28	2.9723	TRUE		TRUE	::::::::::::::::
HVVFGEVVEGLDVVK	3	4.43	0.495	1623	44	CYPH-DROME	TRUE	TRUE	2	1626.9	1.8	24of 28	5.5904	TRUE		TRUE	::::::::::::::::
HVVFGEVVEGLDVVKK	5	5.35	0.453	1624	41.9	CYPH-DROME	TRUE	TRUE	2	1755.1	1.4	24of 30	5.1764	TRUE		TRUE	::::::::::::::::
SIYGNKFPDENFELK	3	4.45	0.374	1419	34.8	CYPH-DROME	TRUE	TRUE	2	1802	1.2	19of 28	3.9336	TRUE		TRUE	::::::::::::::::
VFFDMTADNEPLGR	1	3.71	0.334	838	39.53	CYPH-DROME	TRUE	TRUE	2	1628.8	1.2	16of 26	2.4282	TRUE		TRUE	:::::Oxidation_M::::::::::
SIYGNKFPDENFELK	4	4.45	0.294	1545	34.8	CYPH-DROME	TRUE	TRUE	2	1802	2.7	15of 28	2.5697	TRUE		TRUE	::::::::::::::::
KIIVANSGSL	14	10.1	0.254	362	26.6	CYPH-DROME	TRUE	FALSE	2	1002.2	0.8	15of 18	2.5612	TRUE		TRUE	::::::::::
KIIVANSGSL	15	10.1	0.24	243	26.6	CYPH-DROME	TRUE	FALSE	1	1002.2	2	12of 18	2.4635	TRUE		TRUE	::::::::::
YGNKFPDENFELK	3	4.45	0.214	1424	27.6	CYPH-DROME	TRUE	FALSE	2	1601.8	1	17of 24	2.6077	TRUE		TRUE	::::::::::::::
DLGLASGVANASNSPIPLGSLAHK	10	7.82	0.406	1436	50.2	D3HI-DROME	TRUE	TRUE	2	2290.6	0.9	21of 46	4.6638	TRUE		TRUE	::::::::::::::::::::::::
NIGFVGLGNMGANMASNLIK	14	10.1	0.22	1587	53.66	D3HI-DROME	TRUE	TRUE	2	2022.4	0.4	18of 38	2.7875	TRUE		TRUE	::::::::::::::::::::
AMFTNGLREQGMEVVSIEGIHPKVM	6	5.4	0.023	1891	64.29	D50922	TRUE	FALSE	3	2791.3	-2.2	10of 96	1.2223	TRUE		TRUE	:::::::::::Oxidation_M::::::::::::
SEAKKALCPLGDKYGCDAEADAAALM	3	4.21	0.092	1393	51.43	DCO2-DROME	TRUE	FALSE	3	2773	-1.3	13of100	1.2902	TRUE		TRUE	:::::::Cys_CAM:::::::Cys_CAM:::::::::Oxidation_M:
RRVLPMTISKNVSASSSFGDTSSFSNE	14	10.09	0.025	1596	47.43	DLT-DROME	TRUE	FALSE	3	2922.2	-2.5	21of104	1.6966	TRUE		TRUE	::::::Oxidation_M::::::::::::::::::::
DILEIFGFK	2	4.08	0.263	1588	38.1	DPP3-DROME	TRUE	TRUE	1	1082.3	0.9	12of 16	2.9492	TRUE		TRUE	::::::::::
YPNTDIDDLLESIVEK	1	3.43	0.239	1640	43	DPP3-DROME	TRUE	TRUE	2	1865	0.5	23of 30	3.4383	TRUE		TRUE	::::::::::::::::
FTLASLLAQAVQDIK	6	6.76	0.326	2527	49.3	DYHC-DROME	TRUE	TRUE	2	1618.9	1.5	17of 28	3.1647	TRUE		TRUE	::::::::::::::::
HVPIIYVDYPGETSLK	4	5.22	0.211	1598	43.2	DYHC-DROME	TRUE	TRUE	2	1832.1	1.9	14of 30	1.9143	TRUE		TRUE	::::::::::::::::
ASTIMMDLPVTILK	6	6.76	0.067	1930	50.16	DYHC-DROME	TRUE	FALSE	1	1549.9	-0.1	10of 26	1.4143	TRUE		TRUE	:::::Oxidation_M::::::::::
VTDMADIPNLVAKCGDQSGLPSCAR	4	4.18	0.035	1818	51.43	E2K3-DROME	TRUE	FALSE	3	2692.9	1.4	11of 96	1.0714	TRUE		TRUE	::::Oxidation_M::::::::::Cys_CAM::::::::Cys_CAM:::
VETGVLKPGTVVVFAPANITTEVK	9	7.07	0.486	1880	61	EF11-DROME	TRUE	TRUE	2	2470.9	0	25of 46	5.5615	TRUE		TRUE	::::::::::::::::::::::::
VETGVLKPGTVVVFAPANITTEVK	8	7.07	0.422	2024	61	EF11-DROME	TRUE	TRUE	2	2470.9	-0.6	28of 46	5.4541	TRUE		TRUE	::::::::::::::::::::::::
VETGVLKPGTVVVFAPANITTEVK	7	7.07	0.421	1499	61	EF11-DROME	TRUE	TRUE	2	2470.9	-0.3	1	5.4131	TRUE		TRUE	::::::::::::::::::::::::
VPSKPLCVEAFQEFPPLGR	8	6.44	0.404	2052	54.1	EF11-DROME	TRUE	FALSE	2	2172.5	0.9	17of 36	3.4476	TRUE		TRUE	:::::::Cys_CAM::::::::::::
YYVTIIDAPGHR	10	7.7	0.38	932	30.7	EF11-DROME	TRUE	TRUE	2	1405.6	2.7	17of 22	3.3059	TRUE		TRUE	::::::::::::
YYVTIIDAPGHR	11	7.7	0.373	756	30.7	EF11-DROME	TRUE	TRUE	2	1405.6	-0.8	17of 22	3.5647	TRUE		TRUE	::::::::::::
YYVTIIDAPGHRDFIK	10	7.69	0.354	1236	44.3	EF11-DROME	TRUE	TRUE	2	1909.2	0.6	16of 30	3.2008	TRUE		TRUE	::::::::::::::
EHALLAFTLGVK	10	7.82	0.345	1444	38.7	EF11-DROME	TRUE	TRUE	1	1299.6	1.6	14of 22	3.168	TRUE		TRUE	::::::::::::
EHALLAFTLGVK	11	7.82	0.188	1174	38.7	EF11-DROME	TRUE	TRUE	1	1299.6	0.5	13of 22	1.8329	TRUE		TRUE	::::::::::::
IHINIVVIGHVDSGK	11	7.97	0.08	1843	37.3	EF11-DROME	TRUE	TRUE	2	1601.9	2.1	13of 28	1.7536	TRUE		TRUE	::::::::::::::::
HVDSGKSTTTGHLIYK	13	9.63	0.057	534	17.8	EF11-DROME	TRUE	FALSE	3	1744.9	1.8	18of 60	2.4184	TRUE		TRUE	::::::::::::::::
QTVAVGVIK	14	10.1	0.055	223	22.7	EF11-DROME	TRUE	TRUE	2	915.1	1.1	9of 16	1.3765	TRUE		TRUE	::::::::::
ADLSVFDALGK	1	3.89	0.294	1070	31.2	EF1B-DROME	TRUE	TRUE	2	1136.3	1.2	18of 20	3.1334	TRUE		TRUE	::::::::::
PVGYGINK	15	9.72	0.178	481	15.8	EF1B-DROME	TRUE	FALSE	1	848	0.1	6of 14	1.1264	TRUE		TRUE	::::::::
LVPVGYGINK	14	9.72	0.085	519	28.9	EF1B-DROME	TRUE	TRUE	1	1060.3	-0.5	9of 18	1.5135	TRUE		TRUE	::::::::::
IDGVTLDDGLNSELAK	1	3.51	0.345	918	37.7	EF1D-DROME	TRUE	TRUE	2	1660.8	0.8	13of 30	2.4468	TRUE		TRUE	::::::::::::::::
SHYSPLVSEIAK	9	7.74	0.337	1396	25.3	EF1D-DROME	TRUE	TRUE	1	1331.5	-0.7	16of 22	3.4052	TRUE		TRUE	::::::::::::
FVPVAFGIQK	15	10.1	0.246	1052	35.3	EF1D-DROME	TRUE	TRUE	1	1106.4	-0.6	12of 18	2.5675	TRUE		TRUE	::::::::::
ALIAAQYSGAQVK	15	9.72	0.383	467	30.5	EF1G-DROME	TRUE	TRUE	2	1320.5	0.5	20of 24	4.8432	TRUE		TRUE	::::::::::::
LQDATFLAGER	2	4.08	0.314	600	29.4	EF1G-DROME	TRUE	TRUE	2	1221.4	0.8	16of 20	3.1508	TRUE		TRUE	::::::::::::
VKGTLYTYPENFR	14	9.53	0.201	744	31	EF1G-DROME	TRUE	FALSE	2	1588.8	1.3	14of 24	2.3686	TRUE		TRUE	::::::::::::
WFVTILNQK	15	10.1	0.183	1331	35.3	EF1G-DROME	TRUE	TRUE	1	1149.4	0.5	11of 16	2.6733	TRUE		TRUE	::::::::::
YLSEKYDYDVTEAR	2	4.07	0.44	549	28.9	EF2-DROME	TRUE	TRUE	2	1752.9	0.4	22of 26	4.0623	TRUE		TRUE	::::::::::::::
NMSVIAHVDHGK	10	7.97	0.357	296	17.83	EF2-DROME	TRUE	TRUE	2	1308.5	1.8	16of 22	3.0779	TRUE		TRUE	::::::::::::
MEMLYEGPHDDEAAIAVK	2	3.92	0.353	781	43.36	EF2-DROME	TRUE	TRUE	2	2020.3	2.2	24of 34	4.5295	TRUE		TRUE	::::::::::::::::
SFCMYILDPIYK	6	6.09	0.326	1926	48.03	EF2-DROME	TRUE	TRUE	2	1550.8	0.2	17of 22	4.3381	TRUE		TRUE	:::Cys_CAM::::::::::
GSVGFGSGLHGWAFTLK	15	10.1	0.31	1423	43.2	EF2-DROME	TRUE	TRUE	2	1722	0.1	16of 32	2.4683	TRUE		TRUE	::::::::::::::::
DLEEDHACIPLKK	3	4.54	0.3	1011	26.5	EF2-DROME	TRUE	TRUE	2	1568.7	-0.1	19of 24	4.1001	TRUE		TRUE	:::::::Cys_CAM::::::
EGILADENLR	1	3.83	0.261	584	26.6	EF2-DROME	TRUE	TRUE	1	1130.2	-0.3	10of 18	1.941	TRUE		TRUE	::::::::::
GHVFEENQVVGTPMFVVK	5	5.3	0.256	1618	46.33	EF2-DROME	TRUE	TRUE	2	2018.3	1.2	17of 34	3.0736	TRUE		TRUE	::::::::::::::::
VFDAIMNYK	6	6.68	0.233	1362	30.03	EF2-DROME	TRUE	TRUE	1	1101.3	0.4	12of 16	2.3236	TRUE		TRUE	::::::::::
ETVSEESDQMCLSK	1	3.69	0.23	372	22.63	EF2-DROME	TRUE	TRUE	2	1643.7	1.7	13of 26	2.1751	TRUE		TRUE	:::::::::Cys_CAM::::
KEEIGTLLEK	3	4.56	0.222	1116	23.1	EF2-DROME	TRUE	TRUE	2	1160.4	0.8	15of 18	3.264	TRUE		TRUE	::::::::::
ALPMPDGLPEDIDNGDVSAK	1	3.37	0.151	986	42.73	EF2-DROME	TRUE	TRUE	2	2055.3	1.5	14of 38	1.625	TRUE		TRUE	::::::::::::::::::
FYAFGR	14	9.85	0.145	567	21.9	EF2-DROME	TRUE	TRUE	1	760.9	2	8of 10	1.3446	TRUE		TRUE	::::::
CLYAAAITAK	13	8.88	0.068	707	29.1	EF2-DROME	TRUE	TRUE	2	1082.3	2.1	12of 18	1.9386	TRUE		TRUE	:Cys_CAM:::::::::
EEIGTLLEK	1	3.97	0.01	661	25.2	EF2-DROME	TRUE	TRUE	1	1032.2	0.4	10of 16	1.6449	TRUE		TRUE	::::::::::
VNQIGTVTESIAAHLLAK	10	7.82	0.519	1713	44.1	ENO-DROME	TRUE	TRUE	2	1866.2	2.4	18of 34	4.6664	TRUE		TRUE	::::::::::::::::
VNQIGTVTESIAAHLLAK	11	7.82	0.459	1434	44.1	ENO-DROME	TRUE	TRUE	2	1866.2	2	19of 34	3.746	TRUE		TRUE	::::::::::::::::
FGLDATAVGDEGGFAPNIQSNK	1	3.71	0.376	1009	42.5	ENO-DROME	TRUE	TRUE	2	2209.4	0.4	19of 42	3.4147	TRUE		TRUE	::::::::::::::::::::
GTVTESIAAHLLAK	10	7.82	0.374	1717	32.3	ENO-DROME	TRUE	FALSE	2	1411.6	2.3	16of 26	2.5036	TRUE		TRUE	::::::::::::::
EIILPVPAFNVINGGSHAGNK	11	7.82	0.308	1345	50.7	ENO-DROME	TRUE	TRUE	2	2148.5	0.2	15of 40	3.0091	TRUE		TRUE	::::::::::::::::::
HIADLAGNK	9	7.82	0.274	377	14.7	ENO-DROME	TRUE	TRUE	1	939.1	-0.4	12of 16	2.6727	TRUE		TRUE	::::::::::
KHIADLAGNKEIILPVPAFNVINGGSHAGNK	14	9.76	0.25	1580	63.3	ENO-DROME	TRUE	FALSE	3	3196.7	0.2	26of120	2.7334	TRUE		TRUE	::::::::::::::::::::::::::::
IEEEIGAGVK	2	3.97	0.16	218	22.6	ENO-DROME	TRUE	TRUE	1	1045.2	-0.5	14of 18	2.6316	TRUE		TRUE	::::::::::
EIILPVPAFNVINGGSHAGNK	10	7.82	0.108	1612	50.7	ENO-DROME	TRUE	TRUE	2	2148.5	0.2	13of 40	1.8142	TRUE		TRUE	::::::::::::::::::
EALNLISDAIAK	2	4.08	0.02	974	35.4	ENO-DROME	TRUE	TRUE	2	1258.5	1.4	18of 22	2.2563	TRUE		TRUE	::::::::::::
KHIADLAGNKEIILPVPAFNVINGGSHAGNK	15	9.76	0.013	1689	63.3	ENO-DROME	TRUE	FALSE	3	3196.7	-0.8	22of120	2.0467	TRUE		TRUE	::::::::::::::::::::::::::::
YTKDHSSLMT	10	7.74	0.027	664	14.93	EYA-DROME	TRUE	FALSE	2	1199.3	-2	11of 18	1.6362	TRUE		TRUE	:::::::::Oxidation_M::
TAHVLYHITTEAYTQK	10	7.84	0.342	828	30.7	FAS1-DROME	TRUE	TRUE	2	1877.1	0.4	18of 30	2.6208	TRUE		TRUE	::::::::::::::::
LSEGRRVGQLD	9	7.05	0.102	930	20.7	FBP1-DROME	TRUE	FALSE	2	1230.4	2.5	10of 20	1.5304	TRUE		TRUE	::::::::::::
VTVHYTGTLDDGTKFDSSR	5	5.2	0.499	1276	28.1	FKB1-DROME	TRUE	TRUE	2	2100.2	1.8	22of 36	5.339	TRUE		TRUE	::::::::::::::::::
VTVHYTGTLDDGTK	5	5.1	0.474	977	20.8	FKB1-DROME	TRUE	TRUE	2	1507.6	0.9	20of 26	3.9713	TRUE		TRUE	::::::::::::::::
GHPGVIPPNSTLTFDVELLK	5	5.22	0.265	1859	52.9	FKB1-DROME	TRUE	TRUE	2	2135.5	1.2	20of 38	3.3255	TRUE		TRUE	::::::::::::::::::::
GVQVVPIAPGDGSTYPK	6	6.68	0.125	1251	32.8	FKB1-DROME	TRUE	FALSE	2	1685.9	1.9	14of 32	1.6887	TRUE		TRUE	::::::::::::::::::
GHPGVIPPNSTLTFDVELLKVE	3	4.43	0.058	1819	59	FKB1-DROME	TRUE	FALSE	2	2363.7	0.5	13of 42	2.0365	TRUE		TRUE	::::::::::::::::::::
AKAKAEAEQMAMKAEAYR	13	9.56	0.091	1216	25.96	FLT1-DROME	TRUE	FALSE	2	2014.3	2.5	7of 34	0.8982	TRUE		TRUE	:::::::::Oxidation_M:::::::::
GTVAAEGGFLVVNGQK	7	6.95	0.466	1095	33.4	G3P1-DROME	TRUE	TRUE	2	1547.8	0.2	1	4.9494	TRUE		TRUE	::::::::::::::::
GTVAAEGGFLVVNGQK	8	6.95	0.419	1675	33.4	G3P1-DROME	TRUE	TRUE	2	1547.8	-0.4	23of 30	4.8656	TRUE		TRUE	::::::::::::::::

VINDNFEIVEGLMTTVHATTATQK	3	4.43	0.382	1931	55.33	G3P1-DROME	TRUE	TRUE	2	2634	1.1	22of 46	4.8736	TRUE	TRUE	::::::::::::::::::::::
VPTPNVSVVDLTVR	7	6.79	0.382	1307	37.1	G3P1-DROME	TRUE	TRUE	2	1496.7	0.3	1	3.491	TRUE	TRUE	::::::::::::::
FKGTVAAEGGFLVVNGQK	14	9.89	0.375	864	39.4	G3P1-DROME	TRUE	TRUE	2	1823.1	0.5	22of 34	3.746	TRUE	TRUE	::::::::::::::::::
VPTPNVSVVDLTVR	8	6.79	0.368	1855	37.1	G3P1-DROME	TRUE	TRUE	2	1496.7	0.9	19of 26	3.7445	TRUE	TRUE	::::::::::::::
VINDNFEIVEGLMTTVHATTATQK	4	4.43	0.313	2053	55.33	G3P1-DROME	TRUE	TRUE	2	2634	0	19of 46	3.9357	TRUE	TRUE	::::::::::::::::::::::
VPTPNVSVVDLTVR	9	6.79	0.308	1728	37.1	G3P1-DROME	TRUE	TRUE	2	1496.7	1.9	13of 26	2.2549	TRUE	TRUE	::::::::::::::
LISWYDNEFGYSNR	2	4.08	0.245	1052	40.3	G3P1-DROME	TRUE	TRUE	2	1764.9	2.3	11of 26	2.1203	TRUE	TRUE	::::::::::::::
FKGTVAAEGGFLVVNGQK	15	9.89	0.245	943	39.4	G3P1-DROME	TRUE	TRUE	2	1823.1	1.2	17of 34	2.5936	TRUE	TRUE	::::::::::::::::::
VPTPNVSVVDLTVR	6	6.79	0.188	1518	37.1	G3P1-DROME	TRUE	TRUE	2	1496.7	0.3	16of 26	3.1158	TRUE	TRUE	::::::::::::::
LISWYDNEFGYSNR	3	4.08	0.176	1604	40.3	G3P1-DROME	TRUE	TRUE	2	1764.9	1.4	13of 26	1.9641	TRUE	TRUE	::::::::::::::
GILGYTDEEVVSTDFLSDTHSSVFDAK	1	3.69	0.107	1685	60.7	G3P1-DROME	TRUE	TRUE	3	2934.1	1.9	19of104	1.7046	TRUE	TRUE	::::::::::::::::::::::::::
ILLSNFLAQTEALMAGK	8	6.95	0.472	2752	58.03	G6PI-DROME	TRUE	TRUE	2	1821.2	0.6	24of 32	5.3282	TRUE	TRUE	::::::::::::::::::
TFTTQETITNATSAK	6	6.95	0.385	1019	21.3	G6PI-DROME	TRUE	TRUE	2	1614.7	1.5	20of 28	4.4102	TRUE	TRUE	::::::::::::::::
KVSPFTLGALIALYEHK	15	9.63	0.335	1635	50.3	G6PI-DROME	TRUE	TRUE	3	1888.3	3	32of 64	4.306	TRUE	TRUE	::::::::::::::::::
ILLSNFLAQTEALMAGK	7	6.95	0.253	2194	58.03	G6PI-DROME	TRUE	TRUE	2	1821.2	2.2	1	2.2924	TRUE	TRUE	::::::::::::::::::
VSPFTLGALIALYEHK	11	7.74	0.162	1633	52.4	G6PI-DROME	TRUE	TRUE	3	1760.1	2.8	22of 60	1.3636	TRUE	TRUE	::::::::::::::::::
FVYSSSATVYGEPK	7	6.81	0.473	970	29.9	GALE-DROME	TRUE	TRUE	2	1535.7	1	1	4.1838	TRUE	TRUE	::::::::::::::
RPSLSVYGSDFPTHDGTGVR	10	7.76	0.443	925	31.8	GALE-DROME	TRUE	TRUE	2	2149.3	0.4	16of 38	3.8383	TRUE	TRUE	::::::::::::::::::::
DYIHIVDLAEGHVK	5	5.12	0.322	1598	34.4	GALE-DROME	TRUE	TRUE	2	1609.8	1.6	19of 26	3.7394	TRUE	TRUE	::::::::::::::
IGEDPNGEPNNLMPYIAQVAVGR	1	3.83	0.285	1320	52.33	GALE-DROME	TRUE	TRUE	2	2455.7	3	18of 44	2.7202	TRUE	TRUE	::::::::::::::::::::::
IDMVAHFAALK	10	7.82	0.241	1210	36.13	GALE-DROME	TRUE	TRUE	2	1216.5	1.2	16of 20	2.6839	TRUE	TRUE	::::::::::::
IDMVAHFAALK	11	7.82	0.212	969	36.13	GALE-DROME	TRUE	TRUE	2	1216.5	2.1	16of 20	2.694	TRUE	TRUE	::::::::::::
YFNPVGAHISGR	15	9.85	0.203	548	25.1	GALE-DROME	TRUE	TRUE	2	1318.5	0.9	14of 22	1.9358	TRUE	TRUE	::::::::::::
YFNPVGAHISGR	14	9.85	0.2	587	25.1	GALE-DROME	TRUE	TRUE	2	1318.5	0.7	15of 22	2.1854	TRUE	TRUE	::::::::::::
EGLKERFNDVIVELQQ	1	4.17	0.066	512	41.7	GAS8-DROME	TRUE	FALSE	2	1918.2	2.4	7of 30	0.8147	TRUE	TRUE	::::::::::::::
NLYTLEHNDIINALCFSPNR	5	5.22	0.476	1986	54.9	GBLP-DROME	TRUE	TRUE	2	2405.6	1.6	23of 38	6.454	TRUE	TRUE	::::::::::::::Cys_CAM::::::
EELRPEVVSPTSK	3	4.56	0.282	1076	22.9	GBLP-DROME	TRUE	FALSE	2	1471.7	0.9	15of 24	2.9339	TRUE	TRUE	::::::::::::
GTLIGHNGWVTQIATNPKDPDTIISASR	10	7.82	0.254	1417	55.3	GBLP-DROME	TRUE	TRUE	3	2964.3	0.7	29of108	3.1098	TRUE	TRUE	::::::::::::::::::::::::::
LTEIINETHENVK	3	4.54	0.296	1027	27	GPDA-DROAE	TRUE	TRUE	2	1540.7	0.3	16of 24	3.1992	TRUE	TRUE	::::::::::::
ELFSLFNHK	11	7.82	0.257	1104	28.5	GS1-DROME	TRUE	TRUE	1	1135.3	1.1	8of 16	1.6065	TRUE	TRUE	::::::::::
IVEMAASGVRPCVI	5	6.29	0.072	1506	44.03	GSBN-DROME	TRUE	FALSE	2	1518.8	-2.7	7of 26	1.0207	TRUE	TRUE	:::Oxidation_M::::::::Cys_CAM:::
GTLYQSFANYYYPQVFAK	15	9.3	0.342	1607	50.8	GTT1-DROER	TRUE	FALSE	2	2161.4	0.5	15of 34	2.1185	TRUE	TRUE	::::::::::::::::::
AIQVYLVEK	8	6.87	0.313	1644	31	GTT1-DROER	TRUE	TRUE	2	1063.3	-0.2	13of 16	3.1682	TRUE	TRUE	::::::::::
APADPEAFKK	9	6.99	0.244	408	15.2	GTT1-DROER	TRUE	TRUE	2	1074.2	1.7	16of 18	2.387	TRUE	TRUE	::::::::::
LYFDMGTLYQSFANYYYPQVFAK	6	6.51	0.213	2242	77.23	GTT1-DROER	TRUE	TRUE	2	2847.2	1.1	15of 44	1.8349	TRUE	TRUE	:::::Oxidation_M:::::::::::::::::
LLNLQAGEHLKPEFLK	10	7.8	0.428	1334	47.7	GTT1-DROMA	TRUE	TRUE	2	1851.2	-0.3	17of 30	5.081	TRUE	TRUE	::::::::::::::::
LLNLQAGEHLKPEFLK	11	7.8	0.315	1093	47.7	GTT1-DROMA	TRUE	TRUE	2	1851.2	0.8	18of 30	3.8497	TRUE	TRUE	::::::::::::::::
KLLNLQAGEHLKPEFLK	14	9.76	0.254	1027	45.6	GTT1-DROMA	TRUE	TRUE	3	1979.4	2.1	24of 64	2.922	TRUE	TRUE	::::::::::::::::::
NLQAGEHLKPEFLK	10	7.8	0.166	1353	31.5	GTT1-DROMA	TRUE	FALSE	2	1624.9	1.6	18of 26	3.8542	TRUE	TRUE	::::::::::::::
VDFYYLPGSSPCR	6	6.09	0.027	1488	35.8	GTT1-DROME	TRUE	FALSE	2	1561.7	0.7	12of 24	1.6671	TRUE	TRUE	::::::::::Cys_CAM::
AFTTGQFGSEEDYKK	3	4.45	0.348	1065	21.5	GTT3-DROME	TRUE	TRUE	2	1708.8	1.7	18of 28	3.2492	TRUE	TRUE	::::::::::::::
LNPQHTIPTLVDNGFAIWESR	5	5.22	0.313	2099	57.1	GTT4-DROME	TRUE	TRUE	2	2409.7	2.4	22of 40	3.8501	TRUE	TRUE	::::::::::::::::::::
FSAIHEFQNLHAVAK	10	7.97	0.333	1132	36.7	GYS-DROME	TRUE	TRUE	2	1712.9	2	15of 28	2.9773	TRUE	TRUE	::::::::::::::
DNIQGITKPAIR	15	10.09	0.104	215	23.5	H4-DROME	TRUE	TRUE	2	1326.5	0.7	12of 22	2.0646	TRUE	TRUE	::::::::::::
VCYYYDSDIGNYYYGQGHPMKPHR	11	7.29	0.259	844	43.63	HDA1-DROME	TRUE	TRUE	3	2985.2	1.3	24of 92	2.6968	TRUE	TRUE	::Cys_CAM:::::::::::::::::::::
YNLPFLMVGGGGYTIR	15	9.59	0.043	1654	51.83	HDA1-DROME	TRUE	TRUE	2	1759.1	1.4	14of 30	1.5115	TRUE	TRUE	::::::::::::::::
YNLPFLMVGGGGYTIR	14	9.59	0.041	1542	51.83	HDA1-DROME	TRUE	TRUE	2	1759.1	0.3	16of 30	1.7666	TRUE	TRUE	::::::::::::::::
CVALSQLLTEQNFPAIGIHR	9	7.16	0.375	2053	58.8	HE47-DROME	TRUE	TRUE	2	2268.6	0.1	22of 38	4.4882	TRUE	TRUE	:Cys_CAM:::::::::::::::::::
GTYVSIHSSGFR	15	9.85	0.273	216	21.9	HE47-DROME	TRUE	TRUE	2	1311.4	2.7	17of 22	2.292	TRUE	TRUE	::::::::::::
LTLHGLQQHYVNLK	15	9.72	0.255	924	35.4	HE47-DROME	TRUE	TRUE	2	1664.9	1.6	16of 26	2.459	TRUE	TRUE	::::::::::::::
DFLLKPEILR	7	7.02	0	1375	40.4	HE47-DROME	TRUE	TRUE	2	1244.5	1.2	21	2.5175	TRUE	TRUE	::::::::::
EGASLPFFASGVSAVIHPR	10	7.85	0.435	1664	49.1	HEM6-DROME	TRUE	TRUE	2	1943.2	2.7	18of 36	3.4154	TRUE	TRUE	::::::::::::::::::::
EGASLPFFASGVSAVIHPR	11	7.85	0.384	1380	49.1	HEM6-DROME	TRUE	TRUE	2	1943.2	2.5	17of 36	3.3186	TRUE	TRUE	::::::::::::::::::::
YESILMSLPLHAR	10	7.77	0.352	1392	43.73	HEM6-DROME	TRUE	TRUE	2	1546.8	2	17of 24	3.1385	TRUE	TRUE	:::::Oxidation_M:::::::
AVIPSYVPLVR	15	9.85	0.093	1152	40.2	HEM6-DROME	TRUE	TRUE	2	1214.5	1.5	13of 20	2.2938	TRUE	TRUE	::::::::::::
SPSIYNPYISTLAALR	13	9.59	0.055	691	46.8	HLES-DROME	TRUE	FALSE	3	1767	-1.5	17of 60	1.986	TRUE	TRUE	::::::::::::::::
CGDHPAAIISNVHHPQHSMYQPSS	8	6.48	0.015	1800	32.63	HLES-DROME	TRUE	FALSE	3	2671.9	-2.5	9of 92	0.9677	TRUE	TRUE	:Cys_CAM:::::::::::::::::::::
IKAQQQETDLLHMQQRIDELMKSTA	6	5.39	0.029	2605	50.86	HOOK-DROVI	TRUE	FALSE	3	2989.4	2.2	15of 96	1.436	TRUE	TRUE	::::::::::::Oxidation_M::::::::Oxidation_M::::::
SPIYELGLGLHPHSR	10	7.92	0.161	1165	35.7	HS26-DROME	TRUE	TRUE	2	1676.9	1.9	18of 28	4.0402	TRUE	TRUE	::::::::::::::::
SQIHDIVLVGGSTR	9	7.85	0.139	1405	30.2	HS68-DROME	TRUE	TRUE	2	1482.7	0.6	16of 26	2.4875	TRUE	TRUE	::::::::::::::
DAKMDKSQIHDIVLVGGSTR	9	7.79	0.043	1616	33.93	HS68-DROME	TRUE	TRUE	3	2187.5	-2.8	17of 76	2.6556	TRUE	TRUE	:::::Oxidation_M:::::::::::::::
IINEPTAAALAYGLDK	2	4.08	0.346	972	44.5	HS71-DROSI	TRUE	TRUE	2	1660.9	1.9	19of 30	3.7699	TRUE	TRUE	::::::::::::::::
GQIHDIVLVGGSTR	10	7.85	0.3	1173	30.2	HS71-DROSI	TRUE	TRUE	1	1452.7	0.4	14of 26	2.5561	TRUE	TRUE	::::::::::::::
VEIIANDQGNR	2	4.08	0.086	189	21.1	HS71-DROSI	TRUE	FALSE	2	1229.3	0.4	15of 20	3.2483	TRUE	TRUE	::::::::::::
SINPDEAVAYGAAVQAAILHGDK	3	4.3	0.406	1863	47.5	HS7A-DROME	TRUE	TRUE	3	2311.6	-0.2	30of 88	3.3455	TRUE	TRUE	::::::::::::::::::::
ITPSYVAFTADGER	2	4.08	0.448	709	32.5	HS7C-DROME	TRUE	TRUE	2	1527.7	0.7	19of 26	3.4415	TRUE	TRUE	::::::::::::::
SQVFSTASDNQHTVTIQVYEGERPMTK	6	5.35	0.389	1243	43.13	HS7C-DROME	TRUE	TRUE	3	3071.3	2.9	33of104	4.6943	TRUE	TRUE	::::::::::::::::::::::Oxidation_M:::
VFAPEEISAMVLGK	2	4.27	0.336	1289	44.83	HS7C-DROME	TRUE	TRUE	2	1491.8	1.6	22of 26	4.193	TRUE	TRUE	::::::::::::::
TKLESAIDESIK	3	4.45	0.314	1155	23.3	HS7C-DROME	TRUE	TRUE	2	1334.5	1.7	18of 22	3.6827	TRUE	TRUE	::::::::::::
AKFEELNLDLFR	3	4.45	0.288	1695	41.6	HS7C-DROME	TRUE	TRUE	2	1495.7	2.1	18of 22	3.6669	TRUE	TRUE	::::::::::::
VTHAVVTVPAYFNDAQR	10	7.76	0.283	1096	38.7	HS7C-DROME	TRUE	TRUE	2	1889.1	1.9	17of 32	3.451	TRUE	TRUE	::::::::::::::::
DVHEIVLVGGSTR	5	5.22	0.225	1313	29.1	HS7C-DROME	TRUE	TRUE	2	1382.6	0.4	17of 24	3.5112	TRUE	TRUE	::::::::::::
ITPSYVAFTADGER	3	4.08	0.156	1307	32.5	HS7C-DROME	TRUE	TRUE	2	1527.7	1.6	15of 26	1.6536	TRUE	TRUE	::::::::::::
DLEAIVQPVIAK	1	4.08	0.152	1020	38.1	HS7C-DROME	TRUE	TRUE	1	1296.5	-0.1	16of 22	2.9431	TRUE	TRUE	::::::::::::
DLEAIVQPVIAK	2	4.08	0.145	1001	38.1	HS7C-DROME	TRUE	TRUE	1	1296.5	2.6	14of 22	1.9521	TRUE	TRUE	::::::::::::
FDLTGIPPAPR	6	6.79	0.04	1395	31.6	HS7C-DROME	TRUE	TRUE	1	1184.4	0.5	11of 20	1.557	TRUE	TRUE	::::::::::::
KTFFPEEISSMVLTK	7	7.07	0.391	1560	43.03	HS7D-DROME	TRUE	TRUE	2	1758.1	1.2	1	4.6486	TRUE	TRUE	::::::::::::::::
LVTHFVQEFK	10	7.82	0.374	1036	31.8	HS7D-DROME	TRUE	TRUE	2	1248.5	1.9	16of 18	3.3477	TRUE	TRUE	::::::::::::
FEELNADLFR	2	3.83	0.298	992	35.6	HS7D-DROME	TRUE	TRUE	2	1254.4	0.4	15of 18	3.0714	TRUE	TRUE	::::::::::::
SVIHDIVLVGGSTR	9	7.85	0.298	1618	35.2	HS7D-DROME	TRUE	TRUE	1	1453.7	0.2	16of 26	2.9049	TRUE	TRUE	::::::::::::::
TTPSYVAFTDTER	3	4.08	0.295	1219	24.5	HS7D-DROME	TRUE	TRUE	2	1488.6	2.8	14of 24	2.4796	TRUE	TRUE	::::::::::::::
TTPSYVAFTDTER	2	4.08	0.276	632	24.5	HS7D-DROME	TRUE	TRUE	2	1488.6	1.5	16of 24	2.1878	TRUE	TRUE	::::::::::::::
DAGTIAGLNVLR	6	6.79	0.249	1471	31.8	HS7D-DROME	TRUE	TRUE	2	1200.4	2	19of 22	3.2994	TRUE	TRUE	::::::::::::

ARFEELNADLFR	3	4.45	0.248	1483	37	HS7D-DROME	TRUE	TRUE	2	1481.7	2.1	18of 22	3.3237	TRUE		TRUE	::::::::::::
LVTHFVQEFK	11	7.82	0.235	804	31.8	HS7D-DROME	TRUE	TRUE	2	1248.5	0.7	13of 18	2.0219	TRUE		TRUE	::::::::::
SVIHDIVLVGGSTR	10	7.85	0.233	1172	35.2	HS7D-DROME	TRUE	TRUE	2	1453.7	0	18of 26	3.5668	TRUE		TRUE	::::::::::::::
LLQDLFNGK	7	6.76	0.23	1233	29.7	HS7D-DROME	TRUE	TRUE	2	1048.2	2.9	3	2.7349	TRUE		TRUE	::::::::
HWPFEVVSADGKPK	9	7.8	0.18	1585	27.5	HS7D-DROME	TRUE	TRUE	2	1597.8	1.6	11of 26	1.6258	TRUE		TRUE	::::::::::::::
LLQDLFNGK	6	6.76	0.121	1487	29.7	HS7D-DROME	TRUE	TRUE	1	1048.2	0.3	11of 16	2.2748	TRUE		TRUE	::::::::::
FELSGIPPAPR	6	6.98	0.06	1346	31.7	HS7D-DROME	TRUE	TRUE	2	1184.4	0.5	13of 20	1.7376	TRUE		TRUE	::::::::::::
QAVTNSANTFYATK	14	9.72	0.346	266	21.9	HS7E-DROME	TRUE	TRUE	2	1516.7	1.3	17of 26	3.4413	TRUE		TRUE	::::::::::::::
VYSPSQIGAFILMK	15	9.72	0.26	1571	47.33	HS7E-DROME	TRUE	TRUE	2	1554.9	1.3	19of 26	3.9155	TRUE		TRUE	::::::::::::::
TAGTLTIIDTGIGMTK	6	6.76	0.402	1634	38.33	HS83-DROAV	TRUE	TRUE	2	1593.9	1.7	23of 30	3.6325	TRUE		TRUE	::::::::::::::::
DQVSNSAFVER	2	4.08	0.401	229	19.8	HS83-DROAV	TRUE	TRUE	2	1252.3	0.5	16of 20	3.4601	TRUE		TRUE	::::::::::::
GFEVVYMTEPIDEYVIQHLK	2	4.16	0.379	1532	62.23	HS83-DROAV	TRUE	TRUE	2	2411.8	1.8	21of 38	4.3974	TRUE		TRUE	::::::::::::::::::::
NPDDISQEEYGEFYK	1	3.51	0.372	728	27.1	HS83-DROAV	TRUE	TRUE	2	1834.9	2	23of 28	5.1046	TRUE		TRUE	::::::::::::::::
TMELIEELTEDKENYKK	2	4.2	0.357	932	33.63	HS83-DROAV	TRUE	TRUE	2	2114.4	1.4	18of 32	4.6118	TRUE		TRUE	::::::::::::::::
HFSVEGQLEFR	5	5.3	0.357	1414	28.4	HS83-DROAV	TRUE	TRUE	2	1349.5	1.9	18of 20	3.341	TRUE		TRUE	::::::::::::
IKEDQTDYLEESK	2	3.93	0.317	231	19.9	HS83-DROAV	TRUE	FALSE	2	1598.7	1.7	22of 24	3.8169	TRUE		TRUE	::::::::::::::
KQLEINPDHPIVETLR	6	5.35	0.314	1256	37.6	HS83-DROAV	TRUE	TRUE	2	1903.2	0.2	19of 30	3.7715	TRUE		TRUE	::::::::::::::::
HFSVEGQLEFR	4	5.3	0.31	1445	28.4	HS83-DROAV	TRUE	TRUE	2	1349.5	1.3	18of 20	3.7564	TRUE		TRUE	::::::::::::
DQVSNSAFVER	1	4.08	0.3	296	19.8	HS83-DROAV	TRUE	TRUE	2	1252.3	0.7	15of 20	3.3198	TRUE		TRUE	::::::::::::
RTPFDLFENQK	7	7.02	0.279	1235	24.9	HS83-DROAV	TRUE	TRUE	2	1395.6	0.6	7	4.3499	TRUE		TRUE	::::::::::::
SDLVNNLGTIAK	6	6.76	0.25	1282	27.7	HS83-DROAV	TRUE	TRUE	1	1245.4	-0.5	12of 22	1.6273	TRUE		TRUE	::::::::::::
QLEINPDHPIVETLR	3	4.43	0.248	1395	39.7	HS83-DROAV	TRUE	TRUE	2	1775	1.5	17of 28	2.9487	TRUE		TRUE	::::::::::::::
HVYFITGESK	9	7.74	0.238	1229	22.1	HS83-DROAV	TRUE	TRUE	1	1181.3	-0.6	13of 18	3.049	TRUE		TRUE	::::::::::
GFEVVYMTEPIDEYVIQHLK	3	4.16	0.095	2106	62.23	HS83-DROAV	TRUE	TRUE	2	2411.8	1.3	15of 38	1.9059	TRUE		TRUE	::::::::::::::::::::
ELISNASDALDK	1	3.71	0	562	26	HS83-DROAV	TRUE	TRUE	1	1276.4	1.9	12of 22	2.9423	TRUE		TRUE	::::::::::::
HSQFIGYPIK	13	9.72	0	791	24.8	HS83-DROAV	TRUE	TRUE	2	1190.4	0.8	11of 18	1.7879	TRUE		TRUE	::::::::::
HSQFIGYPIK	14	9.72	0	598	24.8	HS83-DROAV	TRUE	TRUE	1	1190.4	-0.8	13of 18	2.6195	TRUE		TRUE	::::::::::
HSQFIGYPIK	15	9.72	0	384	24.8	HS83-DROAV	TRUE	TRUE	1	1190.4	-0.5	12of 18	2.085	TRUE		TRUE	::::::::::
FHTSASGDDFCSLADYVSR	2	4.17	0.524	956	37.9	HS83-DROME	TRUE	TRUE	2	2136.2	0.5	25of 36	5.7702	TRUE		TRUE	:::::::::Cys_CAM::::::::
HSQFIGYPXK	15	9.72	0.438	451	17.4	HS83-DROPB	TRUE	TRUE	2	1190.4	2.1	12of 18	2.1035	TRUE		TRUE	::::::::::
HSQFIGYPXK	14	9.72	0.368	558	17.4	HS83-DROPB	TRUE	TRUE	2	1190.4	2.9	15of 18	3.759	TRUE		TRUE	::::::::::
ADIECSCYGYEGIDAVK	1	3.59	0.011	737	37.9	IF2A-DROME	TRUE	TRUE	2	1951	2	11of 32	1.8342	TRUE		TRUE	:::::Cys_CAM::Cys_CAM::::::::::
LFFLQCESCGSR	7	6.14	0.412	1275	37.5	IF2B-DROME	TRUE	TRUE	2	1504.6	2.3	1	3.3298	TRUE		TRUE	::::::Cys_CAM:::Cys_CAM::::
FVQGTVAEGAPIIPISAQLK	6	6.95	0.175	1670	57.4	IF2G-DROME	TRUE	TRUE	2	2040.4	2.1	14of 38	2.6981	TRUE		TRUE	::::::::::::::::::
IVSLFAEQNELQYAVPGGLIGVGTK	3	4.27	0.035	1968	71.8	IF2G-DROME	TRUE	TRUE	2	2605	0	13of 48	2.0159	TRUE		TRUE	::::::::::::::::::::::
VGQEIEVRPGVVTK	9	7.1	0.009	1158	29.1	IF2G-DROME	TRUE	TRUE	2	1511.8	1.8	13of 26	2.6571	TRUE		TRUE	::::::::::::::
GHFGPINSLAFHPDGK	11	7.97	0.398	888	30.2	IF32-DROME	TRUE	TRUE	2	1694.9	1.1	20of 30	4.0379	TRUE		TRUE	::::::::::::::
LGHVVMGTQPLSPYQQLVEK	10	7.74	0.396	1306	50.23	IF36-DROME	TRUE	TRUE	2	2225.6	0.6	18of 38	3.2638	TRUE		TRUE	::::::::::::::::::
HLTFPLLEFLCGK	8	7.16	0.355	2611	50.5	IF36-DROME	TRUE	TRUE	2	1575.9	0.9	18of 24	2.9775	TRUE		TRUE	:::::::::Cys_CAM:::
SLTSLPHTDFVMAK	10	7.82	0.045	1025	35.63	IF3B-DROME	TRUE	TRUE	2	1563.8	1.7	13of 26	1.601	TRUE		TRUE	:::::::::::Oxidation_M:::
VLITTDLLAR	7	6.79	0.374	1303	39.5	IF4A-DROME	TRUE	TRUE	2	1115.4	2.7	1	2.9885	TRUE		TRUE	::::::::::
VVMALGEYMK	7	6.87	0.36	1209	34.46	IF4A-DROME	TRUE	TRUE	1	1141.4	-0.5	1	2.442	TRUE		TRUE	::::::::::
GIYGYGFEKPSAIQQR	15	9.53	0.347	819	33.5	IF4A-DROME	TRUE	TRUE	2	1815	0.1	16of 30	2.9503	TRUE		TRUE	::::::::::::::
KEELTLEGIK	3	4.56	0.211	1151	23.1	IF4A-DROME	TRUE	TRUE	2	1160.4	0.4	16of 18	3.0315	TRUE		TRUE	::::::::::
LFVLDEADEMLSR	1	3.59	0.13	1422	46.73	IF4A-DROME	TRUE	TRUE	2	1538.8	-1.2	14of 24	2.3154	TRUE		TRUE	::::::::::::
QFYVNVK	14	9.72	0.094	392	19.9	IF4A-DROME	TRUE	TRUE	2	898	1.8	10of 12	1.3952	TRUE		TRUE	::::::::
DQIQDVFK	1	3.89	0.074	650	18.8	IF4A-DROME	TRUE	TRUE	1	993.1	-0.2	9of 14	1.5298	TRUE		TRUE	::::::::
VHMVGIDIFSNK	10	7.82	0.381	1333	33.43	IF5A-DROME	TRUE	TRUE	2	1360.6	0.3	19of 22	3.653	TRUE		TRUE	::::::::::::
LDFDSGKDLLCTVLK	2	4.18	0.257	1250	44.7	IF5A-DROME	TRUE	TRUE	2	1725	2.2	19of 28	4.2006	TRUE		TRUE	:::::::::Cys_CAM:::::
ACGEECVIAIK	2	4.27	0.211	480	28.9	IF5A-DROME	TRUE	TRUE	1	1250.4	-0.8	12of 20	2.2739	TRUE		TRUE	::Cys_CAM:::Cys_CAM:::::
DLLCTVLK	6	6.1	0.083	1498	30.6	IF5A-DROME	TRUE	TRUE	1	962.1	-0.2	9of 14	1.6742	TRUE		TRUE	::::Cys_CAM:::::
QTIADNSLVGSYAVLSNQGGMVHPK	10	7.74	0.264	1349	48.83	IF6-DROME	TRUE	TRUE	3	2587.9	1.7	30of 96	3.9869	TRUE		TRUE	::::::::::::::::::::::::
LAATTALHNSLEFTK	10	7.82	0.397	1133	36.3	IMB-DROME	TRUE	TRUE	2	1617.8	1.3	17of 28	3.4335	TRUE		TRUE	::::::::::::::::
GALQFLTPVLVEK	8	6.95	0.118	2223	45.8	IMB-DROME	TRUE	TRUE	2	1415.7	2.8	17of 24	2.6775	TRUE		TRUE	::::::::::::::
GKLPIVNQAGELVAMIAR	15	10.09	0.177	1713	51.93	IMDH-DROME	TRUE	TRUE	2	1881.3	1.9	16of 34	1.998	TRUE		TRUE	::::::::::::::::
SELDDLDSNQVAEEAPSAIVR	1	3.38	0.302	929	43.7	IML2-DROME	TRUE	TRUE	2	2259.4	1.3	16of 40	2.6206	TRUE		TRUE	::::::::::::::::::::
CCLKSCTMDEVLRYCAAK	9	7.84	0.155	1361	42.53	INL3-DROME	TRUE	FALSE	3	2266.5	3	20of 68	1.7974	TRUE		TRUE	:Cys_CAM:Cys_CAM:::Cys_CAM::::::::Cys_CAM::::
TADGQLQVHPQTTSLK	10	7.82	0.471	404	22.6	INO1-DROME	TRUE	TRUE	2	1724.9	2	21of 30	3.9404	TRUE		TRUE	::::::::::::::::
FDFSTITNEPPLKR	7	7.02	0.388	1319	34.7	INO1-DROME	TRUE	TRUE	2	1665.9	0	1	3.3289	TRUE		TRUE	::::::::::::::
MKPTNNSTLEVISPK	13	9.89	0.378	598	26.53	INO1-DROME	TRUE	FALSE	2	1675.9	0.5	19of 28	3.2747	TRUE		TRUE	:Oxidation_M:::::::::::::
PSIYDPDFIAANQSDR	1	3.6	0.352	869	34.4	INO1-DROME	TRUE	TRUE	2	1809.9	1.2	20of 30	3.6053	TRUE		TRUE	::::::::::::::::
RAEVLDVALQDQIYDQLAQLRPR	3	4.46	0.338	1893	62.2	INO1-DROME	TRUE	TRUE	3	2712.1	2	34of 88	4.4218	TRUE		TRUE	::::::::::::::::::::
TADGQLQVHPQTTSLK	9	7.82	0.279	1054	22.6	INO1-DROME	TRUE	TRUE	2	1724.9	0.7	18of 30	3.0771	TRUE		TRUE	::::::::::::::::
VQVDDEFITTDYDYQTSHVK	2	3.77	0.258	848	38.8	INO1-DROME	TRUE	TRUE	3	2404.5	2.4	20of 76	2.8202	TRUE		TRUE	::::::::::::::::::
MKPTNNSTLEVISPK	14	9.89	0.213	352	26.53	INO1-DROME	TRUE	FALSE	2	1659.9	-0.2	17of 28	2.3657	TRUE		TRUE	::::::::::::::::
NVFIAGDDFK	1	3.89	0.205	840	28.1	INO1-DROME	TRUE	TRUE	1	1126.3	0.6	13of 18	2.1377	TRUE		TRUE	::::::::::
YVPYVGDSKR	14	9.53	0.118	138	18.1	INO1-DROME	TRUE	TRUE	2	1184.3	0.1	11of 18	2.2026	TRUE		TRUE	::::::::::
IIAIDVNDPLASK	2	3.89	0.267	969	38.8	IPYR-DROME	TRUE	TRUE	2	1369.6	1.4	19of 24	3.4602	TRUE		TRUE	::::::::::::
TIYNMVVEVPR	6	6.89	0.235	1510	34.93	IPYR-DROME	TRUE	TRUE	2	1321.6	1.3	15of 20	2.8813	TRUE		TRUE	::::::::::::
NSPSYSLYFK	13	9.53	0.157	954	23.9	IPYR-DROME	TRUE	TRUE	1	1206.3	1.6	10of 18	2.5182	TRUE		TRUE	::::::::::
VNDIADVDQYFPGLLR	1	3.6	0.129	1460	49.4	IPYR-DROME	TRUE	TRUE	2	1836.1	0.8	12of 30	1.9559	TRUE		TRUE	::::::::::::::::
NSPSYSLYFK	14	9.53	0.114	823	23.9	IPYR-DROME	TRUE	TRUE	1	1206.3	0	10of 18	1.8554	TRUE		TRUE	::::::::::
VYGYSQGFGK	14	9.53	0.169	354	19.2	JANA-DROER	TRUE	TRUE	2	1106.2	1.3	12of 18	1.9645	TRUE		TRUE	::::::::::
AMLSGPGQFAENEANEVHFR	4	4.54	0.354	1654	41.63	JC5794	TRUE	TRUE	2	2205.4	1	22of 38	3.4822	TRUE		TRUE	::::::::::::::::::
IYLPK	14	9.72	0.034	190	19.9	JC6316	TRUE	FALSE	1	633.8	-0.2	6of 8	1.6091	TRUE		TRUE	::::::
QITSAAFGGPNLDILYVTTAAK	6	6.68	0.515	1954	57.3	JC7250	TRUE	TRUE	2	2252.6	2.3	24of 42	5.3317	TRUE		TRUE	::::::::::::::::::::
VTGLNATGYPGVNLK	14	9.72	0.344	816	32	JC7250	TRUE	TRUE	2	1504.7	0.6	19of 28	3.2577	TRUE		TRUE	::::::::::::::::
SYDYDFETGVASNPK	1	3.71	0.329	657	24.9	JC7250	TRUE	TRUE	2	1693.8	1.6	19of 28	3.5119	TRUE		TRUE	::::::::::::::::
VTGLNATGYPGVNLKV	14	9.72	0.295	1059	37	JC7250	TRUE	FALSE	2	1603.9	0.8	14of 30	3.0919	TRUE		TRUE	::::::::::::::::
VTGLNATGYPGVNLK	15	9.72	0.043	883	32	JC7250	TRUE	TRUE	1	1504.7	-0.7	13of 28	1.7054	TRUE		TRUE	::::::::::::::::
VTGLNATGYPGVNLKV	15	9.72	0.029	1131	37	JC7250	TRUE	FALSE	1	1603.9	-0.9	13of 30	1.7554	TRUE		TRUE	::::::::::::::::
YMGLSFTTISASGPNGSVIHYHPK	14	9.53	0.391	1144	49.43	JC7827	TRUE	TRUE	2	2565.9	2	16of 46	3.8097	TRUE		TRUE	::::::::::::::::::::::
NDVEIAGFINSHIR	5	5.22	0.373	1658	34.3	JC7827	TRUE	TRUE	2	1585.8	2.2	23of 26	4.245	TRUE		TRUE	::::::::::::::

DKYMGLSFTTISASGPNGSVIHYHPK	14	9.47	0.372	1071	47.53	JC7827	TRUE	TRUE	3	2809.2	2.9	32of100	4.1906	TRUE	TRUE	::::::::::::::::::::::::
VEDIVQIVPGQVAHNFSNR	5	5.22	0.36	1662	43.9	JC7827	TRUE	TRUE	2	2123.4	1.9	20of 36	4.7103	TRUE	TRUE	::::::::::::::::::
LLNSYHQQVWDTLSPILSR	10	7.76	0.306	1662	57	JC7827	TRUE	TRUE	2	2271.6	1.6	17of 36	2.8546	TRUE	TRUE	::::::::::::::::::
IWIAPTSSYYLTALIPK	15	9.53	0.297	1805	62.9	JC7827	TRUE	TRUE	2	1938.3	1.2	22of 32	3.0373	TRUE	TRUE	::::::::::::::::
LPTDFVQHQK	11	7.82	0.283	484	19.8	JC7827	TRUE	TRUE	2	1213.4	2	13of 18	2.1549	TRUE	TRUE	::::::::::
AIKNDVEIAGFINSHIR	11	7.82	0.253	1133	41.6	JC7827	TRUE	TRUE	2	1898.2	1.8	16of 32	2.874	TRUE	TRUE	::::::::::::::::
GQLSFGSTVFPAK	15	10.1	0.108	1064	31	JC7827	TRUE	TRUE	1	1339.5	-0.5	13of 24	1.9453	TRUE	TRUE	::::::::::::::
IWIAPTSSYYLTALIPK	14	9.53	0.024	1709	62.9	JC7827	TRUE	TRUE	2	1938.3	0.3	16of 32	2.2859	TRUE	TRUE	::::::::::::::::
NTRNEISEMNRAIQRLQAEI	7	7.21	0.006	1352	39.93	K2C7	TRUE	FALSE	3	2387.7	-2.5	42	2.1487	TRUE	TRUE	::::::::::::::::::
SPDTATLLGIVSR	6	6.79	0.302	1623	32.8	K6PF-DROME	TRUE	TRUE	2	1330.5	1.6	17of 24	2.4985	TRUE	TRUE	::::::::::::
ALDYCHSMGIMHR	12	7.32	0.405	1007	30.66	KC2A-DROME	TRUE	TRUE	2	1591.8	1.7	16of 24	2.7885	TRUE	TRUE	:::::Cys_CAM::::::::
FVHSDNQHLVSPEALDFLDK	3	4.43	0.24	1584	48.9	KC2A-DROME	TRUE	TRUE	3	2312.5	2.7	30of 76	3.6285	TRUE	TRUE	::::::::::::::::::
GGTNIITLLAVVKDPVSR	15	10.09	0.116	1575	47.5	KC2A-DROME	TRUE	TRUE	3	1854.2	0.2	26of 68	2.3018	TRUE	TRUE	::::::::::::::::::
YYLFELLK	6	6.81	0.009	1947	40.4	KC2A-DROME	TRUE	TRUE	1	1089.3	-0.2	10of 14	1.6187	TRUE	TRUE	::::::::
FHDILQR	9	7.85	0.004	1257	21.1	KC2A-DROME	TRUE	TRUE	1	929.1	-0.1	8of 12	1.6035	TRUE	TRUE	::::::::
GYIKITDFGF	6	6.68	0.031	1240	33.8	KDC1-DROME	TRUE	FALSE	1	1161.3	2.6	4of 18	0.5809	TRUE	TRUE	::::::::::
QVRSASFDEMQ	3	4.08	0.054	950	20.93	KDGE-DROME	TRUE	FALSE	2	1298.4	2	9of 20	1.4653	TRUE	TRUE	::::::::::
HLCSVHRNV	12	9.02	0.087	861	15.1	KEN-DROME	TRUE	FALSE	2	1122.2	0.2	9of 16	1.2632	TRUE	TRUE	:::Cys_CAM::::::
SHSVFLINVK	15	10.1	0.102	888	28.4	KINH-DROME	TRUE	TRUE	2	1144.4	1.2	8of 18	1.4546	TRUE	TRUE	::::::::::
REYETLQSEMAR	3	4.56	0.029	1025	22.63	KINH-DROME	TRUE	TRUE	2	1513.7	0.5	12of 22	1.7374	TRUE	TRUE	::::::::::::
TLGENHPAVAATLNNLAVLYGK	10	7.74	0.459	1578	52.8	KLC-DROME	TRUE	TRUE	2	2267.6	2.2	23of 42	4.3943	TRUE	TRUE	::::::::::::::::::::
TLHNLVIQYASQGR	14	9.85	0.339	880	32	KLC-DROME	TRUE	TRUE	2	1600.8	1.7	19of 26	3.8242	TRUE	TRUE	::::::::::::::
DRGKSYELGQSTVKCMR	14	9.66	0.04	910	21.43	KPBB-DROME	TRUE	FALSE	2	2016.2	-2.1	12of 32	1.2758	TRUE	TRUE	:::::::::::::Cys_CAM:::
MNFSHGSHEYHAATVANVR	11	8	0.603	490	27.13	KPYK-DROME	TRUE	TRUE	2	2129.3	0.2	22of 36	6.1553	TRUE	TRUE	::::::::::::::::::
GAGTIDASHAAAIAAVEAATK	5	5.22	0.567	1534	35.5	KPYK-DROME	TRUE	TRUE	2	1897.1	2.5	21of 40	4.5216	TRUE	TRUE	::::::::::::::::::
MNFSHGSHEYHAATVANVR	10	8	0.375	528	27.13	KPYK-DROME	TRUE	TRUE	3	2129.3	1.7	29of 72	4.4207	TRUE	TRUE	::::::::::::::::::
KGVNLPGVPVDLPAVSEK	8	6.99	0.337	1896	40.1	KPYK-DROME	TRUE	TRUE	2	1820.1	0.4	18of 34	2.531	TRUE	TRUE	::::::::::::::::::
KGVNLPGVPVDLPAVSEK	7	6.99	0.325	1359	40.1	KPYK-DROME	TRUE	TRUE	2	1820.1	0.7	1	3.0419	TRUE	TRUE	::::::::::::::::::
GDLGIEIPAEK	1	3.83	0.309	724	26.8	KPYK-DROME	TRUE	TRUE	1	1142.3	1.1	15of 20	2.7188	TRUE	TRUE	::::::::::::
IENQQGMHNLDEIIEAGDGIMVAR	2	3.92	0.255	1262	56.96	KPYK-DROME	TRUE	TRUE	2	2655	0.8	19of 46	3.7987	TRUE	TRUE	::::::::::::::::::::::
LQFDSPVPHVR	11	7.85	0.219	733	27.5	KPYK-DROME	TRUE	TRUE	3	1295.5	2.3	23of 40	2.5389	TRUE	TRUE	::::::::::
GSLEIVYVDYENIVNVVKPGNR	3	4.45	0.143	1991	56.2	KPYK-DROME	TRUE	TRUE	2	2478.8	1.1	11of 42	1.8401	TRUE	TRUE	::::::::::::::::::::
LQFDSPVPHVR	10	7.85	0.14	918	27.5	KPYK-DROME	TRUE	TRUE	3	1295.5	0.9	20of 40	2.3188	TRUE	TRUE	::::::::::::
VQFGLQVGK	15	10.1	0.115	697	23.7	KPYK-DROME	TRUE	TRUE	2	976.2	2.2	14of 16	1.589	TRUE	TRUE	::::::::::
LSGIVCTIGPASSSVEMLEK	3	4.27	0.096	1628	52.63	KPYK-DROME	TRUE	TRUE	2	2079.4	-0.6	11of 38	1.675	TRUE	TRUE	::::::Cys_CAM:::::::::::::
GLVPLIYK	15	9.72	0.04	1056	32.8	KPYK-DROME	TRUE	TRUE	1	903.2	-0.3	7of 14	1.6052	TRUE	TRUE	::::::::
KLLVEEEEELQAKRKNPNVISVEEDDEDSS	2	3.9	0.001	1318	51.4	KZ-DROME	TRUE	FALSE	3	3473.7	0.5	22of116	2.299	TRUE	TRUE	::::::::::::::::::::::::::
GFPLDSQISELLDFAANYDK	1	3.51	0.453	1964	56.8	LA-DROME	TRUE	TRUE	2	2244.5	0	24of 38	5.0119	TRUE	TRUE	::::::::::::::::::
NAIVVFEGAPETSSR	3	4.27	0.442	1293	32.5	LA-DROME	TRUE	TRUE	2	1577.7	1.4	21of 28	4.1434	TRUE	TRUE	::::::::::::::
SEEGLVEISEDKLSLR	2	4.01	0.389	938	37.8	LA-DROME	TRUE	TRUE	2	1805	1.7	20of 30	3.8123	TRUE	TRUE	::::::::::::::
NAIVVFEGAPETSSR	2	4.27	0.388	689	32.5	LA-DROME	TRUE	TRUE	2	1577.7	0.8	17of 28	3.2711	TRUE	TRUE	::::::::::::::
IKDFEVAYIEFAK	3	4.45	0.371	1588	42.7	LA-DROME	TRUE	TRUE	2	1573.8	1.6	20of 24	4.706	TRUE	TRUE	::::::::::::::
LASLSTDLSEIVAALNK	2	4.08	0.252	1684	49.4	LA-DROME	TRUE	TRUE	1	1746	1	15of 32	3.7145	TRUE	TRUE	::::::::::::::::
KDPAPAAEEAAGGFTK	3	4.45	0.219	965	20.5	LA-DROME	TRUE	TRUE	2	1560.7	1.7	24of 30	3.0481	TRUE	TRUE	::::::::::::::::
EAKPEPAFELPK	3	4.56	0.126	1179	25.3	LA-DROME	TRUE	TRUE	3	1356.6	1.1	17of 44	2.4379	TRUE	TRUE	::::::::::::
GSIFLTFETK	7	6.95	0.066	1376	31.5	LA-DROME	TRUE	TRUE	1	1143.3	0.2	6	1.517	TRUE	TRUE	::::::::::
VTIVGIGQVGMASAFSILAQNVSK	15	10.1	0.555	2114	66.63	LDH-DROME	TRUE	TRUE	2	2391.8	0.4	28of 46	5.6924	TRUE	TRUE	::::::::::::::::::::::
DSLLAQVAEVLPSSGHK	5	5.22	0.34	1918	36.6	LDH-DROME	TRUE	TRUE	2	1752	2.4	20of 32	3.4139	TRUE	TRUE	::::::::::::::::
SANIMSDVQAGLK	6	6.76	0.212	1408	26.93	LDH-DROME	TRUE	TRUE	1	1334.5	-0.4	14of 24	3.6197	TRUE	TRUE	::::::::::::
EVCLIDVCADK	1	3.71	0.183	725	32.1	LDH-DROME	TRUE	TRUE	1	1322.4	-0.5	15of 20	2.6087	TRUE	TRUE	:::Cys_CAM:::::Cys_CAM::::
VIGSGTNLDSSR	9	6.79	0.121	661	19.1	LDH-DROME	TRUE	TRUE	2	1206.3	1.1	13of 22	1.8058	TRUE	TRUE	::::::::::::
QVVDSAYEVIK	2	4.08	0.098	617	27.9	LDH-DROME	TRUE	TRUE	2	1251.4	0.6	10of 20	2.2047	TRUE	TRUE	::::::::::::
KLYEEVNTLVLPIK	7	7	0.187	1387	46.2	LMA-DROME	TRUE	TRUE	2	1660	1	3	2.733	TRUE	TRUE	::::::::::::::
LQINSLPVK	15	10.1	0.065	705	27.7	LMA-DROME	TRUE	TRUE	2	1012.2	0.8	11of 16	2.0063	TRUE	TRUE	::::::::::
YYYGISNMVVR	14	9.44	0.148	1000	34.83	LMB1-DROME	TRUE	TRUE	2	1365.6	1.5	10of 20	1.2692	TRUE	TRUE	::::::::::::
LSDDHVQFLVYQILR	5	5.1	0.387	2078	51.8	M14A-DROME	TRUE	FALSE	2	1847.1	1.8	18of 28	3.4842	TRUE	TRUE	::::::::::::::::
TITLEVEPSDTXENVKAK	2	4.17	0.108	756	29.8	M33016	TRUE	TRUE	2	1988.2	0	16of 34	2.9791	TRUE	TRUE	::::::::::::::::
TFTHSTMADIGPAAR	9	7.85	0.425	1272	27.93	MCA2-DROME	TRUE	TRUE	2	1576.8	1.3	19of 28	4.2119	TRUE	TRUE	::::::::::::::
DHSELLFFILR	5	5.22	0.252	2154	46.3	MCM2-DROME	TRUE	TRUE	2	1390.6	2.5	17of 20	2.9878	TRUE	TRUE	::::::::::::
ALALALFGGESK	8	6.95	0.242	2007	36.8	MCM2-DROME	TRUE	TRUE	1	1177.4	0.7	14of 22	2.251	TRUE	TRUE	::::::::::::
SQMLQYVFNLVPR	14	9.85	0.429	1679	44.93	MCM4-DROME	TRUE	TRUE	2	1595.9	1.5	19of 24	4.2679	TRUE	TRUE	::::::::::::::
NIIDNVQLPHTLLSR	9	7.85	0.357	1862	42.8	MCM4-DROME	TRUE	TRUE	2	1734	0.8	21of 28	4.4773	TRUE	TRUE	::::::::::::::
IDVGILTTGLSTAAR	7	6.79	0.281	1472	40.8	MCM4-DROME	TRUE	TRUE	2	1488.7	2.6	1	3.1121	TRUE	TRUE	::::::::::::::
AIAPSIYENDDIKK	3	4.31	0.05	1080	29.2	MCM4-DROME	TRUE	TRUE	2	1577.8	0.1	13of 26	1.882	TRUE	TRUE	::::::::::::::
EAAQIMHEICAAVDYLHSR	5	5.18	0.43	2087	45.93	MKK2-DROME	TRUE	TRUE	3	2215.5	1.7	35of 72	4.7893	TRUE	TRUE	:::::::::Cys_CAM:::::::::::
ISFEVFLPIYQAISK	8	6.87	0.289	2695	58.6	MLC2-DROME	TRUE	TRUE	1	1756.1	-0.3	16of 28	3.197	TRUE	TRUE	::::::::::::::
ISFEVFLPIYQAISK	7	6.87	0.215	2108	58.6	MLC2-DROME	TRUE	TRUE	3	1756.1	2.1	9	3.847	TRUE	TRUE	::::::::::::::
HLLTTLGEK	9	7.82	0.203	1212	22.2	MLC2-DROME	TRUE	TRUE	2	1012.2	2.4	11of 16	2.2039	TRUE	TRUE	::::::::::
NIQFEAFHVFK	9	7.82	0.382	1836	35	MO25-DROME	TRUE	TRUE	2	1380.6	0	17of 20	3.5194	TRUE	TRUE	::::::::::::
TVVVGLIGPNITK	15	10.1	0.332	1083	38	MODU-DROME	TRUE	TRUE	1	1311.6	0.6	14of 24	2.4882	TRUE	TRUE	::::::::::::
DLVALFAK	6	6.76	0.179	1644	31.4	MODU-DROME	TRUE	TRUE	1	877.1	0.6	10of 14	1.6999	TRUE	TRUE	::::::::
ALTLGDNVLSVSQPR	7	6.79	0.153	1281	37.3	MODU-DROME	TRUE	TRUE	2	1570.8	1.4	1	2.0843	TRUE	TRUE	::::::::::::::
LHSTELFSR	10	7.85	0.138	572	22.9	MODU-DROME	TRUE	TRUE	2	1090.2	-0.1	13of 16	1.9545	TRUE	TRUE	::::::::::
TTHTAGFLANDR	9	7.85	0.421	1013	18.7	MOEH-DROME	TRUE	TRUE	2	1304.4	0.6	17of 22	2.9744	TRUE	TRUE	::::::::::::
APDFMFFAPR	7	6.79	0.315	1569	37.43	MOEH-DROME	TRUE	TRUE	2	1199.4	0.5	6	3.3356	TRUE	TRUE	::::::::::
DLLEAQDMIR	1	3.71	0.217	892	32.03	MOEH-DROME	TRUE	TRUE	1	1204.4	0.3	12of 18	2.1487	TRUE	TRUE	::::::::::
LKLEEEIMAK	3	4.56	0.131	1231	30.23	MOEH-DROME	TRUE	TRUE	2	1204.5	1.2	14of 18	2.5761	TRUE	TRUE	::::::::::
FYPEDVAEELIQDITLR	1	3.51	0.091	2017	56.3	MOEH-DROME	TRUE	TRUE	2	2052.3	1.5	14of 32	1.6876	TRUE	TRUE	::::::::::::::::
QLQAAKDELELR	3	4.45	0.086	1096	28	MOEH-DROME	TRUE	TRUE	3	1414.6	2.9	20of 44	2.0359	TRUE	TRUE	::::::::::::
KRLAASYKCMG	15	10.19	0.05	1041	19.53	MST2-DROHY	TRUE	FALSE	2	1285.5	-1.4	7of 20	1.1369	TRUE	TRUE	:::::::::Cys_CAM:::
PSMNASIPVKFSSVFF	14	10.1	0.06	2545	49.73	MTHB-DROME	TRUE	FALSE	3	1759.1	2	9of 60	0.8892	TRUE	TRUE	::::::::::::::::
RPYWGQARRWVGDYLANSQENSGYEA	6	6.97	0.047	2058	50.6	MY1A-DROME	TRUE	FALSE	3	3075.3	-2.8	21of100	2.1779	TRUE	TRUE	::::::::::::::::::::::::
ELSSITAKLEDEQVVVLKHQ	3	4.63	0.072	2194	46.1	MYSA-DROME	TRUE	FALSE	2	2267.6	-3	12of 38	1.6903	TRUE	TRUE	::::::::::::::::::

GVADFAIVHYAGR	11	7.76	0.44	920	33.1	MYSN-DROME	TRUE	TRUE	2	1376.6	1.4	20of 24	3.852	TRUE	TRUE	::::::::::::::
GVADFAIVHYAGR	12	7.76	0.355	1283	33.1	MYSN-DROME	TRUE	TRUE	2	1376.6	2.3	16of 24	2.8218	TRUE	TRUE	::::::::::::::
EHGDEVEVELAETGKR	2	4.19	0.334	437	21.2	MYSN-DROME	TRUE	TRUE	2	1798.9	0.5	13of 30	2.224	TRUE	TRUE	::::::::::::::::
TFHIFYQLLAGATPEQR	9	7.77	0.32	2080	49.7	MYSN-DROME	TRUE	TRUE	2	1993.3	1.4	19of 32	3.3078	TRUE	TRUE	::::::::::::::::
IAHLLGLSVTDMTR	10	7.85	0.317	1374	42.53	MYSN-DROME	TRUE	TRUE	2	1527.8	2.6	19of 26	3.4594	TRUE	TRUE	::::::::::::::
REEELTQTLLR	3	4.56	0.215	1207	27.6	MYSN-DROME	TRUE	TRUE	2	1388.6	0.4	15of 20	2.921	TRUE	TRUE	::::::::::::
RHEVPPHVFAITDSAYR	10	7.92	0.11	914	34.3	MYSN-DROME	TRUE	TRUE	2	1996.2	0.4	17of 32	2.613	TRUE	TRUE	::::::::::::::::
SEVLLDRAAARQLQIEQLTTELANEK	4	4.36	0.053	1669	62.6	MYSN-DROME	TRUE	FALSE	3	2941.3	-0.7	21of100	2.9055	TRUE	TRUE	::::::::::::::::::::::::
CTKLQQEAENITNQLEEAELKASAAVKSASNME	4	4.26	0.021	2359	55.93	MYSN-DROME	TRUE	FALSE	3	3654	-1.8	17of128	1.802	TRUE	TRUE	:Cys_CAM::::::::::::::::::::::::::::::::Oxidation_M::
TFIMVKPDGVQR	13	10.09	0.3	820	30.93	NDKA-DROME	TRUE	TRUE	2	1391.7	2	14of 22	2.1346	TRUE	TRUE	::::::::::::
TFIMVKPDGVQR	15	10.09	0.294	607	30.93	NDKA-DROME	TRUE	TRUE	2	1391.7	1.2	17of 22	3.5916	TRUE	TRUE	::::::::::::
TFIMVKPDGVQR	14	10.09	0.276	622	30.93	NDKA-DROME	TRUE	TRUE	2	1391.7	0.4	15of 22	3.1012	TRUE	TRUE	::::::::::::
QMLGATNPADSLPGTIR	6	6.79	0.263	1402	36.73	NDKA-DROME	TRUE	TRUE	2	1743	2.5	21of 32	3.7296	TRUE	TRUE	::::::::::::::::
NIIHGSDAVESAEKEIALWFNEK	3	4.36	0.234	2048	54.7	NDKA-DROME	TRUE	TRUE	2	2601.9	-0.2	18of 44	2.9988	TRUE	TRUE	::::::::::::::::::::::
GDFCIQVGR	6	6.1	0.192	1151	22.3	NDKA-DROME	TRUE	TRUE	1	1052.1	-0.5	7of 16	1.1885	TRUE	TRUE	::::Cys_CAM::::::
HYADLSAR	9	7.76	0.075	385	13.9	NDKA-DROME	TRUE	TRUE	1	933	-0.3	11of 14	1.6599	TRUE	TRUE	::::::::
SQITSIQQEIER	3	4.27	0.165	1301	24	NHPX-DROME	TRUE	TRUE	2	1432.6	2.8	17of 22	2.8686	TRUE	TRUE	::::::::::::
AVNPDVEFYESK	2	3.83	0.371	604	26.1	NLP-DROME	TRUE	TRUE	2	1398.5	0.2	17of 22	3.0706	TRUE	TRUE	::::::::::::
ENEFNVVEVNTPK	1	3.97	0.346	700	25.1	NLP-DROME	TRUE	TRUE	2	1519.7	0.5	19of 24	3.4252	TRUE	TRUE	::::::::::::
ENEFNVVEVNTPK	2	3.97	0.29	676	25.1	NLP-DROME	TRUE	TRUE	2	1519.7	1.3	18of 24	3.1706	TRUE	TRUE	::::::::::::
DSVQIPIAVLK	6	6.76	0.188	1570	34.8	NLP-DROME	TRUE	TRUE	1	1183.4	-0.4	14of 20	2.5161	TRUE	TRUE	::::::::::::
QILLGAEAK	6	6.95	0.062	944	26.4	NLP-DROME	TRUE	TRUE	2	943.1	1.2	11of 16	1.3972	TRUE	TRUE	::::::::::
YTATLPVLR	15	9.85	0.246	904	30.3	NPC2-DROME	TRUE	TRUE	2	1034.2	1.7	12of 16	2.1709	TRUE	TRUE	::::::::::
ISGPELPLGHVGFSLVQR	10	7.85	0.257	1553	51.2	NSF2-DROME	TRUE	TRUE	2	1907.2	1.1	12of 34	2.2985	TRUE	TRUE	::::::::::::::::::
FGNQADHFLGSLAFAK	10	7.82	0.445	1464	41.3	OFU1-DROME	TRUE	TRUE	2	1723.9	0.3	21of 30	4.5599	TRUE	TRUE	::::::::::::::::
NPRLAADRVFSLLSEIKTSAE	8	7.14	0.012	2357	51.3	ORC2-DROME	TRUE	FALSE	2	2318.6	2.4	8of 40	1.0764	TRUE	TRUE	::::::::::::::::::::
NVVTIFSAPNYCYR	13	8.83	0.118	1235	39.7	P2A-DROME	TRUE	TRUE	2	1704.9	0.5	12of 26	1.8336	TRUE	TRUE	::::::::::Cys_CAM:::
NSDFYTHNSVR	9	7.76	0.325	877	14.1	P2B2-DROME	TRUE	TRUE	2	1340.4	1.1	15of 20	2.8005	TRUE	TRUE	::::::::::::
AKVEEAVAVLQVHR	11	7.83	0.433	682	31.5	PABP-DROME	TRUE	TRUE	2	1549.8	1.2	20of 26	4.3321	TRUE	TRUE	::::::::::::::
IAFSPYGNITSAK	15	9.72	0.219	919	30.7	PABP-DROME	TRUE	TRUE	2	1369.6	2.2	14of 24	1.9728	TRUE	TRUE	::::::::::::::
LFTNVYVK	15	9.72	0.012	753	28.6	PABP-DROME	TRUE	TRUE	1	984.2	0.9	10of 14	1.9455	TRUE	TRUE	::::::::
FSASGDVGTANIK	6	6.76	0.422	906	21.8	PCNA-DROME	TRUE	TRUE	2	1267.4	2.1	22of 24	3.5702	TRUE	TRUE	::::::::::::::
VLVSSNFESVALDK	2	4.08	0.472	881	39.3	PDI-DROME	TRUE	TRUE	2	1508.7	1.4	21of 26	4.1756	TRUE	TRUE	::::::::::::::
DLTSVADAEQFLKDNEIAIIGFFK	2	3.85	0.447	1960	71.9	PDI-DROME	TRUE	TRUE	2	2686	0.1	22of 46	4.772	TRUE	TRUE	::::::::::::::::::::::
IFEFFGMNKEEVPTIR	3	4.56	0.386	1731	52.03	PDI-DROME	TRUE	TRUE	2	1958.3	-0.2	18of 30	3.6798	TRUE	TRUE	::::::::::::::::
KFAQVQSLPLIVDFNHESASK	10	7.8	0.354	1461	49.6	PDI-DROME	TRUE	TRUE	3	2359.7	1.5	31of 80	4.8435	TRUE	TRUE	::::::::::::::::::
MDSTANELESIK	1	3.83	0.309	557	22.93	PDI-DROME	TRUE	TRUE	2	1338.5	2.3	17of 22	3.3431	TRUE	TRUE	::::::::::::
DLTSVADAEQFLK	1	3.71	0.248	1136	33.1	PDI-DROME	TRUE	TRUE	2	1437.6	2.1	19of 24	2.8852	TRUE	TRUE	::::::::::::::
SVFEGELNEENLK	2	3.8	0.151	704	30	PDI-DROME	TRUE	TRUE	2	1508.6	1.3	16of 24	2.6578	TRUE	TRUE	::::::::::::::
LIKLEEDMAK	3	4.45	0.076	1118	29.33	PDI-DROME	TRUE	TRUE	2	1190.4	1.4	12of 18	1.7498	TRUE	TRUE	::::::::::
YKPESDDLSAETIEAFLKK	3	4.29	0.076	1672	39.8	PDI-DROME	TRUE	TRUE	3	2185.4	1.5	25of 72	2.193	TRUE	TRUE	::::::::::::::::::
IFEFFGMNK	7	6.95	0.053	1505	35.43	PDI-DROME	TRUE	TRUE	2	1133.4	1.1	1	2.2578	TRUE	TRUE	::::::::::
KQGGLGSMDIPLLADK	7	6.88	0.381	1377	36.63	PDX1-DROME	TRUE	TRUE	2	1643.9	2.6	1	4.4382	TRUE	TRUE	::::::::::::::::
INCEVIGCSTDSQFTHLAWINTPR	5	5.22	0.357	1806	60	PDX1-DROME	TRUE	TRUE	2	2821.1	0.7	15of 46	2.1993	TRUE	TRUE	:::Cys_CAM::::Cys_CAM::::::::::::::::
DYGVLDEETGIPFR	1	3.59	0.222	1096	37.3	PDX1-DROME	TRUE	TRUE	1	1611.7	-0.7	13of 26	2.6238	TRUE	TRUE	::::::::::::::
GLFIIDDKQNLR	7	6.9	0.209	1179	36	PDX1-DROME	TRUE	TRUE	2	1432.7	0.6	27	3.1653	TRUE	TRUE	::::::::::::
KQGGLGSMDIPLLADK	6	6.88	0.141	1355	36.63	PDX1-DROME	TRUE	TRUE	2	1659.9	0.7	13of 30	1.8926	TRUE	TRUE	:::::::Oxidation_M:::::::::
GLFIIDDK	2	3.89	0.103	842	29.1	PDX1-DROME	TRUE	TRUE	1	921.1	0.9	10of 14	2.4018	TRUE	TRUE	::::::::
ASGGAVAGGCLVVGAGTDKTSELIPGK	5	6.36	0.06	2171	47.7	PER-DROWI	TRUE	FALSE	3	2473.8	1.7	16of104	1.4282	TRUE	TRUE	:::::::::Cys_CAM:::::::::::::::::
FYVEEEGKGLDASGGK	2	4.17	0.512	464	26	PGK-DROME	TRUE	TRUE	2	1686.8	0.2	23of 30	5.0475	TRUE	TRUE	::::::::::::::::
NNVQLHLPVDFVCGDK	5	5.1	0.448	1675	38.7	PGK-DROME	TRUE	TRUE	2	1856.1	2.4	19of 30	3.6241	TRUE	TRUE	:::::::::::::Cys_CAM::::
YFSQALDKPPNPFLAILGGAK	15	9.63	0.408	1675	59.2	PGK-DROME	TRUE	TRUE	2	2248.6	-0.9	25of 40	4.6424	TRUE	TRUE	::::::::::::::::::::
YFSQALDKPPNPFLAILGGAK	14	9.63	0.35	1568	59.2	PGK-DROME	TRUE	TRUE	2	2248.6	1.3	25of 40	4.7807	TRUE	TRUE	::::::::::::::::::::
YTLAPVAAELK	6	6.87	0.191	1375	33.3	PGK-DROME	TRUE	TRUE	1	1176.4	-0.3	12of 20	2.0328	TRUE	TRUE	::::::::::::
LIVWNGPPGVFEFPNFANGTK	7	6.95	0.158	1944	63.8	PGK-DROME	TRUE	TRUE	2	2305.6	0.5	459	1.8836	TRUE	TRUE	::::::::::::::::::::
MATHLETTANLLK	10	7.82	0.272	905	31.93	PHS-DROME	TRUE	TRUE	2	1443.7	1.6	17of 24	2.9885	TRUE	TRUE	::::::::::::::
IYDFPATLEDAAEEAK	1	3.51	0.057	1186	40.3	PNUT-DROME	TRUE	TRUE	2	1783.9	1	8of 30	1.4595	TRUE	TRUE	::::::::::::::
TFTDCFNCLPVAAIVDEK	1	3.71	0.357	1364	52.9	PP11-DROME	TRUE	TRUE	2	2101.3	1.8	18of 34	2.8331	TRUE	TRUE	:::::Cys_CAM:::Cys_CAM::::::::::
PSGMRRPSRPSEREYENMPTV	15	9.84	0.022	1141	28.66	PR2-DROME	TRUE	FALSE	3	2493.8	1	9of 80	0.9869	TRUE	TRUE	::::Oxidation_M:::::::::::::::
LISGFDQQDGLTSNGVTLAGQR	2	3.89	0.45	936	46	PROF-DROME	TRUE	TRUE	2	2278.5	1.8	26of 42	5.93	TRUE	TRUE	::::::::::::::::::::
YIYLSGTDR	6	6.64	0.2	985	24.3	PROF-DROME	TRUE	TRUE	2	1088.2	2.5	12of 16	2.5793	TRUE	TRUE	::::::::::
ACIAGHDGNIWAQSSGFEVTKEELSK	4	4.63	0.146	1589	49.4	PROF-DROME	TRUE	TRUE	3	2836.1	1.8	29of100	2.7295	TRUE	TRUE	::Cys_CAM:::::::::::::::::::::
LISGFDQQDGLTSNGVTLAGQR	1	3.89	0.115	942	46	PROF-DROME	TRUE	TRUE	2	2278.5	1.4	15of 42	2.2797	TRUE	TRUE	::::::::::::::::::::
VHVTQEDFEMAVAK	3	4.43	0.269	1243	31.43	PRS8-DROME	TRUE	TRUE	2	1604.8	1.5	15of 26	2.8594	TRUE	TRUE	::::::::::::::
GVLLYGPPGTGK	15	9.72	0.221	708	27.4	PRS8-DROME	TRUE	TRUE	1	1159.4	-0.7	8of 22	1.6121	TRUE	TRUE	::::::::::::
ICMLDNHVVMAFAGLTADAR	5	5.1	0.523	2076	60.86	PS71-DROME	TRUE	TRUE	2	2206.5	1.6	21of 38	4.627	TRUE	TRUE	::Cys_CAM:::::::::::::::::
AVTIFSPDGHLLQVEYAQEAVR	3	4.43	0.489	1687	59.1	PS71-DROME	TRUE	TRUE	2	2444.7	0.4	23of 42	5.6332	TRUE	TRUE	::::::::::::::::::::
LNVEDPVTLEYITR	1	3.83	0.287	1108	42.5	PS71-DROME	TRUE	TRUE	2	1662.9	1.4	16of 26	2.5426	TRUE	TRUE	::::::::::::::
RPYGVGLLVAGYDER	7	6.9	0.338	1263	38.7	PSA1-DROME	TRUE	TRUE	2	1665.9	0.7	1	3.9141	TRUE	TRUE	::::::::::::::::
HSYDTTYPVSR	9	7.7	0.324	876	14.3	PSA1-DROME	TRUE	TRUE	2	1326.4	0.3	16of 20	2.9568	TRUE	TRUE	::::::::::::
FLDSSKDEIIR	3	4.31	0.203	1135	29.4	PSA1-DROME	TRUE	TRUE	2	1323.5	2.5	14of 20	2.9644	TRUE	TRUE	::::::::::::
NKDYAVLVALCKPTSELSDTQRK	13	8.83	0.057	1058	42.2	PSA1-DROME	TRUE	TRUE	3	2638	0.8	24of 88	2.1493	TRUE	TRUE	:::::::::Cys_CAM:::::::::::
YSFSLTTFSPSGK	15	9.72	0.38	1220	28.9	PSA2-DROME	TRUE	TRUE	2	1422.6	0.7	19of 24	3.5536	TRUE	TRUE	::::::::::::::
VEMIYNHIGMVYSGMGPDYR	5	5.22	0.357	1715	54.09	PSA2-DROME	TRUE	TRUE	2	2333.7	0.2	20of 38	3.8282	TRUE	TRUE	::::::::::::::::::
YSFSLTTFSPSGK	14	9.72	0.298	1140	28.9	PSA2-DROME	TRUE	TRUE	1	1422.6	1.5	12of 24	2.2611	TRUE	TRUE	::::::::::::::
IEPSGSSFGYFACASGK	7	6.28	0.409	1176	34.3	PSA3-DROME	TRUE	TRUE	2	1765.9	0.9	1	2.7329	TRUE	TRUE	:::::::::::::Cys_CAM:::::
VAGYVHAYTLY	10	7.65	0.288	1138	33.9	PSA3-DROME	TRUE	FALSE	1	1257.4	1.6	11of 20	2.029	TRUE	TRUE	::::::::::::
LNDNMVCSVAGITSDANVLTSELR	1	3.71	0.438	1504	58.33	PSA4-DROME	TRUE	TRUE	2	2580.8	1.5	21of 46	3.566	TRUE	TRUE	::::::Cys_CAM:::::::::::::::::
TVYSVLEKPDVEK	3	4.45	0.422	1156	28.2	PSA4-DROME	TRUE	TRUE	2	1507.7	0	17of 24	3.5925	TRUE	TRUE	::::::::::::::
LFQVEYAIEAIK	3	4.27	0.301	1772	44.6	PSA5-DROME	TRUE	TRUE	2	1424.7	1.7	19of 22	3.7831	TRUE	TRUE	::::::::::::::
NIVPETVTHLFR	9	7.85	0.203	1800	34.6	PSA6-DROME	TRUE	TRUE	2	1426.7	2.1	17of 22	2.7247	TRUE	TRUE	::::::::::::::
AIAQENITTVALK	8	6.95	0.127	1635	33.5	PSA6-DROME	TRUE	TRUE	2	1372.6	0.9	17of 24	3.1432	TRUE	TRUE	::::::::::::::
FFPYYVSNILAGIDNEGK	2	4.08	0.426	1552	54.5	PSB1-DROME	TRUE	TRUE	2	2048.3	2.7	22of 34	4.6658	TRUE	TRUE	::::::::::::::::::

AGGTAGTLLQPVLDNQIGHK	11	7.82	0.313	1008	38.5	PSB1-DROME	TRUE	TRUE	2	1991.3	0.3	15of 38	2.7364	TRUE		TRUE	::::::::::::::::::::
AGGTAGTLLQPVLDNQIGHK	12	7.82	0.06	1359	38.5	PSB1-DROME	TRUE	TRUE	2	1991.3	-0.6	13of 38	1.8254	TRUE		TRUE	::::::::::::::::::::
FGIQAQTISTDFKK	14	9.89	0.337	835	29.8	PSB3-DROME	TRUE	TRUE	2	1584.8	1.4	21of 26	4.5634	TRUE		TRUE	::::::::::::::
FGIQAQTISTDFKK	15	9.89	0.293	897	29.8	PSB3-DROME	TRUE	TRUE	2	1584.8	1.7	18of 26	3.4029	TRUE		TRUE	::::::::::::::
SAMMSSFLYEHR	10	7.77	0.103	485	31.56	PSB3-DROME	TRUE	FALSE	2	1491.7	0.7	11of 22	1.6403	TRUE		TRUE	:::Oxidation_M:Oxidation_M::::::::
NILLGGSGDFADIQSIKR	6	6.9	0.4	1603	44.6	PSB4-DROME	TRUE	TRUE	2	1905.2	1.6	16of 34	2.7055	TRUE		TRUE	::::::::::::::::::
SYEDYVVATGFAR	2	4.08	0.356	898	32	PSB4-DROME	TRUE	TRUE	2	1478.6	1.4	19of 24	3.0164	TRUE		TRUE	::::::::::::::
DRDFTAVEASELIR	2	4.07	0.289	860	34.4	PSB4-DROME	TRUE	TRUE	2	1622.8	0.4	18of 26	3.8784	TRUE		TRUE	::::::::::::::
IVVFVGSPINHEEGDLVK	3	4.43	0.363	1475	50	PSD4-DROME	TRUE	TRUE	2	1953.2	0.9	17of 34	3.6048	TRUE		TRUE	::::::::::::::::::
DGTGSHLVSVPR	10	7.85	0.183	388	17.4	PSD4-DROME	TRUE	TRUE	2	1225.3	0.6	13of 22	2.8661	TRUE		TRUE	::::::::::::
LDYLIHPHYR	11	7.85	0.23	670	30	PSD6-DROME	TRUE	TRUE	2	1327.5	1.4	14of 18	2.6227	TRUE		TRUE	::::::::::
ILGYTQLLESYR	7	6.83	0.161	1515	41.4	PSD6-DROME	TRUE	TRUE	2	1456.7	0.4	1	2.7981	TRUE		TRUE	::::::::::::
SIIALHNLINNK	14	10.1	0.276	962	34.2	PSD7-DROME	TRUE	TRUE	2	1350.6	2.8	18of 22	3.053	TRUE		TRUE	::::::::::::
VIVHPLVLLSVVDHFNR	11	8	0.263	1464	61.4	PSD7-DROME	TRUE	TRUE	3	1958.4	-0.5	25of 64	3.1932	TRUE		TRUE	::::::::::::::::
KLNDTHLNFTLEFTEVYK	5	5.35	0.118	2128	46.7	PTP6-DROME	TRUE	FALSE	2	2213.5	2.4	5of 34	1.0458	TRUE		TRUE	::::::::::::::::::
CPISFVGVVTGDGR	5	6.1	0.456	1664	34.5	PUR4-DROME	TRUE	TRUE	2	1464.6	1.1	20of 26	4.0832	TRUE		TRUE	:Cys_CAM::::::::::::
VGELLGDFNLFSEK	1	3.83	0.362	1453	44.6	PURA-DROME	TRUE	TRUE	2	1568.8	2.1	20of 26	3.7475	TRUE		TRUE	::::::::::::::
VGDGPFPTEQLNDIGDLLQTR	1	3.51	0.297	1488	49.9	PURA-DROME	TRUE	TRUE	2	2286.5	2.3	19of 40	2.9167	TRUE		TRUE	::::::::::::::::::::
AHLVFDFHQHVDGMQEAEK	5	5.12	0.284	1328	37.83	PURA-DROME	TRUE	TRUE	3	2255.5	0.9	24of 72	3.6698	TRUE		TRUE	:::::::::::::Oxidation_M::::::
LDILDTLPEIK	1	3.71	0.199	1293	41.1	PURA-DROME	TRUE	TRUE	1	1270.5	-0.3	12of 20	2.2305	TRUE		TRUE	::::::::::::
SERPPPGFPGVETILPLLLQAVHEGR	6	5.4	0.249	2379	69.7	PYR1-DROME	TRUE	TRUE	3	2811.3	2.8	38of100	4.4481	TRUE		TRUE	::::::::::::::::::::::::::
CEELNLSGHFYR	5	5.3	0.271	1370	29.9	R13A-DROME	TRUE	TRUE	3	1525.6	1.6	25of 44	3.3194	TRUE		TRUE	:Cys_CAM:::::::::::::
FLAYLR	14	9.85	0.024	798	30.2	R13A-DROME	TRUE	TRUE	1	783	0.2	8of 10	1.5866	TRUE		TRUE	::::::
CNLTFVFSKPEEK	6	6.44	0.245	1348	31.7	R27A-DROME	TRUE	TRUE	2	1599.8	0.2	18of 24	3.9376	TRUE		TRUE	:Cys_CAM:::::::::::::
LAPITYPQGLAMAK	15	9.72	0.028	1073	41.93	RAC1-DROME	TRUE	TRUE	2	1474.8	2.1	10of 26	1.553	TRUE		TRUE	::::::::::::::
AEQIFSALNFTSHIFK	11	7.82	0.389	1485	47.7	RFA1-DROME	TRUE	TRUE	2	1854.1	0.8	21of 30	4.7497	TRUE		TRUE	::::::::::::::::
IMHGEVVDAPVLQILAIK	5	5.22	0.293	2031	61.83	RFA1-DROME	TRUE	TRUE	2	1947.4	2.1	18of 34	3.2105	TRUE		TRUE	::::::::::::::::::
CNALFPNFK	13	8.97	0.001	1100	27.6	RFA1-DROME	TRUE	TRUE	1	1111.3	0.7	8of 16	1.1544	TRUE		TRUE	:Cys_CAM:::::::::
INAFAYLECSAK	7	6.28	0.194	1367	34.9	RHO1-DROME	TRUE	TRUE	2	1387.5	1	1	2.5507	TRUE		TRUE	::::::::Cys_CAM::::
SVETHMLHDFNCDLYGQTLK	5	5.12	0.248	1648	45.43	RIFK-DROME	TRUE	TRUE	3	2409.6	2.7	24of 76	3.1056	TRUE		TRUE	:::::::::::Cys_CAM:::::::::
VPLVSEFHYNVVK	11	7.74	0.433	976	38.8	RIR1-DROME	TRUE	TRUE	2	1531.8	0.2	15of 24	3.2966	TRUE		TRUE	::::::::::::
VLSGEFQVVNHHLLR	11	8	0.363	932	42.7	RIR1-DROME	TRUE	TRUE	2	1749	0.4	14of 28	3.0144	TRUE		TRUE	::::::::::::::::
IIDINYYPLPEAR	2	4.08	0.05	1041	45.4	RIR1-DROME	TRUE	TRUE	2	1577.8	1.9	10of 24	1.5619	TRUE		TRUE	::::::::::::
DQFHIR	10	7.85	0.001	318	13	RL10-DROME	TRUE	TRUE	2	815.9	2	8of 10	1.9067	TRUE		TRUE	::::::
LILFPINEK	7	6.95	0.069	1380	39.5	RL13-DROME	TRUE	TRUE	2	1087.3	1.7	184	2.2135	TRUE		TRUE	::::::::::
LVAIVDVIDQNR	2	3.89	0.35	1042	39.1	RL14-DROVI	TRUE	TRUE	2	1355.6	2	18of 22	3.3321	TRUE		TRUE	::::::::::::
VLVDGPLTGVPR	6	6.79	0.133	1339	35	RL14-DROVI	TRUE	TRUE	2	1223.5	2.4	17of 22	2.7761	TRUE		TRUE	::::::::::::
VLVDGPLTGVPR	7	6.79	0.048	1127	35	RL14-DROVI	TRUE	TRUE	2	1223.5	1.2	2	1.3079	TRUE		TRUE	::::::::::::
DLTVGGAVTQCYR	6	6.09	0.344	1168	27.6	RL1X-DROME	TRUE	TRUE	2	1440.6	1.5	18of 24	2.8408	TRUE		TRUE	:::::::::Cys_CAM:::
DLTVGGAVTQCYR	5	6.09	0.049	1321	27.6	RL1X-DROME	TRUE	TRUE	2	1440.6	0.1	14of 24	1.9967	TRUE		TRUE	:::::::::Cys_CAM:::
LIVSSDVHFSK	10	7.82	0.15	808	29	RL22-DROME	TRUE	TRUE	1	1232.4	-0.6	13of 20	2.8049	TRUE		TRUE	::::::::::::
LIVSSDVHFSK	11	7.82	0.097	656	29	RL22-DROME	TRUE	TRUE	1	1232.4	-0.4	11of 20	1.8866	TRUE		TRUE	::::::::::::
LPAAGVGDMFVATVK	7	6.76	0.44	1413	43.03	RL23-DROME	TRUE	TRUE	2	1476.8	0.1	1	3.707	TRUE		TRUE	::::::::::::::::
NLYYIAVHGIR	14	9.85	0.42	942	35.9	RL23-DROME	TRUE	TRUE	2	1255.5	1	18of 20	3.3504	TRUE		TRUE	::::::::::::
ISLGLPVGAVMNCADNTGAK	6	6.1	0.311	1699	46.43	RL23-DROME	TRUE	TRUE	2	1989.3	0.9	18of 38	3.7533	TRUE		TRUE	:::::::::::Cys_CAM:::::::::
LPAAGVGDMFVATVK	8	6.76	0.273	1972	43.03	RL23-DROME	TRUE	TRUE	2	1476.8	1.4	13of 28	2.1828	TRUE		TRUE	::::::::::::::::
NLYYIAVHGIR	13	9.85	0.241	1066	35.9	RL23-DROME	TRUE	TRUE	2	1255.5	-0.2	14of 20	2.5572	TRUE		TRUE	::::::::::::
KPFSTEPNNLASVSSYR	14	9.72	0.385	695	28.7	RL28-DROME	TRUE	TRUE	2	1898.1	0.9	21of 32	3.7436	TRUE		TRUE	::::::::::::::::::
KPFSTEPNNLASVSSYR	15	9.72	0.171	719	28.7	RL28-DROME	TRUE	TRUE	2	1898.1	0	15of 32	2.0462	TRUE		TRUE	::::::::::::::::::
NNNAFLLK	14	10.1	0.123	478	22.4	RL28-DROME	TRUE	TRUE	2	934.1	0.9	11of 14	1.6522	TRUE		TRUE	::::::::
NLLIGSK	14	10.1	0.028	240	20.5	RL28-DROME	TRUE	TRUE	1	744.9	0	10of 12	1.748	TRUE		TRUE	::::::::
RHESTLGMDVK	9	7.82	0.138	900	15.33	RL29-DROME	TRUE	TRUE	2	1273.4	2.3	14of 20	1.9503	TRUE		TRUE	::::::::::::
LYTYVTYVPVSTFK	14	9.4	0.452	1215	46.2	RL31-DROME	TRUE	TRUE	1	1682	1	16of 26	3.0117	TRUE		TRUE	::::::::::::::::
LYTYVTYVPVSTFK	15	9.4	0.052	1300	46.2	RL31-DROME	TRUE	TRUE	1	1682	-1.2	11of 26	1.4155	TRUE		TRUE	::::::::::::::::
KREELSNILTQLR	15	10.09	0.15	1068	30.4	RL36-DROME	TRUE	TRUE	2	1600.9	0.5	17of 24	3.1602	TRUE		TRUE	::::::::::::::
LKEEAAATTAAAAAATTTSA	2	4.27	0.186	565	31	RL3-DROME	TRUE	FALSE	2	1822	0.6	20of 38	3.9409	TRUE		TRUE	::::::::::::::::::::
YALVSAIAASGVPALVQSK	14	9.72	0.342	1402	52.2	RL4-DROME	TRUE	TRUE	2	1846.2	2.4	27of 36	4.9497	TRUE		TRUE	::::::::::::::::::
APIRPDVVNEVHQLLR	11	7.85	0.292	1180	42	RL4-DROME	TRUE	TRUE	3	1857.2	1.3	33of 60	5.4774	TRUE		TRUE	::::::::::::::
PLVSVYTEK	9	6.87	0.259	1276	24	RL4-DROME	TRUE	TRUE	1	1036.2	-0.5	12of 16	2.3048	TRUE		TRUE	::::::::::
VPPPIHQFSQTLDK	10	7.82	0.332	920	31	RL7A-DROME	TRUE	TRUE	2	1607.8	1.2	14of 26	2.5082	TRUE		TRUE	::::::::::::::
NFGIGQNVQPK	14	10.1	0.296	382	18.8	RL7A-DROME	TRUE	TRUE	2	1202.4	0.8	15of 20	2.4758	TRUE		TRUE	::::::::::::
NFGIGQNVQPK	13	10.1	0.163	646	18.8	RL7A-DROME	TRUE	TRUE	2	1202.4	1.6	14of 20	2.5623	TRUE		TRUE	::::::::::::
TCTTLALTTVDNNDK	2	3.89	0.102	570	25.9	RL7A-DROME	TRUE	TRUE	2	1667.8	1.1	11of 28	1.8112	TRUE		TRUE	::Cys_CAM:::::::::::::
GVTFGFQYK	15	9.72	0.181	947	23.8	RL9-DROME	TRUE	TRUE	1	1047.2	0	9of 16	1.9412	TRUE		TRUE	::::::::::
TSFFQALSIPTK	15	10.1	0.272	1393	34.4	RLA0	TRUE	TRUE	2	1340.6	-0.3	15of 22	2.8619	TRUE		TRUE	::::::::::::
TSFFQALSIPTK	14	10.1	0.25	1310	34.4	RLA0	TRUE	TRUE	2	1340.6	-0.3	17of 22	3.6571	TRUE		TRUE	::::::::::::
GTIEIINDVPILKPGDK	3	4.31	0.114	1613	43.6	RLA0	TRUE	TRUE	2	1823.1	2	15of 32	1.7388	TRUE		TRUE	::::::::::::::::
PGAIAPLHVIIPAQNTGLGPEK	12	7.82	0.072	1469	53.7	RLA0-DROME	TRUE	TRUE	2	2194.6	1.5	13of 42	2.1756	TRUE		TRUE	::::::::::::::::::::
YVAAYLLAVLGGK	15	9.53	0.482	1750	46.8	RLA2-DROME	TRUE	TRUE	2	1338.6	2	22of 24	4.4769	TRUE		TRUE	::::::::::::
YVAAYLLAVLGGK	14	9.53	0.464	1644	46.8	RLA2-DROME	TRUE	TRUE	2	1338.6	0.2	22of 24	4.7247	TRUE		TRUE	::::::::::::
ILSSVGVEVDAER	2	3.83	0.282	768	33.7	RLA2-DROME	TRUE	TRUE	2	1374.5	1.6	12of 24	1.5598	TRUE		TRUE	::::::::::::
NFYQEHPNVANR	9	7.77	0.087	992	18.2	RM62-DROME	TRUE	TRUE	2	1489.6	0.3	10of 22	1.6194	TRUE		TRUE	::::::::::::
NSLGGNYVNCGVFK	13	8.88	0.206	914	28.6	RP16-DROME	TRUE	TRUE	2	1529.7	0.8	15of 26	2.4037	TRUE		TRUE	:::::::::Cys_CAM:::::
NQLLKDPNVLFAGYK	13	9.63	0.241	1202	40.5	RPBY-DROME	TRUE	TRUE	2	1721	2	16of 28	2.6641	TRUE		TRUE	::::::::::::::
VAIYEYLFK	7	6.81	0.226	1585	38.6	RS10-DROME	TRUE	TRUE	2	1146.4	0.4	1	2.5009	TRUE		TRUE	::::::::::
SLIADGLVHGIHQACK	10	7.32	0.562	1112	35.9	RS12-DROME	TRUE	TRUE	2	1719.9	1.7	23of 30	5.3543	TRUE		TRUE	:::::::::::::::Cys_CAM:::
DFGEETPALDVVK	1	3.59	0.386	836	31.1	RS12-DROME	TRUE	TRUE	2	1420.6	1.7	20of 24	3.6376	TRUE		TRUE	::::::::::::::
GISQSALPYR	15	9.85	0.256	268	22.8	RS13-DROME	TRUE	TRUE	1	1092.2	-0.5	10of 18	1.5742	TRUE		TRUE	::::::::::
TLGITALHIK	15	10.1	0.344	917	29.8	RS14-DROME	TRUE	TRUE	2	1067.3	1.7	14of 18	2.3379	TRUE		TRUE	::::::::::
EEVQVQLGPQVR	2	4.27	0.322	577	26.5	RS14-DROME	TRUE	TRUE	2	1382.6	2.1	12of 22	2.3272	TRUE		TRUE	::::::::::::
TLGITALHIK	14	10.1	0.15	843	29.8	RS14-DROME	TRUE	TRUE	1	1067.3	0.1	9of 18	2.21	TRUE		TRUE	::::::::::
IEDVTPIPSDSTR	1	3.71	0.106	434	25.5	RS14-DROME	TRUE	TRUE	2	1430.6	1.5	15of 24	2.1207	TRUE		TRUE	::::::::::::
LLDFHNIR	10	7.85	0.148	1029	28.6	RS17-DROME	TRUE	TRUE	2	1028.2	1.3	13of 14	2.5724	TRUE		TRUE	::::::::

LLDFHNIR	11	7.85	0.101	786	28.6	RS17-DROME	TRUE	TRUE	2	1028.2	1.5	13of 14	2.5137	TRUE	TRUE	::::::::
LTLDFHTNK	11	7.82	0.001	648	20.9	RS17-DROME	TRUE	TRUE	1	1089.2	0.7	9of 16	1.7423	TRUE	TRUE	::::::::
HGYIGEFEIVDDHR	3	4.53	0.272	1311	29.8	RS1A-DROME	TRUE	TRUE	3	1687.8	2.2	29of 52	4.3757	TRUE	TRUE	::::::::::::::
QFGYVVLTTSGGIMDHEEAR	3	4.43	0.165	1564	45.73	RS1A-DROME	TRUE	TRUE	3	2211.5	2	20of 76	2.509	TRUE	TRUE	::::::::::::::::::
IIDLHSPSEIVKK	11	7.8	0.344	653	31.9	RS20-DROME	TRUE	TRUE	2	1479.8	-0.1	16of 24	3.1564	TRUE	TRUE	::::::::::::::
AFVAIGDNNGHIGLGVK	10	7.82	0.431	1192	39	RS2-DROME	TRUE	TRUE	2	1682.9	1.2	22of 32	4.3954	TRUE	TRUE	::::::::::::::::
AFVAIGDNNGHIGLGVK	11	7.82	0.416	948	39	RS2-DROME	TRUE	TRUE	2	1682.9	1.7	20of 32	3.7686	TRUE	TRUE	::::::::::::::::
LLTMAGIEDCYTSAR	2	4.08	0.14	982	41.73	RS2-DROME	TRUE	TRUE	2	1701.9	0.5	9of 28	1.6876	TRUE	TRUE	:::::::::Cys_CAM::::::
NVLCNFHGMDLTTDKYR	9	7.16	0.511	1624	37.33	RS3A-DROME	TRUE	TRUE	2	2085.3	2	23of 32	4.6849	TRUE	TRUE	::::Cys_CAM::::::::::::::
IYPLHDVYIR	10	7.7	0.315	1085	36.4	RS3A-DROME	TRUE	TRUE	1	1289.5	-0.7	12of 18	2.2935	TRUE	TRUE	::::::::::
VFEVSLADLQK	2	4.08	0.242	988	35.3	RS3A-DROME	TRUE	TRUE	1	1249.4	0.7	14of 20	3.0887	TRUE	TRUE	::::::::::::
PLHDVYIR	10	7.76	0.052	1088	24.5	RS3A-DROME	TRUE	FALSE	2	1013.2	0.8	10of 14	1.9915	TRUE	TRUE	::::::::
ELAEDGYSGVEVR	1	3.69	0.367	492	26.9	RS3-DROME	TRUE	TRUE	2	1424.5	0.9	18of 24	3.3375	TRUE	TRUE	::::::::::::::
IPPPSKPLDDLSEAK	3	4.31	0.306	1127	30.5	RS3-DROME	TRUE	TRUE	2	1607.8	1.6	17of 28	2.3747	TRUE	TRUE	::::::::::::::::
GLCAIAQAESLR	7	6.29	0.144	1125	32.3	RS3-DROME	TRUE	TRUE	2	1289.4	1.2	1	2.5192	TRUE	TRUE	:::Cys_CAM:::::::::
ERHPGSFDIVHIK	11	7.97	0.442	650	23.9	RS4-DROME	TRUE	TRUE	3	1535.7	1.8	27of 48	3.1994	TRUE	TRUE	::::::::::::
HPGSFDIVHIK	10	7.97	0.296	854	23.4	RS4-DROME	TRUE	TRUE	1	1250.4	-0.8	11of 20	1.6738	TRUE	TRUE	::::::::::
TDPTYPAGYMDVITLEK	1	3.71	0.186	1140	42.03	RS4-DROME	TRUE	TRUE	2	1915.2	0.4	11of 32	1.6222	TRUE	TRUE	::::::::::::::::
GVPFLVTHDGR	11	7.85	0.185	705	25.9	RS4-DROME	TRUE	TRUE	2	1198.4	0.4	16of 20	2.3237	TRUE	TRUE	::::::::::
DIPGLTDTTIPR	1	3.89	0.369	824	28.3	RS6-DROME	TRUE	TRUE	2	1299.5	0.5	15of 22	2.929	TRUE	TRUE	::::::::::::
MKLDYVLGLK	14	9.63	0.169	1046	35.13	RS9-DROME	TRUE	TRUE	2	1180.5	2.1	16of 18	2.7306	TRUE	TRUE	::::::::::
MKLDYVLGLK	13	9.63	0.021	972	35.13	RS9-DROME	TRUE	TRUE	2	1196.5	0.5	11of 18	1.3062	TRUE	TRUE	:Oxidation_M:::::::::
RADGVNILNLGK	15	10.09	0.244	845	26.5	RSP4-DROME	TRUE	TRUE	2	1270.5	0.2	17of 22	3.9425	TRUE	TRUE	::::::::::::
CNNVLYIK	13	8.88	0.004	703	24.3	RUXF-DROME	TRUE	TRUE	2	1024.2	1	10of 14	1.8939	TRUE	TRUE	:Cys_CAM:::::::
DDLEGEFTKYGKLNSVW	3	4.07	0.154	2094	40.4	RX21-DROME	TRUE	FALSE	3	2002.2	-1.5	15of 64	1.2937	TRUE	TRUE	::::::::::::::::
EEPSDLGCTSMNVMRDNYSMGGSVSAVR	3	4.07	0.015	1305	49.99	S05661	TRUE	FALSE	3	3067.3	0	20of108	1.6151	TRUE	TRUE	:::::::Cys_CAM:::Oxidation_M:::::::::::::::::
CEGKILKIADFGLARNIEGDCYR	7	6.36	0.108	1360	56.2	S18014	TRUE	FALSE	3	2700	0.8	17	2.2679	TRUE	TRUE	:Cys_CAM::::::::::::::::Cys_CAM:::
NTQDFTGHALALFR	9	7.85	0.497	1822	34.3	S36746	TRUE	TRUE	2	1591.8	0.3	19of 26	4.2278	TRUE	TRUE	::::::::::::::
KSDIYVSLVSSTHQVAAK	15	9.63	0.46	815	32.7	S36746	TRUE	TRUE	3	1934.2	1.5	36of 68	5.2911	TRUE	TRUE	::::::::::::::::
YYGGESASITPLEELFQR	2	3.97	0.454	1344	47.2	S36746	TRUE	TRUE	2	2061.3	2.4	20of 34	3.0101	TRUE	TRUE	::::::::::::::::
SPYLYPMYGLGELPQGFAR	6	6.78	0.356	2006	59.13	S36746	TRUE	TRUE	2	2160.5	0.1	18of 36	2.963	TRUE	TRUE	::::::::::::::::
SPYLYPMYGLGELPQGFAR	7	6.78	0.27	1809	59.13	S36746	TRUE	TRUE	2	2160.5	0.2	1	2.7057	TRUE	TRUE	::::::::::::::::
EALASDLMGMFEK	1	3.83	0.229	1478	39.26	S36746	TRUE	TRUE	2	1442.7	0.9	14of 24	1.7898	TRUE	TRUE	::::::::::::
KSDIYVSLVSSTHQVAAK	14	9.63	0.188	787	32.7	S36746	TRUE	TRUE	2	1934.2	0.4	18of 34	2.0708	TRUE	TRUE	::::::::::::::::
FLMANGQLVK	15	10.1	0.116	864	33.93	S36746	TRUE	TRUE	1	1121.4	-0.5	10of 18	1.6547	TRUE	TRUE	::::::::::
DGLSTQIIIPQK	6	6.76	0.073	1315	30.6	S36746	TRUE	TRUE	1	1313.5	-0.4	15of 22	2.5565	TRUE	TRUE	::::::::::::
CVSTLLDLIQTK	5	6.1	0.207	1930	38.4	S39295	TRUE	TRUE	2	1391.6	0.1	15of 22	3.3331	TRUE	TRUE	:Cys_CAM:::::::::::
LHFFMPGFAPLTAK	15	10.1	0.196	1514	50.23	S39821	TRUE	FALSE	2	1577.9	0.7	18of 26	3.6995	TRUE	TRUE	::::::::::::::
TDISSHHHIFVGDLSPEIETETLR	4	4.66	0.127	1593	51.3	S41644	TRUE	TRUE	3	2735	1.1	31of 92	3.6367	TRUE	TRUE	::::::::::::::::::::::
STSVAQLLHATIVLDTINFAPAAK	9	7.82	0.443	2299	66	S42578	TRUE	TRUE	2	2482.9	1.4	18of 46	4.3753	TRUE	TRUE	::::::::::::::::::::::
EVAAANSYR	9	6.89	0.083	890	15.2	S42989	TRUE	FALSE	2	981.1	-2.8	10of 16	1.2809	TRUE	TRUE	::::::::::
CVMSMHDGIVLYTTPSITDVLGYPR	5	5.1	0.031	2559	71.36	S52955	TRUE	FALSE	3	2859.2	-2.2	15of 96	1.6714	TRUE	TRUE	:Cys_CAM::Oxidation_M::Oxidation_M:::::::::::::::::::
AHGIGVHSAEEIEEFGKDDLK	3	4.43	0.42	1347	35.6	S58776	TRUE	TRUE	3	2282.5	2.3	31of 80	3.94	TRUE	TRUE	::::::::::::::::::::
LPNSILNFFFK	15	10.1	0.175	1928	46.4	S58776	TRUE	TRUE	2	1340.6	0.7	18of 20	2.8213	TRUE	TRUE	::::::::::::
DIIYLYQFSR	6	6.64	0.057	1735	39.4	S58776	TRUE	TRUE	1	1318.5	-0.2	11of 18	1.5348	TRUE	TRUE	::::::::::
KAQLQIEQLTTELANEK	4	4.56	0.435	1669	35.4	S61477	TRUE	TRUE	2	1958.2	2.5	25of 32	6.0301	TRUE	TRUE	::::::::::::::::
IVMSHDQEGADLLNREVRD	1	4.2	0.004	1856	39.63	S64733	TRUE	FALSE	2	2214.4	1.7	8of 36	1.0668	TRUE	TRUE	:::Oxidation_M:::::::::::::::
FEGSSESDLSTFVK	2	3.83	0.385	757	29.2	S68280	TRUE	TRUE	2	1533.6	1.3	19of 26	3.4064	TRUE	TRUE	::::::::::::::
YALKDEFSVENLQDFVEK	2	3.93	0.325	1212	47.6	S68280	TRUE	TRUE	2	2175.4	1.6	23of 34	4.1356	TRUE	TRUE	::::::::::::::::
ENFHGLVGHR	11	8	0.313	356	16.5	S68280	TRUE	TRUE	2	1166.3	1	15of 18	2.4387	TRUE	TRUE	::::::::::
DTTLFGYFSDSDSK	1	3.6	0.31	1161	27.7	S68280	TRUE	TRUE	2	1583.6	1.1	16of 26	2.357	TRUE	TRUE	::::::::::::
YSVSGYPTLK	14	9.53	0.283	568	22	S68280	TRUE	TRUE	1	1115.3	1.6	10of 18	2.5272	TRUE	TRUE	::::::::::
YSVSGYPTLK	15	9.53	0.232	576	22	S68280	TRUE	TRUE	2	1115.3	1.9	12of 18	2.2388	TRUE	TRUE	::::::::::
FEGSSESDLSTFVK	1	3.83	0.195	789	29.2	S68280	TRUE	TRUE	2	1533.6	0.6	12of 26	2.3068	TRUE	TRUE	::::::::::::::
DFQNPLITAYYSVDYQK	1	3.89	0.145	1370	44.2	S68280	TRUE	TRUE	2	2066.3	2.8	12of 32	2.2821	TRUE	TRUE	::::::::::::::::
LLANELEPYIK	3	4.27	0.05	1545	39.7	S68280	TRUE	TRUE	2	1303.5	0.2	16of 20	3.2674	TRUE	TRUE	::::::::::::
YKSDVYLLPK	14	9.47	0.329	602	28	SAH2-DROME	TRUE	TRUE	2	1226.5	0.9	15of 18	2.598	TRUE	TRUE	::::::::::
ILDEEVASLHLEK	2	4.16	0.395	812	37.8	SAHH-DROME	TRUE	TRUE	2	1496.7	1.2	19of 24	3.9775	TRUE	TRUE	::::::::::::::
QATYLGVSQTGPFKPDHYR	14	9.53	0.373	759	32.2	SAHH-DROME	TRUE	TRUE	2	2166.4	-0.5	14of 36	3.593	TRUE	TRUE	::::::::::::::::::
TTTGVHNLYK	13	9.72	0.242	430	14.4	SAHH-DROME	TRUE	FALSE	2	1134.3	0	12of 18	2.3164	TRUE	TRUE	::::::::::
FVQLGGK	15	10.1	0.03	800	18.7	SCAL-DROME	TRUE	FALSE	1	748.9	-0.2	9of 12	1.232	TRUE	TRUE	:::::::
DVSFVIHNLPVIAK	10	7.82	0.26	1541	45.2	SELD-DROME	TRUE	TRUE	2	1552.9	1	17of 26	3.2754	TRUE	TRUE	::::::::::::
GFSSIETPGYVGFANLPNQVHR	11	7.77	0.402	1172	49	SEP1-DROME	TRUE	TRUE	2	2391.6	1.9	18of 42	3.4266	TRUE	TRUE	::::::::::::::::::::
INFHFDENPYFENK	3	4.43	0.348	1519	34.6	SET-DROME	TRUE	TRUE	2	1815	1.4	16of 26	2.825	TRUE	TRUE	::::::::::::
CNGCAKRDALCQDLNGVLRNLER	10	8.02	0.038	600	44.6	SGS3-DROME	TRUE	FALSE	3	2733.9	1.5	21of 88	2.624	TRUE	TRUE	:Cys_CAM:::Cys_CAM::::::Cys_CAM::::::::::::
LAPADTTAVSTAQIELK	2	4.08	0.198	746	39.4	SH3B-DROME	TRUE	TRUE	1	1730	-1.2	13of 32	1.7353	TRUE	TRUE	::::::::::::::
LQKTASPIQP	13	10.1	0.08	1186	19.8	SIF2-DROME	TRUE	FALSE	2	1083.3	1.6	7of 18	1.2404	TRUE	TRUE	::::::::::
ENHSPGPRTITA	11	7.85	0.085	410	12	SIMA-DROME	TRUE	FALSE	2	1280.4	1.9	9of 22	1.3703	TRUE	TRUE	::::::::::::
NRDPVHLETLSIR	9	7.85	0.317	1440	28.4	SMD1-DROME	TRUE	TRUE	2	1550.8	1.8	17of 24	3.1377	TRUE	TRUE	::::::::::::
FLILPDMLK	6	6.76	0.158	1898	45.43	SMD3-DROME	TRUE	TRUE	1	1090.4	0	11of 16	2.1778	TRUE	TRUE	::::::::::
ITLFGADSIIGR	6	6.79	0.307	1747	40	SODC-DROMD	TRUE	TRUE	2	1263.5	1.6	20of 22	2.8852	TRUE	TRUE	::::::::::::
ITLFGADSIIGR	7	6.79	0.111	1524	40	SODC-DROMD	TRUE	TRUE	2	1263.5	0.9	5	2.6053	TRUE	TRUE	::::::::::::
TVVVHADADDLGQGGHELSK	3	4.43	0.484	1031	30.4	SODC-DROME	TRUE	TRUE	2	2049.2	-0.1	22of 38	5.9345	TRUE	TRUE	::::::::::::::::::
GTVFFEQESSGTPVK	3	4.27	0.265	1267	28.7	SODC-DROME	TRUE	TRUE	2	1613.8	0.9	15of 28	2.6118	TRUE	TRUE	::::::::::::::
DQLINASHAQSPAILK	10	7.82	0.391	892	34	SPCA-DROME	TRUE	TRUE	2	1706.9	1.6	20of 30	4.4927	TRUE	TRUE	::::::::::::::::
MQHNLEQQIQAR	9	7.85	0.036	969	20.83	SPCA-DROME	TRUE	TRUE	2	1512.7	1.7	15of 22	1.9946	TRUE	TRUE	:Oxidation_M:::::::::::
LFVGGLSWETTEK	3	4.27	0.168	1580	38.8	SQD-DROME	TRUE	TRUE	2	1467.7	2	14of 24	2.033	TRUE	TRUE	::::::::::::::
YGEIESINVK	2	4.27	0.124	540	23.4	SQD-DROME	TRUE	TRUE	2	1152.3	2	12of 18	2.8532	TRUE	TRUE	::::::::::
ARNVLIGENNVAK	15	10.09	0.009	1139	25.9	SR64-DROME	TRUE	FALSE	1	1398.6	1.5	10of 24	1.4257	TRUE	TRUE	::::::::::::::
PGTVIFNASVYK	14	9.72	0.024	706	31.5	STAN-DROME	TRUE	FALSE	1	1296.5	0.4	10of 22	1.5025	TRUE	TRUE	::::::::::::
FGMEAIASL	1	3.3	0.003	1150	33.83	STIM-DROME	TRUE	FALSE	1	955.1	-1.1	8of 16	1.1079	TRUE	TRUE	:::Oxidation_M:::::::
LLDMVINPPLSENKR	7	7.02	0.025	1724	43.43	SUS-DROME	TRUE	FALSE	2	1756.1	1.4	92	0.9964	TRUE	TRUE	::::Oxidation_M:::::::::::
KIPALLETIHESMLNK	10	7.8	0.216	1313	44.33	SYEP-DROME	TRUE	TRUE	2	1854.2	1	15of 30	2.9003	TRUE	TRUE	::::::::::::Oxidation_M::::

NIDALPAVHIGNPK	9	7.82	0.325	1532	30.5	SYFB-DROME	TRUE	TRUE	2	1459.7	0.9	17of 26	3.0866	TRUE	TRUE	::::::::::::::
TAGFEVVHGLLDR	5	5.22	0.262	1639	35.1	SYFB-DROME	TRUE	TRUE	2	1414.6	0.1	14of 24	2.5122	TRUE	TRUE	::::::::::::
RLVVLEPLK	15	10.09	0.171	873	34.7	SYQ-DROME	TRUE	TRUE	2	1067.4	1.6	13of 16	2.005	TRUE	TRUE	::::::::::
ILLCEATAAVLR	7	6.29	0.331	1435	46.4	SYR-DROME	TRUE	TRUE	2	1330.6	1.1	1	3.255	TRUE	TRUE	::::Cys_CAM::::::::
VLVDFSSPNIAK	7	6.76	0.203	1168	34.7	SYR-DROME	TRUE	TRUE	2	1290.5	1.5	7	2.0336	TRUE	TRUE	::::::::::::
LHDILIK	10	7.82	0.042	594	27	SYR-DROME	TRUE	TRUE	2	852.1	1.2	10of 12	1.5896	TRUE	TRUE	::::::::
ASFALPLHYPR	15	9.85	0.073	1053	33.9	T08434	TRUE	TRUE	2	1272.5	1.3	11of 20	1.7559	TRUE	TRUE	::::::::::::
LSSAPTPTPSNPFAVLSSLIDK	7	6.76	0.017	2085	54.5	T09072	TRUE	TRUE	2	2243.6	2	2	1.4726	TRUE	TRUE	::::::::::::::::::::::
NHMESGGVAGR	9	7.85	0.024	648	9.53	T13158	TRUE	FALSE	2	1131.2	-0.8	10of 20	1.3672	TRUE	TRUE	:::Oxidation_M:::::::::
YPILMGPNFFQNLGLK	14	9.72	0.361	1773	58.23	T13174	TRUE	TRUE	2	1853.2	1.8	24of 30	4.4985	TRUE	TRUE	::::::::::::::::
YPILMGPNFFQNLGLK	15	9.72	0.334	1869	58.23	T13174	TRUE	TRUE	2	1853.2	0.6	23of 30	4.0988	TRUE	TRUE	::::::::::::::::
VVDTTGAGDAFIGALAHNLAR	5	5.1	0.498	1998	49.4	T13380	TRUE	TRUE	2	2070.3	1.2	23of 40	3.6329	TRUE	TRUE	::::::::::::::::::::
VNAGHVPGTDVGPVISAASR	10	7.85	0.211	877	33.9	T13418	TRUE	TRUE	2	1905.1	2.1	17of 38	2.5762	TRUE	TRUE	::::::::::::::::::
IEINFPAEYPFKPPK	8	7	0.141	2020	42.9	T13578	TRUE	TRUE	2	1791.1	-0.3	16of 28	1.977	TRUE	TRUE	::::::::::::::
ECKDRQSFTWWPASHVVAPKQPLF	12	8.94	0.081	1588	59.1	T13711	TRUE	FALSE	3	2916.3	-2	13of 92	1.6553	TRUE	TRUE	::Cys_CAM::::::::::::::::::::
FVANIKSPLEVDSGVGTPLSPPSTASNSSGGSIFSRMG	9	7.02	0.047	2323	75.53	T13718	TRUE	FALSE	3	3753.2	-2.2	22of148	1.5046	TRUE	TRUE	::::::::::::::::::::::::::::::::::::
SGSLTTLLLSFTGTSLPVSYAR	14	9.85	0.383	1906	62.5	T13719	TRUE	TRUE	2	2272.6	2.2	18of 42	3.8475	TRUE	TRUE	::::::::::::::::::::::
IILNDFSLTTLK	7	6.76	0.217	1576	45.7	T13798	TRUE	TRUE	2	1378.7	1.5	4	3.4708	TRUE	TRUE	::::::::::::
LIEPIDNLLDQLSLTFGEQSSK	1	3.59	0.108	1978	65.1	T13798	TRUE	TRUE	2	2461.8	0.6	13of 42	1.8269	TRUE	TRUE	::::::::::::::::::::::
MPNMPNALGMLQSLP	6	6.02	0.061	2046	47.29	T13828	TRUE	FALSE	2	1631	2.8	6of 28	0.9775	TRUE	TRUE	::::Oxidation_M:::::::::::
YTSGLDPRLLDMAYP	1	3.89	0.063	2210	44.83	T13928	TRUE	FALSE	3	1713	0.4	8of 56	1.0789	TRUE	TRUE	::::::::::::::
ALVATGDAHSHTSFTK	12	7.97	0.449	688	22.3	T13930	TRUE	TRUE	2	1643.8	0.2	22of 30	4.493	TRUE	TRUE	::::::::::::::::
ALVATGDAHSHTSFTK	11	7.97	0.423	364	22.3	T13930	TRUE	TRUE	2	1643.8	1	21of 30	4.1546	TRUE	TRUE	::::::::::::::::
VAQHPFTYILNPAEK	10	7.74	0.358	1180	38	T13930	TRUE	TRUE	2	1729	1.9	18of 28	4.2859	TRUE	TRUE	::::::::::::::
GVEAHNPNAYVMHAGR	11	7.92	0.305	316	22.73	T13930	TRUE	TRUE	3	1739.9	2.4	24of 60	2.2432	TRUE	TRUE	::::::::::Oxidation_M:::::
GVEAHNPNAYVMHAGR	12	7.92	0.304	735	22.73	T13930	TRUE	TRUE	3	1723.9	1.8	29of 60	4.067	TRUE	TRUE	::::::::::::::::
VDPTGLQPGVHSAVIR	10	7.85	0.297	773	34	T13930	TRUE	TRUE	2	1646.9	2	16of 30	2.3845	TRUE	TRUE	::::::::::::::::
VDPTGLQPGVHSAVIR	11	7.85	0.277	632	34	T13930	TRUE	TRUE	2	1646.9	1	16of 30	1.8808	TRUE	TRUE	::::::::::::::::
MLFDANKALVATGDAHSHTSFTK	12	7.94	0.218	688	43.53	T13930	TRUE	FALSE	3	2463.8	1.7	18of 88	2.9963	TRUE	TRUE	::::::::::::::::::::::
SQLMNGTSMAAPHVAGAVALLISGLK	14	10.1	0.211	1733	67.46	T13930	TRUE	TRUE	3	2539	2.3	23of100	2.4934	TRUE	TRUE	::::::::::::::::::::::
ISEANLVASFK	7	6.95	0.168	1211	30.6	T13930	TRUE	TRUE	2	1179.4	1.8	10	1.7696	TRUE	TRUE	::::::::::
DHFVELAAINGALGHEHIR	5	5.75	0.154	1482	44.6	T13930	TRUE	TRUE	3	2100.3	2.4	31of 72	3.6882	TRUE	TRUE	::::::::::::::::::
AAGDGISVQNDPPVDSSGSPASPKKGKANADDYAESFR	3	4.24	0.068	2289	42	T13930	TRUE	FALSE	3	3808	-1.5	23of148	2.3997	TRUE	TRUE	::::::::::::::::::::::::::::::::::
KLLACEQELQPLNEIMPSMPEERQQW	3	4.09	0.011	2436	72.26	T13944	TRUE	FALSE	3	3231.6	-1	10of100	1.4073	TRUE	TRUE	:::::Cys_CAM::::::::::Oxidation_M:::Oxidation_M::::::::
INNGNISPGDGLPTK	9	6.76	0.021	1061	23	T13998	TRUE	FALSE	2	1497.6	0.1	11of 28	1.4179	TRUE	TRUE	::::::::::::::
EPQYGFVAKDFIPFR	7	6.94	0.1	2039	45.6	T2D5-DROME	TRUE	FALSE	2	1815.1	1.1	16	1.1779	TRUE	TRUE	::::::::::::::
KFEALKDPGVISVTNIYNYYK	14	9.32	0.465	1276	52.5	TAL1-DROME	TRUE	TRUE	2	2463.8	-0.7	25of 40	5.1052	TRUE	TRUE	::::::::::::::::::
ALAGCDLLTISPALLK	8	6.1	0.147	2267	56.8	TAL1-DROME	TRUE	TRUE	2	1657	1.1	12of 30	2.4529	TRUE	TRUE	:::::Cys_CAM:::::::::::
TVGGGDDSFNTFFSETGAGK	1	3.71	0.567	1041	30.5	TBA1-DROME	TRUE	TRUE	2	1995.1	1.3	24of 38	4.8456	TRUE	TRUE	::::::::::::::::::
IHFPLVTYAPVISAEK	9	7.74	0.489	1914	50.8	TBA1-DROME	TRUE	TRUE	1	1786.1	-0.2	19of 30	4.0744	TRUE	TRUE	::::::::::::::::
IHFPLVTYAPVISAEK	10	7.74	0.462	1509	50.8	TBA1-DROME	TRUE	TRUE	1	1786.1	-1.2	17of 30	3.2977	TRUE	TRUE	::::::::::::::::
AYHEQLSVAEITNACFEPANQMVK	3	4.54	0.408	1573	54.53	TBA1-DROME	TRUE	TRUE	2	2752	1.1	24of 46	5.5581	TRUE	TRUE	::::::::::::::Cys_CAM:::::::::
TIQFVDWCPTGFK	6	6.1	0.398	1782	41.1	TBA1-DROME	TRUE	TRUE	2	1599.8	1.8	17of 24	3.6974	TRUE	TRUE	:::::::Cys_CAM::::::
PTVVDEVR	2	4.08	0.258	1125	18.3	TBA1-DROME	TRUE	FALSE	1	915	0.3	10of 14	1.8433	TRUE	TRUE	::::::::
DIERPTYTNLNR	6	6.96	0.247	1166	22.1	TBA1-DROME	TRUE	FALSE	2	1492.6	0.4	13of 22	2.3817	TRUE	TRUE	::::::::::::
QLFHPEQLITGK	10	7.82	0.242	1204	31	TBA1-DROME	TRUE	TRUE	2	1411.6	0.8	13of 22	2.3109	TRUE	TRUE	::::::::::::
EIVDLVLDR	1	3.71	0.229	1001	34.5	TBA1-DROME	TRUE	TRUE	2	1072.2	2	13of 16	2.1772	TRUE	TRUE	::::::::::
FDGALNVDLTEFQTNLVPYPR	1	3.71	0.213	1516	61.7	TBA1-DROME	TRUE	TRUE	2	2410.7	1	20of 40	2.7453	TRUE	TRUE	::::::::::::::::::::
QLFHPEQLITGKEDAANNYAR	6	5.35	0.209	1426	41	TBA1-DROME	TRUE	TRUE	2	2416.7	0.9	11of 40	2.1557	TRUE	TRUE	::::::::::::::::::::
NLDIERPTYTNLNR	6	6.96	0.178	1162	29.6	TBA1-DROME	TRUE	TRUE	2	1719.9	0.3	14of 26	2.8132	TRUE	TRUE	::::::::::::::
AVCMLSNTTAIAEAWAR	8	6.29	0.055	1940	48.33	TBA1-DROME	TRUE	TRUE	2	1882.1	1.4	13of 32	1.7153	TRUE	TRUE	:::Cys_CAM:Oxidation_M::::::::::::
IMNTYSVVPSPK	15	9.72	0.389	285	28.93	TBB1-DROME	TRUE	TRUE	2	1352.6	1.3	17of 22	2.9887	TRUE	TRUE	::Oxidation_M:::::::::::
MSATFIGNSTAIQELFK	7	6.95	0.388	1792	47.63	TBB1-DROME	TRUE	TRUE	2	1859.1	0.8	1	4.2728	TRUE	TRUE	::::::::::::::::::
ISEQFTAMFR	7	6.98	0.387	1311	32.03	TBB1-DROME	TRUE	TRUE	2	1230.4	2.4	1	3.569	TRUE	TRUE	::::::::::
SLGGGTGSGMGTLLISK	14	10.1	0.341	958	34.53	TBB1-DROME	TRUE	FALSE	2	1536.8	0.7	17of 32	2.8433	TRUE	TRUE	::::::::::::::::
GHYTEGAELVDSVLDVVRK	4	4.54	0.303	1913	40.5	TBB1-DROME	TRUE	TRUE	3	2088.3	0.8	28of 72	2.8677	TRUE	TRUE	::::::::::::::::::
IMNTYSVVPSPK	14	9.72	0.3	438	28.93	TBB1-DROME	TRUE	TRUE	2	1352.6	1.1	18of 22	2.6234	TRUE	TRUE	::Oxidation_M:::::::::::
MSATFIGNSTAIQELFK	8	6.95	0.294	2351	47.63	TBB1-DROME	TRUE	TRUE	2	1859.1	1.5	15of 32	2.964	TRUE	TRUE	::::::::::::::::::
SGPFGQIFRPDNFVFGQSGAGNNWAK	15	10.09	0.285	1574	55.9	TBB1-DROME	TRUE	TRUE	3	2800.1	0.5	30of100	4.2041	TRUE	TRUE	::::::::::::::::::::::
YLTVAAIFR	14	9.85	0.279	1267	37.1	TBB1-DROME	TRUE	TRUE	2	1054.3	0.8	15of 16	2.777	TRUE	TRUE	::::::::::
GHYTEGAELVDSVLDVVR	2	4.06	0.272	1300	42.6	TBB1-DROME	TRUE	TRUE	2	1960.2	0.6	28of 34	6.4355	TRUE	TRUE	::::::::::::::::
YLTVAAIFR	15	9.85	0.244	1359	37.1	TBB1-DROME	TRUE	TRUE	2	1054.3	2.2	15of 16	2.6635	TRUE	TRUE	::::::::::
AVLVDLEPGTMDSVR	1	3.71	0.226	969	41.83	TBB1-DROME	TRUE	TRUE	2	1602.8	2.4	19of 28	3.3033	TRUE	TRUE	::::::::::::::::
FPGQLNADLRK	15	10.09	0.211	257	25	TBB1-DROME	TRUE	TRUE	2	1259.5	0.6	16of 20	2.0993	TRUE	TRUE	::::::::::
SGPFGQIFRPDNFVFGQSGAGNNWAK	14	10.09	0.205	1482	55.9	TBB1-DROME	TRUE	TRUE	2	2800.1	-0.4	20of 50	2.8268	TRUE	TRUE	::::::::::::::::::::::
NSSYFVEWIPNNVK	6	6.87	0.163	1746	37.6	TBB1-DROME	TRUE	TRUE	1	1697.9	-0.1	12of 26	2.3199	TRUE	TRUE	::::::::::::
ALTVPELTQQMFDAK	2	4.08	0.07	913	41.23	TBB1-DROME	TRUE	TRUE	2	1709	2.1	11of 28	1.4625	TRUE	TRUE	::::::::::Oxidation_M::::::
VSVYYNEASAVTR	7	6.83	0.42	916	28.1	TBB3-DROME	TRUE	TRUE	2	1459.6	0.8	1	3.2109	TRUE	TRUE	::::::::::::
EIVHLQAGQCGNQIGAK	12	7.16	0.193	749	30.2	TBB3-DROME	TRUE	TRUE	3	1824	0.1	25of 64	2.6883	TRUE	TRUE	::::::::::Cys_CAM:::::::::
TQNVMAALSISNIVK	15	10.1	0.445	1439	39.33	TCPA-DROME	TRUE	TRUE	2	1589.9	-0.1	21of 28	4.9501	TRUE	TRUE	::::::::::::::
TQNVMAALSISNIVK	14	10.1	0.379	1343	39.33	TCPA-DROME	TRUE	TRUE	2	1589.9	-0.2	19of 28	3.0016	TRUE	TRUE	::::::::::::::
YFVEAGAMAVR	6	6.89	0.304	1024	34.43	TCPA-DROME	TRUE	TRUE	2	1230.4	1.3	17of 20	2.7082	TRUE	TRUE	:::::::Oxidation_M::::
GPNDFYCDEMER	1	3.59	0.261	597	23.93	TCPA-DROME	TRUE	TRUE	2	1533.6	0.8	17of 22	2.9843	TRUE	TRUE	::::::Cys_CAM::::::
SVHDALCVVK	9	7.16	0.234	1132	23.5	TCPA-DROME	TRUE	TRUE	1	1128.3	-0.7	13of 18	2.4416	TRUE	TRUE	::::::Cys_CAM::::
ESVLIPGYALNCTIASQQMPK	7	6.28	0.204	1539	55.03	TCPA-DROME	TRUE	TRUE	2	2321.7	0.4	5	2.8893	TRUE	TRUE	::::::::::Cys_CAM:::::::::
MGVQVLINDPDKLEAIR	3	4.31	0.11	1557	48.53	TCPA-DROME	TRUE	TRUE	3	1912.3	2.6	22of 64	2.4484	TRUE	TRUE	::::::::::::::::
YISEHLTAPVDELGR	3	4.43	0.044	1316	37	TCPA-DROME	TRUE	TRUE	3	1700.9	1	28of 56	2.5978	TRUE	TRUE	::::::::::::::::
FATEAAITILR	6	6.98	0.035	1522	38.7	TCPA-DROME	TRUE	TRUE	1	1206.4	0.3	12of 20	1.8826	TRUE	TRUE	::::::::::::
KGESQTNVEIIGEQDFTR	2	4.17	0.418	674	28.7	TCPG-DROME	TRUE	TRUE	2	2052.2	0.4	24of 34	3.4934	TRUE	TRUE	::::::::::::::::::
GPYTAVAHALEIIPR	12	7.77	0.402	1639	41.2	TCPG-DROME	TRUE	TRUE	3	1608.9	2.7	18of 56	2.3496	TRUE	TRUE	::::::::::::::::
GPYTAVAHALEIIPR	11	7.77	0.365	1300	41.2	TCPG-DROME	TRUE	TRUE	2	1608.9	1.1	19of 28	3.1031	TRUE	TRUE	::::::::::::::::
LVAGGGAVEMAASQLLTR	7	6.98	0.361	1617	48.13	TCPG-DROME	TRUE	TRUE	3	1745	1.6	2	4.1693	TRUE	TRUE	::::::::::::::::::
ICADIIAVKPDLVFTEK	3	4.31	0.258	1643	54.9	TCPG-DROME	TRUE	TRUE	2	1933.3	1.5	17of 32	3.3685	TRUE	TRUE	::Cys_CAM:::::::::::::::

GVSDLAQHYLLK	11	7.74	0.248	960	31.4	TCPG-DROME	TRUE	TRUE	2	1344.6	1.1	16of 22	3.0873	TRUE		TRUE	::::::::::::
TAVETAILLLR	6	6.98	0.223	1796	42.4	TCPG-DROME	TRUE	TRUE	2	1200.5	1.7	18of 20	3.4227	TRUE		TRUE	::::::::::
IVLLDCSLEYK	2	4.08	0.198	948	42.8	TCPG-DROME	TRUE	TRUE	2	1353.6	1.2	17of 20	3.2701	TRUE		TRUE	::::::Cys_CAM::::::
NLQDALHVAR	10	7.85	0.12	754	22.1	TCPG-DROME	TRUE	TRUE	2	1137.3	1.4	10of 18	1.503	TRUE		TRUE	::::::::::
IPGGAIEESCVLK	3	4.27	0.051	1216	34	TCPG-DROME	TRUE	TRUE	2	1373.6	0.9	16of 24	1.8436	TRUE		TRUE	:::::::::Cys_CAM::::
NLQDALHVAR	9	7.85	0.035	1317	22.1	TCPG-DROME	TRUE	TRUE	1	1137.3	-0.4	8of 18	1.3893	TRUE		TRUE	::::::::::
IYKDIITGDEMFADTYK	2	3.97	0.298	984	45.33	TCTP-DROME	TRUE	TRUE	2	2024.3	1.6	22of 32	4.4877	TRUE		TRUE	::::::::::::::::
LTECFAFGDK	2	4.08	0.298	652	28.5	TCTP-DROME	TRUE	TRUE	2	1188.3	2.2	14of 18	2.8505	TRUE		TRUE	::::Cys_CAM:::::::
EINGDSVPVLMFFK	1	4.08	0.254	1550	47.43	TCTP-DROME	TRUE	TRUE	2	1596.9	2.2	13of 26	2.2045	TRUE		TRUE	::::::::::::::::
LVDDVIYEVYGK	1	3.71	0.253	1054	38.7	TCTP-DROME	TRUE	TRUE	1	1413.6	1.6	14of 22	3.0397	TRUE		TRUE	::::::::::::
SPDQVDIFK	1	3.89	0.047	646	20.6	TCTP-DROME	TRUE	TRUE	1	1049.2	0.8	9of 16	1.4347	TRUE		TRUE	::::::::::
SYLHHIATNESVSSSLLSIHNVAYQLR	10	7.94	0.235	1502	62.6	TGT-DROME	TRUE	TRUE	3	3041.4	2.8	33of104	4.5897	TRUE		TRUE	::::::::::::::::::::::::::
DDDQSLFPIVQGGLDVPLR	1	3.43	0.017	1466	53.4	TGT-DROME	TRUE	TRUE	2	2085.3	2.6	10of 36	1.4506	TRUE		TRUE	::::::::::::::::::
VEEFAGANAK	2	4.27	0	116	18.4	THI2-DROME	TRUE	TRUE	2	1036.1	2.3	16of 18	2.7024	TRUE		TRUE	::::::::::
FVFIK	15	10.1	0	949	26.5	THIT-DROME	TRUE	FALSE	1	653.8	0.4	6of 8	1.1112	TRUE		TRUE	::::::
AKLVVLSVGALWMMM	13	10.1	0.065	2542	66.19	TLD-DROME	TRUE	FALSE	2	1698.2	-0.8	5of 28	0.7468	TRUE		TRUE	::::::::::::Oxidation_M:Oxidation_M:Oxidation_M:
VIACIGETLEER	2	3.97	0.444	708	35.6	TPIS-DROME	TRUE	TRUE	2	1390.5	1.5	19of 22	3.9688	TRUE		TRUE	::::Cys_CAM:::::::::
NLLPCELGLAGQNAYK	6	6.28	0.375	1572	42.9	TPIS-DROME	TRUE	TRUE	2	1762	2.2	20of 30	3.7761	TRUE		TRUE	:::::Cys_CAM::::::::::::
AIFGESDALIAEK	2	3.83	0.348	865	36.9	TPIS-DROME	TRUE	TRUE	2	1364.5	1.5	20of 24	3.541	TRUE		TRUE	::::::::::::::
NVVVAYEPVWAIGTGK	6	6.87	0.217	1711	45.3	TPIS-DROME	TRUE	TRUE	1	1704	-0.9	14of 30	1.953	TRUE		TRUE	::::::::::::::::
GAFTGEISPAMLK	7	6.95	0.109	1264	34.13	TPIS-DROME	TRUE	TRUE	2	1322.6	0.7	28	2.2004	TRUE		TRUE	::::::::::::::
IVELEEELR	2	3.8	0.112	678	32.4	TPM1-DROME	TRUE	TRUE	1	1130.3	-0.5	10of 16	1.9258	TRUE		TRUE	::::::::::
DHINTIGGNTVISQSP	3	4.94	0.05	1304	26.5	TRA1-DROME	TRUE	FALSE	2	1653.8	-2.8	9of 30	1.2357	TRUE		TRUE	::::::::::::::::
KGLVDDLNLPNAGVTVQK	7	6.88	0.403	1276	38.5	TRX1-DROME	TRUE	TRUE	2	1882.2	2	1	3.9391	TRUE		TRUE	::::::::::::::::
KVEYINGLGSFVDSHTLLAK	10	7.73	0.376	1476	50.5	TRX1-DROME	TRUE	TRUE	2	2192.5	1.6	22of 38	4.6115	TRUE		TRUE	::::::::::::::::::
VYGLHYIGPVAGEVIQGFAAALK	10	7.69	0.364	2006	69.2	TRX1-DROME	TRUE	TRUE	2	2374.8	1	23of 44	4.335	TRUE		TRUE	::::::::::::::::::::
GFDQQMAELVAASMEER	1	3.69	0.317	1497	40.76	TRX1-DROME	TRUE	TRUE	2	1913.1	2.6	15of 32	3.1832	TRUE		TRUE	::::::::::::::::
YPDIPGAVEYGITSDDLFSLDREPGK	1	3.69	0.299	1470	61	TRX1-DROME	TRUE	TRUE	3	2856.1	1.6	30of100	3.174	TRUE		TRUE	::::::::::::::::::::::::
VYGLHYIGPVAGEVIQGF	5	5.13	0.237	2080	57.2	TRX1-DROME	TRUE	FALSE	2	1920.2	2.9	17of 34	3.3863	TRUE		TRUE	::::::::::::::::::
GLVDDLNLPNAGVTVQK	2	3.89	0.171	1008	40.6	TRX1-DROME	TRUE	TRUE	1	1754	-1.1	14of 32	2.4143	TRUE		TRUE	::::::::::::::::
TTIQNSSSTLTALDVGRNYTVDHTNPNSKEVQ	5	5.28	0.097	2342	44	TRX-DROME	TRUE	FALSE	3	3492.7	0.1	21of124	1.88	TRUE		TRUE	::::::::::::::::::::::::::::::
DPKKISGPHLLYE	10	7.73	0.245	561	26.7	TRX-DROVI	TRUE	FALSE	3	1497.7	2.5	19of 48	2.429	TRUE		TRUE	::::::::::::::
SLQGSYSSTRANDLQLKFWK	13	10.18	0.027	1583	42.1	U140-DROME	TRUE	FALSE	3	2330.6	-1.4	19of 76	1.8856	TRUE		TRUE	::::::::::::::::::
VIIFVK	15	10.1	0.114	948	30.8	U90426	TRUE	FALSE	1	719	1.6	8of 10	2.0716	TRUE		TRUE	::::::::
TITLEVEPSDTIENVK	1	3.69	0.283	890	37.3	UBIQ-DROME	TRUE	TRUE	1	1789	-0.2	13of 30	2.7954	TRUE		TRUE	::::::::::::::::
ESTLHLVLR	11	7.85	0.231	709	28.1	UBIQ-DROME	TRUE	TRUE	2	1068.3	1.2	13of 16	2.7497	TRUE		TRUE	::::::::::
ESTLHLVLR	10	7.85	0.204	880	28.1	UBIQ-DROME	TRUE	TRUE	2	1068.3	0.4	12of 16	2.3615	TRUE		TRUE	::::::::::
QLEDGRTLSDYNIQKESTLHLVLR	6	5.39	0.128	1516	54.6	UBIQ-DROME	TRUE	TRUE	3	2830.2	2.1	23of 92	3.4088	TRUE		TRUE	::::::::::::::::::::
TITLEVEPSDTIENVKAK	2	4.17	0.042	761	37.2	UBIQ-DROME	TRUE	TRUE	3	1988.2	1.2	22of 68	1.8711	TRUE		TRUE	::::::::::::::::::
TLSDYNIQKESTLHLVLR	10	7.75	0.03	1261	46	UBIQ-DROME	TRUE	TRUE	3	2131.4	0.4	23of 68	2.2531	TRUE		TRUE	::::::::::::::::::
VIHHFIALVNK	15	10.1	0.179	659	36.1	UBL-DROME	TRUE	TRUE	2	1291.6	0.7	13of 20	2.0171	TRUE		TRUE	::::::::::::
AFILLFPCSETYEK	3	4.27	0.154	1827	51.4	UBL-DROME	TRUE	TRUE	2	1719	0.1	16of 26	3.2714	TRUE		TRUE	:::::::Cys_CAM:::::::
YNVGEHNLFPGPIDNSGLFSDPESQTLK	3	4.06	0.084	2100	59.4	UBPN	TRUE	FALSE	3	3077.3	-0.9	18of108	1.4379	TRUE		TRUE	::::::::::::::::::::::::::
GHKVEIPSYDYR	10	7.69	0.125	621	19.5	UCK-DROME	TRUE	TRUE	3	1464.6	2	20of 44	2.2855	TRUE		TRUE	::::::::::::
LSESFVIHQAPIR	10	7.85	0.426	1022	38	UGGG-DROME	TRUE	TRUE	2	1497.7	1	18of 24	3.5856	TRUE		TRUE	::::::::::::
LSESFVIHQAPIR	11	7.85	0.41	797	38	UGGG-DROME	TRUE	TRUE	2	1497.7	0.7	14of 24	2.4324	TRUE		TRUE	::::::::::::
ILFLDVLFPLNVR	7	6.79	0.219	2386	67	UGGG-DROME	TRUE	TRUE	2	1559.9	0.5	1	3.3309	TRUE		TRUE	::::::::::::
DLYGLVHENTLVK	5	5.22	0.16	1703	35.7	VAA2-DROME	TRUE	FALSE	2	1501.7	2.1	10of 24	1.8644	TRUE		TRUE	::::::::::::
AVVQVFEGTSGIDAK	2	4.08	0.387	745	33.7	VATB-DROME	TRUE	TRUE	2	1521.7	1.7	21of 28	3.496	TRUE		TRUE	::::::::::::::
RIPASILAEFYPR	14	9.85	0.309	1324	43.2	VATB-DROME	TRUE	TRUE	2	1533.8	1.2	19of 24	3.0768	TRUE		TRUE	::::::::::::
QIYPPVNVLPSLSR	14	9.85	0.255	1218	42.5	VATB-DROME	TRUE	TRUE	2	1583.9	2.3	16of 26	2.5642	TRUE		TRUE	::::::::::::
QIYPPVNVLPSLSR	15	9.85	0.245	1303	42.5	VATB-DROME	TRUE	TRUE	2	1583.9	1.6	13of 26	2.3673	TRUE		TRUE	::::::::::::
IPASILAEFYPR	8	6.89	0.216	2224	43.8	VATB-DROME	TRUE	TRUE	2	1377.6	0.2	18of 22	2.9537	TRUE		TRUE	::::::::::::
IPASILAEFYPR	7	6.89	0.024	1675	43.8	VATB-DROME	TRUE	TRUE	2	1377.6	0.9	36	1.5605	TRUE		TRUE	::::::::::::
YGLPVNFQAILIEPNKK	14	9.63	0.424	1391	50.1	VATC-DROME	TRUE	TRUE	2	1945.3	1.4	17of 32	3.4797	TRUE		TRUE	::::::::::::::
LIVQGLFQIMEPK	7	6.95	0.365	1856	50.43	VATE-DROME	TRUE	TRUE	2	1516.9	0.5	1	4.0914	TRUE		TRUE	::::::::::::
VREDHVSSVLDDAR	3	4.44	0.194	993	23.1	VATE-DROME	TRUE	TRUE	3	1598.7	1.2	24of 52	3.3763	TRUE		TRUE	::::::::::::
KDPFILEILQYVYNISPEVHK	6	5.35	0.256	2487	64.8	VATG-DROME	TRUE	TRUE	3	2547	1.4	32of 80	5.0601	TRUE		TRUE	::::::::::::::::::
PAVPANSLKQYKEQDGFGKR	14	10.05	0.114	972	26.9	VIT3-DROME	TRUE	FALSE	2	2234.5	0.5	11of 38	2.0542	TRUE		TRUE	::::::::::::::::::
SADIEIVFDGAEHK	3	4.06	0.064	1313	29.9	VP26-DROME	TRUE	FALSE	2	1531.7	2.5	15of 26	2.4539	TRUE		TRUE	::::::::::::
VFLYDGTSSELVGEFGSPAHK	3	4.43	0.487	1617	48.5	WDR1-DROME	TRUE	TRUE	2	2241.5	0.8	23of 40	4.545	TRUE		TRUE	::::::::::::::::::
VELDHLGAVTDVSYSPDLK	2	3.97	0.311	946	45.3	WDR1-DROME	TRUE	TRUE	2	2059.3	1.4	20of 36	3.8834	TRUE		TRUE	::::::::::::::::::
NIYATLPR	13	9.85	0.216	742	23.4	WDR1-DROME	TRUE	TRUE	2	948.1	0.9	10of 14	2.2149	TRUE		TRUE	::::::::::
NFLYTNGNSVIIR	13	9.85	0.205	1138	38.3	WDR1-DROME	TRUE	TRUE	2	1511.7	0.1	16of 24	2.7159	TRUE		TRUE	::::::::::::
KYEVTLNFLHEVDPEK	4	4.63	0.337	1678	38	YC17-DROME	TRUE	TRUE	3	1962.2	2.6	31of 60	3.7119	TRUE		TRUE	::::::::::::::::
IITHPNFNGNTLDNDIMLIK	5	5.1	0.454	1794	56.23		TRUE	TRUE	2	2284.6	1.5	22of 38	5.0916	TRUE		TRUE	::::::::::::::::::
LGEHNIDVLEGNEQFINAAK	2	4.16	0.348	940	45.2		TRUE	TRUE	2	2212.4	0.3	28of 38	6.7561	TRUE		TRUE	::::::::::::::::::
AASDIAMNDLPPTHPIR	6	5.1	0.281	1214	37.93	143E-DROME	TRUE	TRUE	2	1820.1	0.8	17of 32	3.4706	FALSE		TRUE	::::::::::::::::
DICSDILNVLEK	2	3.71	0.136	1473	37.2	143E-DROME	TRUE	TRUE	2	1419.6	1.4	18of 22	3.5334	FALSE		TRUE	:::Cys_CAM:::::::::
NLLSVAYK	12	9.72	0.06	1124	24.8	143E-DROME	TRUE	TRUE	2	908.1	1.4	8of 14	1.5877	FALSE		TRUE	::::::::
DSTLIMQLLR	5	6.79	0.009	2046	37.23	143E-DROME	TRUE	TRUE	2	1190.4	0.9	15of 18	3.4981	FALSE		TRUE	::::::::::
ALAEAIQEATAMNPDMTVEKIE	4	3.59	0.159	1361	54.06	41-DROME	TRUE	FALSE	3	2376.7	-2.5	22of 84	2.6712	FALSE		TRUE	::::::::::::::::::::
FTNGPIEGYRLRLSSSEGNA	11	7.04	0.03	586	39.4	7LES-DROME	TRUE	FALSE	3	2169.4	0.4	19of 76	1.9013	FALSE		TRUE	::::::::::::::::::
NSVHVALAVGHTPK	12	10.1	0.164	856	22.4	A36A-DROME	TRUE	TRUE	2	1430.6	2.4	13of 26	1.5434	FALSE		TRUE	::::::::::::::
GTFIALDR	11	6.79	0.039	328	25.6	A49502	TRUE	FALSE	1	893	-2.1	7of 14	1.2499	FALSE		TRUE	::::::::::
IGVGSGVQATVVASTSSSSSSSAKQLK	13	10.6	0.068	686	36.3	A56721	TRUE	FALSE	3	2437.7	-1.2	8of100	0.9063	FALSE		TRUE	::::::::::::::::::::::::
GNINICLMGDPGVAKSQL	12	6.1	0.056	1577	44.23	AB010109	TRUE	FALSE	2	1888.2	1.8	10of 34	1.2121	FALSE		TRUE	::::::Cys_CAM:::::::::::
CSSHAVILPAAKS	9	8.97	0.041	1170	26.3	AB030450	TRUE	FALSE	2	1341.5	-1.9	10of 24	1.408	FALSE		TRUE	:Cys_CAM:::::::::::
PNLGREGR	15	10.89	0.002	625	9	AB035447	TRUE	TRUE	1	899	1.7	3of 14	0.5684	FALSE		TRUE	::::::::
APLSCSHTLITDK	11	7.16	0.276	492	27	AB035891	TRUE	TRUE	2	1443.6	-0.1	15of 24	2.8154	FALSE		TRUE	::::::Cys_CAM:::::::::
AYHYLVDETEKPQMFNGPLDSR	5	4.54	0.058	1562	47.23	AB035891	TRUE	FALSE	3	2627.9	0.9	23of 84	2.5558	FALSE		TRUE	::::::::::::Oxidation_M:::::::::
ERFHCAVCNKSY	13	8.29	0.101	612	20.3	AB107277	TRUE	FALSE	2	1571.7	-1.4	10of 22	1.2314	FALSE		TRUE	::::::Cys_CAM::::Cys_CAM:::::
AMGGLPVSEALDVISR	5	4.08	0.18	1584	45.03	ABS-DROME	TRUE	FALSE	2	1615.9	1.7	12of 30	1.4824	FALSE		TRUE	::::::::::::::::

LCYVALDFEQEMATAASSSSLEK	2	3.69	0.316	2205	59.23	ACT1-DROME	TRUE	TRUE	2	2551.8	1.4	19of 44	2.6602	FALSE		TRUE	::Cys_CAM::::::::::::::::::::
LCYVALDFEQEMATAASSSSLEKS	4	3.69	0.159	1947	59.03	ACT1-DROME	TRUE	FALSE	2	2654.9	1.1	14of 46	2.8333	FALSE		TRUE	::Cys_CAM::::::::::Oxidation_M::::::::::::
VAPEEHPVLLTEAPLNPK	1	4.54	0.149	804	45.4	ACT1-DROME	TRUE	TRUE	2	1955.3	2.4	15of 34	1.6409	FALSE		TRUE	::::::::::::::::
SYELPDGQVITIGNER	3	3.83	0.114	1548	35.6	ACT1-DROME	TRUE	TRUE	2	1792	0.6	15of 30	1.9695	FALSE		TRUE	::::::::::::::::
SGDGVSHTVPIYEGYALPHAILR	8	6.03	0.111	1935	54.1	ACT1-DROME	TRUE	FALSE	2	2453.8	0.2	18of 44	2.5076	FALSE		TRUE	::::::::::::::::::::
AVFPSIVGR	15	11.05	0.044	929	28.5	ACT1-DROME	TRUE	TRUE	1	946.1	-0.1	9of 16	1.3118	FALSE		TRUE	::::::::::
RGILTLKYPIEHGMVKNWDEM	8	7.73	0.013	2869	57.46	ACTY-DROME	TRUE	FALSE	2	2548	0.1	10of 40	1.1496	FALSE		TRUE	::::::::::::::::::Oxidation_M:
IIHLLNDQHMGVVTAATSLIDALVK	8	6.02	0.149	2685	75.43	ADA-DROME	TRUE	TRUE	3	2674.2	1.7	25of 96	3.4896	FALSE		TRUE	::::::::::::::::::::::::
VPSSASITVNGVSQQLEVLHHDNTVVVR	9	6.03	0.356	1806	58.1	AE003122	TRUE	TRUE	3	2987.3	2.3	34of108	4.1457	FALSE		TRUE	::::::::::::::::::::::::
TENESKLILNEEGYPYHYVLK	1	4.71	0.011	1178	49.3	AE003420	TRUE	FALSE	3	2540.8	0.2	8of 80	1.0685	FALSE		TRUE	::::::::::::::::::::
TPTQTPSQAQTPTSIPMADHQDLAIYPKR	7	7.74	0.135	1361	47.13	AE003421	TRUE	FALSE	3	3195.6	2.7	295	1.4624	FALSE		TRUE	::::::::::::::::::::::::
FVMSELGGNDFLEATAAWCTR	3	3.83	0.017	1989	62.13	AE003422	TRUE	FALSE	2	2376.6	-3	8of 40	1.0616	FALSE		TRUE	::::::::::::::::::Cys_CAM:::
RMMCSTGLSDVIQ	9	6.1	0.034	1314	33.76	AE003423	TRUE	FALSE	2	1498.7	1.7	10of 24	1.3531	FALSE		TRUE	::::Cys_CAM:::::::::
PVAPKSAPCDNTFCLETPVKALK	13	8.29	0.11	1384	48.9	AE003424	TRUE	FALSE	3	2544.9	-1	18of 88	1.7665	FALSE		TRUE	::::::::Cys_CAM::::Cys_CAM:::::::::
LLGDFELAAHDLR	2	4.3	0.297	1021	43.1	AE003429	TRUE	TRUE	2	1470.7	1.3	18of 24	3.2434	FALSE		TRUE	::::::::::::::
GQTLYVPLQQQQSYDGGRAGGGSPSNALSALITD	3	3.89	0.104	2274	62.2	AE003429	TRUE	FALSE	3	3451.7	0.5	29of132	2.096	FALSE		TRUE	::::::::::::::::::::::::::::::::
LNLPIQPIKPK	15	10.6	0.043	1019	32.2	AE003432	TRUE	FALSE	2	1261.6	2.5	9of 20	1.1035	FALSE		TRUE	::::::::::::
VAGGAAGGASGGGTSTASSPSN	12	6.02	0.106	727	15.2	AE003433	TRUE	FALSE	3	1721.7	-2.2	23of 84	1.7153	FALSE		TRUE	::::::::::::::::::::::
YPYGALQRASFM	12	9.59	0.138	951	35.73	AE003434	TRUE	FALSE	2	1404.6	-2.1	10of 22	1.5122	FALSE		TRUE	::::::::::::
NRNGEQFTGEELQLLIQGMEDTR	5	4.01	0.019	1784	48.13	AE003434	TRUE	FALSE	2	2679.9	1.9	11of 44	1.4653	FALSE		TRUE	::::::::::::::::::::::::
IMGLDLPDGGHLTHGFFTPTK	8	6.02	0.234	2109	52.53	AE003435	TRUE	TRUE	2	2255.6	2.4	19of 40	2.3366	FALSE		TRUE	::::::::::::::::::::::
SPGSSPGGGSGPGMPGMPGMGGGMSGLMLGAGGSGGSSKK	14	10.6	0.052	1180	46.65	AE003435	TRUE	FALSE	3	3444.8	0.7	21of156	1.8214	FALSE		TRUE	::::::::::::Oxidation_M::::::Oxidation_M:::::Oxidation_M:::::Oxidation_M::::::::::::
TPILLLCGK	15	8.97	0.109	400	34.6	AE003436	TRUE	FALSE	2	1015.2	1.8	8of 16	1.0851	FALSE		TRUE	::::::Cys_CAM:::
FLLLAYRRSSSDLIR	15	11.05	0.105	2761	52.2	AE003436	TRUE	FALSE	3	1811.1	-0.6	12of 56	1.4015	FALSE		TRUE	::::::::::::::
GHTSQSQESCTAAAAASTATAASGQAPGGK	10	7.16	0.249	529	20.1	AE003437	TRUE	TRUE	2	2762.8	-0.8	25of 58	3.2478	FALSE		TRUE	::::::::Cys_CAM:::::::::::::::::::
APASGYGKCGQLGFTTLTETCECVTKFFK	8	8.01	0.036	2659	61.7	AE003439	TRUE	FALSE	3	3260.6	-0.7	19of112	1.3906	FALSE		TRUE	::::::::Cys_CAM::::::::::Cys_CAM::Cys_CAM::::::
IERLLKLSEHSMPKEDIKKPSTGAVPKSR	14	10.38	0.024	836	46.93	AE003440	TRUE	FALSE	3	3276.9	-2.5	21of112	1.9197	FALSE		TRUE	::::::::::::::::::::::::::::
FSMTLMR	15	11.05	0.007	383	27.06	AE003440	TRUE	TRUE	1	902.1	-1.8	3of 12	0.5903	FALSE		TRUE	::::::Oxidation_M::
SKHPTNPNVKLQMTVSPP	15	10.6	0.021	979	24.93	AE003441	TRUE	FALSE	3	1992.3	2.3	17of 68	1.7995	FALSE		TRUE	::::::::::::Oxidation_M:::::
QHHIAAMAKSSLA	12	10.1	0.051	1256	22.33	AE003443	TRUE	FALSE	2	1381.6	2.8	9of 24	1.2842	FALSE		TRUE	::::::Oxidation_M::::::
SLHDALCVLAATVK	10	7.16	0.402	1604	39.3	AE003446	TRUE	TRUE	2	1498.7	1.2	19of 26	3.4183	FALSE		TRUE	::::::Cys_CAM::::::::
NAVTQFLCSVLK	14	8.97	0.354	1770	36.6	AE003446	TRUE	TRUE	2	1380.6	0.2	16of 22	3.1544	FALSE		TRUE	:::::::Cys_CAM:::::
DSPDIEDLLSLNPRVKTQCSVVPTK	1	4.46	0.106	1148	52.2	AE003446	TRUE	TRUE	3	2813.1	2.5	17of 96	2.3817	FALSE		TRUE	::::::::::::::::::Cys_CAM:::::::
REINDRAAIFHDQGAVRAALNGRVLVLDGV	8	7.86	0.025	2021	72.6	AE003446	TRUE	FALSE	3	3247.7	-0.6	22of116	2.1825	FALSE		TRUE	::::::::::::::::::::::::::::
MKLTLLKTIVALAQK	15	10.85	0.002	1799	49.23	AE003446	TRUE	TRUE	2	1672.2	2.9	10of 28	1.3554	FALSE		TRUE	::::::::::::::
GSQYEDSHGMDSQYK	2	4.3	0.011	78	10.83	AE003450	TRUE	FALSE	2	1732.8	-2.7	7of 28	0.8478	FALSE		TRUE	::::::::::::::
QQRGAAGATTGAGDSGN	11	6.79	0.071	545	7	AE003451	TRUE	FALSE	2	1519.5	1.1	11of 32	1.3919	FALSE		TRUE	::::::::::::::::
STMETVQKDFVK	10	6.99	0.086	1212	21.73	AE003453	TRUE	FALSE	2	1413.6	2.9	8of 22	0.9675	FALSE		TRUE	::::::::::::
TRIAFENLANRMASG	15	10.89	0.084	1814	34.03	AE003453	TRUE	FALSE	2	1667.9	1.6	7of 28	1.3277	FALSE		TRUE	::::::::::Oxidation_M::::
QLHTLQNFQNLKPQEENQKHR	12	9.89	0.04	1512	26.4	AE003453	TRUE	TRUE	3	2631.9	0.9	21of 80	2.4926	FALSE		TRUE	::::::::::::::::::
PTVDAMVPVGGM	1	3.1	0.028	816	32.46	AE003453	TRUE	FALSE	2	1190.4	-0.6	9of 22	1.4877	FALSE		TRUE	::::::Oxidation_M::::::
DISGLRAILDSR	12	6.93	0.022	1021	31.6	AE003453	TRUE	FALSE	2	1316.5	-0.7	12of 22	1.502	FALSE		TRUE	::::::::::::
AWSAKNSRYNLILVSGILA	12	10.4	0.056	1493	58.7	AE003456	TRUE	FALSE	3	2077.4	-2.9	21of 72	1.9224	FALSE		TRUE	::::::::::::::::::
WNEVCQQSHVQMP	3	5.13	0.037	1241	27.13	AE003457	TRUE	FALSE	3	1643.8	-0.1	15of 48	1.5723	FALSE		TRUE	:::::Cys_CAM::::::::
QPAALVQQKAQLSGLIDEEKFKTT	6	7.08	0.019	1572	49.7	AE003457	TRUE	FALSE	3	2645	0.7	22of 92	2.4759	FALSE		TRUE	::::::::::::::::::::::
SFGFGGFTG	12	6.02	0.204	1157	23.9	AE003459	TRUE	FALSE	1	876.9	-1.7	7of 16	1.3106	FALSE		TRUE	::::::::::
DCSLGGGGGPGGVGGGGGGGGGGGMR	9	6.1	0.146	649	19.23	AE003459	TRUE	TRUE	2	1964	-0.2	16of 48	1.5468	FALSE		TRUE	::Cys_CAM::::::::::::::::::::Oxidation_M::
TSTVTPTTNTVTPGEAAKPGLSIF	12	6.95	0.002	851	45.4	AE003459	TRUE	FALSE	3	2391.7	2.3	22of 92	1.9039	FALSE		TRUE	::::::::::::::::::::::
AKSDDLQFVSGMKVLRNR	13	10.58	0.073	1247	35.63	AE003460	TRUE	FALSE	2	2081.4	1	8of 34	0.944	FALSE		TRUE	::::::::::Oxidation_M::::::
SNHNLLEGVDIKTEMTQYMNSPSMNMYK	3	5.35	0.127	2624	55.82	AE003461	TRUE	FALSE	3	3309.7	-1	19of108	1.6212	FALSE		TRUE	::::::::::::::::::::Oxidation_M::Oxidation_M:::
FESLMFLKDEEIPADKKFK	5	4.73	0.135	1375	52.53	AE003462	TRUE	FALSE	3	2316.7	-2.5	18of 72	1.5649	FALSE		TRUE	::::::::::::::::::
DKPINYEAINKPGKDKLYAK	12	9.75	0.093	1177	29.5	AE003462	TRUE	FALSE	3	2306.7	0.6	20of 76	1.502	FALSE		TRUE	::::::::::::::::::
HGGFLGVLQR	15	11.05	0.046	489	26	AE003462	TRUE	TRUE	2	1084.3	1.2	13of 18	1.4601	FALSE		TRUE	::::::::::
RFRGNLKDAGAPDMSSGSSQCETWEQF	6	4.56	0.009	1544	45.13	AE003462	TRUE	FALSE	3	3063.3	0.4	23of104	2.064	FALSE		TRUE	::::::::::::::::::Cys_CAM:::::::
NTTLIISRIPIAHPTKKGWEPPA	15	10.59	0.033	1115	53.5	AE003463	TRUE	FALSE	3	2542	-0.9	25of 88	1.5969	FALSE		TRUE	::::::::::::::::::::::
RSELQKLKDEEASLQKEYDS	2	4.44	0.062	231	28.1	AE003465	TRUE	FALSE	3	2397.6	2.6	19of 76	2.2882	FALSE		TRUE	::::::::::::::::::::
IQKIQSLNESLPEDTELL	4	3.69	0.039	2365	50.2	AE003469	TRUE	FALSE	2	2071.3	-1.8	8of 34	1.1888	FALSE		TRUE	::::::::::::::::::
AGLPIQVPAYGINMLCGSGLK	15	8.88	0.291	1645	61.03	AE003471	TRUE	TRUE	2	2160.5	0.6	22of 40	3.0607	FALSE		TRUE	::::::::::::::Cys_CAM:::::::
SPVYSMSYNPALNAVLICTR	14	8.83	0.442	1382	56.93	AE003472	TRUE	TRUE	2	2257.6	2.3	24of 38	5.3867	FALSE		TRUE	::::::::::::::::Cys_CAM:::
TLFLQNYACSR	14	8.9	0.415	902	32.6	AE003472	TRUE	TRUE	2	1373.5	0.4	14of 20	2.7201	FALSE		TRUE	::::::::Cys_CAM:::
TPQRAPRTDSHSEALLLAR	15	10.8	0.106	115	32.5	AE003472	TRUE	FALSE	2	2120.4	-2.4	6of 36	0.7922	FALSE		TRUE	::::::::::::::::::
FDEHDGPVRGVAFHQQMPLFVSGGDDYK	5	4.53	0.077	1592	57.43	AE003472	TRUE	TRUE	3	3150.5	-2.4	25of108	2.605	FALSE		TRUE	::::::::::::::::::::::::
KLLMIGVP	12	10.1	0.049	1428	33.83	AE003472	TRUE	FALSE	2	887.2	0	9of 14	1.5388	FALSE		TRUE	::::Oxidation_M:::::
LQQLLACEPDESTVLFDIR	4	3.59	0.134	2539	61.9	AE003473	TRUE	FALSE	2	2248.5	-1.9	12of 36	1.7386	FALSE		TRUE	::::::Cys_CAM:::::::::::
MGLLLGRNGTLTEVSSVKTGMD	12	7.02	0.079	977	52.06	AE003473	TRUE	FALSE	3	2280.7	-2.5	23of 84	2.2318	FALSE		TRUE	::::::::::::::::::
TVLAAFTLLVVGTGLFVMG	4	6.02	0.046	2544	79.33	AE003473	TRUE	FALSE	2	1910.4	-0.6	11of 36	1.4549	FALSE		TRUE	::::::::::::::::::
LTEEATKDGDEVASSTRR	2	4.29	0.103	230	18.7	AE003474	TRUE	FALSE	2	1966.1	2.2	12of 34	2.2675	FALSE		TRUE	::::::::::::::::::
PAMEPPQPPPNASPNPPMRAQA	11	6.98	0.1	1229	36.16	AE003475	TRUE	FALSE	3	2312.6	-1.1	21of 84	1.6684	FALSE		TRUE	::::::::::::::::::Oxidation_M:::::
NVDIVVTATGNK	5	6.76	0.339	1208	22.3	AE003476	TRUE	TRUE	1	1231.4	-0.2	15of 22	2.968	FALSE		TRUE	::::::::::::
HYDSANIQTILQGVLAR	8	7.76	0.249	2293	41.6	AE003477	TRUE	TRUE	2	1900.1	0	19of 32	2.9591	FALSE		TRUE	::::::::::::::::
RTKIVNDNEASVLVIHQVAL	8	7.82	0.072	2095	50.7	AE003477	TRUE	FALSE	2	2220.6	1.1	12of 38	1.9083	FALSE		TRUE	::::::::::::::::::
FLYLFLAVM	7	5.93	0.013	1501	57.53	AE003477	TRUE	FALSE	1	1133.4	-0.5	319	1.793	FALSE		TRUE	::::::::Oxidation_M:
AGVVCVLGHVDTGK	11	7.16	0.47	673	28.7	AE003478	TRUE	TRUE	2	1412.6	1.3	20of 26	3.7743	FALSE		TRUE	:::::Cys_CAM:::::::::
RNTQGYYIADLTLLLR	12	9.85	0.014	2335	50.7	AE003478	TRUE	FALSE	3	1847.2	-2.1	11of 60	1.135	FALSE		TRUE	::::::::::::::::
PEAFQDDYTPTPPSPR	2	3.71	0.082	446	26.5	AE003479	TRUE	FALSE	2	1818.9	0.9	7of 30	1.2728	FALSE		TRUE	::::::::::::::::
HAIDVGYR	8	7.76	0	29	16.2	AE003479	TRUE	FALSE	2	931	2.6	10of 14	1.6944	FALSE		TRUE	::::::::
IMKDISDVVEIKTAKELK	5	7.1	0.072	1800	42.43	AE003481	TRUE	FALSE	2	2061.5	2	11of 34	1.8135	FALSE		TRUE	::::::::::::::::::
LKTLDFGWNQIAK	12	9.89	0.075	1508	38.3	AE003482	TRUE	TRUE	2	1534.8	2.9	10of 24	1.2315	FALSE		TRUE	::::::::::::
VLLGSPIDDKKNDNGQVSVEPATFDK	5	4.13	0.015	1756	46.9	AE003483	TRUE	FALSE	3	2788.1	-0.2	8of100	0.8784	FALSE		TRUE	::::::::::::::::::::::::
LQQDTERGMYDAIIHVGD	4	3.97	0.087	1949	39.13	AE003484	TRUE	FALSE	2	2078.3	-2	7of 34	0.9137	FALSE		TRUE	::::::::Oxidation_M:::::::::
QYATSWAKLQELSGPM	5	6.87	0.035	1384	40.03	AE003486	TRUE	FALSE	2	1827.1	-2.6	8of 30	1.184	FALSE		TRUE	::::::::::::::Oxidation_M:
HNYLPFIVELLK	8	7.74	0.311	2444	47.6	AE003488	TRUE	TRUE	2	1486.8	0.9	17of 22	3.0816	FALSE		TRUE	::::::::::::
PIPATSASSVVK	12	10.1	0.106	681	23.3	AE003488	TRUE	FALSE	2	1157.4	-2.9	12of 22	1.3715	FALSE		TRUE	::::::::::::

EGNVSGCFR	12	6.29	0.026	455	15	AE003489	TRUE	FALSE	2	1026.1	-0.3	7of 16	1.2312	FALSE	TRUE	::::::Cys_CAM:::
KDHLVVILMGSASDISHSEK	8	6.03	0.424	1831	40.63	AE003490	TRUE	TRUE	3	2167.5	1.9	34of 76	5.3987	FALSE	TRUE	::::::::::::::::::
SASSHSTATPPETIIYNVPVAHPQR	8	7.92	0.048	2181	40	AE003490	TRUE	FALSE	3	2661.9	1.9	11of 96	1.2688	FALSE	TRUE	::::::::::::::::::::
PRPTQSLIVAQVTSE	11	6.98	0.052	1226	32.8	AE003492	TRUE	FALSE	2	1626.9	-1.7	8of 28	1.0664	FALSE	TRUE	::::::::::::
LPDCLKTNIKFIRPFK	12	10.32	0.006	1839	47.1	AE003493	TRUE	FALSE	2	1991.4	-1.2	8of 30	1.0111	FALSE	TRUE	::::Cys_CAM::::::::::::
LIEQATRPNVPR	15	10.89	0.044	1179	26.4	AE003497	TRUE	FALSE	2	1394.6	1	13of 22	2.4056	FALSE	TRUE	::::::::::::
RSLGSLGYPGGK	14	10.4	0.042	594	18.8	AE003497	TRUE	FALSE	2	1192.4	1.1	15of 22	2.296	FALSE	TRUE	::::::::::::
FPSPLLDIFM	1	3.1	0.001	916	49.33	AE003497	TRUE	FALSE	1	1196.4	-1.5	9of 18	1.4768	FALSE	TRUE	:::::::::Oxidation_M:
TFDCATLAAGLVLQAVDSVLRG	3	3.89	0.239	2892	66.5	AE003498	TRUE	FALSE	2	2278.6	0.5	10of 42	1.7564	FALSE	TRUE	::::Cys_CAM::::::::::::::::::
ATDKLEVTKEVPSAKTEASAIGSTTEISTIG	1	4.36	0.121	2036	51	AE003498	TRUE	FALSE	3	3136.5	2.3	17of120	1.5302	FALSE	TRUE	::::::::::::::::::::::::::::::
AVTTAAPFVTKLDR	12	10.09	0.006	1131	33.5	AE003498	TRUE	TRUE	2	1490.7	-0.1	11of 26	1.7238	FALSE	TRUE	::::::::::::::
TRSFSSEMQ	11	6.98	0.091	350	14.13	AE003499	TRUE	FALSE	2	1073.2	0.6	10of 16	1.4737	FALSE	TRUE	::::::::::
EEINYVSQQMELGQTLMGPRSMAGNSFSSTK	5	4.56	0.06	1736	60.79	AE003499	TRUE	FALSE	3	3454.8	1.7	21of120	1.6298	FALSE	TRUE	::::::::::::::::Oxidation_M:::::Oxidation_M:::::::::::
DGNVLLHEMQIQHPTASMIAR	8	6.03	0.419	1879	49.16	AE003500	TRUE	TRUE	2	2362.7	1	21of 40	5.7253	FALSE	TRUE	::::::::::::::::::::
DLMESNTIASALKMYLRN	5	6.94	0.076	1867	48.86	AE003500	TRUE	FALSE	2	2103.4	1.4	11of 34	2.0481	FALSE	TRUE	:::Oxidation_M::::::::::Oxidation_M:::::
ETGIDEIMLFSQMSLHDQH	4	4.06	0.005	2459	48.56	AE003500	TRUE	FALSE	2	2232.5	-3	9of 36	1.3153	FALSE	TRUE	::::::::::::::::::::
PSKEALHEEPEDSVVATNFEVPYDPFDLMEK	3	3.82	0.177	2199	69.93	AE003501	TRUE	FALSE	3	3580.9	-1.3	21of120	1.9158	FALSE	TRUE	::::::::::::::::::::::::::Oxidation_M:::
PVLSTTSSGLPKWPTTRTLEK	14	10.59	0.003	1862	42.6	AE003501	TRUE	FALSE	2	2300.7	2.3	13of 40	2.1653	FALSE	TRUE	::::::::::::::::::::
NASSETYINRFL	5	6.89	0.017	1528	29.6	AE003502	TRUE	FALSE	2	1415.5	-0.8	11of 22	0.9973	FALSE	TRUE	::::::::::::
RILNLLESYSTPLIDAK	12	6.94	0.004	2264	53.9	AE003502	TRUE	FALSE	2	1947.3	2.9	10of 32	1.1773	FALSE	TRUE	::::::::::::::::
LPLAEDELLEVTAK	2	3.69	0.322	1090	45.4	AE003507	TRUE	TRUE	2	1541.8	2.2	14of 26	2.5636	FALSE	TRUE	::::::::::::::
TAFSPDSLNFAPFVLVPSSFPR	5	6.79	0.222	2394	69.4	AE003507	TRUE	TRUE	2	2397.7	0.4	17of 42	3.1585	FALSE	TRUE	::::::::::::::::::
LIFVLSTGSDPMSGFLK	12	6.76	0.029	1624	58.13	AE003507	TRUE	FALSE	3	1813.2	-0.1	23of 64	1.9437	FALSE	TRUE	::::::::::::::::
IFTEISGPDMSGASLPMS	1	3.01	0.09	1602	48.76	AE003508	TRUE	FALSE	3	1841.1	-1.8	14of 68	1.5677	FALSE	TRUE	::::::::::::::::
TSDVEVYVASAHK	6	5.22	0.428	927	20.8	AE003509	TRUE	TRUE	3	1406.5	1.1	24of 48	2.9396	FALSE	TRUE	::::::::::::
EAVQHQQVAAIEEHVAVVA	6	4.52	0.03	1135	41.5	AE003511	TRUE	FALSE	3	2029.3	-1.8	24of 72	2.3305	FALSE	TRUE	::::::::::::::::
RCVEFLLRMGASRTER	15	10.75	0.003	1189	39.43	AE003511	TRUE	FALSE	3	1982.3	2.3	21of 60	1.9635	FALSE	TRUE	::Cys_CAM:::::::::::::
DSLNTRGEGFSLLDMFGS	4	3.71	0.038	1733	45.73	AE003513	TRUE	FALSE	2	1947.1	-2.2	8of 34	1.1832	FALSE	TRUE	::::::::::::::::
KQIVREFITVKKVLHLPPE	13	10.32	0.013	1722	51.9	AE003514	TRUE	FALSE	2	2275.8	-0.2	10of 36	1.3922	FALSE	TRUE	::::::::::::::::
GDFESGVEHLANA	5	3.83	0.013	1415	24.3	AE003515	TRUE	FALSE	1	1346.4	2.5	7of 24	1.1835	FALSE	TRUE	::::::::::::
PGMAPNQMNQMNMGGQGMSQ	9	6.02	0.008	836	30.85	AE003515	TRUE	FALSE	3	2158.4	-0.3	22of 76	1.8749	FALSE	TRUE	::::::::::Oxidation_M::Oxidation_M:::::Oxidation_M:::
VDNMEMQLMDLKEQVDASLG	4	3.43	0.067	2349	52.59	AE003516	TRUE	FALSE	2	2283.6	-1.2	10of 38	1.1807	FALSE	TRUE	::::::Oxidation_M:::::::::::::
KVSSSSESSGNKSSSDSDSEAKNSVR	11	7.12	0.061	144	3.9	AE003519	TRUE	FALSE	2	2647.7	1.1	9of 50	1.1261	FALSE	TRUE	::::::::::::::::::::::
IAQELDYVNHHVR	9	6.03	0.411	1208	27.9	AE003522	TRUE	TRUE	2	1594.8	1.7	18of 24	3.1615	FALSE	TRUE	::::::::::::::
KENGIISTAHATAAYLKRR	12	10.7	0.036	992	29.2	AE003522	TRUE	FALSE	3	2101.4	-2.4	20of 72	1.4836	FALSE	TRUE	::::::::::::::::
YLSKYKYVAATKKDV	12	9.97	0.039	848	27.8	AE003526	TRUE	FALSE	3	1778.1	1	17of 56	1.6295	FALSE	TRUE	::::::::::::::::
KLLENILPV	10	6.95	0.089	400	37.1	AE003527	TRUE	FALSE	2	1039.3	-2.8	8of 16	1.1754	FALSE	TRUE	::::::::::
QIKGLAIFDLIVDDD	4	3.43	0.045	1386	52	AE003527	TRUE	FALSE	3	1675.9	1.5	19of 56	1.7105	FALSE	TRUE	::::::::::::::::
ERLLLAKHLSEK	12	9.89	0.011	1487	29.5	AE003527	TRUE	FALSE	2	1437.7	2.3	10of 22	2.1631	FALSE	TRUE	::::::::::::
LCLCGEESFGTGSNHIR	6	5.3	0.436	1206	35.4	AE003528	TRUE	TRUE	2	1938	0.6	18of 32	3.009	FALSE	TRUE	::Cys_CAM::Cys_CAM:::::::::::::
ALGGIVLTASHNPGGPENDFGIK	6	5.22	0.379	1598	47.4	AE003528	TRUE	TRUE	2	2265.5	1.1	18of 44	2.863	FALSE	TRUE	::::::::::::::::::::
LLVGQNGILSTPAVSSLIR	15	11.05	0.303	1548	59.6	AE003528	TRUE	TRUE	2	1939.3	-0.3	12of 36	2.4515	FALSE	TRUE	::::::::::::::::::::
ERLPESSENVESIRSPQKTEPV	1	4.43	0.012	1748	32.9	AE003528	TRUE	FALSE	2	2512.7	2.3	5of 42	0.9599	FALSE	TRUE	::::::::::::::::::::
LPFAVAQIGNSFR	15	11.05	0.371	1383	41.1	AE003532	TRUE	TRUE	2	1420.7	1.5	20of 24	3.3784	FALSE	TRUE	::::::::::::
IMYSLLEHSFQCR	10	7.16	0.344	1373	42.33	AE003532	TRUE	TRUE	2	1684.9	-0.4	17of 24	3.303	FALSE	TRUE	:::::::::::Cys_CAM::
CYFTLPPLVAPIK	14	8.88	0.342	1478	50.3	AE003532	TRUE	TRUE	2	1519.8	-0.1	16of 24	2.9238	FALSE	TRUE	:Cys_CAM:::::::::::
SIHPHGSSDKLPYATMGSGSLAAMTVFESR	8	7.89	0.284	2256	56.06	AE003532	TRUE	FALSE	3	3136.5	1.2	21of116	2.8962	FALSE	TRUE	::::::::::::::::::::::::::::
IQQFLLAIGIKPECLR	15	8.97	0.277	1495	59.4	AE003532	TRUE	TRUE	2	1900.3	1	20of 30	3.8077	FALSE	TRUE	::::::::::::Cys_CAM:::
EPSFGIGRIMYSLLEHSFQCR	10	7.16	0.099	1373	59.73	AE003532	TRUE	FALSE	3	2528.9	-2.5	21of 80	2.7717	FALSE	TRUE	::::::::::::::::::Cys_CAM::
QTSSQNSNCSESSLLKKQVTF	9	8.94	0.008	1402	27.6	AE003532	TRUE	FALSE	3	2374.5	0.1	24of 80	2.0774	FALSE	TRUE	::::::::Cys_CAM:::::::::::
IPITPTNGIS	12	6.02	0.005	677	26.4	AE003532	TRUE	FALSE	2	1013.2	-2.4	10of 18	1.3942	FALSE	TRUE	::::::::::
LRTVAKTDSFVILDWNK	12	9.89	0.01	2638	48.5	AE003533	TRUE	TRUE	3	2007.3	-1.7	11of 64	1.0923	FALSE	TRUE	::::::::::::::::
GQEEHDEGDPETPVEAILEMVHSPSFLNS	4	3.68	0.178	2495	57.03	AE003534	TRUE	FALSE	3	3211.4	2.7	22of112	2.6272	FALSE	TRUE	::::::::::::::::::Oxidation_M:::::::::
PPRTSLTPLQPRSMMIPPPPPPPLDQESDTDS	4	3.97	0.073	2182	64.26	AE003534	TRUE	FALSE	3	3415.9	1.8	21of120	2.2409	FALSE	TRUE	::::::::::::Oxidation_M:::::::::::::::::
FNDPHVQHELTSIPAR	9	6.03	0.361	1313	30.9	AE003536	TRUE	TRUE	2	1862.1	2.2	19of 30	2.9191	FALSE	TRUE	::::::::::::::::
LQLDDIHSVEIVGGSSR	2	4.3	0.31	869	38.8	AE003536	TRUE	TRUE	2	1826	0.7	20of 32	3.2757	FALSE	TRUE	::::::::::::::::
VSALQTLHAAPTSHIVSPIK	12	10.1	0.093	1427	45.3	AE003536	TRUE	FALSE	2	2071.4	-1.4	6of 38	1.0257	FALSE	TRUE	::::::::::::::::
TMSMCITPVTPTPVVTPSPLHGTPP	6	7.16	0.013	2593	59.06	AE003536	TRUE	FALSE	3	2620.1	1.3	11of 96	1.5532	FALSE	TRUE	:::::Cys_CAM:::::::::::::::::::
CAALITTLALVLYTCRHRIR	12	9.89	0.038	1660	65.8	AE003538	TRUE	FALSE	3	2402.8	1.4	13of 76	1.2227	FALSE	TRUE	:Cys_CAM::::::::::::Cys_CAM::::::
DVPTGTCAVLITGTHR	11	7.16	0.293	676	31.6	AE003539	TRUE	TRUE	2	1698.9	2	22of 30	3.1935	FALSE	TRUE	::::::Cys_CAM:::::::::
SLRASLNNEVPAIQPEPVINTV	5	4.27	0.041	1604	56	AE003540	TRUE	FALSE	3	2362.7	-2	20of 84	2.0339	FALSE	TRUE	::::::::::::::::::::
QLSNFGLDYIDLYLMHMPVGYK	6	5.1	0.102	2336	74.46	AE003541	TRUE	TRUE	2	2619.1	-0.5	13of 42	2.396	FALSE	TRUE	::::::::::::::::::::
NLHLVVPASAIQPEYLIFVR	8	7.77	0.019	2323	72.3	AE003542	TRUE	TRUE	2	2280.7	3	7of 38	0.8097	FALSE	TRUE	::::::::::::::::::::
HIDCAYVYQNEDEVGDGVEAK	2	3.76	0.409	612	36.7	AE003544	TRUE	TRUE	2	2412.5	-0.5	23of 40	3.6498	FALSE	TRUE	::::Cys_CAM:::::::::::::::::
LVPLLNQYGHPHHPFEKDEY	7	5.75	0.371	1200	45.6	AE003544	TRUE	FALSE	2	2434.7	-0.7	1	3.4538	FALSE	TRUE	::::::::::::::::::
PPVTNQIECHPYLTQK	6	7.16	0.321	1612	31.1	AE003544	TRUE	FALSE	2	1926.1	1.9	17of 30	3.9892	FALSE	TRUE	::::::::Cys_CAM:::::::
VLEVATIPPVTNQIECHPYLTQK	6	5.3	0.178	1610	60.3	AE003544	TRUE	TRUE	2	2652	1	18of 44	2.4192	FALSE	TRUE	::::::::::::::Cys_CAM:::::::
ESSIIWTKSSSSMLTDGAWSYTKV	12	6.92	0.038	1887	54.83	AE003544	TRUE	FALSE	2	2682	1.6	7of 46	1.0167	FALSE	TRUE	::::::::::::Oxidation_M:::::::::::
SSDSFPGILSGVLVMK	5	6.76	0.044	2092	46.13	AE003545	TRUE	TRUE	2	1653.9	1.5	9of 30	1.2265	FALSE	TRUE	::::::::::::::Oxidation_M::
MTAPGPRPLVLCGPSGSGKSTL	12	10.11	0.015	2118	44.53	AE003547	TRUE	FALSE	3	2200.5	0.8	18of 84	1.4505	FALSE	TRUE	:Oxidation_M::::::::::Cys_CAM:::::::::::
LSAATGATQSPQTAAAAAAAAASMAASANAANN	12	6.02	0.109	1709	46.63	AE003548	TRUE	FALSE	3	2805	1.1	8of124	0.9125	FALSE	TRUE	::::::::::::::::::::::::::::::
AILTHGIFSGPAISR	15	11.05	0.305	1325	41.5	AE003551	TRUE	FALSE	2	1540.8	-1.2	14of 28	2.5306	FALSE	TRUE	::::::::::::::
AQAQRGLRNYEEAINDLKTAHNLL	6	7.75	0.068	1847	47.9	AE003551	TRUE	FALSE	3	2740.1	0.2	20of 92	1.9865	FALSE	TRUE	::::::::::::::::::::
VEFVMEVTDKTR	2	4.45	0.071	566	29.53	AE003552	TRUE	FALSE	2	1470.7	2.1	7of 22	1.3227	FALSE	TRUE	:::::Oxidation_M:::::::
SGLPAGSLAVSILPVTLDTPMNR	5	6.79	0.338	2178	64.53	AE003553	TRUE	TRUE	2	2310.7	1	17of 44	3.3191	FALSE	TRUE	::::::::::::::::::::
GALGSACVDHFK	11	7.16	0.208	508	23.2	AE003553	TRUE	TRUE	2	1262.4	0.6	11of 22	2.0311	FALSE	TRUE	::::::Cys_CAM:::::::
QALLFSK	12	10.1	0.002	1108	24	AE003553	TRUE	FALSE	1	807	0.4	7of 12	1.5101	FALSE	TRUE	::::::::
IVADKRSERATPRKQQKIENAHV	13	10.81	0.11	328	24.8	AE003555	TRUE	FALSE	2	2676.1	-0.2	5of 44	0.9099	FALSE	TRUE	::::::::::::::::::::
SIDFKGESITFRATTSGV	12	7.02	0.12	1573	37.4	AE003556	TRUE	FALSE	2	1917.1	-0.7	6of 34	0.837	FALSE	TRUE	::::::::::::::::::
SMAGNIIPAIATTNAITAGISVMR	15	11.05	0.075	1800	64.26	AE003556	TRUE	TRUE	2	2374.8	1.4	17of 46	2.0842	FALSE	TRUE	::::::::::::::::::::
TYPEEESIARTWTHKLK	6	7.73	0.045	1311	30.8	AE003557	TRUE	FALSE	2	2090.3	-2.7	10of 32	1.5251	FALSE	TRUE	::::::::::::::::
LTVCALHVTQTAR	15	9.02	0.205	381	31.9	AE003559	TRUE	TRUE	2	1470.7	2.5	9of 24	1.5592	FALSE	TRUE	::::Cys_CAM:::::::::
AMFEPEPTGTPAKDQLRGR	5	7.14	0.021	1526	31.63	AE003560	TRUE	FALSE	2	2118.4	0.5	12of 36	1.679	FALSE	TRUE	::Oxidation_M:::::::::::::::

RAEGGQLPAALTAENVCRIADDESERDEAEG	4	3.82	0.017	2222	49.8	AE003561	TRUE	FALSE	3	3331.5	-0.8	17of120	1.4091	FALSE	TRUE	::::::::::::::Cys_CAM::::::::::::::
DVVISFCMSDRGGAIR	9	6.25	0.054	1921	41.43	AE003562	TRUE	FALSE	3	1784	-0.6	14of 60	1.5989	FALSE	TRUE	::::::Cys_CAM::::::::
GGGKILTNASYEENMQELRK	5	7.09	0.179	1642	32.73	AE003563	TRUE	FALSE	2	2239.5	1.3	15of 38	3.1085	FALSE	TRUE	::::::::::::::::::
AVIGLCVVDASVR	7	6.1	0.476	1296	41.3	AE003565	TRUE	TRUE	2	1359.6	2.4	1	3.8633	FALSE	TRUE	::::::Cys_CAM::::::::
LQLLALIANGVEPRQVG	12	6.98	0.008	2732	55.3	AE003571	TRUE	FALSE	3	1792.1	-2.8	10of 64	1.0306	FALSE	TRUE	::::::::::::::::::
LPLLTQ	9	6.02	0	1273	26.9	AE003571	TRUE	FALSE	1	684.9	0.1	8of 10	1.6238	FALSE	TRUE	::::::::
AGGGRDMFASVGADGSVRMFDLR	6	7.02	0.117	1806	48.76	AE003574	TRUE	TRUE	3	2389.7	-0.9	23of 88	2.6826	FALSE	TRUE	::::::Oxidation_M:::::::::::::::
FTLEEPSQVLVEHMEREALAVK	1	4.42	0.093	1378	60.03	AE003574	TRUE	FALSE	2	2572.9	-2.2	5of 42	0.8811	FALSE	TRUE	::::::::::::::Oxidation_M:::::::::
EFSKEDRELINPCNSKSITQALDF	2	4.29	0.085	2346	51.5	AE003574	TRUE	FALSE	3	2843.1	1.8	13of 92	1.3456	FALSE	TRUE	::::::::::::::Cys_CAM::::::::::::
QTTLMDMQTEMKIRYK	12	9.63	0.021	1200	34.89	AE003575	TRUE	FALSE	3	2034.4	-0.4	16of 60	1.1704	FALSE	TRUE	:::::Oxidation_M:::::::::::
DTLTEHFDIPKVSWTK	6	5.28	0.002	1715	36.2	AE003576	TRUE	FALSE	2	1918.2	3	5of 30	0.9189	FALSE	TRUE	::::::::::::::::::
GSTNHSLQMSISLIENIK	7	7.82	0.071	1763	39.23	AE003578	TRUE	FALSE	3	1973.3	-2.1	335	1.4071	FALSE	TRUE	::::::::::::::::::
PKVADFPPPLTLNQTELDILKIQR	5	7.05	0.19	2531	67.6	AE003579	TRUE	FALSE	2	2748.2	1.6	10of 46	1.6906	FALSE	TRUE	::::::::::::::::::::::::
SDHDCKPVPASSTTSSR	11	7.16	0.1	132	9.4	AE003579	TRUE	FALSE	2	1832.9	-1.9	6of 32	0.8046	FALSE	TRUE	:::::Cys_CAM:::::::::::
TCEHLFASGHIERAIERHR	7	7.42	0.064	1483	33	AE003579	TRUE	TRUE	2	2320.5	-1.5	218	1.367	FALSE	TRUE	::Cys_CAM:::::::::::::::
VICAILETHQTETGIK	6	5.3	0.351	1230	39.5	AE003581	TRUE	TRUE	2	1814.1	0.6	22of 30	4.8569	FALSE	TRUE	:::Cys_CAM::::::::::::
MNAAVDYVHMLNATMCAATR	10	7.16	0.297	1676	49.29	AE003581	TRUE	TRUE	2	2241.6	0.8	18of 38	3.3243	FALSE	TRUE	::::::::::::::Cys_CAM:::::
DGVILVAAK	12	6.76	0.16	1423	27.4	AE003581	TRUE	FALSE	1	886.1	1.2	9of 16	1.3646	FALSE	TRUE	::::::::::
FIHEDDKCVAFHDVAPQAPTHFLVIPR	8	5.75	0.398	1900	70.1	AE003582	TRUE	TRUE	3	3161.6	2.5	40of104	6.3887	FALSE	TRUE	::::::::Cys_CAM::::::::::::::::::
MPKPKIETVWK	14	10.32	0.097	1522	26.13	AE003582	TRUE	FALSE	2	1357.7	1.6	11of 20	2.0654	FALSE	TRUE	::::::::::::
VIEFKEQFPLLSFRHL	6	7.83	0.037	2436	60.2	AE003582	TRUE	FALSE	2	2004.4	-2.7	10of 30	1.4593	FALSE	TRUE	::::::::::::::::
YDVQRVSYERLPFTNQLA	10	6.9	0.011	2053	47.2	AE003583	TRUE	FALSE	2	2200.5	-0.8	7of 34	0.9499	FALSE	TRUE	::::::::::::::::::
NSLSGGSSSIVPGGVGIGLGGGATGANSMSG	7	6.02	0.067	1461	48.33	AE003585	TRUE	FALSE	3	2606.8	-0.4	136	1.7061	FALSE	TRUE	::::::::::::::::::::::::::::::
ELSTLLDFFPHNHHYHSIIMN	4	6.02	0.04	1586	59.23	AE003586	TRUE	FALSE	3	2582.9	1.8	13of 80	1.3175	FALSE	TRUE	::::::::::::::::::Oxidation_M::
HSLPQAYLDQVANFIIK	8	7.74	0.379	2383	49.8	AE003587	TRUE	TRUE	2	1958.3	1	23of 32	3.8139	FALSE	TRUE	::::::::::::::::
IGGDVAQHAELVK	6	5.22	0.285	910	26.2	AE003587	TRUE	TRUE	2	1337.5	0.9	18of 24	3.7965	FALSE	TRUE	::::::::::::::
SALFAQINQGADITK	5	6.76	0.214	1502	34.7	AE003587	TRUE	TRUE	2	1577.8	1.7	17of 28	2.5108	FALSE	TRUE	::::::::::::::
MLESDGAINMKSLINLAQDR	1	4.31	0.002	1545	51.16	AE003587	TRUE	FALSE	3	2236.6	1.9	24of 76	2.3572	FALSE	TRUE	::::::::::Oxidation_M:::::::::::
ITCDFAASGGRTWAMGRY	9	8.9	0.024	1392	42.33	AE003588	TRUE	FALSE	3	2021.2	-2.7	19of 68	1.7091	FALSE	TRUE	:::Cys_CAM:::::::::::::::
DMAKPETPSKHGLR	12	9.89	0.084	451	14.23	AE003589	TRUE	FALSE	2	1567.8	2.6	11of 26	1.5225	FALSE	TRUE	::::::::::::::
NPQMMPMGAGGGAPVPG	12	6.02	0.067	789	31.99	AE003589	TRUE	FALSE	3	1601.9	-2.9	19of 64	1.92	FALSE	TRUE	::::Oxidation_M:Oxidation_M:::::::::::::
LLESGIIQIH	6	5.13	0.293	1436	37	AE003590	TRUE	FALSE	2	1123.3	2.4	16of 18	3.5287	FALSE	TRUE	::::::::::
MISYKTGLPINSLPGWELIP	5	6.87	0.287	2821	69.53	AE003590	TRUE	FALSE	2	2230.7	2.7	10of 38	1.3145	FALSE	TRUE	::::::::::::::::::
KAQAAYQKALELDPNNAEAIEGYR	1	4.65	0.237	853	43.9	AE003590	TRUE	FALSE	3	2664.9	1.1	21of 92	2.5646	FALSE	TRUE	::::::::::::::::::::::
DAGHYALSIACK	10	7.15	0.127	758	24.2	AE003590	TRUE	TRUE	2	1306.4	-0.4	12of 22	1.5924	FALSE	TRUE	:::::::::Cys_CAM:::
SEFDTNFRPGRSFCLAIVCT	4	6.22	0.103	2421	54.1	AE003590	TRUE	FALSE	2	2378.6	-2.9	11of 38	1.2718	FALSE	TRUE	::::::::::::Cys_CAM::::Cys_CAM::
DAVNAIYGKSSCPK	15	8.85	0.061	355	20.3	AE003590	TRUE	TRUE	3	1510.7	-1.5	14of 52	1.6523	FALSE	TRUE	::::::::::Cys_CAM:::
IKGVSVLPSLNILTANSTLTERTTSSTPDFST	5	7.02	0.003	2150	71.5	AE003590	TRUE	FALSE	3	3352.8	2.3	27of124	3.0473	FALSE	TRUE	::::::::::::::::::::::::::::::
RATLLMQESMEEDIISPL	3	3.69	0.09	1949	57.26	AE003592	TRUE	FALSE	2	2077.4	-0.7	11of 34	2.2952	FALSE	TRUE	::::::::::::::::::
VAAPQNFAGAVPNHL	8	7.85	0.029	1863	34.7	AE003594	TRUE	FALSE	2	1506.7	1.5	11of 28	1.2327	FALSE	TRUE	::::::::::::::
QAVHFMATKGDTCSVPLSKEGPVHCVKWSPK	9	9.05	0.041	1982	54.63	AE003595	TRUE	FALSE	3	3499.9	2.8	9of120	1.085	FALSE	TRUE	::::::Oxidation_M::::::Cys_CAM::::::::::::Cys_CAM::::::
LLDMELAWSIYNSEQLAAKKAAELTARK	5	7.1	0.034	2729	74.93	AE003596	TRUE	FALSE	3	3165.7	1.1	18of108	1.7438	FALSE	TRUE	::::::::::::::::::::::::::::
GVKIAQVLVTK	14	10.6	0.013	124	28.7	AE003596	TRUE	FALSE	2	1156.5	2.8	9of 20	1.4763	FALSE	TRUE	::::::::::::
NLIASGLVLAADGQK	5	6.76	0.379	1711	39.6	AE003597	TRUE	TRUE	2	1470.7	2.1	24of 28	4.9522	FALSE	TRUE	::::::::::::::::
LLGGGGGDNGGGGGLLGGR	11	6.79	0.01	786	29	AE003600	TRUE	FALSE	3	1541.7	2.4	26of 72	2.2896	FALSE	TRUE	::::::::::::::::::
LCTLNPSSTVAYFFEVVNQHAAPIPQGGR	10	7.16	0.289	2038	71.5	AE003602	TRUE	TRUE	3	3175.5	2.3	37of112	2.4749	FALSE	TRUE	::Cys_CAM:::::::::::::::::::::::::
AILNPLCQVDYR	7	6.09	0.148	1301	38.7	AE003602	TRUE	TRUE	2	1462.7	2.4	27	1.4613	FALSE	TRUE	::::::Cys_CAM:::::::
ELDQAGSSSSANLLPTPSLGKHQPSQFNFP	3	5.22	0.068	1944	55.5	AE003602	TRUE	FALSE	3	3156.4	1.7	12of116	1.2592	FALSE	TRUE	::::::::::::::::::::::::::::
FERNVLEKFEAEQRK	10	7.22	0.015	1289	29.7	AE003602	TRUE	FALSE	2	1924.2	-0.8	12of 28	2.0615	FALSE	TRUE	::::::::::::::::
AAVAGGTTMII	9	6.02	0.008	869	32.13	AE003602	TRUE	FALSE	2	1005.2	-2.3	11of 20	1.2952	FALSE	TRUE	::::::::::::
LHKNSNGMGLSIVAAKGAGQEK	14	10.32	0.074	987	30.43	AE003603	TRUE	TRUE	2	2211.5	-0.2	11of 42	1.1145	FALSE	TRUE	::::::::::::::::::::
VIVTEPEPDVQSELLNSLAK	2	3.69	0.24	1188	53.7	AE003605	TRUE	TRUE	2	2182.5	2.1	14of 38	2.092	FALSE	TRUE	::::::::::::::::::
ILYHDKENETAIHK	9	6.04	0.156	853	23.4	AE003605	TRUE	FALSE	2	1711.9	0	17of 26	2.602	FALSE	TRUE	::::::::::::::
FAALMAISAIGEGCHK	10	7.16	0.075	1458	43.43	AE003605	TRUE	TRUE	2	1676.9	1.6	13of 30	1.5896	FALSE	TRUE	::::::::::::Cys_CAM:::
VTHLLGNIQNGQQSEEAR	3	5.3	0.026	1052	28.9	AE003605	TRUE	TRUE	3	1995.2	2.8	29of 68	3.3768	FALSE	TRUE	::::::::::::::::::
VNTHCEALYHDIAR	9	6.02	0.275	1205	28.1	AE003606	TRUE	TRUE	3	1699.8	1.8	30of 52	3.6832	FALSE	TRUE	:::::Cys_CAM:::::::::
MAAHVLLATLSIPLPSAHPEFDR	8	6.03	0.223	2231	69.13	AE003606	TRUE	TRUE	2	2487.9	0.4	19of 44	2.8312	FALSE	TRUE	::::::::::::::::::::
VGIGFNNIFNR	15	11.05	0.193	1297	33.2	AE003606	TRUE	TRUE	2	1251.4	-0.1	14of 20	2.3489	FALSE	TRUE	::::::::::
MFLQNGSMKPSERDEQGAYLIDRSP	1	4.56	0.073	1181	50.96	AE003606	TRUE	FALSE	3	2903.2	2.1	13of 96	1.4855	FALSE	TRUE	:Oxidation_M::::::Oxidation_M:::::::::::::::::
INRINPDNFTDLSEF	2	3.71	0.094	1006	40.6	AE003608	TRUE	FALSE	1	1795.9	-2.9	12of 28	2.0996	FALSE	TRUE	::::::::::::::
MANTFTGLKLKGDLGRFGKT	13	10.83	0.088	1163	41.73	AE003608	TRUE	FALSE	2	2156.6	-2.3	14of 38	2.5272	FALSE	TRUE	::::::::::::::::::
AEDEVISPPMPLTVNLENVR	3	3.69	0.011	2476	54.23	AE003608	TRUE	FALSE	2	2224.5	-1.2	11of 38	1.739	FALSE	TRUE	::::::::::::::::::
SQFIQPPPPPYPGLGAATASSV	12	5.93	0.028	913	50.7	AE003609	TRUE	FALSE	3	2183.5	-2	20of 84	1.6225	FALSE	TRUE	::::::::::::::::::::
IPVLFFNGQFLCMHR	9	9.02	0.025	2518	59.53	AE003612	TRUE	FALSE	3	1880.2	-0.2	11of 56	1.0031	FALSE	TRUE	::::::::::Cys_CAM::::
EYDCNYLLDAQKTKLQISK	9	6.41	0.01	2224	40.3	AE003612	TRUE	FALSE	2	2331.6	-0.8	9of 36	1.3521	FALSE	TRUE	:::Cys_CAM:::::::::::::::
NPGDNYCSAIYR	9	6.09	0.093	974	21	AE003613	TRUE	FALSE	2	1430.5	1	10of 22	1.5027	FALSE	TRUE	::::::Cys_CAM::::::
VYRIPFPVITICNR	12	9.87	0.073	1971	50.2	AE003613	TRUE	FALSE	2	1749.1	-0.2	8of 26	1.006	FALSE	TRUE	::::::::::Cys_CAM:::
YGSQESLRHYNTMGSMSMLQTPTSGVSREAA	7	7.71	0.014	1921	51.09	AE003614	TRUE	FALSE	3	3394.7	-0.8	350	1.8935	FALSE	TRUE	::::::::::::::::Oxidation_M:::::::::::::
YNSTTTTPFMRIAPLKEEEIS	1	4.56	0.006	961	48.43	AE003614	TRUE	FALSE	2	2328.6	0.8	7of 38	1.1909	FALSE	TRUE	::::::::::::::::::
ESNTSAKFYLQPGAALDPMPVPEL	4	3.83	0.042	2810	61.13	AE003615	TRUE	FALSE	3	2592.9	1	17of 92	1.3679	FALSE	TRUE	::::::::::::::::Oxidation_M:::::
ELEENMDEIKSMLTYMFK	5	4.01	0.013	2527	52.99	AE003615	TRUE	FALSE	2	2284.6	3	11of 34	1.3066	FALSE	TRUE	::::::Oxidation_M::::::Oxidation_M:::::::
ASSEQDNSDLSEHSEKSPLVSARLDNLAR	1	4.37	0.015	1300	41.3	AE003618	TRUE	FALSE	3	3157.3	2.1	22of112	2.5271	FALSE	TRUE	::::::::::::::::::::::::::::
SLEALMPLIGHIAQHQ	12	6.02	0.128	885	47.13	AE003619	TRUE	FALSE	2	1759.1	1.8	5of 30	1.0026	FALSE	TRUE	::::::::::::::::
VFLGDIIK	11	6.76	0.186	294	33.9	AE003620	TRUE	FALSE	2	905.1	-0.4	10of 14	1.401	FALSE	TRUE	::::::::
SPPAKGTMLSRKSDCGLPEIRIK	14	10.32	0.085	1474	40.53	AE003620	TRUE	FALSE	2	2543	1.9	11of 44	2.6117	FALSE	TRUE	::::::::::::::Cys_CAM:::::::::
ATYMASCCEPKVSLIAFDA	4	4.08	0.04	2742	53.23	AE003620	TRUE	FALSE	2	2151.4	0.8	8of 36	1.0504	FALSE	TRUE	::::Oxidation_M:::Cys_CAM:Cys_CAM:::::::::::
NHSATHALNHCLLQVLGK	15	8.98	0.435	967	34.6	AE003621	TRUE	TRUE	2	2014.3	1.2	18of 34	3.5893	FALSE	TRUE	::::::::::Cys_CAM:::::::::
NVADMGLNILFK	5	6.76	0.21	2035	40.93	AE003621	TRUE	TRUE	1	1335.6	-0.7	13of 22	2.1829	FALSE	TRUE	::::::::::::
LSFYELLQAVNAHCFK	11	7.16	0.184	1629	52.7	AE003621	TRUE	TRUE	2	1941.2	1	14of 30	2.0723	FALSE	TRUE	::::::::::::::Cys_CAM:::
IFCLSSVPK	15	8.97	0.123	905	30.7	AE003621	TRUE	TRUE	2	1051.2	1.7	10of 16	1.6263	FALSE	TRUE	:::Cys_CAM:::::::
TIYETLGRAMVTAAV	12	6.89	0.119	847	43.63	AE003621	TRUE	FALSE	3	1596.9	0.7	20of 56	1.9229	FALSE	TRUE	::::::::::::::::
NHSATHALNHCLLQVLGK	14	8.98	0.076	908	34.6	AE003621	TRUE	TRUE	3	2014.3	2.2	23of 68	2.1411	FALSE	TRUE	::::::::::Cys_CAM:::::::
LSFYELLQAVNAHCFK	10	7.16	0.028	1890	52.7	AE003621	TRUE	TRUE	2	1941.2	0.9	11of 30	1.6774	FALSE	TRUE	::::::::::::::Cys_CAM:::

HLFNDGGGVGEALNETQYGKGLIARGKL	7	7.73	0.043	2346	54.9	AE003622	TRUE	FALSE	3	2916.3	-2.6	481	1.6248	FALSE	TRUE	::::::::::::::::::::::::::::
NLVEIEWQVGPIEREE	4	3.68	0.022	1953	47.8	AE003622	TRUE	FALSE	2	1941.1	1.3	11of 30	1.2762	FALSE	TRUE	::::::::::::::::
ISPAVQYLSLLGIRE	12	6.89	0.2	1717	52.5	AE003623	TRUE	FALSE	2	1660	-1.1	7of 28	1.2705	FALSE	TRUE	::::::::::::::::
KFLTSSHIMDLLSRLMQE	7	7.82	0.048	2301	55.46	AE003624	TRUE	FALSE	2	2150.6	-0.1	285	1.1571	FALSE	TRUE	::::::::::::::::
NFDLPFVPLR	5	6.79	0.12	2019	40.4	AE003626	TRUE	TRUE	2	1218.4	0.4	10of 18	2.326	FALSE	TRUE	::::::::::
INGRLLRSY	15	11.14	0.029	601	25.9	AE003626	TRUE	FALSE	2	1092.3	-2.1	8of 16	1.2716	FALSE	TRUE	::::::::::
SSIPRRRKPKNYDLPYFAPLV	14	10.77	0.07	1632	48.9	AE003627	TRUE	FALSE	3	2519	2	15of 80	1.8914	FALSE	TRUE	::::::::::::::::::::
TADDINGFNAVVQREPVVAAR	1	4.31	0.036	2366	45	AE003627	TRUE	FALSE	2	2243.5	-0.3	7of 40	0.9381	FALSE	TRUE	::::::::::::::::::::
AAASHALGAVSVGSLQTYLPLILHEIEVQPK	8	6.03	0.328	2650	84.3	AE003628	TRUE	TRUE	3	3214.7	0	34of120	3.1969	FALSE	TRUE	::::::::::::::::::::::::::::::
DMECNESDLTDSDREDDPTFPSKMAK	2	3.69	0.032	877	35.56	AE003628	TRUE	FALSE	3	3067.2	-2.2	12of100	1.163	FALSE	TRUE	::Oxidation_M::Cys_CAM::::::::::::::::::Oxidation_M:::
DLERERELLMSRSLPGIQNQNVSSE	1	4.36	0.019	2388	52.93	AE003628	TRUE	FALSE	2	2918.2	2.8	5of 48	0.7681	FALSE	TRUE	:::::::::Oxidation_M:::::::::::::
MPQPQPRCPSGHVVVLVELRR	14	10.81	0.177	1411	49.13	AE003629	TRUE	FALSE	2	2472.9	-2	12of 40	1.6594	FALSE	TRUE	:Oxidation_M::::::Cys_CAM::::::::::::
MLVGVYR	12	9.85	0.112	1115	27.33	AE003631	TRUE	FALSE	1	854.1	-0.2	8of 12	1.922	FALSE	TRUE	:Oxidation_M::::::
SNKPLKLFHSKALAEMTYR	12	10.45	0.076	1571	40.13	AE003631	TRUE	TRUE	2	2235.7	1.8	13of 36	2.064	FALSE	TRUE	::::::::::::::::::
ETASQIISEQTPAKLEKI	6	4.56	0.03	1228	36.2	AE003631	TRUE	FALSE	3	1987.3	-2.7	16of 68	1.5281	FALSE	TRUE	::::::::::::::::::
SNQSIGKSTIGEVDISKA	12	6.99	0.148	1077	25.1	AE003633	TRUE	FALSE	3	1835	1.5	16of 68	1.7419	FALSE	TRUE	::::::::::::::::::
GDPLKGYYDFVITEGS	3	3.71	0.071	1476	38.8	AE003634	TRUE	FALSE	2	1761.9	2.6	12of 30	1.6791	FALSE	TRUE	::::::::::::::::
ILALDCMVYFAR	7	6.09	0.027	1285	52.93	AE003635	TRUE	FALSE	2	1472.8	1.7	218	1.5851	FALSE	TRUE	::::::Cys_CAM::::::::
EHVNVVFIGHVDAGK	8	6.03	0.399	1605	31.5	AE003636	TRUE	TRUE	3	1621.8	0.8	30of 56	4.1479	FALSE	TRUE	::::::::::::::::
GEVLSAYVGSGPPPDTGLHR	6	5.22	0.474	1290	36.7	AE003637	TRUE	TRUE	2	2010.2	-0.1	18of 38	3.0688	FALSE	TRUE	::::::::::::::::::::
PHEDIHTWLKYASLCRKS	15	8.85	0.05	1868	36	AE003638	TRUE	FALSE	2	2242.5	-0.3	13of 34	2.1539	FALSE	TRUE	::::::::::::::Cys_CAM::::
HQIEAVPTVIFFAK	8	7.82	0.412	1997	44.5	AE003639	TRUE	TRUE	1	1600.9	0.2	17of 26	3.7614	FALSE	TRUE	::::::::::::::
IGLCAFSGYK	15	8.88	0.034	959	30	AE003640	TRUE	TRUE	1	1116.3	0.9	10of 18	1.8491	FALSE	TRUE	::::Cys_CAM:::::::
CSTCPYLGMPAFKPGEK	13	8.28	0.269	1006	36.33	AE003646	TRUE	TRUE	2	1944.2	-0.5	16of 32	2.2813	FALSE	TRUE	:Cys_CAM:::Cys_CAM::::::::::::
RLAEQGDTALALRK	12	10.09	0.016	737	28.7	AE003648	TRUE	FALSE	3	1542.8	2.8	15of 52	1.8324	FALSE	TRUE	::::::::::::::
IQALFCGGSMAKE	9	6.29	0.024	496	34.13	AE003649	TRUE	FALSE	2	1412.6	-2.2	8of 24	1.1349	FALSE	TRUE	::::::Cys_CAM::::::::
TQMGMAAMAHMLAPPPPPPPTPSEGR	6	7.85	0.287	2457	53.22	AE003650	TRUE	FALSE	3	2704.2	2	10of100	1.5554	FALSE	TRUE	:::Oxidation_M::::::::Oxidation_M:::::::::::::::
NFTVAVVDKDGVR	5	6.9	0.237	1314	27.6	AE003652	TRUE	TRUE	2	1420.6	0.8	17of 24	2.9413	FALSE	TRUE	::::::::::::::
EYGSCSAWKFRCSVDRCPYRTNR	15	9.09	0.047	1552	38.7	AE003652	TRUE	FALSE	3	2957.1	0.1	22of 88	3.2803	FALSE	TRUE	:::::Cys_CAM::::::Cys_CAM::::Cys_CAM::::::::
RHSMMATGAPTSYMSLNHMSSPTTK	13	10.4	0.046	2003	36.42	AE003652	TRUE	FALSE	3	2774.1	-1.2	14of 96	1.3815	FALSE	TRUE	::::Oxidation_M:Oxidation_M::::::::Oxidation_M:::::::::::
VTVISEGAAGLYKGFGAMILQ	4	6.87	0.055	1901	63.73	AE003657	TRUE	FALSE	3	2126.5	0.6	21of 80	1.892	FALSE	TRUE	::::::::::::::::::::
ALYDYFIDTDK	2	3.6	0.033	861	33.7	AE003660	TRUE	FALSE	1	1364.5	-0.5	7of 20	1.2886	FALSE	TRUE	::::::::::
DQMMAVCSHTIEKD	2	4.3	0.02	79	25.76	AE003660	TRUE	FALSE	2	1697.8	1.6	6of 26	1.001	FALSE	TRUE	:::Oxidation_M:Oxidation_M:::Cys_CAM::::::::
PTIYVDTKDPNAAEPYEPAAK	4	4.07	0.353	1443	36.4	AE003661	TRUE	FALSE	3	2291.5	1.2	24of 80	2.9225	FALSE	TRUE	::::::::::::::::::::
IPLIVNGNVESYR	11	6.89	0.096	982	38.3	AE003661	TRUE	FALSE	2	1474.7	1.7	10of 24	1.2141	FALSE	TRUE	::::::::::::
DENTLAHGETFADAANAIW	2	3.59	0.002	1786	42.7	AE003661	TRUE	FALSE	2	2047.1	-0.6	4of 36	0.6534	FALSE	TRUE	::::::::::::::::::
TTVAHDSHVFHSGAGGPTQAVGFSAESASASAAPVVR	9	6.31	0.467	1472	55.4	AE003663	TRUE	TRUE	3	3565.8	2.6	44of144	4.2131	FALSE	TRUE	::::::::::::::::::::::::::::::::
LVLSPLTTLGNLPFR	15	11.05	0.351	1764	57.2	AE003664	TRUE	TRUE	2	1642	1.2	14of 28	2.1447	FALSE	TRUE	::::::::::::::::
SYLGLGASGSSAMNASDSMDVCCVPSCESK	4	3.71	0.137	2679	54.16	AE003664	TRUE	FALSE	3	3145.3	-2.5	17of116	1.6234	FALSE	TRUE	:::::::::::::::::Oxidation_M:::Cys_CAM:Cys_CAM:::Cys_CAM:::
NYIPMAGPPRFPMSSAQR	15	11.14	0.046	553	40.66	AE003666	TRUE	TRUE	3	2021.4	2.4	20of 68	2.325	FALSE	TRUE	::::::::::::::::::
FYLPGLAPVNFCK	14	8.88	0.24	1418	47.6	AE003667	TRUE	FALSE	2	1526.8	0.2	19of 24	2.3907	FALSE	TRUE	::::::::::Cys_CAM:::
VAVPSTVHCDHLIEAQIGGPK	9	6.02	0.323	1469	43.5	AE003669	TRUE	TRUE	2	2229.5	-0.1	20of 40	3.1503	FALSE	TRUE	::::::::Cys_CAM::::::::::::
RLNDSQSALRNSTSESEVHEEEPQD	4	4.02	0.024	1495	26.2	AE003669	TRUE	FALSE	3	2858.9	1.7	11of 96	1.1984	FALSE	TRUE	::::::::::::::::::::::::
DETLEALSDAQVVAPAAQTVDLHSADH	3	3.69	0.067	2146	52.9	AE003671	TRUE	FALSE	3	2805	-0.7	18of104	1.6036	FALSE	TRUE	::::::::::::::::::::::::::
ALAAAEDSGLPENLGLPR	5	3.83	0.038	2051	45	AE003675	TRUE	FALSE	3	1795	-0.9	20of 68	1.8873	FALSE	TRUE	::::::::::::::::::
SRYCYAAMR	12	9.62	0.015	1064	19.73	AE003675	TRUE	FALSE	2	1178.3	1.1	8of 16	1.0885	FALSE	TRUE	::::Cys_CAM:::::::
IVGSLVMSVAYRTK	14	10.4	0.101	1072	39.83	AE003678	TRUE	FALSE	2	1524.9	1.8	8of 26	1.2872	FALSE	TRUE	::::::::::::::
TVAFVSTFATFFTR	15	11.05	0.443	1884	48	AE003680	TRUE	TRUE	2	1595.8	0.7	18of 26	4.039	FALSE	TRUE	::::::::::::::
FNLFQGCPNAK	14	8.97	0.164	871	27.4	AE003680	TRUE	TRUE	2	1296.4	2.1	14of 20	2.0831	FALSE	TRUE	::::::Cys_CAM::::::
NSASGFAGGVGYI	9	5.93	0.176	1114	27.2	AE003681	TRUE	FALSE	2	1200.3	1.7	11of 24	1.3453	FALSE	TRUE	::::::::::::::
IGFPAAQAAPAISSTFPFIFGNR	15	11.05	0.437	1908	69.2	AE003682	TRUE	TRUE	2	2381.7	-0.5	24of 44	4.3105	FALSE	TRUE	::::::::::::::::::::::::
CALIHSTFFPALQGAK	14	8.97	0.363	1178	46.4	AE003682	TRUE	TRUE	2	1762	2.7	21of 30	3.8841	FALSE	TRUE	:Cys_CAM:::::::::::::::
LAVETLTPIVEQHQAAR	6	5.3	0.046	1342	42.3	AE003682	TRUE	TRUE	2	1877.2	1.3	11of 32	2.0502	FALSE	TRUE	::::::::::::::::
EPIVMHIRNSTALVPAPPRLDEQTKAITMQ	6	7.83	0.107	2590	71.46	AE003683	TRUE	FALSE	3	3358.9	2.9	23of116	1.9949	FALSE	TRUE	::::::::::::::::::::::::::::::
VSKYDLGKFIIDSLEQPEHYRK	6	7.66	0.233	1324	48.1	AE003684	TRUE	FALSE	3	2667	-1.9	22of 84	2.2759	FALSE	TRUE	::::::::::::::::::::::::
SSSGTPTISDAAGGGGGGGVFSRFR	13	10.89	0.045	1466	32	AE003685	TRUE	FALSE	2	2343.5	1.9	10of 50	1.2152	FALSE	TRUE	::::::::::::::::::::::::::
LEGKLSPLVTSTDLVLTI	4	4.08	0.191	2379	60.3	AE003687	TRUE	FALSE	2	1900.3	-2.5	6of 34	0.9838	FALSE	TRUE	::::::::::::::::::
FSLCIK	15	8.97	0.032	792	23.9	AE003688	TRUE	TRUE	1	767.9	-0.1	7of 10	1.2272	FALSE	TRUE	::::Cys_CAM:::
QISLCINMLHRM	14	9.02	0.01	1230	41.16	AE003691	TRUE	FALSE	2	1532.8	2.6	9of 22	2.1075	FALSE	TRUE	:::::Cys_CAM:::Oxidation_M:::::
SPIYSHLSATITGLPT	6	7.76	0.17	1919	40.4	AE003692	TRUE	FALSE	2	1658.9	0.7	8of 30	1.1137	FALSE	TRUE	::::::::::::::
TTEQILLTEKALQK	10	7.07	0.007	626	33.5	AE003692	TRUE	FALSE	2	1616.9	2.6	11of 26	1.4404	FALSE	TRUE	::::::::::::::
EIEMCGTNSPRR	9	6.44	0.05	802	18.13	AE003693	TRUE	FALSE	3	1450.6	2.6	16of 44	1.5909	FALSE	TRUE	:::::Cys_CAM:::::::
GITAFLTPKDVPGLSIAKKESKMGMRA	12	10.55	0.05	1759	57.66	AE003695	TRUE	FALSE	3	2848.4	3	16of104	1.28	FALSE	TRUE	::::::::::::::::::::::::::
FFSVPPCGLIK	9	8.97	0.087	404	40.8	AE003696	TRUE	FALSE	2	1265.5	-2.7	8of 20	1.2197	FALSE	TRUE	::::::Cys_CAM:::::
LHFAQLHEPIDTLAEAVR	6	5.18	0.35	1658	51	AE003697	TRUE	TRUE	2	2061.3	0.7	19of 34	4.0192	FALSE	TRUE	::::::::::::::::
VKPAVDAVLIFSCK	15	8.94	0.252	1180	43	AE003697	TRUE	TRUE	1	1547.8	0.2	17of 26	3.1154	FALSE	TRUE	::::::::::Cys_CAM:::
CIFASGSPFAPVTYNNK	14	8.88	0.132	1135	40.4	AE003697	TRUE	TRUE	2	1874.1	-0.1	13of 32	1.9507	FALSE	TRUE	:Cys_CAM:::::::::::::::
LAELVSKDDLAK	2	4.31	0.096	460	30.4	AE003697	TRUE	TRUE	2	1302.5	1.1	15of 22	2.0965	FALSE	TRUE	::::::::::::
ESIVYHDGSNYHAVAPLTFR	9	6.03	0.542	1589	44.5	AE003698	TRUE	TRUE	2	2277.5	1.5	23of 38	5.5488	FALSE	TRUE	::::::::::::::::::
FLAQVIGFTLGDANIEK	4	4.08	0.044	1665	55	AE003698	TRUE	FALSE	2	1837.1	0.6	9of 32	1.3016	FALSE	TRUE	::::::::::::::::
GVIMVEANPRPNR	14	10.89	0.022	1330	27.43	AE003698	TRUE	FALSE	2	1453.7	1	11of 24	1.9936	FALSE	TRUE	::::::::::::::
DAQEKLDLLEAGYTST	3	3.59	0.058	1144	34.1	AE003699	TRUE	FALSE	2	1754.9	1.5	10of 30	1.9559	FALSE	TRUE	::::::::::::::::
GLSGSVLCINRNYQLPNIEEQLLR	4	6.43	0.151	2362	67.8	AE003700	TRUE	FALSE	3	2788.1	-2.6	15of 92	1.6542	FALSE	TRUE	:::::::Cys_CAM:::::::::::::::
YTHIDIAGSAGEHPAMPTAAPLVSLVK	8	6.03	0.298	1867	62.43	AE003701	TRUE	TRUE	3	2764.2	-0.1	31of104	3.261	FALSE	TRUE	::::::::::::::Oxidation_M:::::::::::
VELGQPGVLTLVSATYAEEEEENH	3	3.58	0.048	1448	54.3	AE003701	TRUE	FALSE	3	2615.8	0.4	15of 92	1.3117	FALSE	TRUE	::::::::::::::::::::::::
KKSNPNVKLEIAVGGWAEGGSKYSQMVAVRDRR	13	10.62	0.039	1418	51.93	AE003701	TRUE	FALSE	3	3649.2	-1	21of128	1.7057	FALSE	TRUE	:::::::::::::::::::::::::::::::Oxidation_M:::::::
KTVNDCGISFSVVY	12	6.09	0.017	1239	35.1	AE003703	TRUE	FALSE	2	1589.8	-0.3	10of 26	1.2906	FALSE	TRUE	:::::Cys_CAM:::::::::
LIAVNFRAVALELR	13	10.89	0.104	2164	55.1	AE003708	TRUE	TRUE	3	1585.9	2.1	10of 52	1.3207	FALSE	TRUE	::::::::::::::
GEQPWEEGIEGFRRDFYSR	2	4.36	0.045	657	40.9	AE003708	TRUE	FALSE	3	2359.5	1.4	23of 72	1.5838	FALSE	TRUE	::::::::::::::::::
DNMMPGMGGRGQPGKNARPASPTLLDNTGHPA	12	10.09	0.024	1503	41.79	AE003708	TRUE	FALSE	3	3279.6	-2.7	22of124	1.8472	FALSE	TRUE	:::Oxidation_M:Oxidation_M:::::::::::::::::::::::::::
VITKDSNVVLVAMAGKC	9	8.94	0.101	1609	43.23	AE003711	TRUE	FALSE	2	1806.1	0.1	5of 32	0.8489	FALSE	TRUE	::::::::::::::::Cys_CAM:
KIECDRSEVKAENQKLEAKLSELTVDLAEER	2	4.48	0.07	2424	56.5	AE003711	TRUE	FALSE	3	3633	0.9	17of120	1.5824	FALSE	TRUE	::::Cys_CAM:::::::::::::::::::::::::
KYVFVVR	13	10.4	0.011	834	24.9	AE003711	TRUE	FALSE	1	911.1	-0.1	7of 12	1.391	FALSE	TRUE	::::::::

LWFVVPESPR	11	6.98	0.049	582	39.3	AE003712	TRUE	FALSE	2	1230.5	1.5	9of 18	1.1013	FALSE	TRUE	::::::::::
RTKDMMALGLDSDSED	4	3.77	0.05	1390	28.46	AE003718	TRUE	FALSE	2	1785	-2.7	11of 30	1.3382	FALSE	TRUE	::::::::::::::::
SGAVEQATLRCRQISGKTK	14	10.58	0.028	639	23.2	AE003718	TRUE	FALSE	3	2091.3	2.5	13of 72	1.182	FALSE	TRUE	:::::::::::Cys_CAM::::::::
ESPAICCYTIDKK	9	6.21	0.072	1269	26	AE003719	TRUE	FALSE	3	1585.7	-1.3	17of 48	1.8672	FALSE	TRUE	::::::Cys_CAM:Cys_CAM::::::
TLMITGMMLFSGCMYYR	14	8.83	0.114	2793	65.42	AE003728	TRUE	FALSE	2	2124.5	2.2	6of 32	0.8955	FALSE	TRUE	:::Oxidation_M:::::Oxidation_M:::::Cys_CAM:Oxidation_M::::
GLFRPNSKIGQEVK	15	10.59	0.088	808	25.7	AE003728	TRUE	FALSE	3	1573.8	1.1	14of 52	1.3285	FALSE	TRUE	::::::::::::::
HSMVKQTGDSTFDALLK	7	7.79	0.037	1753	31.53	AE003728	TRUE	FALSE	2	1879.1	-2.7	422	1.4397	FALSE	TRUE	::::::::::::::::::
VTRDGLEDQLLAEVVKAER	5	4.29	0.075	1862	44.1	AE003733	TRUE	FALSE	2	2142.4	-0.4	10of 36	2.0362	FALSE	TRUE	::::::::::::::::::::
NTLFSTLNYCVIGDHHTEVK	8	6.02	0.062	1913	44	AE003733	TRUE	TRUE	2	2349.6	2.7	14of 38	1.542	FALSE	TRUE	::::::::::Cys_CAM::::::::::
RDAGVQKLMVHGTSVKSSK	15	10.83	0.015	81	21.43	AE003734	TRUE	FALSE	2	2029.4	-1.8	7of 36	0.9565	FALSE	TRUE	::::::::::::::::::::
IVKALQGNKVVTVEQSR	13	10.59	0.108	1446	33.4	AE003736	TRUE	FALSE	2	1870.2	1.5	8of 32	1.2939	FALSE	TRUE	::::::::::::::::::
LHNYLVDNQFTAANPSKLFEAIAK	8	7.73	0.008	1618	61	AE003736	TRUE	FALSE	3	2706.1	1.6	11of 92	1.1946	FALSE	TRUE	::::::::::::::::::::::::
LLLPELGKQCPTSVSDCI	4	4.08	0.049	2764	53.2	AE003738	TRUE	FALSE	3	2031.3	-1.2	10of 68	1.1008	FALSE	TRUE	::::::::::Cys_CAM::::::Cys_CAM::
LAQHVPTLHPTSEELSIGNMR	9	6.03	0.046	1453	45.63	AE003738	TRUE	TRUE	3	2347.7	0.9	21of 80	2.4246	FALSE	TRUE	::::::::::::::::::Oxidation_M::
FMTVAEAAHQLLSIVEK	6	5.3	0.453	2378	51.63	AE003739	TRUE	TRUE	2	1888.2	1	25of 32	4.7653	FALSE	TRUE	::::::::::::::::::
VILKVNGTDVHRYTTK	12	10.18	0.115	1212	29.3	AE003739	TRUE	FALSE	2	1845.2	-2.9	7of 30	1.2072	FALSE	TRUE	::::::::::::::::
SYPSQQEYEHILSFFK	6	5.3	0.433	1911	40.1	AE003740	TRUE	TRUE	2	2004.2	2.7	18of 30	3.0532	FALSE	TRUE	::::::::::::::::
ISERFSVVVPLNMSR	15	10.89	0.059	687	44.83	AE003741	TRUE	FALSE	3	1751.1	1.8	15of 56	1.4587	FALSE	TRUE	:::::::::::::Oxidation_M:::
RLLCKGNVNLNDAAASTD	12	6.24	0.041	1721	34	AE003746	TRUE	FALSE	2	1933.1	-3	4of 34	0.6796	FALSE	TRUE	::::Cys_CAM::::::::::::::
LRTTNTMNLNAEGRASAGTQTPIVEDKENR	10	7.21	0.039	477	41.73	AE003748	TRUE	FALSE	3	3305.6	-1.3	8of116	0.8955	FALSE	TRUE	:::::::Oxidation_M::::::::::::::::::::::
VHDMISTSKIQRYRT	13	10.39	0.003	916	25.43	AE003748	TRUE	FALSE	3	1852.1	0.8	16of 56	1.7948	FALSE	TRUE	::::Oxidation_M::::::::::::
VTVVCEAVDYDR	2	3.71	0.369	614	30.6	AE003749	TRUE	TRUE	2	1426.5	0.9	17of 22	3.1598	FALSE	TRUE	:::::Cys_CAM::::::::
SPASAKGDHYASIMFRARVK	15	10.7	0.151	249	32.43	AE003751	TRUE	FALSE	3	2193.5	1.6	25of 76	2.2026	FALSE	TRUE	::::::::::::::::::::
HQRVSELRWDLRDTKDWEHM	7	6.05	0.086	1935	39.43	AE003751	TRUE	FALSE	3	2638.9	1.1	20	1.3789	FALSE	TRUE	::::::::::::::::::::
SASFENFVGDSAEGADFQMKMYNNPRYR	5	4.56	0.007	1914	53.86	AE003751	TRUE	FALSE	3	3249.5	-2.3	10of108	1.1558	FALSE	TRUE	::::::::::::::::::Oxidation_M:::::::::
SGASSPMSDADADLQARLDKLR	1	4.35	0.022	1268	36.33	AE003754	TRUE	FALSE	2	2305.5	2.9	11of 42	1.9496	FALSE	TRUE	::::::::::::::::::::
SRSSEDLLEQSQSLSSGR	1	4.45	0.022	304	23.9	AE003756	TRUE	FALSE	2	1967.1	0.3	10of 34	1.3083	FALSE	TRUE	::::::::::::::::
QQFDSLGGSSR	12	6.79	0.033	819	14.8	AE003757	TRUE	FALSE	2	1182.2	-1.4	9of 20	0.9374	FALSE	TRUE	::::::::::::
APLVSLEHCIAPFLESCDSNKDHR	6	5.22	0.25	1730	52.5	AE003758	TRUE	TRUE	3	2797	0.9	28of 92	3.5304	FALSE	TRUE	::::::::Cys_CAM::::::::Cys_CAM:::::::
MVKSNLVSAAEALGNKMQASKGGAPKKPQ	13	10.71	0.012	1375	39.46	AE003758	TRUE	FALSE	3	2958.5	0.7	10of112	0.9494	FALSE	TRUE	::::::::::::::::Oxidation_M::::::::::::
GKKITASTKSIDASS	13	10.32	0.05	798	12.9	AE003759	TRUE	FALSE	2	1494.7	-1.9	12of 28	1.236	FALSE	TRUE	::::::::::::::
GLDITDNGIMAIENLIGR	3	3.71	0.013	1010	53.03	AE003759	TRUE	FALSE	3	1916.2	1	22of 68	2.4035	FALSE	TRUE	::::::::::::::::::
KSLAAHTGYKDKRMTSASNTSSLPSTSESPVWK	12	10.3	0.088	2183	40.23	AE003760	TRUE	FALSE	2	3571	-2.9	8of 64	1.2468	FALSE	TRUE	::::::::::::::Oxidation_M::::::::::::::::
AADIRARVAPPNSHLCGGGGMPMPGGVGSSGGAIVGVA	15	9.02	0.059	1896	70.26	AE003760	TRUE	FALSE	3	3519	0.7	26of148	2.5588	FALSE	TRUE	::::::::::::::::Cys_CAM:::::Oxidation_M:::::::::::::::::
YQPGYCSYYTKQEKCTAARPG	15	8.87	0.066	1563	28.1	AE003761	TRUE	FALSE	3	2529.7	-2.1	10of 80	1.2154	FALSE	TRUE	::::::Cys_CAM::::::::Cys_CAM:::::::
LTIKLLQQSAGIFQY	12	9.72	0.003	1701	51.8	AE003762	TRUE	FALSE	2	1724.1	-0.6	4of 28	0.5635	FALSE	TRUE	::::::::::::::::
ALHIMDSGIGMTHQDLINNLGTIAK	8	6.02	0.522	2087	62.26	AE003763	TRUE	TRUE	2	2665.1	0	26of 48	5.6809	FALSE	TRUE	::::::::::::::::::::::::
YLTVACIFR	14	8.9	0.215	1232	37.7	AE003763	TRUE	TRUE	2	1143.3	1.8	11of 16	2.0479	FALSE	TRUE	::::::Cys_CAM::::
ALHIMDSGIGMTHQDLINNLGTIAK	9	6.02	0.01	1741	62.26	AE003763	TRUE	TRUE	3	2697.1	1	28of 96	2.2219	FALSE	TRUE	:::::Oxidation_M:::::Oxidation_M:::::::::::::
LMLIACGTSYHSAVATR	15	8.9	0.3	912	45.13	AE003765	TRUE	TRUE	2	1852.1	0.5	16of 32	3.0632	FALSE	TRUE	::::::Cys_CAM::::::::::::
GQDYSLPIDTHIGIAHTR	9	6.02	0.262	1582	35	AE003765	TRUE	TRUE	2	1995.2	0.1	16of 34	2.6815	FALSE	TRUE	::::::::::::::::::
TVLSIGAAQGNVETVRQ	11	6.98	0.122	1721	35	AE003766	TRUE	FALSE	2	1744	1.1	10of 32	1.493	FALSE	TRUE	::::::::::::::::::
NSGARKQDSKWPPMDASSVCHSVRDA	9	8.94	0.032	284	28.23	AE003766	TRUE	FALSE	3	2904.1	0.3	15of100	1.2754	FALSE	TRUE	::::::::::::::Oxidation_M:::::Cys_CAM:::::::
LRGYYRSSYVDPVANETRC	9	8.77	0.116	1506	37.1	AE003768	TRUE	FALSE	3	2307.5	-2.9	18of 72	2.1731	FALSE	TRUE	::::::::::::::::::Cys_CAM:
SLPKSYDIKSIMDSWTLQTGYPVIN	12	6.75	0.067	1845	66.53	AE003768	TRUE	FALSE	3	2874.3	2.3	13of 96	1.2785	FALSE	TRUE	::::::::::::Oxidation_M::::::::::::::
SLLTSGPSSAVANQPVITMK	12	10.1	0.01	907	44.63	AE003768	TRUE	FALSE	3	2002.3	0.4	18of 76	1.7286	FALSE	TRUE	::::::::::::::::::::
DEFDSGDVGLAILHSTTMTGMCQWGM	4	3.5	0.005	1929	66.89	AE003768	TRUE	FALSE	3	2893.2	-0.9	13of100	1.2934	FALSE	TRUE	::::::::::::::::::::Oxidation_M:Cys_CAM:::Oxidation_M:
VTSNLVSIANQVVDTCLHK	11	7.16	0.237	1385	43.8	AE003770	TRUE	TRUE	2	2099.4	-0.2	16of 36	2.7138	FALSE	TRUE	::::::::::::::::Cys_CAM::::
FSKTHETLGSDFESPSSSPRSYRTTSPC	5	7.16	0.085	1276	35	AE003771	TRUE	FALSE	3	3150.3	2.3	24of108	3.2566	FALSE	TRUE	::::::::::::::::::::::::::::Cys_CAM:
DYGQIGFSYLNDLDR	4	3.6	0.049	1982	39.5	AE003771	TRUE	TRUE	2	1776.9	-0.8	7of 28	1.039	FALSE	TRUE	::::::::::::::::
SLVSSESTKNCSGNAMDVFYDLNAHKAK	5	7.16	0	1738	43.63	AE003771	TRUE	TRUE	3	3091.3	2.1	21of108	2.5166	FALSE	TRUE	::::::::::Cys_CAM:::::Oxidation_M::::::::::::
RPYIDQSHICAEIGK	10	7.16	0.161	772	29.4	AE003775	TRUE	TRUE	3	1788	1.9	21of 56	3.218	FALSE	TRUE	::::::::::Cys_CAM:::::::
HLTTDAVCHVSGVCASR	10	7.17	0.099	496	28.3	AE003775	TRUE	TRUE	3	1871	1	25of 64	2.3711	FALSE	TRUE	:::::::Cys_CAM:::::Cys_CAM::::
VLTHCNTGSLATAGYGTALGVVR	15	8.9	0.601	1035	50.5	AE003778	TRUE	TRUE	2	2319.6	1.4	29of 44	5.4954	FALSE	TRUE	:::::Cys_CAM:::::::::::::::
MLSPAFSILQLFCSSPK	15	8.97	0.459	1959	59.13	AE003778	TRUE	TRUE	2	1943.3	1.6	21of 32	3.867	FALSE	TRUE	:Oxidation_M::::::::::Cys_CAM:::::
MLSPAFSILQLFCSSPK	14	8.97	0.408	2013	59.13	AE003778	TRUE	TRUE	2	1927.3	0.3	19of 32	3.7198	FALSE	TRUE	::::::::::::Cys_CAM:::::
NAAVSCAALVSSLR	14	9.01	0.32	890	35	AE003778	TRUE	TRUE	2	1419.6	0.8	18of 26	2.895	FALSE	TRUE	:::::Cys_CAM:::::::::
SPYAVCMLIR	14	8.9	0.288	1063	36.33	AE003778	TRUE	TRUE	1	1210.4	-0.5	13of 18	2.4179	FALSE	TRUE	:::::Cys_CAM:::::
DAVAAEEVAAEK	2	3.69	0.453	209	21.4	AE003781	TRUE	TRUE	2	1203.3	2.3	19of 22	4.5698	FALSE	TRUE	::::::::::::
NAAQNIALNSSVAAPR	15	11.05	0.289	547	29.7	AE003781	TRUE	TRUE	2	1597.8	1.4	21of 30	3.7481	FALSE	TRUE	::::::::::::::::
RRCRPFSEE	15	9.01	0.004	551	12.9	AE003784	TRUE	FALSE	2	1237.3	1.5	4of 16	0.7888	FALSE	TRUE	:::Cys_CAM::::::
YPSLSVHGIEGAFYEPGAK	6	5.3	0.42	1643	42.6	AE003785	TRUE	TRUE	2	2023.3	1.2	20of 36	3.5556	FALSE	TRUE	::::::::::::::::::
LSLSNLGLEYVDLYLMHMPVGQK	6	5.22	0.341	2400	76.36	AE003790	TRUE	TRUE	2	2622.1	0.9	16of 44	2.7716	FALSE	TRUE	::::::::::::::::::::::
TKLEILTGGCAGTMK	14	8.94	0.16	698	31.83	AE003795	TRUE	TRUE	2	1580.8	0.4	16of 28	3.2058	FALSE	TRUE	::::::::Cys_CAM:::::
VVTMIENGGLPIVATSK	12	6.95	0.033	1300	46.43	AE003795	TRUE	FALSE	2	1730.1	-2.4	10of 32	1.1989	FALSE	TRUE	::::::::::::::
SILGEEGALFPHIVTK	6	5.3	0.334	1718	46.1	AE003798	TRUE	TRUE	2	1712	0.8	18of 30	3.1895	FALSE	TRUE	::::::::::::::
VIVTIEHPNRAMGNAPNPSQRI	14	10.89	0.119	1895	43.93	AE003798	TRUE	FALSE	3	2431.8	0.3	17of 84	1.7263	FALSE	TRUE	::::::::::Oxidation_M::::::::::
TCLELEQQGVHILIAL	5	4.25	0.045	2194	57.3	AE003798	TRUE	FALSE	2	1838.1	2.8	11of 30	1.2598	FALSE	TRUE	::Cys_CAM::::::::::::::
VADIEAIAQLVHGVR	6	5.22	0.341	1806	42.3	AE003799	TRUE	TRUE	2	1591.9	1	22of 28	4.8765	FALSE	TRUE	::::::::::::::
YMNGHTDVVMGGITMNSEK	6	5.22	0.31	1246	34.79	AE003799	TRUE	TRUE	2	2085.4	0.7	17of 36	2.342	FALSE	TRUE	::::::::::::::::::
LYYDCGHLFPR	10	7.15	0.308	1124	35.2	AE003799	TRUE	TRUE	2	1441.6	2.5	16of 20	3.3525	FALSE	TRUE	:::::Cys_CAM:::::::
FLQNAVGIVPSPFDCYQVNR	9	6.09	0.238	2004	57.8	AE003799	TRUE	TRUE	2	2325.6	2.6	16of 38	2.7645	FALSE	TRUE	::::::::::::::Cys_CAM:::::::
LSVGLEDADDLIKDLEQALEIASK	2	3.63	0.187	2064	65.6	AE003799	TRUE	TRUE	2	2586.9	2.3	14of 46	2.5921	FALSE	TRUE	::::::::::::::::::::::
LYYDCGHLFPR	11	7.15	0.141	880	35.2	AE003799	TRUE	TRUE	2	1441.6	2.1	12of 20	1.7913	FALSE	TRUE	:::::Cys_CAM:::::::
YDAIIEIYDFVETFLK	3	3.59	0.064	2661	63.6	AE003799	TRUE	TRUE	2	1980.3	0.6	13of 30	2.2067	FALSE	TRUE	::::::::::::::::
SIDLGLGVRNVKEKSSEYIVEKF	5	7.1	0.079	1554	53.6	AE003802	TRUE	FALSE	3	2612	1.1	12of 88	1.3395	FALSE	TRUE	::::::::::::::::::::
PTVSASSTTEAAVTEASGGSGFKVVFP	1	4.27	0.059	1956	49.1	AE003802	TRUE	FALSE	2	2585.8	2.5	6of 52	0.9702	FALSE	TRUE	::::::::::::::::::::::::
ILGGVGGISGGGGRGGHYESSDYEPDYGR	1	4.54	0.038	598	39.9	AE003803	TRUE	FALSE	3	2871	-1.7	15of112	1.2739	FALSE	TRUE	::::::::::::::::::::::::::
SLAGTVLLADPLLYAQSTFK	4	6.68	0.068	2302	64.8	AE003806	TRUE	FALSE	2	2109.5	-0.7	13of 38	1.522	FALSE	TRUE	::::::::::::::::::
AVGHVEGFQSAASEYFNRYILELNR	8	5.4	0.061	2145	62.8	AE003806	TRUE	FALSE	3	2872.2	1.3	12of 96	1.1963	FALSE	TRUE	::::::::::::::::::::::
IKGLSAFDKVVGGMTWCI	14	8.94	0.037	2707	55.73	AE003807	TRUE	FALSE	3	1983.3	2.3	12of 68	1.3487	FALSE	TRUE	::::::::::::::::Cys_CAM::
DIYNQILKDMAAFPENTI	4	3.71	0.012	2588	53.23	AE003807	TRUE	FALSE	2	2097.4	-0.8	9of 34	1.0938	FALSE	TRUE	::::::::::::::::
YFLHTGHLTIAGCK	15	8.88	0.334	847	35.3	AE003808	TRUE	TRUE	2	1618.8	0.7	18of 26	3.1093	FALSE	TRUE	:::::::::::::Cys_CAM::

DFGSTLGIPLHVFGPETHMTAICGMALGK	8	6.02	0.316	2415	77.56	AE003808	TRUE	TRUE	3	3059.5	0.5	31of112	3.8518	FALSE		TRUE	:::::::::::::::::::::Cys_CAM::::::
YFLHTGHLTIAGCK	14	8.88	0.283	803	35.3	AE003808	TRUE	TRUE	2	1618.8	0	14of 26	2.0698	FALSE		TRUE	:::::::::::Cys_CAM::
TGIDPTQEQWTELADLMEKK	5	3.93	0.085	1815	43.03	AE003808	TRUE	FALSE	3	2334.6	0.7	21of 76	2.61	FALSE		TRUE	::::::::::::::::::
ERIEQSSVMDIVVK	2	4.45	0.008	473	34.63	AE003808	TRUE	FALSE	3	1633.9	-0.4	16of 52	1.7635	FALSE		TRUE	::::::::::::::
LLQSFAQAVLHFETNIERISARLS	6	7.86	0	1994	72.7	AE003808	TRUE	FALSE	3	2745.2	0.4	16of 92	2.3005	FALSE		TRUE	::::::::::::::::::::::
EDEIQFILNEIK	3	3.69	0.009	1308	39.2	AE003809	TRUE	FALSE	2	1491.7	-1.8	12of 22	1.9493	FALSE		TRUE	::::::::::::
TEMGVGTGAGSGFTRR	15	10.89	0.021	976	21.13	AE003810	TRUE	FALSE	2	1600.7	-0.9	11of 30	1.7822	FALSE		TRUE	:::Oxidation_M:::::::::::::
VQVAHVAESIQLPMPQVEK	6	5.3	0.341	1555	46.83	AE003813	TRUE	TRUE	2	2104.5	0.9	22of 36	4.0013	FALSE		TRUE	::::::::::::::::::
SPTEPGALTMDYYHDLAELCF	3	3.59	0.142	1915	58.83	AE003813	TRUE	FALSE	2	2447.6	2.8	11of 40	1.7196	FALSE		TRUE	:::::::::Oxidation_M::::::::::Cys_CAM::
TEMVHFDDVSLYGTPKEEPMPNIPIVSEK	5	4.13	0.132	2674	68.06	AE003815	TRUE	FALSE	3	3320.8	-1.9	18of112	1.7336	FALSE		TRUE	:::::::::::::::::::Oxidation_M:::::::::::
NDCGMPPPPPPPR	9	6.1	0.056	440	20.93	AE003815	TRUE	FALSE	2	1448.6	0.7	11of 24	1.2571	FALSE		TRUE	:::Cys_CAM::Oxidation_M:::::::::
QLVTPNLTFDISNRGIGPASSC	12	6.1	0.069	1752	51.3	AE003817	TRUE	FALSE	3	2348.6	1.1	24of 84	1.6845	FALSE		TRUE	:::::::::::::::::::::Cys_CAM:
AVPQIPLSDDGSNMNGNAARLARK	12	10.09	0.062	1113	40.63	AE003817	TRUE	FALSE	3	2512.8	1.5	8of 92	0.8801	FALSE		TRUE	:::::::::::::Oxidation_M:::::::::::
PGCDVAMGQTLVAYDNRR	12	6.24	0.066	1043	35.53	AE003818	TRUE	FALSE	3	2024.2	-1.3	20of 68	1.8246	FALSE		TRUE	:::Cys_CAM:::::::::::::::
ENWAKINKQVTTGGLAVAK	13	10.32	0.008	1726	34.7	AE003818	TRUE	FALSE	2	2029.3	0.3	7of 36	0.9852	FALSE		TRUE	::::::::::::::::::
RVPFFERSLLIEYWG	6	7.04	0.004	2190	60.7	AE003818	TRUE	FALSE	2	1913.2	1.8	5of 28	1.0034	FALSE		TRUE	::::::::::::::::
PPPNVTGSLHLGHALTNAIEDAITR	8	6.03	0.453	2577	52.6	AE003819	TRUE	FALSE	3	2595.9	1.1	36of 96	4.1822	FALSE		TRUE	::::::::::::::::::::::::
FVMIIPPPNVTGSLHLGHALTNAIEDAITR	8	6.03	0.141	2658	86.03	AE003819	TRUE	TRUE	3	3199.7	2.3	27of116	1.9429	FALSE		TRUE	::::::::::::::::::::::::::::
DTSATVRKTVINFMLK	12	10.59	0.033	897	37.53	AE003819	TRUE	FALSE	2	1841.2	1.2	5of 30	0.922	FALSE		TRUE	:::::::::::::Oxidation_M:::::
SGAGGAAGSSAADAGDDDVPDLVENFEEVAIADTK	1	3.13	0.349	1684	57.4	AE003820	TRUE	TRUE	2	3323.4	0.8	21of 68	4.1846	FALSE		TRUE	::::::::::::::::::::::::::::
ASKVDLMNSLPE	5	4.08	0.031	1608	28.93	AE003820	TRUE	FALSE	2	1304.5	1	11of 22	1.8161	FALSE		TRUE	::::::::::::
PFYTMPDPNNPVYSNSYDMFMRG	5	3.89	0.003	1967	57.29	AE003820	TRUE	FALSE	3	2745.1	2	18of 88	1.8207	FALSE		TRUE	::::::::::::::::::
KLQVVLRTKEK	13	10.83	0.058	1255	21	AE003822	TRUE	FALSE	2	1342.7	-1.3	9of 20	1.1664	FALSE		TRUE	::::::::::::
SIHDAICVVR	10	7.16	0	642	26.7	AE003823	TRUE	TRUE	1	1170.3	0.4	11of 18	1.8373	FALSE		TRUE	::::::Cys_CAM::::
PNANGGQTLMITPAPQPAPK	12	10.1	0.041	1401	34.53	AE003824	TRUE	FALSE	3	2004.3	0.1	24of 76	2.5861	FALSE		TRUE	::::::::::::::::::
FATNSVTMGDYERPLNISHFIGDLNTGFR	6	5.28	0.467	1987	71.53	AE003829	TRUE	TRUE	3	3274.6	2.9	32of112	4.8686	FALSE		TRUE	::::::::::::::::::::::::::
LQIIHSDLSQISAACGLAR	10	7.16	0.447	1337	51.8	AE003829	TRUE	TRUE	2	2054.3	0.8	25of 36	5.87	FALSE		TRUE	:::::::::::::Cys_CAM:::::
NMTNMFGRSRPTISVC	13	10.9	0.012	1291	34.36	AE003830	TRUE	FALSE	2	1888.1	2.9	7of 30	0.8441	FALSE		TRUE	::Oxidation_M::::::::::::Cys_CAM:
GVLFYGPPGCGK	15	8.88	0.177	843	29.4	AE003831	TRUE	TRUE	1	1252.4	-0.4	12of 22	1.9733	FALSE		TRUE	:::::::::Cys_CAM:::
IIEAIDAISSTAYSHQR	6	5.22	0.147	1438	38.7	AE003831	TRUE	TRUE	2	1876.1	-0.2	14of 32	1.9352	FALSE		TRUE	::::::::::::::::
SSHLIVMAATNRPNSIDPALR	15	10.89	0.061	969	47.23	AE003831	TRUE	TRUE	2	2264.6	1.8	14of 40	2.3894	FALSE		TRUE	::::::::::::::::::::
VSIPSSPSTVCSRISTQPAEDK	12	6.36	0.056	1396	34	AE003831	TRUE	FALSE	3	2347.6	0.1	21of 84	1.9281	FALSE		TRUE	:::::::::Cys_CAM:::::::::::
DLQQDVYHMASKMAEGVSRGLILRN	6	7.75	0.055	2396	55.96	AE003831	TRUE	FALSE	2	2865.3	2	5of 48	0.8924	FALSE		TRUE	:::::::::Oxidation_M:::Oxidation_M:::::::::::::
LDSPATLHVAFNALSCYR	10	7.16	0.307	1488	49.6	AE003832	TRUE	TRUE	2	2036.3	0.3	22of 34	3.4643	FALSE		TRUE	:::::::::::::::Cys_CAM:::::
DSFYPTLPWSYCR	12	6.09	0.307	865	40.4	AE003832	TRUE	FALSE	3	1692.8	-2.5	17of 48	1.8934	FALSE		TRUE	:::::::::::Cys_CAM:::
LDSPATLHVAFNALSCYR	11	7.16	0.293	1249	49.6	AE003832	TRUE	TRUE	2	2036.3	-0.2	21of 34	3.0273	FALSE		TRUE	:::::::::::::::Cys_CAM:::::
TVSHTGPLTEEFLR	6	5.3	0.292	1330	32.2	AE003832	TRUE	TRUE	2	1587.8	0.6	15of 26	2.7822	FALSE		TRUE	::::::::::::
APSVMDPMLGGSGGGGGSGSMQR	12	6.79	0.005	1608	33.09	AE003834	TRUE	FALSE	2	2069.3	-2.3	5of 42	0.7484	FALSE		TRUE	:::::Oxidation_M::::::::::::Oxidation_M:::
KQAMLAAYEMNLIREDDFEGHNI	5	4.28	0.068	1524	58.16	AE003835	TRUE	FALSE	3	2742.1	-2	16of 88	1.7586	FALSE		TRUE	:::Oxidation_M::::::Oxidation_M:::::::::::::
LVDGALDCLAQFT	1	2.93	0.008	996	44.8	AE003835	TRUE	FALSE	2	1423.6	-2.1	10of 24	1.0095	FALSE		TRUE	:::::::Cys_CAM::::::
GFMFYTDWTPSLSRSLLDGSNR	12	6.85	0.022	1567	59.93	AE003838	TRUE	TRUE	3	2551.8	-1.6	9of 84	1.065	FALSE		TRUE	::::::::::::::::::::
IGGTPIIGGQYVVSCDLIPQLPVIK	8	6.09	0.262	2487	79	AE003839	TRUE	TRUE	2	2639.1	-0.1	18of 48	3.1116	FALSE		TRUE	:::::::::::::::Cys_CAM:::::::::::
YQYTPDCDLAARFVVQR	12	6.24	0.01	2091	43.6	AE003839	TRUE	FALSE	3	2103.3	-0.3	22of 64	2.2311	FALSE		TRUE	::::::Cys_CAM:::::::::::
RSEPVNLFGTICKFYIKDKRLLA	12	10.05	0.108	2107	64.8	AE003840	TRUE	FALSE	3	2770.3	2.2	18of 88	1.7699	FALSE		TRUE	:::::::::::Cys_CAM:::::::::::
AKACANLISNEILSMR	15	8.97	0.02	529	41.93	AE003840	TRUE	FALSE	3	1792.1	-2.2	21of 60	2.1559	FALSE		TRUE	:::::Cys_CAM::::::::::::
GFGHIGIMVPDVYAACQR	10	7.16	0.316	1460	48.43	AE003841	TRUE	TRUE	2	1992.3	1.9	17of 34	2.9587	FALSE		TRUE	:::::::::::::::Cys_CAM:::::
AQAGENVGALLRGIK	12	10.09	0.088	792	31.8	AE003841	TRUE	FALSE	2	1497.7	1.8	12of 28	1.5924	FALSE		TRUE	::::::::::::::::
VRKHMGLSVDDASTDSPSPPPLDLT	2	4.34	0.019	1430	46.03	AE003847	TRUE	FALSE	3	2636.9	0.3	14of 96	1.2187	FALSE		TRUE	::::::::::::::::::::::
ELIKIKSEINLVQSDMK	5	7.08	0.053	1687	44.03	AE017256	TRUE	TRUE	3	2005.4	2.8	23of 64	1.932	FALSE		TRUE	:::::::::::::::Oxidation_M::
HAGDVITRTPR	14	10.89	0.031	711	14.3	AE017256	TRUE	FALSE	2	1223.4	-2.7	5of 20	1.0408	FALSE		TRUE	::::::::::::
EKMLRVAKENDILKDILDATTTIKHSDSR	6	7.76	0.024	1931	53.13	AE017256	TRUE	FALSE	3	3342.8	0.7	27of112	2.9453	FALSE		TRUE	::::::::::::::::::::::::::
DVYNEFRNYVGSQNMDDLFNLYSDTKSEFKIR	5	4.31	0.018	2465	71.93	AE017256	TRUE	FALSE	3	3910.3	1.9	22of124	2.286	FALSE		TRUE	::::::::::::::::::::::::::::
FDEISGVLSSYLEKACPS	3	3.83	0.044	1276	47.1	AE017257	TRUE	FALSE	3	2003.2	1.4	18of 68	1.7066	FALSE		TRUE	:::::::::::::::Cys_CAM:::
GVSACATCDGAFFR	9	5.95	0.143	508	32	AE017258	TRUE	FALSE	3	1519.6	-2.4	16of 52	1.744	FALSE		TRUE	:::::Cys_CAM:::Cys_CAM::::::
DISDDNVHDVSVHQQTDGHNCGIWAYENAR	5	4.23	0.096	2071	42.9	AE017258	TRUE	FALSE	3	3454.5	-1.6	21of116	1.8542	FALSE		TRUE	:::::::::::::::::::Cys_CAM:::::::::::
LKERAVQLEDHLRRAVADNENVK	8	7.8	0.018	1908	39.7	AE017258	TRUE	FALSE	3	2705	-2.8	15of 88	1.4238	FALSE		TRUE	::::::::::::::::::::
VIATGSDVISLPGINIDEK	2	3.71	0.003	1057	50.3	AE017258	TRUE	FALSE	2	1942.2	-1.6	10of 36	1.1984	FALSE		TRUE	::::::::::::::::::
PVIKLIKEFADTIG	11	6.99	0.011	1080	44.9	AE017259	TRUE	FALSE	3	1544.9	-0.9	17of 52	1.5929	FALSE		TRUE	::::::::::::::
EAKFDIMYNEGISKLGEIIDMGAKLG	5	4.29	0.008	2763	69.26	AE017259	TRUE	FALSE	3	2860.3	2.9	19of100	1.8807	FALSE		TRUE	:::::::::::::::::::Oxidation_M:::::
VGDEKIEMILSSEKAESFGKIMVHMDDKSCE	1	4.34	0.169	1822	63.99	AE017260	TRUE	FALSE	3	3577	1.3	11of120	1.1319	FALSE		TRUE	:::::::::::::::::::Oxidation_M:::Oxidation_M:::::Cys_CAM::
FNLKPIPNLQSK	12	10.6	0.007	1383	30.1	AE017260	TRUE	FALSE	2	1399.7	1.2	11of 22	1.9878	FALSE		TRUE	::::::::::::
DNVTWHHSESMVEAIESAKSQMPEEAAMQM	5	4.19	0.043	2537	56.92	AF045793	TRUE	FALSE	3	3405.8	-0.6	17of116	1.3999	FALSE		TRUE	::::::::::::::::::::::::
WVITAAHCVATTPNSN	6	7.16	0.016	1904	35.1	AF053915	TRUE	FALSE	2	1742.9	1.9	5of 30	0.893	FALSE		TRUE	:::::::Cys_CAM:::::::::
LSAITMPSVARHT	15	11.05	0.04	343	30.13	AF195418	TRUE	FALSE	3	1400.6	-0.9	12of 48	1.6095	FALSE		TRUE	:::::Oxidation_M:::::::
FPLKLNHMKTK	14	10.85	0.005	888	23.43	AF310892	TRUE	FALSE	1	1357.7	0.3	4of 20	0.7163	FALSE		TRUE	::::::::::
IFTDHQPLTFAVSESNPNAKIKRWKAR	13	10.82	0.002	1714	54.2	AF364549	TRUE	FALSE	3	3156.6	-2.4	18of104	1.5107	FALSE		TRUE	::::::::::::::::::::::
CLIDTGSSINLMSKNF	12	6.1	0.241	1782	43.93	AF364550	TRUE	FALSE	2	1817	-1.6	9of 30	1.3632	FALSE		TRUE	:Cys_CAM::::::::Oxidation_M:::::
MSVDETLMCSFYVLKPSKKPGLRK	12	9.96	0.009	1878	56.66	AF427494	TRUE	FALSE	3	2832.4	-2	16of 92	1.4369	FALSE		TRUE	:::::::Oxidation_M:Cys_CAM:::::::::::::
PMTLKLKKGAIIDTKCKEYIESFE	14	8.79	0.137	2051	56.93	AJ009736	TRUE	FALSE	3	2860.3	-2.5	13of 92	1.6662	FALSE		TRUE	::Oxidation_M::::::::::::Cys_CAM::::::::
YQSINPNCIMFK	15	8.88	0.122	1348	34.03	AJ302712	TRUE	TRUE	1	1531.7	0.3	8of 22	1.1721	FALSE		TRUE	:::::::Cys_CAM::Oxidation_M:::
LQIDMKPEVPREKLASRPTRPPEPR	13	10.56	0.016	1679	45.43	AK091465	TRUE	FALSE	3	2942.5	-1.8	11of 96	1.1962	FALSE		TRUE	::::::::::::::::::::::
RFETAYRGIKTFGFSQKVLNFCVKLPKN	12	10.62	0.019	2412	68	AL009193	TRUE	FALSE	2	3350.9	0.1	9of 54	0.9978	FALSE		TRUE	:::::::::::::::::::Cys_CAM:::::::
ATSRAAPIPRFEVLHPSPIACLSWK	12	10.11	0.013	1846	67.2	AL355930	TRUE	FALSE	3	2806.2	-2.7	19of 96	1.9022	FALSE		TRUE	:::::::::::::::::::Cys_CAM:::::
AHMHAVSPGGSSSSVGNFVVAVPAAHHAS	13	8.16	0.178	1338	43.83	AL512294	TRUE	FALSE	3	2786.1	1	23of112	1.8043	FALSE		TRUE	:::Oxidation_M:::::::::::::::::::::
GLPAFQPGENVKLNL	10	6.95	0.095	617	40.8	AL844507	TRUE	FALSE	2	1597.9	-0.5	10of 28	1.4157	FALSE		TRUE	::::::::::::::
QQILYDEFINNKNVQNTLNTGNYIGLMNI	4	4.08	0.016	2589	77.33	AL844507	TRUE	FALSE	3	3402.8	2.3	26of112	2.1323	FALSE		TRUE	:::::::::::::::::::::::::::Oxidation_M:::
NTPSYQSILENANVLAR	5	6.89	0.518	1839	38	ALF-DROME	TRUE	TRUE	2	1891.1	2	23of 32	4.6666	FALSE		TRUE	::::::::::::::::
LAENISGVILFHETLYQK	6	5.3	0.413	1756	56.3	ALF-DROME	TRUE	TRUE	2	2076.4	0.5	21of 34	4.2974	FALSE		TRUE	::::::::::::::::
ALSDHHVYLEGTLLKPN	9	6.03	0.372	1576	40.5	ALF-DROME	TRUE	FALSE	2	1908.2	1.5	16of 32	2.9703	FALSE		TRUE	::::::::::::::::
ALSDHHVYLEGTLLKPN	8	6.03	0.004	1685	40.5	ALF-DROME	TRUE	FALSE	3	1908.2	0.6	22of 64	2.3147	FALSE		TRUE	::::::::::::::::
WSPCTKENNYSYHK	9	8.79	0.069	643	16.2	ATB2-DROME	TRUE	FALSE	2	1814.9	3	6of 26	1.0694	FALSE		TRUE	:::Cys_CAM:::::::::
PLPETRIDVEIPRISADLGKEQHFIK	3	5.47	0.003	2457	63.3	ATU-DROME	TRUE	FALSE	3	3003.5	-1.7	17of100	1.5651	FALSE		TRUE	::::::::::::::::::::
MHGQANRNSHTLTLDENTS	9	6.03	0.033	934	19.63	AY035777	TRUE	FALSE	3	2143.3	-2.3	18of 72	1.9587	FALSE		TRUE	:Oxidation_M:::::::::::::::::

ENDSGNRIRGLYSYLDDVGERHSVR	8	5.42	0.11	1887	38.5	AY051482	TRUE	FALSE	3	2909.1	0.2	15of 96	1.6506	FALSE	TRUE	::::::::::::::::::::::::
AGSGAGAPPPLQHPHCDR	6	7.32	0.036	1131	19.3	AY051643	TRUE	FALSE	2	1825.9	-0.2	10of 34	1.5505	FALSE	TRUE	:::::::::::::Cys_CAM:::
KCSIVREEDEDESATECTAVGN	3	3.74	0.053	1435	29.8	AY052073	TRUE	FALSE	3	2500.5	2.6	7of 84	0.838	FALSE	TRUE	::Cys_CAM::::::::::::Cys_CAM::::::
GMGIPSTSGAGPAPDIVFHPVK	8	7.82	0.082	2495	45.83	AY052093	TRUE	FALSE	2	2136.5	2.5	9of 42	1.2572	FALSE	TRUE	::::::::::::::::::::
SNRLRRRLQESEVDSFDVSDI	5	4.65	0.134	1996	40.7	AY069039	TRUE	FALSE	3	2522.7	0	11of 80	1.2284	FALSE	TRUE	::::::::::::::::::::
NQEENKTKTFRPLK	13	10.32	0.005	868	13.5	AY069562	TRUE	FALSE	3	1734	-1	12of 52	1.4322	FALSE	TRUE	::::::::::::::
RIRIELSNEN	6	7.13	0.017	1184	22.5	AY071474	TRUE	FALSE	2	1244.4	-0.9	8of 18	1.214	FALSE	TRUE	::::::::::::
LQLQPTPVSLKPGTPQMQLQLPPQTAAK	15	10.6	0.023	1757	64.23	AY075176	TRUE	FALSE	3	3012.6	1.6	19of108	1.7567	FALSE	TRUE	::::::::::::::::::::::::::::
RELLVCHDMMGNYLEDRHFY	6	5.22	0.032	1879	56.46	AY075262	TRUE	FALSE	3	2599.9	-2.9	9of 76	1.1527	FALSE	TRUE	::::::Cys_CAM:::::::::::::::
LHGDVANIRKQERKLE	12	9.88	0.051	1431	24.7	AY075270	TRUE	FALSE	3	1907.2	1.3	19of 60	1.7449	FALSE	TRUE	::::::::::::::::
NVDRKNGLDIQHTEA	3	5.28	0	1064	18.4	AY075449	TRUE	FALSE	3	1710.8	1.6	20of 56	2.3395	FALSE	TRUE	::::::::::::::::
DKLGDRIEKRAKSDGLLTLYQLKEELPTGMI	6	7.13	0.099	2123	72.13	AY089480	TRUE	FALSE	3	3533.1	1.8	9of120	1.1794	FALSE	TRUE	::::::::::::::::::::::::::::::
TYAPVPAAIGADTYAPEKFIPQDVQEAHYK	5	4.54	0.043	1948	63.7	AY089627	TRUE	FALSE	3	3292.7	2.1	23of116	2.8296	FALSE	TRUE	::::::::::::::::::::::::::::
PSALKTHLFSSDSEMFGGSHDPNPVESSSMK	3	5.22	0.113	1837	48.66	AY094638	TRUE	FALSE	3	3340.6	1.8	27of120	2.5369	FALSE	TRUE	::::::::::::::Oxidation_M:::::::::::::Oxidation_M::
GGGGSDIAKPYGCDVCRR	13	8.28	0.004	1182	22	AY095100	TRUE	FALSE	2	1926	2.3	13of 34	1.8549	FALSE	TRUE	:::::::::::Cys_CAM:::Cys_CAM:::
LSSPTYGDLNHLVSVTMSGVTTCLR	10	7.16	0.094	1835	60.13	AY118611	TRUE	TRUE	2	2710	0.9	11of 48	1.912	FALSE	TRUE	:::::::::::::::::::::Cys_CAM:::
VTPDIELIPRQVHRVV	6	7.85	0.066	2266	45.5	AY119270	TRUE	FALSE	2	1872.2	-2.3	6of 30	0.8764	FALSE	TRUE	::::::::::::::::
VLIQVSVHYIESKKSSSEV	6	7.73	0.047	1291	42.3	AY122267	TRUE	FALSE	3	2133.4	-2.2	21of 72	2.1152	FALSE	TRUE	::::::::::::::::::
FTKEFASGMGDKSCKVK	12	9.7	0.113	1136	24.03	AY219209	TRUE	FALSE	2	1921.2	-2.3	6of 32	1.0549	FALSE	TRUE	:::::::::::::Cys_CAM::::
ILHGSTNLESMALSVQCLLR	10	7.16	0.155	1796	60.63	AY231684	TRUE	TRUE	3	2243.6	1.1	20of 76	2.6664	FALSE	TRUE	::::::::::::::::Cys_CAM::::
YCLGYK	14	8.81	0.07	174	17.4	AY231694	TRUE	TRUE	1	803.9	-0.2	8of 10	1.4455	FALSE	TRUE	::Cys_CAM:::::
QMVCDVLHPGLSSVNK	10	7.16	0.241	1016	36.13	AY231786	TRUE	TRUE	2	1785	2.6	16of 30	3.14	FALSE	TRUE	::::Cys_CAM::::::::::::
QMVCDVLHPGLSSVNK	5	7.16	0.013	1442	36.13	AY231786	TRUE	TRUE	2	1785	0.7	18of 30	1.887	FALSE	TRUE	::::Cys_CAM::::::::::::
NLTPGTVLILLAGR	15	11.05	0.3	1749	48.4	AY231788	TRUE	TRUE	2	1438.8	1.9	20of 26	3.6094	FALSE	TRUE	::::::::::::::
FVNFVQGFGR	15	11.05	0.268	1212	32.7	AY231796	TRUE	TRUE	1	1171.3	0.4	12of 18	2.5515	FALSE	TRUE	::::::::::
LQEPLLLLGKEKF	12	7.07	0.047	1379	48.4	AY231801	TRUE	FALSE	2	1528.9	0	8of 24	1.1837	FALSE	TRUE	::::::::::::::
LRESLPLLIFLR	15	10.89	0.411	1730	57.7	AY231807	TRUE	TRUE	2	1470.8	0	18of 22	3.9692	FALSE	TRUE	::::::::::::
VVCAAYSHELPK	10	7.16	0.312	393	27.9	AY231809	TRUE	TRUE	2	1374.5	1.3	17of 22	3.3104	FALSE	TRUE	:::Cys_CAM:::::::::
NSIVVIDATPFR	5	6.79	0.398	1619	36.3	AY231815	TRUE	TRUE	2	1332.5	0.9	15of 22	3.3991	FALSE	TRUE	::::::::::::
RKVDQLTQEMSLHNFTVSAMHGDMEQR	8	6.04	0.385	1816	47.99	AY231884	TRUE	TRUE	3	3190.6	1.6	35of104	4.8463	FALSE	TRUE	::::::::::::::::::::::::::
SYLLDLLSSIR	5	6.7	0.192	2367	43.3	AY231903	TRUE	TRUE	2	1280.5	2.1	15of 20	3.5134	FALSE	TRUE	::::::::::
DVTFEFPDNYLNV	1	2.88	0.034	1514	41.7	AY231915	TRUE	FALSE	1	1573.7	0.2	13of 24	2.0245	FALSE	TRUE	::::::::::::
AHQCATIQLDFQLPIR	10	7.16	0.38	1512	45.8	AY231919	TRUE	TRUE	2	1912.2	1.1	22of 30	4.5733	FALSE	TRUE	::::Cys_CAM:::::::::::
VNINCINQNNGVVDHR	11	7.16	0.373	517	26.7	AY232007	TRUE	TRUE	2	1867	0.4	17of 30	3.7723	FALSE	TRUE	:::::Cys_CAM:::::::::::
NILFVINNPDVYK	5	6.68	0.243	1838	43.8	AY232038	TRUE	TRUE	2	1549.8	1.8	19of 24	4.7477	FALSE	TRUE	::::::::::::
IIVHSNFIASTVVNDISLIR	7	7.85	0.004	2572	66.5	AY232168	TRUE	FALSE	3	2212.6	2	6	2.5475	FALSE	TRUE	::::::::::::::::::
EGTGTETPHSGCTVSLHYTGR	9	6.03	0.399	1025	21.4	AY232182	TRUE	TRUE	3	2248.3	0	23of 80	3.8026	FALSE	TRUE	:::::::::::Cys_CAM:::::::::
NKLEATTELSR	6	7.1	0.156	706	18.1	AY232198	TRUE	TRUE	2	1262.4	2.3	16of 20	2.9684	FALSE	TRUE	::::::::::::
LLEDKTTYQLTAKEALRKVYQERCDAMQ	4	6.57	0.046	1822	58.53	AY232200	TRUE	FALSE	3	3419.8	-2.2	15of108	1.4947	FALSE	TRUE	:::::::::::::::::::::Cys_CAM::::Oxidation_M::
LLMQAVLDE	1	3.01	0.026	566	38.13	BLM-DROME	TRUE	FALSE	1	1032.2	0.4	6of 16	0.9741	FALSE	TRUE	::::::::::
PYGVWSAPLMSI	9	5.93	0.071	1369	44.73	BT001442	TRUE	FALSE	2	1337.6	-1.5	9of 22	1.2646	FALSE	TRUE	:::::::::Oxidation_M:::
IDDDTDKHGIQFVKSTDVK	2	4.46	0.092	788	26.3	BT001615	TRUE	FALSE	2	2162.4	-2.4	9of 36	1.1814	FALSE	TRUE	::::::::::::::::::
TPMAPMAPMAPMAPMAPMAPMT	7	6.02	0.062	1860	65.91	BT003646	TRUE	FALSE	3	2261.9	1.5	7	1.8605	FALSE	TRUE	::::Oxidation_M:::::::::::::::::
VDGLMCVEDPLYLPPVTRPPRARKTKPRPKSPR	15	10.85	0.031	1708	62.93	BT011057	TRUE	FALSE	3	3845.5	1.4	17of128	1.3595	FALSE	TRUE	:::::Oxidation_M:Cys_CAM::::::::::::::::::::::::::
ELGMFELRPLITNISCK	12	6.44	0.003	1476	56.43	BT011349	TRUE	TRUE	2	2038.4	1.5	9of 32	0.9738	FALSE	TRUE	::::Oxidation_M::::::::::Cys_CAM::
LTGCQSVIAAASGAK	15	8.97	0.345	545	28.8	BT012447	TRUE	TRUE	2	1434.6	0.7	17of 28	2.4515	FALSE	TRUE	::::Cys_CAM:::::::::::
LSSAGLVYCHYGER	10	7.15	0.397	765	32.4	BT012460	TRUE	TRUE	2	1612.7	2	16of 26	2.9625	FALSE	TRUE	:::::::::Cys_CAM::::::
LMSIVTPDAPVSDGALLYRR	10	6.85	0.019	2551	58.93	BX251410	TRUE	FALSE	2	2191.6	0.3	8of 38	0.9988	FALSE	TRUE	::Oxidation_M:::::::::::::::::
TEAGRYASDHLPIAIRI	6	7.77	0.046	2232	41	BX294148	TRUE	FALSE	2	1884.1	-0.8	8of 32	1.1048	FALSE	TRUE	::::::::::::::::::
IMKHLRKMNNYNSY	12	10.34	0.019	1315	26.66	C3G-DROME	TRUE	FALSE	2	1829.1	1.6	6of 26	0.8708	FALSE	TRUE	::::::::Oxidation_M::::::
AKVKKKMLYSSSFDALKK	15	10.6	0.105	836	30.33	CADF-DROME	TRUE	FALSE	3	2089.5	-1.1	17of 68	2.3435	FALSE	TRUE	::::::Oxidation_M:::::::::::
AKVKKKMLYSSSFDALKK	14	10.6	0.056	786	30.33	CADF-DROME	TRUE	FALSE	3	2089.5	-0.4	17of 68	2.3869	FALSE	TRUE	::::::Oxidation_M:::::::::::
AFSLFDKDGDGTITTKELGTVMR	2	4.46	0.049	2264	50.83	CALM-DROME	TRUE	FALSE	3	2503.8	0.9	13of 88	1.2917	FALSE	TRUE	::::::::::::::::::::::
AALDLETLAYTASHYR	6	5.22	0.403	1827	40.9	CAPA-DROME	TRUE	TRUE	2	1796	1.3	17of 30	4.0679	FALSE	TRUE	::::::::::::::::
LGPNYLQIPVNCPYK	15	8.81	0.342	1191	42.7	CATA-DROME	TRUE	TRUE	2	1777	1.3	19of 28	3.3215	FALSE	TRUE	:::::::::::Cys_CAM::::
YADLLHHEFR	9	6.03	0.246	1432	27.3	CATL-DROME	TRUE	TRUE	2	1301.4	1.7	13of 18	2.058	FALSE	TRUE	::::::::::
LCQQYGMLR	15	8.9	0	275	28.03	CC37-DROME	TRUE	TRUE	2	1169.4	1.2	15of 16	3.0949	FALSE	TRUE	::Cys_CAM:::::::
LALGLVLHKHSYLR	12	10.4	0.028	896	44.7	CCAA-DROME	TRUE	FALSE	3	1621	2.4	17of 52	2.227	FALSE	TRUE	::::::::::::::
CSQTQLELADSRIDEKWQQAR	1	4.56	0.061	638	38.5	CCB2-DROME	TRUE	FALSE	3	2563.8	-0.3	20of 80	2.0475	FALSE	TRUE	:Cys_CAM:::::::::::::::::::
KHLVCYYDSASFVK	14	8.79	0.003	702	33.3	CH47-DROME	TRUE	TRUE	2	1717.9	0.6	15of 26	2.3518	FALSE	TRUE	:::::Cys_CAM:::::::::
GASGGVGSMSGSAVGAGATGMTADLLASGGAGAQGR	12	6.79	0.239	1232	50.66	CNC-DROME	TRUE	FALSE	3	3012.3	1.6	20of140	1.8488	FALSE	TRUE	::::::::::::::::::Oxidation_M:::::::::::::::
AALDLIQ	1	3.1	0.065	1180	27.8	COG2-DROME	TRUE	FALSE	1	743.9	1.2	8of 12	1.8807	FALSE	TRUE	::::::::
ALIIEHLIEAFPQIK	6	5.3	0.461	2126	57.9	COPB-DROME	TRUE	TRUE	2	1736.1	1.5	19of 28	5.0429	FALSE	TRUE	::::::::::::::::
VTVNTSFTDLHEYLK	6	5.22	0.438	1576	36.9	COPB-DROME	TRUE	TRUE	2	1768	2.2	15of 28	2.9184	FALSE	TRUE	::::::::::::::::
ASFLDTQQDMSCKR	12	6.24	0.102	1149	24.23	COPB-DROME	TRUE	FALSE	2	1703.8	-2.1	9of 26	1.2023	FALSE	TRUE	::::::::::Oxidation_M::Cys_CAM:::
LPEAAFFARTYLPSQM	11	6.89	0.095	1705	53.33	COPP-DROME	TRUE	FALSE	2	1843.2	2.7	10of 30	1.3792	FALSE	TRUE	::::::::::::::
SILGPQVLASCLPQLIR	15	9.01	0.102	1705	59.6	CSE1-DROME	TRUE	TRUE	2	1866.2	1.1	16of 32	2.096	FALSE	TRUE	:::::::::Cys_CAM:::::::
HTGSGILSMANAGANTNGSQFFICTVK	15	8.97	0.458	1333	52.63	CYPH-DROME	TRUE	TRUE	2	2785.1	2.4	25of 52	6.143	FALSE	TRUE	:::::::::::::::::::::::Cys_CAM::::
VIPNFMCQGGDFTNHNGTGGK	10	7.16	0.453	1152	33.13	CYPH-DROME	TRUE	TRUE	2	2252.4	0.3	18of 40	2.9591	FALSE	TRUE	::::::Cys_CAM:::::::::::::
VIPNFMCQGGDFTNHNGTGGK	11	7.16	0.439	916	33.13	CYPH-DROME	TRUE	TRUE	2	2252.4	1.2	17of 40	2.4272	FALSE	TRUE	::::::Cys_CAM:::::::::::::
HVVFGEVVEGLDVVK	2	4.43	0.421	1085	44	CYPH-DROME	TRUE	TRUE	2	1626.9	1.4	23of 28	4.9725	FALSE	TRUE	::::::::::::::
VFFDMTADNEPLGR	2	3.71	0.355	1028	39.53	CYPH-DROME	TRUE	TRUE	2	1612.8	1.4	17of 26	3.8537	FALSE	TRUE	::::::::::::::
VFGEVVEGLDVVK	3	3.83	0.174	1629	41.1	CYPH-DROME	TRUE	FALSE	1	1390.6	0.3	9of 24	1.4886	FALSE	TRUE	::::::::::::::
PNFMCQGGDFTNHNGTGGK	10	7.16	0.163	1161	20.73	CYPH-DROME	TRUE	FALSE	2	2040.1	2.3	16of 36	1.9698	FALSE	TRUE	:::::Cys_CAM:::::::::::::
KVDALGVGGNKR	13	10.59	0.036	772	14.3	DC11-DROME	TRUE	FALSE	2	1214.4	2.8	10of 22	1.293	FALSE	TRUE	::::::::::::
YIANLGHGITPQTPITSMEVLVEAVHK	9	6.03	0.352	2136	67.93	DCUP-DROME	TRUE	TRUE	3	2920.4	2.5	29of104	3.7389	FALSE	TRUE	::::::::::::::::::::::::::
AGAQMLQVFESSAEHLSK	6	5.3	0.273	1751	38.03	DCUP-DROME	TRUE	TRUE	3	1934.2	1.8	24of 68	3.863	FALSE	TRUE	::::::::::::::::::
LKEQYLTEDTGTRFV	2	4.45	0.025	436	35.1	DPG1-DROME	TRUE	FALSE	3	1801	2	18of 56	2.0705	FALSE	TRUE	::::::::::::::::
MVEQLAEK	1	4.27	0.017	769	20.73	DYNA-DROME	TRUE	FALSE	1	964.1	1	10of 14	1.517	FALSE	TRUE	:Oxidation_M:::::::
VETGVLKPGTVVVFAPANITTEVK	10	7.07	0.325	1481	61	EF11-DROME	TRUE	TRUE	2	2470.9	-0.6	16of 46	3.3163	FALSE	TRUE	::::::::::::::::::::::
IGGIGTVPVGR	15	11.05	0.266	431	26	EF11-DROME	TRUE	TRUE	2	1026.2	0.8	14of 20	2.5417	FALSE	TRUE	::::::::::::
LPLQDVYK	12	6.68	0.178	812	25.8	EF11-DROME	TRUE	TRUE	2	976.2	0.8	13of 14	2.4508	FALSE	TRUE	::::::::
GAADFTAQVIVLNHPGQIANGYTPVLDCHTAH	8	5.72	0.153	2053	69.3	EF11-DROME	TRUE	FALSE	3	3389.7	2.6	25of124	2.4006	FALSE	TRUE	::::::::::::::::::::::::::Cys_CAM::::

GAADFTAQVIVLNHPGQIANGYTPVLD	4	3.88	0.011	2214	68.3	EF11-DROME	TRUE	FALSE	2	2783.1	-1.1	11of 52	2.2711	FALSE		TRUE	::::::::::::::::::::::::::
VFMSCNLITGMFQR	15	9.01	0.35	1614	49.36	EF1G-DROME	TRUE	TRUE	2	1705	-0.3	18of 26	2.6236	FALSE		TRUE	:::::Cys_CAM:::::::::
GHVFEENQVVGTPMFVVK	6	5.3	0.359	1550	46.33	EF2-DROME	TRUE	TRUE	2	2018.3	0.6	19of 34	3.9016	FALSE		TRUE	::::::::::::::::::
EEDHACIPLKK	3	5.35	0.088	1012	18.2	EF2-DROME	TRUE	FALSE	2	1340.5	1.8	12of 20	1.4484	FALSE		TRUE	::::::Cys_CAM::::::
CLYAAAITAK	14	8.88	0.041	492	29.1	EF2-DROME	TRUE	TRUE	2	1082.3	1.2	8of 18	1.4027	FALSE		TRUE	:Cys_CAM:::::::::
FSVSPVVR	15	11.05	0.022	393	24.1	EF2-DROME	TRUE	TRUE	2	891.1	2.6	10of 14	1.8525	FALSE		TRUE	::::::::
AAVPSGASTGVHEALELR	6	5.3	0.511	1267	35.5	ENO-DROME	TRUE	TRUE	2	1766	1.4	24of 34	4.4445	FALSE		TRUE	::::::::::::::::::
FGLDATAVGDEGGFAPNIQSNK	2	3.71	0.482	1000	42.5	ENO-DROME	TRUE	TRUE	2	2209.4	2	25of 42	5.061	FALSE		TRUE	::::::::::::::::::::::
PSGASTGVHEALELR	6	5.3	0.482	1274	26.5	ENO-DROME	TRUE	FALSE	2	1524.7	1.4	23of 28	4.1893	FALSE		TRUE	::::::::::::::::
NGTISVSRPLDRETISHYTLE	3	5.35	0.059	1388	42	FAT2-DROME	TRUE	FALSE	2	2389.6	-0.2	7of 40	1.0177	FALSE		TRUE	::::::::::::::::::::::
VTVHYTGTLDDGTK	6	5.1	0.427	888	20.8	FKB1-DROME	TRUE	TRUE	2	1507.6	0.8	18of 26	3.6194	FALSE		TRUE	::::::::::::::::
VTVHYTGTLDDGTKFDSSR	6	5.2	0.293	1106	28.1	FKB1-DROME	TRUE	TRUE	3	2100.2	2.8	32of 72	4.0761	FALSE		TRUE	::::::::::::::::::
VPTPNVSVVDLTVR	5	6.79	0.47	1595	37.1	G3P1-DROME	TRUE	TRUE	2	1496.7	0.9	19of 26	3.5103	FALSE		TRUE	::::::::::::::::
VPTPNVSVVDLTVR	4	6.79	0.46	1610	37.1	G3P1-DROME	TRUE	TRUE	2	1496.7	1.1	17of 26	3.0671	FALSE		TRUE	::::::::::::::
GANVVAVNDPFIDVNYMVYLFK	4	3.89	0.394	2450	73.53	G3P2-DROME	TRUE	TRUE	2	2489.9	0	20of 42	3.6337	FALSE		TRUE	::::::::::::::::::::::
GANVVAVNDPFIDVNYMVYLFK	3	3.89	0.361	2322	73.53	G3P2-DROME	TRUE	TRUE	2	2489.9	2.1	20of 42	3.5991	FALSE		TRUE	::::::::::::::::::::::
GANVVAVNDPFIDVNYMVYLFK	5	3.89	0.123	2574	73.53	G3P2-DROME	TRUE	TRUE	2	2489.9	2.7	12of 42	1.6987	FALSE		TRUE	::::::::::::::::::::::
GLHSHFVSNIDGTHLAEVLK	9	6.31	0.264	1669	43.9	G6PI-DROME	TRUE	TRUE	2	2175.5	-0.1	16of 38	3.1637	FALSE		TRUE	::::::::::::::::::::
NLYTLEHNDIINALCFSPNR	6	5.22	0.289	1895	54.9	GBLP-DROME	TRUE	TRUE	2	2405.6	0.8	20of 38	3.0051	FALSE		TRUE	:::::::::::::::Cys_CAM::::::
YWLCVAYGPSIK	14	8.81	0.206	1219	42.4	GBLP-DROME	TRUE	TRUE	2	1457.7	2.8	12of 22	1.7842	FALSE		TRUE	::::Cys_CAM::::::::
CTFHHDLELDHKPPTREALLPDMA	6	5.15	0.004	1447	53.63	GCH1-DROME	TRUE	FALSE	3	2845.2	2	21of 92	1.7621	FALSE		TRUE	:Cys_CAM:::::::::::::::::::::
LLTSFTALPVTAQLFR	15	11.05	0.224	1763	60.6	GELS-DROME	TRUE	TRUE	2	1779.1	1.4	16of 30	2.3026	FALSE		TRUE	::::::::::::::::
IYHKQMEYFELG	6	5.3	0.074	1552	35.93	GMDS-DROME	TRUE	FALSE	2	1574.8	-1.3	8of 22	1.2724	FALSE		TRUE	::::::Oxidation_M::::::
HEKPDTTVVAFLIFPTK	8	7.8	0.449	2080	44.5	GYS-DROME	TRUE	TRUE	2	1944.3	-0.1	22of 32	3.7082	FALSE		TRUE	::::::::::::::::::
GATHLAHVFTTVSEITGYEAEHLLK	7	5.76	0.422	1843	57	GYS-DROME	TRUE	TRUE	3	2726.1	2.3	1	5.2733	FALSE		TRUE	::::::::::::::::::::::
GATHLAHVFTTVSEITGYEAEHLLK	8	5.76	0.256	2364	57	GYS-DROME	TRUE	TRUE	3	2726.1	1.8	33of 96	3.4422	FALSE		TRUE	::::::::::::::::::::::
VDVTSEKDVSAALQTAKDKFGR	10	7.07	0.013	446	32.6	HCD2-DROME	TRUE	FALSE	2	2366.6	-1.8	5of 42	0.7961	FALSE		TRUE	::::::::::::::::::::
TAVFVLATLQQLEPSDNNTCHVLVMCHTR	8	6.02	0.168	2281	74.73	HE47-DROME	TRUE	TRUE	3	3356.8	2.7	35of112	3.0855	FALSE		TRUE	:::::::::::::::::::Cys_CAM:::::Cys_CAM::::
IFNGSHSFEPSGVMAVPPHSTVLM	7	6.02	0.07	1497	61.46	HIG-DROME	TRUE	FALSE	3	2542.9	0.5	367	1.3356	FALSE		TRUE	::::::::::::::::::::::
DMFNNLNTEDIVRRVK	12	7.07	0.12	1824	36.13	HMCU-DROME	TRUE	FALSE	2	1965.2	-2.6	9of 30	1.2304	FALSE		TRUE	::::::::::::::::
MVPFYEPYYCQRQR	9	8.77	0.025	2030	38.63	HS23-DROME	TRUE	FALSE	2	1954.2	-1.9	5of 26	0.8411	FALSE		TRUE	:Oxidation_M::::::::Cys_CAM:::::
SPIYELGLGLHPH	9	6.02	0.311	1740	36.5	HS26-DROME	TRUE	FALSE	2	1433.7	2	19of 24	2.9069	FALSE		TRUE	::::::::::::
DAGVIAGLQVMR	5	6.79	0.417	1583	34.23	HS7C-DROME	TRUE	TRUE	1	1230.5	0.5	12of 22	2.3243	FALSE		TRUE	::::::::::::
MIRDAEKFADEDKKLKERV	11	7.18	0.021	133	32.43	HS7C-DROME	TRUE	FALSE	2	2322.7	-0.9	5of 36	0.9727	FALSE		TRUE	::::::::::::::::::
APAVGIDLGTTYSCVGVFQHGK	11	7.15	0.449	1128	47.9	HS7D-DROME	TRUE	TRUE	2	2278.5	1.1	22of 42	4.6153	FALSE		TRUE	:::::::::::Cys_CAM:::::::::
DNNLLGKFELSGIPPAPRGVPQ	12	7.02	0.053	1445	51.4	HS7D-DROME	TRUE	FALSE	3	2320.7	-2.9	23of 84	1.869	FALSE		TRUE	::::::::::::::::::::
TAGTLTIIDTGIGMTK	5	6.76	0.484	1718	38.33	HS83-DROAV	TRUE	TRUE	2	1593.9	0.8	22of 30	3.8028	FALSE		TRUE	::::::::::::::::
GVVDSEDLPLNISR	2	3.71	0.379	876	35.3	HS83-DROAV	TRUE	TRUE	2	1514.7	1.9	20of 26	3.8573	FALSE		TRUE	::::::::::::::::
TAGTLTIIDTGIGMTK	4	6.76	0.242	1713	38.33	HS83-DROAV	TRUE	TRUE	2	1593.9	0.5	14of 30	2.036	FALSE		TRUE	::::::::::::::::
CAIYIGCSPVVAISSLK	13	8.28	0.122	1404	53.1	HTS-DROME	TRUE	TRUE	2	1839.1	1.5	15of 32	1.7441	FALSE		TRUE	:Cys_CAM:::::Cys_CAM:::::::::::
LHTECFIFGNVTK	10	7.16	0.342	1213	36.6	IDE-DROME	TRUE	TRUE	2	1566.8	0.4	15of 24	2.5707	FALSE		TRUE	:::::Cys_CAM:::::::::
ALEVAIEHIR	6	5.3	0.223	1170	31.4	IF2A-DROME	TRUE	TRUE	2	1151.4	1.3	15of 18	3.3065	FALSE		TRUE	::::::::::::
LVTAIDEADLAR	2	3.71	0.214	681	36.1	IF2A-DROME	TRUE	TRUE	2	1287.5	0.3	15of 22	2.4645	FALSE		TRUE	::::::::::::
VFEIILDKNPDMAAGR	2	4.31	0.095	926	45.53	IF2B-DROME	TRUE	TRUE	2	1790.1	0.9	18of 30	3.6114	FALSE		TRUE	::::::::::::::::
FVSHVVGTTFQTIR	15	11.05	0.284	935	37.3	IF3B-DROME	TRUE	TRUE	2	1592.8	2.2	17of 26	3.5124	FALSE		TRUE	::::::::::::::
ILESGCHVVVGTPGR	10	7.16	0.335	585	33.3	IF4A-DROME	TRUE	TRUE	2	1581.8	2.2	20of 28	4.2163	FALSE		TRUE	::::::Cys_CAM:::::::::
LESGCHVVVGTPGR	10	7.16	0.263	601	25.9	IF4A-DROME	TRUE	FALSE	2	1468.6	2.3	14of 26	2.5175	FALSE		TRUE	:::::Cys_CAM:::::::::
LFVLDEADEMLSR	2	3.59	0.199	1353	46.73	IF4A-DROME	TRUE	TRUE	2	1538.8	1.4	21of 24	3.851	FALSE		TRUE	::::::::::::::
VLITTDLLARGIDVQQVS	4	3.89	0.046	2757	56.7	IF4A-DROME	TRUE	FALSE	2	1942.3	1.4	7of 34	1.1767	FALSE		TRUE	::::::::::::::::::
QYIKLFVLDEADEMLSRGFK	5	4.56	0.026	1836	62.33	IF4A-DROME	TRUE	FALSE	3	2419.8	2.8	20of 76	1.8306	FALSE		TRUE	:::::::::::::Oxidation_M::::::
SSHIIDHVLSEAR	9	6.03	0.31	1468	25.8	IML2-DROME	TRUE	TRUE	2	1464.6	0.9	16of 24	2.6926	FALSE		TRUE	::::::::::::::
LLYGPDEHPDHVVVIK	6	5.12	0.444	1218	42.1	INO1-DROME	TRUE	TRUE	2	1832.1	1.3	16of 30	4.4771	FALSE		TRUE	::::::::::::::::
GCIGLPPISHMTLEQR	11	7.16	0.376	1064	41.53	INO1-DROME	TRUE	TRUE	2	1810.1	1.4	17of 30	2.2937	FALSE		TRUE	::Cys_CAM:::::::::::::
GCIGLPPISHMTLEQR	10	7.16	0.055	1060	41.53	INO1-DROME	TRUE	TRUE	2	1826.1	0.7	14of 30	1.7127	FALSE		TRUE	::Cys_CAM::::::::Oxidation_M::::::
EKLRHFTRYAIFVVACREEIPSEK	14	8.85	0.001	1774	58.9	INSR-DROME	TRUE	FALSE	2	2980.4	-2.8	5of 46	0.7518	FALSE		TRUE	:::::::::::::::Cys_CAM:::::::::
NADFANTIIAETHK	6	5.22	0.444	1352	26	IPYR-DROME	TRUE	TRUE	2	1545.7	2.6	18of 26	2.9965	FALSE		TRUE	::::::::::::::
RIQEVTPICVLK	15	8.97	0.27	859	36.5	JC7827	TRUE	TRUE	2	1456.7	1.4	14of 22	2.7235	FALSE		TRUE	::::::::Cys_CAM::::
MNKVELESRLEGLTDEINFLR	2	4.36	0.15	2352	58.73	K2C8	TRUE	FALSE	2	2507.9	-2.9	8of 40	1.3397	FALSE		TRUE	::::::::::::::::::::
AGKPVICATQMLESMVK	15	8.94	0.383	1432	42.26	KPYK-DROME	TRUE	TRUE	2	1864.2	0.6	20of 32	3.1548	FALSE		TRUE	::::::Cys_CAM:::::::::
CPIIAVTR	14	9.01	0.127	262	26.4	KPYK-DROME	TRUE	TRUE	2	930.1	2.5	12of 14	2.4304	FALSE		TRUE	:Cys_CAM:::::::
TSAAGGAASVGAGDGPGSKVMRMSSVIQFAK	12	10.59	0.049	1847	49.36	KRUH-DROME	TRUE	FALSE	3	2929.3	-0.8	12of120	1.2236	FALSE		TRUE	:::::::::::::::::::Oxidation_M::Oxidation_M:::::::::
TVRVQAYTSMGAGPMSTPVQVK	14	10.4	0.273	1766	41.86	LAR-DROME	TRUE	FALSE	2	2325.7	-2.9	11of 42	1.6255	FALSE		TRUE	::::::::Oxidation_M:::::::::::
HEKIIDIYGHVTC	4	6.02	0.008	1363	29.7	LAR-DROME	TRUE	FALSE	3	1585.8	-2.6	17of 48	1.5263	FALSE		TRUE	:::::::::::Cys_CAM:
NPQITASTDFAASANSR	5	6.79	0.517	1306	24.5	LDH-DROME	TRUE	TRUE	2	1751.9	0.9	23of 32	4.7232	FALSE		TRUE	::::::::::::::::
LQGELMDLQHGSNFLK	6	5.22	0.413	1538	41.93	LDH-DROME	TRUE	TRUE	2	1831.1	2.5	20of 30	3.6705	FALSE		TRUE	::::::::::::::::
DSLLAQVAEVLPSSGHK	6	5.22	0.349	1820	36.6	LDH-DROME	TRUE	TRUE	2	1752	1.8	23of 32	5.2571	FALSE		TRUE	::::::::::::::::
LCIVTAGVR	15	9.01	0.054	423	29.9	LDH-DROME	TRUE	TRUE	1	989.2	-0.3	10of 16	1.4693	FALSE		TRUE	::Cys_CAM:::::::
GMPMQMFFMVVPYVA	12	5.93	0.011	1604	63.62	LP1B-DROME	TRUE	FALSE	2	1781.2	0.2	6of 28	1.022	FALSE		TRUE	::Oxidation_M::::::Oxidation_M:::::::
TITLEVEPSDTXENVK	2	3.69	0.231	878	29.9	M33016	TRUE	TRUE	2	1789	2.3	19of 30	3.4015	FALSE		TRUE	::::::::::::::::
HLDIRVMVTTGGTI	7	7.85	0.082	1437	37.33	ME31-DROME	TRUE	FALSE	2	1529.8	-2	393	1.421	FALSE		TRUE	::::::Oxidation_M:::::::
LVQDLKCLVFSLIGLHFK	14	8.94	0.181	2047	70.2	MGN-DROME	TRUE	FALSE	3	2131.6	-1.1	21of 68	2.1746	FALSE		TRUE	::::::Cys_CAM::::::::::
IMLHSDEFFK	6	5.22	0.164	1366	34.13	MO25-DROME	TRUE	TRUE	2	1267.5	-0.1	14of 18	2.3909	FALSE		TRUE	::::::::::
ILALCMGNHELYMR	10	7.16	0.305	1153	49.46	MOEH-DROME	TRUE	TRUE	2	1738	1.2	16of 26	2.1653	FALSE		TRUE	:::::Cys_CAM:Oxidation_M:::::::::
AYALPLMEGRHRDLKSISSE	8	7.75	0.008	2391	43.93	MPIP-DROME	TRUE	FALSE	2	2274.6	-0.4	10of 38	1.7459	FALSE		TRUE	::::::::::::::::::::
DVGCTHLIVSTACGSLR	10	7.01	0.176	1072	38.7	MTAP-DROME	TRUE	TRUE	2	1847	0.2	15of 32	2.8019	FALSE		TRUE	::::Cys_CAM::::::::Cys_CAM:::::
QLRDLETELDEE	3	3.44	0.051	1592	29.1	MYSN-DROME	TRUE	FALSE	2	1490.6	-1	8of 22	1.1977	FALSE		TRUE	::::::::::::
QDMTLLCNSNRENR	9	6.36	0.037	1130	23.03	NBEA-DROME	TRUE	FALSE	3	1767.9	0.5	18of 52	2.0576	FALSE		TRUE	::::Oxidation_M::::Cys_CAM::::::::
LHPTDVHVTAVLVEYK	8	6.03	0.124	1708	40.9	NCPR-DROME	TRUE	TRUE	2	1822.1	2.1	13of 30	1.6019	FALSE		TRUE	::::::::::::::::
ELVTWTPAAK	11	6.95	0.155	728	28.1	NDKA-DROME	TRUE	TRUE	1	1116.3	-0.5	9of 18	1.192	FALSE		TRUE	::::::::::
WIISAAHCVINYGKYFY	9	8.75	0.012	2729	59	NDL-DROME	TRUE	FALSE	3	2106.4	-2.7	12of 64	1.383	FALSE		TRUE	::::::::Cys_CAM:::::::::
DSVQIPIAVLK	5	6.76	0.048	1651	34.8	NLP-DROME	TRUE	TRUE	1	1183.4	0	14of 20	2.3062	FALSE		TRUE	::::::::::
SNDDVELGLGKAGLASMETLD	4	3.43	0.007	1843	46.63	NRT-DROME	TRUE	FALSE	3	2136.3	-0.3	12of 80	1.1992	FALSE		TRUE	::::::::::::::::::::::
FGFNSLFVVLTR	15	11.05	0.025	2254	49.5	O67B-DROME	TRUE	FALSE	3	1400.7	0.7	9of 44	1.1167	FALSE		TRUE	::::::::::::

DSQHLFASPQCLGYK	10	7.15	0.125	1056	30.8	OFU1-DROME	TRUE	TRUE	2	1751.9	1.3	19of 28	3.121	FALSE	TRUE	::::::::::Cys_CAM::::
LPRSNSCPDLSMYR	14	8.9	0.059	344	30.63	ORK1-DROME	TRUE	FALSE	3	1712.9	-1.7	14of 52	1.4867	FALSE	TRUE	::::::Cys_CAM::::Oxidation_M:::
NVVTIFSAPNYCYR	14	8.83	0.131	1143	39.7	P2A-DROME	TRUE	TRUE	2	1704.9	2	13of 26	2.6246	FALSE	TRUE	::::::::::Cys_CAM:::
VEEAVAVLQVHR	6	5.3	0.424	1135	31.6	PABP-DROME	TRUE	TRUE	2	1350.6	1.4	16of 22	2.8421	FALSE	TRUE	::::::::::::
FAQVQSLPLIVDFNHESASK	6	5.22	0.44	1770	51.7	PDI-DROME	TRUE	TRUE	2	2231.5	0.4	24of 38	4.752	FALSE	TRUE	::::::::::::::::::::
DLTSVADAEQFLKDNEIAIIGFFK	3	3.85	0.421	2564	71.9	PDI-DROME	TRUE	TRUE	2	2686	-0.3	18of 46	3.866	FALSE	TRUE	::::::::::::::::::::::::
YKDNEDIVIAK	2	4.31	0.336	223	23	PDI-DROME	TRUE	TRUE	2	1308.5	1.8	15of 20	3.1999	FALSE	TRUE	::::::::::::
SHLLFFVSR	15	11.05	0.273	1163	34.3	PDI-DROME	TRUE	TRUE	1	1106.3	0.2	10of 16	2.0891	FALSE	TRUE	::::::::::
KINCEVIGCSTDSQFTHLAWINTPR	10	7.01	0.349	1412	57.9	PDX1-DROME	TRUE	TRUE	3	2949.2	2.4	29of 96	3.8815	FALSE	TRUE	::::Cys_CAM::::Cys_CAM::::::::::::::::
PQLQKPAPAFAGTAVVNGVFK	15	10.6	0.201	1087	48.7	PDX1-DROME	TRUE	FALSE	2	2141.5	2.2	24of 40	3.8406	FALSE	TRUE	::::::::::::::::::::
YGEVCPANWKPGQK	15	8.85	0.171	264	22.8	PDX1-DROME	TRUE	TRUE	2	1634.8	1.1	15of 26	2.1326	FALSE	TRUE	:::::Cys_CAM:::::::::
LVQAFQYTDK	12	6.68	0.02	804	26.4	PDX1-DROME	TRUE	TRUE	2	1213.4	0.1	10of 18	1.4022	FALSE	TRUE	::::::::::
DTYEISKEANQIHEKLRCRRTENKDKLVEQ	10	7.17	0.129	2101	38.5	PEN-DROME	TRUE	FALSE	3	3733.1	-1.9	23of116	2.0634	FALSE	TRUE	::::::::::::::::Cys_CAM::::::::::::
ATVPDPTTPTTPSPSVIR	11	6.79	0.059	1081	31.6	PHTF-DROME	TRUE	FALSE	3	1838.1	-2.2	17of 68	1.5465	FALSE	TRUE	::::::::::::::::::
VELELWLKGELKTDDDPEEDASAGKPP	4	3.77	0.2	3032	56.2	PIPA-DROME	TRUE	FALSE	2	2983.3	0.7	10of 52	1.5009	FALSE	TRUE	::::::::::::::::::::::::::
IVIDYRKLNE	10	6.94	0.029	908	30.4	POL3-DROME	TRUE	FALSE	1	1263.5	-1.6	7of 18	1.7987	FALSE	TRUE	::::::::::
YMIEHLVKAGANNVNIESDQ	2	4.43	0.002	1909	42.93	POLO-DROME	TRUE	FALSE	2	2246.5	-1.7	10of 38	1.1858	FALSE	TRUE	::::::::::::::::::
GVSFTFGVDVVSKFLN	4	6.76	0.011	1581	49.7	PP1B-DROME	TRUE	FALSE	2	1717	0.8	9of 30	1.0626	FALSE	TRUE	::::::::::::::::
LGDYLITCGY	1	3.1	0.271	1026	35.6	PROF-DROME	TRUE	FALSE	1	1175.3	1.8	13of 18	1.9291	FALSE	TRUE	::::::::Cys_CAM:::
VSACSDRSLEAAAADVAGGSPPRAASVSSLNGGASSGEQ	4	4.07	0.09	2678	53.8	PROS-DROME	TRUE	FALSE	3	3648.8	1.3	15of152	1.6814	FALSE	TRUE	::::Cys_CAM::::::::::::::::::::::::::::::::::
GPHIYQVTPSATFFNCK	15	8.88	0.316	1075	37.7	PSA1-DROME	TRUE	TRUE	2	1968.2	2.4	22of 32	4.6593	FALSE	TRUE	:::::::::::::::::Cys_CAM:::
VTGGLHLINPSELTEK	6	5.3	0.3	1458	36.7	PSA3-DROME	TRUE	TRUE	2	1709	2.2	16of 30	3.5098	FALSE	TRUE	::::::::::::::
ATCIGNNFGAAISMLK	15	8.97	0.148	1408	41.83	PSA4-DROME	TRUE	TRUE	2	1668.9	0.9	15of 30	1.8232	FALSE	TRUE	:::Cys_CAM::::::::::::::
IVEVDKHIGCATSGLMADAR	6	5.28	0.459	1294	43.73	PSA5-DROME	TRUE	TRUE	2	2144.4	1.3	24of 38	4.9485	FALSE	TRUE	:::::::::Cys_CAM:::::::::::
AIAQENITTVALK	12	6.95	0.031	952	33.5	PSA6-DROME	TRUE	TRUE	2	1372.6	1.5	12of 24	1.8502	FALSE	TRUE	::::::::::::
HLAVPLVR	15	11.05	0.115	500	27.5	PSB4-DROME	TRUE	TRUE	2	905.1	0.4	9of 14	1.7725	FALSE	TRUE	::::::::
NYLHYALYDQADKLVK	8	7.63	0.247	1795	40.3	PSD3-DROME	TRUE	TRUE	2	1955.2	0.5	16of 30	2.6515	FALSE	TRUE	::::::::::::::::
GGVPIAGTAGYCVGALHIPGYK	15	8.81	0.229	1259	49.7	PUR4-DROME	TRUE	TRUE	2	2159.5	1.4	16of 42	1.9818	FALSE	TRUE	::::::::::::Cys_CAM:::::::::::
DTICFLHTALR	10	7.16	0.36	1256	35	PURA-DROME	TRUE	TRUE	2	1347.5	1.2	17of 20	3.6725	FALSE	TRUE	::::Cys_CAM:::::::
CGPYICLLK	13	8.28	0.216	1079	33	PYR5-DROME	TRUE	TRUE	2	1124.3	0.1	11of 16	1.7242	FALSE	TRUE	:Cys_CAM::::Cys_CAM::::
LSHEVGWHYQDVIK	9	6.03	0.241	1492	33.4	R13A-DROME	TRUE	TRUE	2	1711.9	-0.6	15of 26	2.7813	FALSE	TRUE	::::::::::::
KLLQQASLHTVESVANATKK	14	10.32	0.045	1042	33.2	RA51-DROME	TRUE	FALSE	2	2167.5	-1.3	14of 38	2.9007	FALSE	TRUE	::::::::::::::::::::
FLLVDEGLELKV	5	3.83	0.198	1851	50.6	RCL1-DROME	TRUE	FALSE	2	1375.6	1.2	10of 22	2.1594	FALSE	TRUE	::::::::::::
LHDAKAALPRPN	12	10.09	0	967	21	RDGB-DROME	TRUE	FALSE	2	1303.5	2.4	9of 22	1.1686	FALSE	TRUE	::::::::::::
VMNAR	15	11.05	0.014	193	11.33	RDGC-DROME	TRUE	FALSE	1	606.7	-0.1	3of 8	0.7979	FALSE	TRUE	::Oxidation_M::::
KAFSDVFEDLYNHVNK	6	5.28	0.228	1723	34.6	RIR1-DROME	TRUE	TRUE	2	1927.1	0.9	15of 30	2.2917	FALSE	TRUE	::::::::::::::
SAGGIGLNVHCIR	15	9.02	0.008	372	28.4	RIR1-DROME	TRUE	TRUE	2	1354.5	2	13of 24	1.6702	FALSE	TRUE	:::::::::Cys_CAM:::
YFEVILIDTHHSAIR	9	6.03	0.449	1780	46.8	RL15-DROME	TRUE	TRUE	2	1815.1	2.5	19of 28	4.2008	FALSE	TRUE	::::::::::::::
ISLGLPVGAVMNCADNTGAK	7	6.1	0.45	1496	46.43	RL23-DROME	TRUE	TRUE	2	1989.3	0.8	1	4.2135	FALSE	TRUE	::::::::::::Cys_CAM::::::::
VYCGEIAHGVSSK	11	7.16	0.427	344	22.6	RL32-DROME	TRUE	TRUE	2	1407.5	1.9	20of 24	3.8898	FALSE	TRUE	:::Cys_CAM:::::::::
DDASKPVHLTCFIGYK	10	7.16	0.43	1105	34	RL3-DROME	TRUE	TRUE	2	1852.1	1.9	19of 30	3.4048	FALSE	TRUE	:::::::::Cys_CAM::::::
SITPMGGFPHYGEVNNDFVMIK	6	5.22	0.084	1772	56.26	RL3-DROME	TRUE	TRUE	2	2454.8	1.9	15of 42	2.3116	FALSE	TRUE	::::::::::::::::::::
NICLPAVFK	14	8.97	0.128	1118	32.5	RL4-DROME	TRUE	TRUE	1	1062.3	-0.5	10of 16	1.8639	FALSE	TRUE	:::Cys_CAM:::::::
TVCSHIENMIK	10	7.16	0.234	901	24.63	RL9-DROME	TRUE	TRUE	2	1332.5	1.5	15of 20	2.9474	FALSE	TRUE	:::Cys_CAM:::::::::
YVAAYLLAVLGGK	12	9.53	0.318	1910	46.8	RLA2-DROME	TRUE	TRUE	2	1338.6	1	16of 24	2.491	FALSE	TRUE	::::::::::::
LVTALCNEHQIPLIR	10	7.16	0.349	1248	49.1	RS12-DROME	TRUE	TRUE	2	1778.1	2.2	18of 28	3.81	FALSE	TRUE	:::::Cys_CAM:::::::::
LVTALCNEHQIPLIR	11	7.16	0.307	998	49.1	RS12-DROME	TRUE	TRUE	2	1778.1	0.9	17of 28	2.8678	FALSE	TRUE	:::::Cys_CAM:::::::::
TALCNEHQIPLIR	10	7.16	0.206	1249	36	RS12-DROME	TRUE	FALSE	2	1565.8	0.7	15of 24	2.735	FALSE	TRUE	::::Cys_CAM:::::::::
SVGLKPDIPEDLYHMIK	6	5.28	0.403	1710	44.83	RS13-DROME	TRUE	TRUE	2	1956.3	2.7	20of 32	3.6817	FALSE	TRUE	::::::::::::::::
ICEEVAIIPTKPLR	9	6.44	0.287	1560	44	RS17-DROME	TRUE	TRUE	2	1639.9	1.8	17of 26	2.9299	FALSE	TRUE	::Cys_CAM:::::::::::
DIEKPHVGDSASVHR	9	6.03	0.342	588	15.4	RS20-DROME	TRUE	TRUE	3	1647.8	2.8	29of 56	3.3667	FALSE	TRUE	::::::::::::
IIDLHSPSEIVK	6	5.22	0.248	1222	34	RS20-DROME	TRUE	TRUE	2	1351.6	0.1	14of 22	3.1731	FALSE	TRUE	::::::::::::
VFCIGFTAK	15	8.97	0.115	1001	31.5	RS3A-DROME	TRUE	TRUE	1	1043.2	-0.2	10of 16	1.6856	FALSE	TRUE	:::Cys_CAM:::::::
MTDIITNEVSGADLK	2	3.71	0.11	850	35.03	RS3A-DROME	TRUE	TRUE	2	1607.8	1.6	12of 28	2.3688	FALSE	TRUE	::::::::::::::
CYPGAMLGSEDTSWAFDGHNVTK	5	4.3	0.033	1288	45.53	RY44-DROME	TRUE	FALSE	2	2560.7	-2.3	10of 44	1.4623	FALSE	TRUE	:Cys_CAM::::Oxidation_M:::::::::::::::
NLRNITLSSGTALKLDANITGEPA	6	7.02	0.111	2075	53	S24600	TRUE	FALSE	3	2470.8	-1.9	16of 92	1.5213	FALSE	TRUE	::::::::::::::::::::::::
PTQRSDSGEYLVTATNTSGKDSVLV	2	4.31	0.08	2017	39.1	S24600	TRUE	FALSE	2	2626.8	-2.4	7of 48	0.9262	FALSE	TRUE	::::::::::::::::::::::
GSIFAAPCAPAPLTK	9	8.97	0.002	1009	38.3	S28400	TRUE	FALSE	2	1501.7	2.8	12of 28	1.1541	FALSE	TRUE	::::::::Cys_CAM:::::::::
TPLLPSLSPYCLK	14	8.88	0.252	1242	43.6	S58776	TRUE	TRUE	2	1489.8	-0.1	14of 24	2.9687	FALSE	TRUE	:::::::::Cys_CAM:::::
TPLLPSLSPYCLK	15	8.88	0.213	1335	43.6	S58776	TRUE	TRUE	2	1489.8	2.5	13of 24	2.5753	FALSE	TRUE	:::::::::Cys_CAM:::::
DKIVLIRAPHLSNKFESSSIK	13	10.32	0.035	710	46.4	S68280	TRUE	FALSE	3	2383.8	-0.9	17of 80	1.9946	FALSE	TRUE	::::::::::::::::::::
PSKTPVHERPYACP	9	8.88	0.055	405	18.8	S69205	TRUE	FALSE	3	1639.8	-1.8	7of 52	1.0507	FALSE	TRUE	::::::::::::Cys_CAM::
SKFDNLYGCR	14	8.88	0.295	235	19.8	SAHH-DROME	TRUE	TRUE	2	1260.4	1.1	15of 18	2.9358	FALSE	TRUE	::::::::Cys_CAM::
FPHVPMNATPIPEHMDKFHPPLLDQMSPDSS	6	5.07	0.064	2627	70.09	SALM-DROVI	TRUE	FALSE	3	3515	-1.5	19of120	1.5366	FALSE	TRUE	::::::::::::::::::::::::::::::
RPFDPTAHDLDASFR	6	5.2	0.123	1244	30	SELD-DROME	TRUE	TRUE	2	1745.9	1.5	12of 28	2.047	FALSE	TRUE	::::::::::::::::
LNGIQRRKELELQHAK	15	10.58	0.07	1155	27.6	SERR-DROME	TRUE	FALSE	3	1934.3	-2.9	20of 60	1.9401	FALSE	TRUE	::::::::::::::::
LTSAVNSLPQLMEKK	12	9.89	0.091	773	35.33	SLY1-DROVI	TRUE	FALSE	3	1660	2.2	21of 56	2.2334	FALSE	TRUE	::::::::::::::::
IQSASNLVEGQYGSMSSK	12	6.87	0.001	873	29.53	SM1A-DROME	TRUE	FALSE	3	1887.1	0.4	16of 68	1.6576	FALSE	TRUE	::::::::::::::::
MLPLLK	12	10.1	0	1551	29.73	SMG-DROME	TRUE	FALSE	1	731	0.1	8of 10	1.2012	FALSE	TRUE	:Oxidation_M:::::
LCSIHADHSDQIR	9	6.01	0.32	874	22.7	SPCA-DROME	TRUE	TRUE	2	1552.7	0	16of 24	2.8561	FALSE	TRUE	::Cys_CAM:::::::::
PTATISVVVPQQMPAVSS	12	6.02	0.022	1540	43.53	SPEN-DROME	TRUE	FALSE	3	1829.1	1.5	18of 68	1.6655	FALSE	TRUE	::::::::::::Oxidation_M:::::
KLVYPKKGLRADDTWQLIVNN	12	10.05	0.046	2188	51.7	SPZ-DROME	TRUE	FALSE	2	2472.9	1.3	10of 40	1.4329	FALSE	TRUE	::::::::::::::::::::
DQKISGNGRPNRRYKMESSFLL	13	10.69	0.004	582	36.83	STAN-DROME	TRUE	FALSE	3	2598	0.3	17of 84	1.8935	FALSE	TRUE	::::::::::::::::::::
PSGGRMWGMSHSLPSGMSRYAFSPED	6	7.77	0.075	2275	50.09	SXL	TRUE	FALSE	3	2877.2	1.9	21of100	1.5808	FALSE	TRUE	::::::Oxidation_M:::Oxidation_M::::::::Oxidation_M:::::::::
LTIADFALFNEMHSR	6	5.22	0.411	1878	47.73	SYEP-DROME	TRUE	TRUE	2	1766	2.8	18of 28	3.8122	FALSE	TRUE	::::::::::::::::
LLVCHSNNDVLR	10	7.16	0.359	628	33	SYEP-DROME	TRUE	TRUE	2	1440.6	1.5	17of 22	2.6517	FALSE	TRUE	::::Cys_CAM::::::::
VTYLVANKLTIADFALFNEMHSR	6	7.75	0.044	1878	70.23	SYEP-DROME	TRUE	FALSE	3	2655.1	-2.4	23of 88	2.6933	FALSE	TRUE	::::::::::::::::::::::::
NPDPASVLTVNTLLNK	5	6.76	0.01	1775	37.6	SYEP-DROME	TRUE	TRUE	2	1696.9	-0.3	9of 30	1.5919	FALSE	TRUE	::::::::::::::::
SIQAHGELVTAETVTHK	9	6.03	0.388	1164	26.8	SYFA-DROME	TRUE	TRUE	2	1822	2.4	20of 32	3.4011	FALSE	TRUE	::::::::::::::::
DAHDTFFVNHPAK	9	6.02	0.29	1154	21.3	SYFA-DROME	TRUE	TRUE	2	1499.6	1.3	15of 24	2.9351	FALSE	TRUE	::::::::::::::
TAGFEVVHGLLDR	6	5.22	0.376	1560	35.1	SYFB-DROME	TRUE	TRUE	2	1414.6	2.4	15of 24	1.97	FALSE	TRUE	::::::::::::::
AININFGYAAAHDGVCYLR	11	7.15	0.432	1220	51.5	SYQ-DROME	TRUE	TRUE	2	2126.3	1	18of 36	3.3284	FALSE	TRUE	::::::::::::::::Cys_CAM::::
NFPHAAPVQLEVPDFPQNPQQGTHK	8	6.03	0.239	1849	42.5	SYQ-DROME	TRUE	TRUE	3	2798.1	1.8	31of 96	3.8703	FALSE	TRUE	::::::::::::::::::::::::

DYASLALSNLLR	5	6.7	0.037	2075	39.5	SYR-DROME	TRUE	TRUE	1	1336.5	-0.1	12of 22	2.1107	FALSE		TRUE	::::::::::::
DNMTAAQVMRILSVEYAK	10	6.94	0.051	1552	45.46	T12678	TRUE	TRUE	2	2057.4	2.2	10of 34	1.3702	FALSE		TRUE	:::Oxidation_M::::::::::::::
LPLPNTPAR	15	11.05	0.031	999	23.6	T13612	TRUE	FALSE	1	979.2	-2.1	9of 16	1.9392	FALSE		TRUE	::::::::::
VLVPPTEVVILDAKGDRIK	5	7.05	0.038	1846	54.1	T13669	TRUE	TRUE	2	2063.5	2.6	13of 36	2.3691	FALSE		TRUE	::::::::::::::::::
VDGLQTLHAICFGAQGK	11	7.16	0.044	1054	39.3	T13691	TRUE	TRUE	2	1816	1.6	11of 32	1.5632	FALSE		TRUE	:::::::::::Cys_CAM::::::
SLDADQKDELVMVIEK	3	3.85	0.021	1089	39.53	T13713	TRUE	FALSE	3	1850.1	2.3	15of 60	1.4356	FALSE		TRUE	:::::::::::Oxidation_M:::::
MANHLLEVMDCALHLLGSGVPASMR	8	6.02	0.087	2754	72.79	T13719	TRUE	TRUE	3	2740.2	-0.5	26of 96	2.9829	FALSE		TRUE	:Oxidation_M::::::::::Cys_CAM::::::::::::::
HCLKSILQLFELL	5	7.16	0.044	2594	55.3	T13719	TRUE	FALSE	3	1614.9	1.6	9of 48	1.2142	FALSE		TRUE	::Cys_CAM::::::::::::
LALSQDEISVLRTSSQRR	13	10.8	0.009	1638	38	T13806	TRUE	TRUE	2	2060.3	-1.9	8of 34	1.1429	FALSE		TRUE	::::::::::::::::::
VETKIYEQHGSRFNLGSSQAVA	6	7.75	0.055	1192	38.5	T13858	TRUE	FALSE	2	2422.7	-0.8	9of 42	1.0374	FALSE		TRUE	::::::::::::::::::::::
DHFVELAAINGALGHEHIR	8	5.75	0.375	1847	44.6	T13930	TRUE	TRUE	3	2100.3	2.5	33of 72	4.9198	FALSE		TRUE	::::::::::::::::::
HLQANLLLIQNIESNQLK	8	7.82	0.284	2072	52.2	T13930	TRUE	TRUE	2	2090.4	2.1	18of 34	3.8382	FALSE		TRUE	::::::::::::::::::
LGYVDPFAQGHGLLNVEK	6	5.22	0.241	1671	46.8	T13930	TRUE	TRUE	2	1958.2	1.7	19of 34	2.7664	FALSE		TRUE	::::::::::::::::::
AFEHLTEHR	9	6.03	0.206	886	16.2	T13930	TRUE	TRUE	2	1140.2	-1	13of 16	2.2991	FALSE		TRUE	::::::::::
VITFIDLAGHER	6	5.22	0.199	1495	37	T44681	TRUE	TRUE	2	1371.6	1.1	13of 22	2.4272	FALSE		TRUE	::::::::::::
TVGGGDDSFNTFFSETGAGK	2	3.71	0.41	1012	30.5	TBA1-DROME	TRUE	TRUE	2	1995.1	0.9	19of 38	3.9251	FALSE		TRUE	::::::::::::::::::::
LIGQIVSSITASLR	15	11.05	0.358	1732	44.6	TBA1-DROME	TRUE	TRUE	2	1458.7	-0.8	20of 26	3.7653	FALSE		TRUE	::::::::::::::
EIVDLVLDR	2	3.71	0.227	964	34.5	TBA1-DROME	TRUE	TRUE	2	1072.2	0.8	13of 16	2.3394	FALSE		TRUE	::::::::::
RSIFVDLEPTVIDDVRNGCMR	1	4.46	0.153	2304	55.63	TBA4-DROME	TRUE	FALSE	3	2493.8	0.4	8of 80	1.2003	FALSE		TRUE	:::::::::::::::::::Cys_CAM:::
LTTPTYGDLNHLVSLTMSGVTTCLR	11	7.16	0.471	1655	64.83	TBB1-DROME	TRUE	TRUE	3	2752.1	2.2	27of 96	4.6304	FALSE		TRUE	:::::::::::::::::::::::Cys_CAM:::
PTYGDLNHLVSLTMSGVTTCLR	10	7.16	0.433	1913	55.53	TBB1-DROME	TRUE	FALSE	2	2436.8	-0.4	21of 42	4.2204	FALSE		TRUE	:::::::::::::::::::Cys_CAM:::
LTTPTYGDLNHLVSLTMSGVTTCLR	10	7.16	0.418	1906	64.83	TBB1-DROME	TRUE	TRUE	2	2752.1	0.4	19of 48	4.5958	FALSE		TRUE	:::::::::::::::::::::::Cys_CAM:::
LHFFMPGFAPLTSR	15	11.05	0.306	1518	49.53	TBB1-DROME	TRUE	TRUE	2	1621.9	0.6	18of 26	3.4269	FALSE		TRUE	::::::::::::::
EIVHIQAGQCGNQIGAK	11	7.16	0.19	524	29.5	TBB1-DROME	TRUE	TRUE	3	1824	2.3	32of 64	3.4083	FALSE		TRUE	:::::::::Cys_CAM::::::::
LAVNMVPFPR	15	11.05	0.173	1165	36.53	TBB1-DROME	TRUE	TRUE	2	1144.4	1.2	14of 18	3.1994	FALSE		TRUE	::::::::::
EIVHIQAGQCGNQIGAK	10	7.16	0.161	602	29.5	TBB1-DROME	TRUE	TRUE	3	1824	1.6	32of 64	4.2878	FALSE		TRUE	:::::::::Cys_CAM::::::::
AVLVDLEPGTMDSVR	2	3.71	0.142	944	41.83	TBB1-DROME	TRUE	TRUE	2	1602.8	2.2	19of 28	3.6305	FALSE		TRUE	::::::::::::::
LTTPTYGDLNHLVSATMSGVTTCLR	10	7.16	0.042	1834	58.73	TBB2-DROER	TRUE	TRUE	3	2710	1.2	23of 96	2.9705	FALSE		TRUE	:::::::::::::::::::::Cys_CAM:::
EIVHLQAGQCGNQIGAK	10	7.16	0.304	600	30.2	TBB3-DROME	TRUE	TRUE	2	1824	-0.1	20of 32	4.6727	FALSE		TRUE	:::::::::Cys_CAM:::::::
EIVHLQAGQCGNQIGAK	11	7.16	0.225	521	30.2	TBB3-DROME	TRUE	TRUE	2	1824	1	20of 32	3.7053	FALSE		TRUE	:::::::::Cys_CAM:::::::
TCLGPQAMLK	15	8.97	0.007	585	26.63	TCPG-DROME	TRUE	TRUE	2	1119.3	2	12of 18	1.9698	FALSE		TRUE	::Cys_CAM::::::::
LVDDVIYEVYGK	2	3.71	0.436	1020	38.7	TCTP-DROME	TRUE	TRUE	2	1413.6	1.6	19of 22	4.6603	FALSE		TRUE	::::::::::::
DDVIYEVYGK	2	3.71	0.189	1025	25.6	TCTP-DROME	TRUE	FALSE	1	1201.3	-0.6	11of 18	1.8243	FALSE		TRUE	::::::::::
AHGHGDHYVHIKIEVPKK	12	9.57	0.038	1189	19.5	TID-DROVI	TRUE	FALSE	3	2066.4	-2.2	18of 68	1.6123	FALSE		TRUE	::::::::::::::::
LIIWTDCDREGENIGYEIIDVCR	4	3.76	0.036	1937	70.9	TP3A-DROME	TRUE	FALSE	3	2841.1	3	8of 88	0.9242	FALSE		TRUE	::::::Cys_CAM::::::::::::::Cys_CAM:::
EMFFYISASVKYIEK	10	6.95	0.031	1036	50.13	TRA1-DROME	TRUE	FALSE	3	1872.2	2.8	26of 56	2.2384	FALSE		TRUE	::Oxidation_M::::::::::::
RVPDWNLMKIALAK	12	10.59	0.024	768	43.73	TRA1-DROME	TRUE	FALSE	3	1656	-0.5	21of 52	2.2024	FALSE		TRUE	::::::::::::
SGLTINTLINTVGIHPTTAEEFTR	6	5.3	0.352	1962	56.8	TRX1-DROME	TRUE	TRUE	2	2586.9	1.7	18of 46	4.0208	FALSE		TRUE	::::::::::::::::::::
VACLDFVKPTPTLGTK	15	8.94	0.321	951	40.5	TRX1-DROME	TRUE	TRUE	2	1748	0.1	20of 30	4.0791	FALSE		TRUE	:::Cys_CAM:::::::::::
YCYLK	14	8.81	0.294	144	17.6	TRX1-DROME	TRUE	TRUE	1	746.8	0.3	6of 8	1.421	FALSE		TRUE	::Cys_CAM:::::
AFLYHEGKHRKVFPCPVCSKEFSRPDK	12	9.57	0.205	2133	48.1	TTKA-DROME	TRUE	FALSE	2	3321.7	-0.8	7of 52	1.197	FALSE		TRUE	:::::::::::::Cys_CAM::::Cys_CAM::::::::::
VTVEITPGTHASELAVNK	6	5.3	0.256	1155	35.3	U195-DROME	TRUE	TRUE	2	1867.1	0.9	19of 34	2.8496	FALSE		TRUE	::::::::::::::::::
MLVIADLDQDGRINYEEFTR	3	3.85	0.091	1312	57.53	U25882	TRUE	FALSE	3	2399.7	1.5	19of 76	2.143	FALSE		TRUE	::::::::::::::::::::
TKVRGLLEIISSAAEYE	1	4.56	0.048	2358	45.1	U520-DROME	TRUE	FALSE	3	1880.1	1.2	7of 64	0.999	FALSE		TRUE	::::::::::::::::::
IYHPNINSNGSICLDILR	10	7.16	0.146	1428	50	UBC1-DROME	TRUE	TRUE	2	2100.3	2.6	18of 34	2.5429	FALSE		TRUE	:::::::::::Cys_CAM::::::
WFFDSSGGNGHALEHYRDMGYP	6	5.12	0.052	1546	46.53	UBP3	TRUE	FALSE	3	2544.7	2.2	23of 84	2.3056	FALSE		TRUE	::::::::::::::::::::::
VWISECIAQRQTDR	4	6.36	0.058	1631	33.7	V0D2-DROME	TRUE	FALSE	2	1762.9	-1.8	5of 26	0.8709	FALSE		TRUE	:::::Cys_CAM:::::::::
TALVANTSNMPVAAR	15	11.05	0.223	543	32.83	VAA1-DROME	TRUE	TRUE	2	1516.8	0.9	17of 28	2.2196	FALSE		TRUE	::::::::::::::::
VGSHITGGDLYGLVHENTLVK	8	6.03	0.474	1852	45.8	VAA2-DROME	TRUE	TRUE	2	2210.5	2.5	25of 40	5.1294	FALSE		TRUE	::::::::::::::::::::
SADIEIVFDGAEHK	4	4.06	0.041	1443	29.9	VP26-DROME	TRUE	FALSE	2	1531.7	-2.8	14of 26	2.3175	FALSE		TRUE	::::::::::::::
YLVACDAHR	10	7.16	0.215	285	21.7	WDR1-DROME	TRUE	TRUE	2	1105.2	2.5	13of 16	2.4449	FALSE		TRUE	:::::Cys_CAM:::::
SDMNPVLSAAGAQLEVASFVDGK	2	3.71	0.028	2272	52.63	XDH-DROME	TRUE	FALSE	3	2307.6	0.1	15of 88	1.5191	FALSE		TRUE	::::::::::::::::::::::
LPDQSLISSMMLDSRCGLNDLY	4	3.6	0.008	2893	66.46	Y07964	TRUE	FALSE	3	2561.8	-1.7	7of 84	0.7229	FALSE		TRUE	:::::::::Oxidation_M:Oxidation_M::::Cys_CAM:::::::
SGGAIVGAGQKSPYWKLDAWEDDAR	5	4.46	0.008	2416	48.3	Y18278	TRUE	FALSE	3	2678.9	2.2	19of 96	1.6953	FALSE		TRUE	::::::::::::::::::::::
QEKTQRLAMFAEEVFLR	6	7.18	0.06	2014	47.53	Y2R2-DROME	TRUE	FALSE	2	2097.4	-1.5	11of 32	1.4923	FALSE		TRUE	::::::::::::::::::
IITHPNFNGNTLDNDIMLIK	6	5.1	0.046	1719	56.23		TRUE	TRUE	2	2284.6	1.8	13of 38	2.0047	FALSE		TRUE	::::::::::::::::::
LSSPATLNSRVATVSLPRSCAAAGTECLISG	9	8.3	0.042	2332	68.5		TRUE	FALSE	3	3148.5	-0.7	13of120	0.9693	FALSE		TRUE	:::::::::::::::::::Cys_CAM::::::Cys_CAM:::::
VATVSLPR	15	11.05	0.001	475	21.9		TRUE	TRUE	2	843	2.9	8of 14	1.0513	FALSE		TRUE	::::::::
AAFDDAIAELDTLSEESYKDSTLIMQLLR	2	3.63	0.421	2108	83.43	143E-DROME	TRUE	TRUE	3	3260.6	0.8	37of112	4.7738	FALSE		FALSE	::::::::::::::::::::::::::::
DAAENSLIAYKAASDIAMNDL	11	3.51	0	1815	51.03	143E-DROME	TRUE	FALSE	2	2213.4	-1.2	6of 40	0.8493	FALSE		FALSE	:::::::::::::::::Oxidation_M::::
QAFDDAIAELDTLNEDSYKDSTLIMQLLR	1	3.58	0.302	1968	80.13	143Z-DROME	TRUE	TRUE	3	3346.7	2.9	27of112	3.002	FALSE		FALSE	:::::::::::::::::::::::Oxidation_M:::::
TSACGLFSVCYPR	14	8.29	0.474	1010	34.3	2AAA-DROME	TRUE	TRUE	2	1518.6	1.3	15of 24	3.2923	FALSE		FALSE	::::Cys_CAM:::::Cys_CAM::::
LAIIEYMPALAGQLGQEFFDQK	2	3.83	0.28	1853	73.23	2AAA-DROME	TRUE	TRUE	2	2483.9	1.1	9of 42	1.5024	FALSE		FALSE	::::::::::::::::::::
DSEGVDIMLGVCASGL	11	2.88	0.043	394	44.23	41-DROME	TRUE	FALSE	3	1623.8	2.6	16of 60	1.8571	FALSE		FALSE	:::::::::::Cys_CAM:::::
MMLCVGIVWLAAACISL	11	5.18	0.001	2601	79.76	5HT1-DROME	TRUE	FALSE	3	1909.3	-2.6	9of 64	0.9124	FALSE		FALSE	::::Cys_CAM::::::::::Cys_CAM::::
DDMAVTDDGQLEDTNNNNNSK	8	3.27	0.007	3413	18.43	5HTA-DROME	TRUE	FALSE	3	2311.3	1.5	14of 80	1.3461	FALSE		FALSE	::::::::::::::::::::
NPFIENSIENTRSCQMQTLYIDFK	7	4.45	0.092	2004	59.83	60A-DROVI	TRUE	FALSE	3	2950.3	-2.5	361	1.5019	FALSE		FALSE	:::::::::::Cys_CAM:::::::::::
NTEMLRNSGNIEEGMT	9	3.97	0.015	2032	28.06	A24786	TRUE	FALSE	2	1829	-2.5	5of 30	0.6817	FALSE		FALSE	::::Oxidation_M::::::::::Oxidation_M::
AGEVVSVEYKLEYGSDTFELQKSAIK	11	4.36	0.016	2019	57.6	A29596	TRUE	FALSE	2	2892.2	0.6	8of 50	0.9865	FALSE		FALSE	::::::::::::::::::::::::
LGLENVSLSTVPEIR	12	4.27	0.046	1636	44.7	A29944	TRUE	TRUE	3	1627.9	2.6	16of 56	1.6803	FALSE		FALSE	::::::::::::::
ESTHKLLKSYLYDR	3	9.47	0.078	2755	27.9	A32713	TRUE	FALSE	3	1754	-1.2	8of 52	1.1414	FALSE		FALSE	::::::::::::::
SLADASSPLSPTRHSRVAEK	7	10.09	0.03	1280	26.7	A37103	TRUE	FALSE	3	2110.3	1.4	116	1.8142	FALSE		FALSE	::::::::::::::::::
VKRIKPVSVAPK	2	11.73	0.056	278	21.3	A37792	TRUE	FALSE	2	1322.7	2.5	7of 22	1.1488	FALSE		FALSE	::::::::::::
WVKIDGSQDSM	8	3.89	0.107	1813	24.43	A37C-DROME	TRUE	FALSE	2	1282.4	2.6	9of 20	1.6449	FALSE		FALSE	:::::::::Oxidation_M:
NNLGTLLYSAGFNSGVGALHK	1	9.72	0.053	1225	47.4	A41054	TRUE	FALSE	2	2134.4	-2	6of 40	0.7848	FALSE		FALSE	::::::::::::::::::::
PDSESVPVQQEDQK	3	3.59	0.071	1477	14.1	A43917	TRUE	FALSE	2	1586.7	1.4	9of 26	1.3828	FALSE		FALSE	::::::::::::::
VDSGLIINGKR	13	10.09	0.094	1873	24.2	A44085	TRUE	FALSE	2	1172.4	1.9	11of 20	1.0683	FALSE		FALSE	::::::::::::
YSPGQYMYACMKMAPLMQK	9	9.4	0.105	945	49.72	A47397	TRUE	FALSE	3	2315.8	1.8	23of 72	2.4779	FALSE		FALSE	:::::::::Cys_CAM::::::Oxidation_M:::
QGYFSNAHGMVRS	9	9.85	0.006	644	21.03	A49502	TRUE	FALSE	2	1454.6	-0.4	10of 24	1.2588	FALSE		FALSE	::::::::::::::
PFRCLGPFQSDALLVPEGCLFDHI	9	4.3	0.028	1645	80.5	A4-DROME	TRUE	FALSE	3	2790.1	-2.6	21of 92	1.9691	FALSE		FALSE	::::Cys_CAM::::::::::::::Cys_CAM::::::
LADPKAAQSFKQRM	14	10.59	0	2785	24.93	A4-DROME	TRUE	FALSE	2	1591.9	-2.8	6of 26	0.2747	FALSE		FALSE	::::::::::::::::
NGNSEDDDFGLSSSCSLNSNM	6	2.79	0.054	1524	30.13	A53970	TRUE	FALSE	3	2251.2	2.2	18of 80	1.4707	FALSE		FALSE	:::::::::::::::Cys_CAM:::::::
RSDYLLQYDDAGALQSLTTPRGHIHA	11	6.02	0.176	1262	52.4	A54148	TRUE	FALSE	3	2900.2	2.1	9of100	1.292	FALSE		FALSE	::::::::::::::::::::::::::

VAFVHDTAGRLET	9	5.22	0.046	613	29.8	A54148	TRUE	FALSE	3	1416.6	-1.4	16of 48	1.485	FALSE	FALSE	::::::::::::::
LTSAVTPTGRVIELSFDLS	14	4.08	0.028	887	55.5	A54148	TRUE	FALSE	2	2007.3	2.3	10of 36	1.1944	FALSE	FALSE	::::::::::::::::::
VLAHSLVGTPNYIAPEV	7	5.13	0.13	1191	49.7	A56155	TRUE	FALSE	3	1781.1	2.5	67	1.9944	FALSE	FALSE	::::::::::::::::
RLVRIGVLKSPHEARLRAG	1	12.41	0.075	2038	41.6	A56687	TRUE	FALSE	2	2129.6	2.6	5of 36	0.6647	FALSE	FALSE	::::::::::::::::::
RRVGILPSGVHGAR	14	12.71	0.172	742	24.8	A56699	TRUE	FALSE	2	1475.7	2.1	16of 26	2.6352	FALSE	FALSE	::::::::::::::
SLQGSVRESPRMVSKRDRDR	7	11.83	0.096	1436	21.03	A56699	TRUE	FALSE	3	2360.7	1.9	486	2.1765	FALSE	FALSE	::::::::::::::::::
RRVGILPSGVHGAR	15	12.71	0.085	779	24.8	A56699	TRUE	FALSE	2	1475.7	0.3	14of 26	2.1453	FALSE	FALSE	::::::::::::::
STGRLRGAVVR	10	12.71	0.003	2320	18.3	A56699	TRUE	FALSE	2	1172.4	-1.3	5of 20	0.7706	FALSE	FALSE	::::::::::
MTTPVKQQQQLPPPPSPLPMQTMQYRQDPATPVTK	6	10.18	0.104	2267	65.49	A56922	TRUE	FALSE	3	3994.6	-0.4	26of136	2.3851	FALSE	FALSE	:Oxidation_M:::::::::::::::::Oxidation_M:::::::::::::::
QRMLGNGSSTAMAG	9	11.05	0.063	429	21.56	A56922	TRUE	FALSE	3	1397.6	2.4	14of 52	1.4225	FALSE	FALSE	:::Oxidation_M:::::::::::
YGRGVPPAPIAGDAR	9	9.85	0.028	1989	27.3	A56922	TRUE	FALSE	1	1497.7	0.2	9of 28	1.375	FALSE	FALSE	::::::::::::::::
LELKSPVGYSIFLKTGDRVYA	1	9.47	0.168	1453	59.1	A59233	TRUE	FALSE	3	2357.8	-1.9	23of 80	2.9826	FALSE	FALSE	::::::::::::::::::::
VLSFKPEEVWSILSLLAAILHLGNL	10	5.3	0.042	101	101	A59233	TRUE	FALSE	3	2764.3	1.1	16of 96	1.8877	FALSE	FALSE	::::::::::::::::::::::
TYMSNWGTGWGFAASDR	15	6.7	0.174	1821	38.93	A60766	TRUE	FALSE	3	1908.1	2.5	16of 64	1.9178	FALSE	FALSE	::::::::::::::::
NGRHCTLPGCENGCSR	5	8.03	0.025	2159	14.3	A61625	TRUE	FALSE	2	1875.9	2.6	9of 30	1.5834	FALSE	FALSE	:::::Cys_CAM::::Cys_CAM::::Cys_CAM:::
APCVCKPGYVINER	3	8.28	0.061	1909	30.7	A62F-DROME	TRUE	FALSE	2	1663.8	-0.1	7of 26	1.2438	FALSE	FALSE	:::Cys_CAM::Cys_CAM:::::::::
IGAEEIVDGNLK	15	3.83	0.031	336	29.2	AACT-DROME	TRUE	FALSE	3	1258.4	0.4	14of 44	1.5657	FALSE	FALSE	::::::::::::
HKIYEMSKDRNLYQNLISSLFPSIYGNDEVKR	6	9.32	0.203	2358	70.83	AB010108	TRUE	FALSE	3	3860.4	-0.1	19of124	3.1147	FALSE	FALSE	::::::::::::::::::::::::::::::::
HLRQRDTGTSGR	5	12.11	0.067	1317	5	AB010108	TRUE	FALSE	3	1384.5	0.1	17of 44	2.334	FALSE	FALSE	::::::::::::
DPLTGEMTLEGGALVLAD	15	2.84	0.17	1375	52.13	AB010109	TRUE	FALSE	2	1803	0.7	14of 34	2.4193	FALSE	FALSE	::::::::::::::::::
GNHMNPGRNGHHR	4	12.41	0.042	1426	-2.37	AB010261	TRUE	FALSE	2	1500.6	1.4	9of 24	1.1947	FALSE	FALSE	::::Oxidation_M:::::::::
YIHSKNRAKLTYTLAVNHLADKTEEELK	4	9.39	0.159	1605	50.5	AB011376	TRUE	TRUE	3	3287.7	-1	20of108	3.0064	FALSE	FALSE	::::::::::::::::::::::::::
ELLKPLQCNIKF	5	8.94	0.059	1503	40.7	AB018079	TRUE	FALSE	2	1503.8	2.6	10of 22	1.0309	FALSE	FALSE	:::::::Cys_CAM:::::
IPEQQRYIEKVEELEDYRK	9	4.5	0.063	1945	39.2	AB026845	TRUE	FALSE	3	2466.8	2	19of 72	2.2511	FALSE	FALSE	::::::::::::::::::
NKLGEAQQQATMIVETRSSIDTSSM	9	4.45	0.025	1638	42.86	AB026845	TRUE	FALSE	3	2743	-2.4	22of 96	1.6476	FALSE	FALSE	:::::::::::::::::::::::Oxidation_M:
TMATGAVYSPPTR	7	9.85	0.012	1704	23.83	AB026979	TRUE	FALSE	1	1368.5	1.5	60	1.152	FALSE	FALSE	::Oxidation_M:::::::::::
DSTHVIPDVNPFDGIHACVIRGQ	2	5.03	0.27	397	49.1	AB026980	TRUE	FALSE	3	2548.8	1.6	18of 88	1.9601	FALSE	FALSE	:::::::::::::::Cys_CAM:::::::
VKEVQYEIFRSLMYWMMVQFDN	1	4.45	0.101	1876	79.99	AB026980	TRUE	FALSE	3	2890.4	1.6	9of 84	1.0523	FALSE	FALSE	:::::::::::::Oxidation_M::Oxidation_M:::::::
VMTYHGSSGLLATKSNEDGWSTFYEYDNYGR	14	4.54	0.01	414	60.43	AB026980	TRUE	FALSE	3	3566.8	-0.7	11of120	1.1784	FALSE	FALSE	::Oxidation_M:::::::::::::::::::::::::::
IVAFYLNEDAGLPEAN	9	2.95	0.008	928	50.2	AB027531	TRUE	FALSE	3	1736.9	-1.4	15of 60	1.7438	FALSE	FALSE	::::::::::::::::
GAAGSAGGAAGTGGVGSGGAGVAGGGGSGTGVAGTPDGR	1	6.79	0.085	58	30	AB029202	TRUE	TRUE	3	2902	0.2	27of152	1.5552	FALSE	FALSE	::::::::::::::::::::::::::::::::::
STGAIAKKEPPK	12	10.32	0.116	895	10.4	AB030577	TRUE	FALSE	2	1227.4	2.8	9of 22	1.3799	FALSE	FALSE	::::::::::::
WMRGDQPIICATNSFGMGVDKPSVR	4	8.97	0.005	2553	57.46	AB031086	TRUE	FALSE	2	2824.2	1.2	4of 48	0.8944	FALSE	FALSE	:::::::::Cys_CAM:::::::::::::
PPSEPPAMKSAGYAQQKFKLS	3	10.05	0.111	2017	34.23	AB032181	TRUE	FALSE	2	2263.6	-2.3	5of 40	0.9708	FALSE	FALSE	::::::::::::::::::
ASPYSHLYSMMPGAALGISPAMHDRMKLEEEHRAR	10	7.93	0.089	258	70.92	AB032181	TRUE	FALSE	3	3974.5	-0.1	17of136	1.5375	FALSE	FALSE	:::::::::Oxidation_M:Oxidation_M::::::::::::::::::::::
SMMPGAALGISPAMHDR	2	7.85	0.053	195	38.79	AB032181	TRUE	FALSE	3	1743.1	-2.2	8of 64	1.1836	FALSE	FALSE	::::::::::::::::
VYWLIDNGGWLGLSRHIR	1	9.85	0.071	2260	61.7	AB032430	TRUE	FALSE	3	2156.5	-0.7	11of 68	1.2424	FALSE	FALSE	::::::::::::::::
MHPRVYTNISRQLSRAPFGELEDSDMAP	10	5.39	0.062	985	60.16	AB032430	TRUE	FALSE	3	3235.6	2.2	19of108	2.3269	FALSE	FALSE	:::::::::::::::::::::::Oxidation_M:::
SGCGQGIAPSDLVRKPR	8	10.11	0.027	2155	25	AB034690	TRUE	FALSE	3	1799	0.5	18of 64	2.2126	FALSE	FALSE	:::Cys_CAM:::::::::::::
MQQQLAHEIYR	11	7.77	0.002	2708	25.93	AB035412	TRUE	TRUE	2	1433.6	2.6	4of 20	0.6833	FALSE	FALSE	:Oxidation_M:::::::::::
PGSHKHGSGTAANAASAAGSQK	13	10.6	0.02	1790	4	AB035419	TRUE	FALSE	3	1993.1	2.6	15of 84	1.3322	FALSE	FALSE	::::::::::::::::::
GWTRWCDKDRDTSDKS	15	6.39	0.022	1913	16.2	AB035891	TRUE	FALSE	2	2014.1	1	12of 30	1.4635	FALSE	FALSE	::::::Cys_CAM:::::::::::
LKSTIGNISLIHRFR	4	12.42	0.032	2381	40.5	AB038236	TRUE	FALSE	2	1756.1	2.3	9of 28	1.2104	FALSE	FALSE	::::::::::::::::
STNKPSNQESQHHRLAIDDMR	7	7.97	0.103	2063	17.83	AB042816	TRUE	FALSE	3	2465.7	-1.2	451	1.6373	FALSE	FALSE	::::::::::::::::::
PPTEAPTALAAAPPAPAAR	8	6.98	0.106	2767	37.8	AB043038	TRUE	FALSE	2	1771	2.1	5of 36	1.0349	FALSE	FALSE	::::::::::::::::::
SALVAQLNSPSPLNSNSKSLSG	9	10.1	0.085	595	39.9	AB044403	TRUE	FALSE	3	2172.4	-0.1	23of 84	2.3347	FALSE	FALSE	::::::::::::::::::
LEDANEVRKENNIKEMFGKMSEMR	13	4.91	0	2403	43.19	AB049435	TRUE	TRUE	2	2932.3	-0.4	5of 46	0.9755	FALSE	FALSE	:::::::::::::::::::Oxidation_M::Oxidation_M::
EDDKPHVVAKRLEL	9	5.39	0.028	624	25.9	AB050622	TRUE	FALSE	3	1649.9	1.4	19of 52	2.3393	FALSE	FALSE	::::::::::::::
NLAAMAYFGLTEYQKMSQYIFEETFNL	2	3.97	0.057	2056	87.36	AB051856	TRUE	FALSE	3	3256.7	0	11of104	1.3919	FALSE	FALSE	:::::Oxidation_M::::::::::Oxidation_M:::::::::::
RKLLQQCHGAGAAGQSRRNVR	8	12.41	0.05	3353	21.8	AB052367	TRUE	TRUE	3	2364.6	2	18of 80	1.4159	FALSE	FALSE	::::::Cys_CAM:::::::::::::
AKDTNVSGGSTVSFGAASPLAATR	5	10.09	0.088	1344	35.5	AB053478	TRUE	FALSE	2	2266.5	2.4	17of 46	2.0251	FALSE	FALSE	::::::::::::::::::::
KKEVPVSSPLSPVEQK	11	9.76	0.018	1414	24.4	AB053478	TRUE	TRUE	2	1753	-1.8	8of 30	1.005	FALSE	FALSE	::::::::::::::::
QYDGIGPVTN	10	3.1	0.034	2707	18.7	AB053480	TRUE	FALSE	2	1064.1	1.7	11of 18	1.8856	FALSE	FALSE	::::::::::
GEATGESQQQQQQLQQHQHQQQQQCPTPNGASY	4	5.13	0.034	2632	20.8	AB054995	TRUE	FALSE	3	3779.9	-2.5	22of128	2.2746	FALSE	FALSE	:::::::::::::::::::::::::Cys_CAM:::::::::
LFIMVSNYENDR	9	4.08	0.066	2307	37.93	AB055857	TRUE	FALSE	2	1501.7	-0.6	9of 22	1.1514	FALSE	FALSE	::::::::::::
NDERGQPMLMRDQRSMMIE	6	4.56	0.004	2848	39.42	AB055857	TRUE	FALSE	3	2386.7	-1.8	15of 72	0.3137	FALSE	FALSE	:::::::::Oxidation_M::::::Oxidation_M:Oxidation_M:::
NPELLQFTGQLSNLESASKTT	6	4.27	0.057	2510	44.4	AB061681	TRUE	FALSE	2	2279.5	-1.2	11of 40	1.4663	FALSE	FALSE	::::::::::::::::::::
QNLPNLMNLLATVLVFAVV	7	6.02	0.022	1576	78.93	AB062670	TRUE	FALSE	3	2070.5	-0.8	450	2.4094	FALSE	FALSE	::::::::::::::::::
TSVGQLQQQQPHQSQQKNSM	2	10.1	0.133	2206	15.63	AB062671	TRUE	FALSE	2	2299.5	-2.2	5of 38	1.0573	FALSE	FALSE	:::::::::::::::::Oxidation_M:
PATPVGMAMGGKGGGGGGGKKMKSVPINVTLQRKKS	10	11.9	0.057	468	42.09	AB069908	TRUE	FALSE	3	3516.2	1.9	12of140	1.0529	FALSE	FALSE	::::::Oxidation_M::Oxidation_M:::::::::::::::::::::::::
SGIADPVTNGGTSTPDGRPRAGSVFRGSTPQPG	8	10.8	0.011	3243	37.7	AB069908	TRUE	FALSE	2	3198.4	2.6	8of 64	1.0661	FALSE	FALSE	::::::::::::::::::::::::::::::::
PLQFMHEFLRMRLETRPVRPNPLSLEQLMK	5	11.16	0.198	2873	90.89	AB069961	TRUE	FALSE	3	3741.5	-0.1	11of116	1.463	FALSE	FALSE	:::::Oxidation_M::::::::::::::::::::::Oxidation_M::
KTANIFLVDGSNSLK	1	9.89	0.119	852	33.5	AB069961	TRUE	FALSE	2	1607.8	2.3	8of 28	1.1867	FALSE	FALSE	::::::::::::::::
RKQKVVNVTASADLPASVGGTPKKTRTARSR	4	12.43	0.054	2683	30.3	AB069961	TRUE	FALSE	3	3281.8	0.8	13of120	1.1723	FALSE	FALSE	::::::::::::::::::::::::::::::
WMFTKLISPMIKGMHTLASQKFCGIISK	11	10.56	0.049	1230	83.69	AB069961	TRUE	FALSE	3	3272	-2.2	20of108	1.8615	FALSE	FALSE	::Oxidation_M::::::::::::::::::Cys_CAM::::::
SAVNSMDSSKPPSMAGSASR	9	10.09	0.015	2197	21.36	AB069961	TRUE	FALSE	2	1984.2	2.6	7of 38	1.0568	FALSE	FALSE	:::::::::::::Oxidation_M:::::::
VHNRGKFNAKSKAKMK	1	11.86	0.046	1605	7.83	AB073024	TRUE	FALSE	3	1861.2	1.6	7of 60	0.9971	FALSE	FALSE	:::::::::::::::Oxidation_M::
MSKSALVILAPGAEEMEF	7	3.97	0.063	1653	56.36	AB079599	TRUE	FALSE	2	1940.3	2.8	15	1.8433	FALSE	FALSE	:::::::::::::::Oxidation_M:::
EGKFYVEDPTGCVQLDL	13	3.59	0.043	1331	44.1	AB102715	TRUE	FALSE	3	1971.1	2.1	19of 64	1.6786	FALSE	FALSE	:::::::::::Cys_CAM:::::::
GIEELYYTIEPLDMLETAYPDLVAAFLKSKEKPAK	11	4.28	0.185	1741	99.73	AB103508	TRUE	TRUE	3	4004.6	1.8	15of136	1.6608	FALSE	FALSE	:::::::::::::Oxidation_M:::::::::::::::::::
QQSKQEKILIQPLEIIKKR	1	10.55	0.033	243	40.8	AB103508	TRUE	FALSE	2	2321.8	-0.7	11of 36	1.3908	FALSE	FALSE	::::::::::::::::::
RLARRKGTLAIATAIATSASATHMMS	8	12.71	0.107	2225	51.66	AB107273	TRUE	FALSE	3	2720.2	-0.2	16of100	1.4354	FALSE	FALSE	:::::::::::::::::::::::Oxidation_M:Oxidation_M::
TAIATSASATHMMSRRK	9	12.42	0.04	2676	22.26	AB107273	TRUE	FALSE	3	1853.1	0.3	15of 64	1.2337	FALSE	FALSE	:::::::::::Oxidation_M:Oxidation_M:::::
KNLSRHLRYECGQLPTE	5	8.88	0.062	2471	29.8	AB107281	TRUE	FALSE	2	2102.3	2.9	9of 32	1.0939	FALSE	FALSE	:::::::::Cys_CAM:::::::
THSSSNHSSNGNG	13	8	0.015	520	-6.8	AB107283	TRUE	FALSE	2	1286.2	2.3	9of 24	1.1796	FALSE	FALSE	::::::::::::
FVFDMVVLSVCSAVG	9	3.1	0.134	623	59.03	AB107958	TRUE	FALSE	3	1630.9	-1.1	20of 56	2.0781	FALSE	FALSE	:::::::::Cys_CAM:::::
IMSKAKYESYEYVTALLISLGMIFFMSGSS	9	6.9	0.126	2412	98.79	AB107958	TRUE	FALSE	3	3385	-2.8	8of116	0.9976	FALSE	FALSE	:::::::::::::::::::::::::Oxidation_M:::::
SCLLAVSVDDAMEKMVEDYFDM	13	3.32	0.013	1286	67.49	AB110069	TRUE	FALSE	3	2601.9	-2.1	9of 84	1.0336	FALSE	FALSE	::Cys_CAM::::::::::Oxidation_M:::Oxidation_M:::::::::
PSDRQLALRAKLKAGWSSSK	3	11.57	0.074	2771	32.8	AB112927	TRUE	FALSE	3	2200.5	2.6	20of 76	1.8987	FALSE	FALSE	::::::::::::::::::
SPTGGSGSSGGGGGGGSSQAK	1	10.1	0.073	1746	-0.7	ABRU-DROME	TRUE	FALSE	2	1637.6	1.3	12of 40	1.3368	FALSE	FALSE	::::::::::::::::::::
YMCILSGCDYLSSLRGIGLAKACK	4	8.54	0.081	2514	67.73	AC004783	TRUE	TRUE	3	2754.1	-1.6	10of 92	1.3129	FALSE	FALSE	::Oxidation_M:Cys_CAM::::Cys_CAM::::::::::::::Cys_CAM::
FRYMC	11	8.9	0.08	437	20.13	AC004783	TRUE	FALSE	1	776.9	-2	5of 8	0.8693	FALSE	FALSE	:::::Cys_CAM:
KKPLDVKKGKKGKK	15	11	0.052	688	-1.9	AC018748	TRUE	TRUE	3	1583	0.5	18of 52	2.1197	FALSE	FALSE	::::::::::::::

FSKTKFGQALMDEMQMNSGGSSP	6	6.99	0	2980	40.59	ACH2-DROME	TRUE	FALSE	2	2511.8	-2.8	6of 44	0.6449	FALSE	FALSE	:::::::::Oxidation_M::::Oxidation_M:::::::
FRCPEALFQPSFLGMEACGIHETTYNSIMK	6	5.4	0.587	1938	82.36	ACT1-DROME	TRUE	TRUE	3	3537	3	42of116	6.7706	FALSE	FALSE	:::Cys_CAM::::::::::::::Cys_CAM::::::::::::
CPEALFQPSFLGMEACGIHETTYNSIMK	3	4.54	0.414	1888	74.86	ACT1-DROME	TRUE	TRUE	3	3233.6	-1.8	33of108	4.4831	FALSE	FALSE	:Cys_CAM::::::::::::::Cys_CAM::::::::::::
PIYEGYALPHAILR	5	7.7	0.414	1898	46.2	ACT1-DROME	TRUE	FALSE	2	1613.9	0.1	21of 26	3.6408	FALSE	FALSE	::::::::::::::
TTGIVLDSGDGVSHTVPIYEGYALPHAILR	7	5.12	0.39	1624	75.8	ACT1-DROME	TRUE	TRUE	3	3153.6	1	1	4.3227	FALSE	FALSE	::::::::::::::::::::::::::::::
TTGIVLDSGDGVSHTVPIYEGYALPHAILR	4	5.12	0.361	1857	75.8	ACT1-DROME	TRUE	TRUE	3	3153.6	0.9	32of116	3.858	FALSE	FALSE	::::::::::::::::::::::::::::::
GYSFTTTAER	8	6.89	0.355	1143	16.5	ACT1-DROME	TRUE	TRUE	2	1133.2	0.8	15of 18	2.8867	FALSE	FALSE	::::::::::
TTGIVLDSGDGVSHTVPIYEGYALPHAILR	6	5.12	0.321	1794	75.8	ACT1-DROME	TRUE	TRUE	3	3153.6	0.5	39of116	4.7615	FALSE	FALSE	::::::::::::::::::::::::::::::
TTGIVLDSGDGVSHTVPIYEGYALPHAILR	9	5.12	0.252	1948	75.8	ACT1-DROME	TRUE	TRUE	3	3153.6	2.4	26of116	3.8096	FALSE	FALSE	::::::::::::::::::::::::::::::
TTGIVLDSGDGVSHTVPIYEGYALPHAILR	5	5.12	0.153	1871	75.8	ACT1-DROME	TRUE	TRUE	2	3153.6	1.1	18of 58	3.3788	FALSE	FALSE	::::::::::::::::::::::::::::::
GYALPHAILR	5	9.85	0.087	1896	31.2	ACT1-DROME	TRUE	FALSE	1	1111.3	0	10of 18	1.3838	FALSE	FALSE	::::::::::
WDDMEKIWHHTFYNELR	8	5.22	0.03	1931	46.93	ACT1-DROME	TRUE	FALSE	3	2337.6	0.7	17of 64	1.7182	FALSE	FALSE	::::Oxidation_M:::::::::::::
EEYDESGPGIVHRKC	13	4.63	0.009	1971	19.6	ACT2	TRUE	FALSE	2	1776.9	-0.7	8of 28	1.09	FALSE	FALSE	::::::::::::::Cys_CAM:
HQGVMVGMGQKDCYVGD	4	5.1	0.035	2203	28.56	ACT4-DROME	TRUE	FALSE	2	1898.1	0.2	11of 32	1.3934	FALSE	FALSE	:::::Oxidation_M::::::::Cys_CAM:::::
KVWHHTFYNELR	8	9.72	0.009	1888	28.7	ACT4-DROME	TRUE	FALSE	3	1630.8	1.7	15of 44	1.6245	FALSE	FALSE	::::::::::::
RKMLYQNIVLSGGSTLFK	4	10.71	0.178	2741	49.23	ACTZ-DROME	TRUE	FALSE	2	2056.5	-1.7	7of 34	0.9383	FALSE	FALSE	::::::::::::::::::
KMLYQNIVLSGGSTLFKGFGDR	12	10.18	0.042	1079	57.13	ACTZ-DROME	TRUE	TRUE	3	2432.8	-2.7	20of 84	1.6572	FALSE	FALSE	::::::::::::::::::::::
ALDLLYGMVSKKNLM	1	9.63	0.168	1382	49.96	ADD-DROME	TRUE	FALSE	2	1697.1	-1.9	11of 28	1.7192	FALSE	FALSE	::::::::::::::::
KDGKKKHKKGKKSK	9	11.06	0.084	2176	-21.4	ADD-DROME	TRUE	FALSE	3	1626	0.9	16of 52	1.6226	FALSE	FALSE	::::::::::::::::
ENIAAGQNELLKRAKANGEAACGNYTAG	10	6.52	0.028	2651	40.6	ADFFR	TRUE	FALSE	3	2893.1	0	14of108	1.2631	FALSE	FALSE	:::::::::::::::::::::::Cys_CAM::::::
SWLDVEPRVGELLLEHPTQTTLECAQNFVK	8	4.36	0.049	2435	81.6	ADH1-DROMN	TRUE	FALSE	3	3511.9	0.3	21of116	2.9206	FALSE	FALSE	:::::::::::::::::::::::Cys_CAM::::::
VCLLGCGISTGYGAALNTAK	14	8.28	0.496	1138	49.9	ADHX-DROME	TRUE	TRUE	2	2027.3	1.8	22of 38	3.981	FALSE	FALSE	::Cys_CAM:::Cys_CAM:::::::::::::
NVINTFKTAEHPRLRYFGNISLGTDVSLR	3	10.39	0.122	2220	68.9	ADRO-DROME	TRUE	TRUE	3	3421.9	2.3	24of116	2.4128	FALSE	FALSE	::::::::::::::::::::::::::::
KGLGGAIKVMIH	9	10.6	0.125	665	28.53	AE001572	TRUE	FALSE	2	1240.6	-0.5	10of 22	1.6464	FALSE	FALSE	:::::::::Oxidation_M:::
RPETDSHSPRRRLEHILLG	9	10.73	0.12	1158	31.5	AE001572	TRUE	FALSE	3	2270.6	-0.8	19of 72	2.4533	FALSE	FALSE	::::::::::::::::::
TRVAVRGQARDSAPPGSAKPLPAFAYGIINPF	12	11.29	0.095	2668	70.9	AE001572	TRUE	FALSE	2	3326.8	-1.2	5of 62	0.8723	FALSE	FALSE	::::::::::::::::::::::::::::
SKALSDRSEEFR	6	7.14	0.039	1280	16.7	AE001572	TRUE	FALSE	2	1425.5	2.3	11of 22	1.519	FALSE	FALSE	::::::::::
RPETDSHSP	12	5.22	0.019	953	2.8	AE001572	TRUE	FALSE	2	1026.1	2.7	8of 16	1.5446	FALSE	FALSE	::::::::
AELKSSDS	3	4.08	0.009	2874	8.7	AE001572	TRUE	FALSE	1	836.9	-0.7	6of 14	1.0456	FALSE	FALSE	::::::::
MLDKSHEKRFNNIDTHNENQENQDR	10	5.32	0.001	2203	20.83	AE001572	TRUE	TRUE	3	3114.3	2.6	15of 96	1.4458	FALSE	FALSE	::::::::::::::::::::::
MSPKSTMKFNR	3	11.64	0.018	2856	15.96	AE002603	TRUE	TRUE	3	1327.6	-2.3	6of 40	0.8457	FALSE	FALSE	::::::::::
SRMGWLTTFLIELVLGVAFMEVLA	11	4.27	0.071	1162	105.16	AE002611	TRUE	FALSE	3	2730.3	-3	8of 92	0.9873	FALSE	FALSE	:::Oxidation_M::::::::::::::Oxidation_M:::::
VTPRYQVLLLR	13	11.14	0.025	2199	40.2	AE002611	TRUE	FALSE	3	1358.7	-1.5	8of 40	1.0487	FALSE	FALSE	::::::::::
HFTAGIDLNDMINVGQTLAETDDYARKGVSMERMIKV	12	4.7	0.022	1341	83.89	AE002611	TRUE	FALSE	3	4173.7	-1.1	23of144	2.302	FALSE	FALSE	:::::::::Oxidation_M::::::::::::::::::::Oxidation_M::::
HFTAGIDLNDMINVGQTLAETDDYARKGVSMERMIKV	11	4.7	0.015	986	83.89	AE002611	TRUE	FALSE	3	4173.7	0.1	23of144	2.5722	FALSE	FALSE	:::::::::Oxidation_M::::::::::::::::::Oxidation_M:::::::
DFYVHESR	14	5.22	0	2078	16	AE002611	TRUE	FALSE	2	1053.1	0.1	4of 14	0.7948	FALSE	FALSE	::::::::
LYVCVGAGAIGAVYYMAR	5	8.77	0.034	1515	58.93	AE002656	TRUE	FALSE	2	1951.3	-0.5	12of 34	1.6898	FALSE	FALSE	:::::Cys_CAM::::::::::Oxidation_M:::
GDTDACNMLMLEK	2	3.71	0.01	2280	31.06	AE002656	TRUE	FALSE	2	1514.7	0.6	6of 24	0.8132	FALSE	FALSE	::::::Cys_CAM::Oxidation_M:::::
GKQKIKLIAAQHRYRNR	3	12.15	0.038	1633	20.4	AE003407	TRUE	TRUE	2	2081.5	2.6	8of 32	1.2285	FALSE	FALSE	::::::::::::::::
SRVNWACWMVDVVLSAR	4	9.01	0.011	1422	55.83	AE003408	TRUE	FALSE	3	2066.4	2.7	17of 64	1.6867	FALSE	FALSE	:::::::Cys_CAM::Oxidation_M:::::::::
FYQVKDSLSTGKTVILQKTSAGKIKND	3	10.19	0.112	1765	45.7	AE003409	TRUE	FALSE	3	2971.4	1.3	24of104	2.3134	FALSE	FALSE	::::::::::::::::::::::::
RSCRVQKSNDSNLSKPLYSTTKRRRAMRMSK	4	12.14	0.055	2536	30.36	AE003411	TRUE	FALSE	3	3760.3	-2.5	20of120	2.2771	FALSE	FALSE	:::Cys_CAM::::::::::::::::::::::Oxidation_M:::::
QVLVPCAPLLGFLDR	15	6.1	0.212	1465	58.5	AE003412	TRUE	FALSE	2	1699	0.9	11of 28	1.695	FALSE	FALSE	::::::Cys_CAM:::::::::
SQRDIENYGAAMLAKSKL	8	9.63	0.094	2746	34.93	AE003417	TRUE	FALSE	2	1996.3	1.1	7of 34	0.9567	FALSE	FALSE	::::::::::::::::::
KPGRKRKLPDEPIDQQQLSD	6	9.76	0.008	2083	23.4	AE003417	TRUE	FALSE	2	2349.7	1.1	6of 38	1.0302	FALSE	FALSE	::::::::::::::::::::
THFGKMGSWYINR	12	10.4	0.01	2044	28.93	AE003418	TRUE	FALSE	2	1597.8	-1.2	6of 24	0.7478	FALSE	FALSE	::::::::::::
SACPTTFMSNMLYACSILYK	14	8.27	0.456	1668	60.86	AE003419	TRUE	TRUE	2	2359.7	0.5	20of 38	3.3324	FALSE	FALSE	:::Cys_CAM::::::::::Cys_CAM::::::
SRLSREPSSNPPRKSQHSSTQRKK	5	12.42	0.19	1751	3	AE003419	TRUE	FALSE	3	2780.1	-1	16of 92	1.8739	FALSE	FALSE	::::::::::::::::::::::::
RNKARKSASTAGCLDAQHIRA	13	11.38	0.126	2348	19.6	AE003419	TRUE	FALSE	3	2312.6	1.7	24of 80	2.0422	FALSE	FALSE	:::::::::::Cys_CAM:::::::::
VNKTNPSASTTRS	11	11.49	0.124	430	6.3	AE003419	TRUE	FALSE	2	1363.5	2.6	12of 24	1.5047	FALSE	FALSE	::::::::::::::
NDSSNSASPRQPA	9	6.79	0.1	2415	5.6	AE003419	TRUE	FALSE	2	1331.3	-1.9	7of 24	1.0194	FALSE	FALSE	::::::::::::::
YDVVSFMAANKEGQKLMVTLER	1	7.04	0.08	1172	56.06	AE003419	TRUE	FALSE	3	2531	2.7	15of 84	1.6355	FALSE	FALSE	::::::::::::::::::::
GLDFLYDDLSVRL	9	3.6	0.004	1430	49.6	AE003419	TRUE	FALSE	3	1526.7	1	15of 48	1.6325	FALSE	FALSE	::::::::::::::
SDDDSETKSQPKGLTPEDEDRR	13	4.01	0.145	247	11.4	AE003420	TRUE	FALSE	3	2506.6	0.1	12of 84	1.1992	FALSE	FALSE	::::::::::::::::::::
KSSEQLTEIKSVLDTNFEEVAKIVA	10	4.36	0.139	1792	56.4	AE003420	TRUE	FALSE	3	2780.1	1.3	15of 96	1.4594	FALSE	FALSE	::::::::::::::::::::::
ASSLSQSEASGSKGNGFPKKVTTLKK	3	10.71	0.115	2875	24.7	AE003420	TRUE	FALSE	3	2639	-0.3	9of100	1.1594	FALSE	FALSE	::::::::::::::::::::::
VDEDDSQDALVRDVGVVGGLSSPDTPPHSSPPPAKR	9	4.05	0.108	2589	53.1	AE003420	TRUE	FALSE	3	3699	0.5	24of140	1.9944	FALSE	FALSE	::::::::::::::::::::::::::::::::::::
AEKSKEETRR	10	9.88	0.102	930	0.3	AE003420	TRUE	FALSE	2	1234.4	-0.5	7of 18	1.0237	FALSE	FALSE	::::::::::
QHTYKVR	10	10.4	0.097	2362	5.3	AE003420	TRUE	FALSE	2	932.1	2	5of 12	1.1576	FALSE	FALSE	::::::::
SLDVVGKIRREIQNLKLF	7	10.58	0.088	1767	52.1	AE003420	TRUE	FALSE	2	2129.6	-2.8	236	1.3471	FALSE	FALSE	::::::::::::::::::
IGYGSAPAHR	9	9.85	0.068	1298	14.6	AE003420	TRUE	FALSE	2	1029.1	-0.9	10of 18	1.1891	FALSE	FALSE	::::::::::
MSTLCSAVTVTSGTSGNSRR	12	10.9	0.045	1433	27.43	AE003420	TRUE	FALSE	3	2073.3	0.2	20of 76	1.9713	FALSE	FALSE	:::::Cys_CAM:::::::::::::::
YTFGYPFGLK	8	9.53	0.024	1785	33.4	AE003420	TRUE	FALSE	2	1193.4	1.4	7of 18	1.3595	FALSE	FALSE	::::::::::
GAKKHKRQGRV	1	12.44	0.011	908	-3	AE003420	TRUE	FALSE	1	1265.5	2.5	5of 20	1.039	FALSE	FALSE	::::::::::
SESQAGQLHSAPSQR	2	7.85	0.161	673	11.5	AE003421	TRUE	FALSE	2	1583.7	0.9	9of 28	1.5785	FALSE	FALSE	::::::::::::::
MDLEMSTRAQKNKK	10	10.32	0.036	554	15.36	AE003421	TRUE	FALSE	3	1697	-1.3	20of 52	2.0001	FALSE	FALSE	:::::Oxidation_M:::::::::
TSAEELVRAENEAFLDWRR	14	4.36	0.008	1621	46.7	AE003421	TRUE	FALSE	3	2293.5	2.6	18of 72	1.567	FALSE	FALSE	::::::::::::::::::
KILVPGAGLGR	15	11.49	0.06	588	29.3	AE003422	TRUE	FALSE	2	1081.3	-0.8	9of 20	1.1665	FALSE	FALSE	::::::::::
DQVAPVRFPDVCPLKNPPK	8	8.93	0.043	1723	40.8	AE003422	TRUE	FALSE	3	2178.5	2.1	21of 72	2.0439	FALSE	FALSE	:::::::::::Cys_CAM:::::::
YCHFVPVERSLSKPCA	9	8.29	0.036	2189	37.8	AE003422	TRUE	FALSE	2	1951.2	2.1	11of 30	1.2839	FALSE	FALSE	::Cys_CAM::::::::::Cys_CAM::
KVARIEAAATALRSFIQFKDGAVLSPLKPAG	11	10.82	0.018	1418	76.9	AE003422	TRUE	FALSE	3	3227.8	-1.5	9of120	1.1942	FALSE	FALSE	::::::::::::::::::::::::::::
YYAEIMVMDPFSLEVIYVLSSKVK	12	4.45	0.003	1564	85.26	AE003422	TRUE	FALSE	3	2826.4	-0.2	8of 92	0.8948	FALSE	FALSE	::::::::::::::::::::::
LLGDVREVRDAIAPPQPPPLPTSLPPPIPELS	14	4.07	0.15	1571	90.7	AE003423	TRUE	FALSE	3	3384	-2.1	9of124	1.1344	FALSE	FALSE	::::::::::::::::::::::::::::
NSFISLLLAVQNKRRQ	13	12.42	0.075	1687	41.9	AE003423	TRUE	FALSE	2	1888.2	3	8of 30	1.2395	FALSE	FALSE	::::::::::::::
CMELLTKQGWSSAYTVEAVIMQIAATLVK	5	6.43	0.063	2649	88.26	AE003423	TRUE	FALSE	3	3243.8	2.9	29of112	1.7449	FALSE	FALSE	:Cys_CAM:::::::::::::::::::::::::::
FRQRAQVETPDTVYWDRLAKP	5	9.72	0.035	2144	46.3	AE003423	TRUE	FALSE	3	2577.9	-1.2	14of 80	1.4603	FALSE	FALSE	::::::::::::::::::
HVYDHAHR	12	8	0.02	2496	4.8	AE003423	TRUE	FALSE	2	1035.1	-2.2	4of 14	0.703	FALSE	FALSE	::::::::
PSSAVTATTTTGTTNSGSTDDVS	8	2.93	0.007	2768	19.2	AE003423	TRUE	FALSE	2	2159.2	-1.4	10of 44	1.2507	FALSE	FALSE	::::::::::::::::::::
GKSESNSGSGSFKR	10	10.59	0.128	793	2.2	AE003424	TRUE	FALSE	1	1428.5	0.2	5of 26	0.9716	FALSE	FALSE	::::::::::::::
TLTYRVRTQPGQNNR	12	12.11	0.039	781	18.2	AE003424	TRUE	FALSE	3	1805	1.1	18of 56	1.846	FALSE	FALSE	::::::::::::::::
VIVNIDMPESPQNLELGMFMVCAEMRDYDS	9	3.38	0.03	2270	90.82	AE003424	TRUE	FALSE	3	3506	1.5	10of116	1.0967	FALSE	FALSE	:::::::::::::::::::::Cys_CAM:::::::::
QELHQSLLDLTEKEMR	9	4.63	0.029	2386	37.03	AE003424	TRUE	FALSE	3	1971.2	-1.3	16of 60	1.7253	FALSE	FALSE	::::::::::::::::
DRVLFITEEPIPIANVVDSC	7	3.59	0.013	1093	63.8	AE003424	TRUE	FALSE	3	2288.6	0.9	94	2.2538	FALSE	FALSE	:::::::::::::::::::Cys_CAM:

TLDVATPTNLGTPR	10	6.79	0.002	653	28.4	AE003424	TRUE	FALSE	2	1456.6	2.4	9of 26	1.1674	FALSE	FALSE	::::::::::::::
PPPGPR	5	11.05	0.096	2852	7.2	AE003425	TRUE	FALSE	1	620.7	-2.8	5of 10	1.0452	FALSE	FALSE	::::::::
IAPGAVVK	10	10.1	0.079	472	21.1	AE003425	TRUE	FALSE	1	754.9	-0.1	7of 14	1.3438	FALSE	FALSE	::::::::::
DAKSPVVTTAPAATCSVSVSDASGAGASVRTTGR	4	8.97	0.025	1663	43.9	AE003425	TRUE	FALSE	3	3236.5	-0.6	8of132	0.9575	FALSE	FALSE	::::::::::::::Cys_CAM::::::::::::::::::
RAPHGLGPIPRMGIR	13	12.71	0.016	2116	31.93	AE003425	TRUE	FALSE	2	1645	2.1	5of 28	0.7521	FALSE	FALSE	::::::::::::Oxidation_M::::
QSPMPDVQMKGATLGVPLAGPVK	4	9.89	0.076	2270	50.06	AE003426	TRUE	FALSE	2	2322.8	-1.8	10of 44	1.3342	FALSE	FALSE	::::::::::::::::::::::
LTSSSASALATSHPSNSQLLPTSKMQAEQGS	2	7.82	0.013	1460	46.03	AE003426	TRUE	FALSE	3	3134.4	0.8	11of120	1.2951	FALSE	FALSE	::::::::::::::::::::::::Oxidation_M::::::
RRRRSSSSSSSSSGSTSSRSGNSRIRRRRARSAR	2	13.01	0.002	1801	1	AE003426	TRUE	TRUE	3	3697	-1.5	10of128	1.0587	FALSE	FALSE	::::::::::::::::::::::::::::::::
LSAHHHTGHGGRR	13	12.41	0.063	2573	0.3	AE003428	TRUE	FALSE	3	1423.5	-1.1	14of 48	1.3853	FALSE	FALSE	::::::::::::::
GMETKLR	9	10.09	0	474	12.43	AE003428	TRUE	FALSE	2	835	-1.2	7of 12	1.1543	FALSE	FALSE	::::::::
NHTNGNDHETSIK	5	6.03	0.08	2226	1.4	AE003429	TRUE	FALSE	2	1467.5	-0.4	11of 24	1.1077	FALSE	FALSE	::::::::::::::
HNKTITKRQHWDHLMAVVAK	5	10.83	0.005	2884	31.43	AE003429	TRUE	TRUE	2	2430.8	1.6	5of 38	0.7997	FALSE	FALSE	::::::::::::::Oxidation_M::::::
FSSERVCLRHRRQCILGHY	9	9.89	0.001	193	40.3	AE003429	TRUE	FALSE	3	2475.8	-2.4	10of 72	0.9192	FALSE	FALSE	::::::Cys_CAM::::::Cys_CAM::::::
DFTTDFSGAPGHIAMLQSVLLATI	2	3.88	0.136	592	73.13	AE003430	TRUE	FALSE	2	2506.9	-1.2	9of 46	1.1612	FALSE	FALSE	::::::::::::::::::::::
GSCEPSAGNSNSNLLQ	6	3.3	0.128	1108	20.9	AE003430	TRUE	FALSE	2	1635.7	-0.7	8of 30	1.1912	FALSE	FALSE	:::Cys_CAM:::::::::::::
GQGHGSGIGLGDPK	13	7.82	0.122	956	12.1	AE003430	TRUE	FALSE	2	1280.4	-0.4	13of 26	1.4531	FALSE	FALSE	::::::::::::::
ATTSAAAAAAATAAATQR	12	11.05	0.116	1052	23.6	AE003430	TRUE	FALSE	2	1576.7	2.1	14of 34	2.1241	FALSE	FALSE	::::::::::::::::::
YSLLPEVE	14	3.13	0.057	951	29.7	AE003430	TRUE	FALSE	2	950.1	1	11of 14	1.8636	FALSE	FALSE	::::::::
QERQQDISASSDQHLNDSG	5	3.97	0.03	2219	14.9	AE003430	TRUE	FALSE	2	2116.1	-2.8	5of 36	0.7526	FALSE	FALSE	::::::::::::::::::::
YSLLPEVE	13	3.13	0.025	1070	29.7	AE003430	TRUE	FALSE	1	950.1	0.8	9of 14	2.0163	FALSE	FALSE	::::::::
PSDDENSEPTPKK	11	4.07	0.014	788	4	AE003430	TRUE	FALSE	2	1444.5	-2.4	9of 24	1.1625	FALSE	FALSE	::::::::::::::
MVKTFKESLKMCRWDAARYSLR	4	10.44	0.181	2446	53.66	AE003431	TRUE	FALSE	3	2794.3	2.5	15of 84	1.4819	FALSE	FALSE	:Oxidation_M::::::::::Cys_CAM::::::::::
SDQTSGSGSDSDDKDAAGGK	3	3.7	0.048	1261	-0.4	AE003431	TRUE	FALSE	3	1885.8	1.5	14of 76	1.4212	FALSE	FALSE	::::::::::::::::::
HNASGDFVGIEPGCGGGGGGGGRVLVVPRPRQP	1	9.01	0.046	966	50.6	AE003431	TRUE	FALSE	2	3215.5	2.2	10of 64	1.0932	FALSE	FALSE	::::::::::::Cys_CAM::::::::::::::::::
GECPYSLSPVSAKSQKLLR	11	9.66	0.038	1520	37.7	AE003431	TRUE	FALSE	2	2121.4	-1.3	10of 36	1.4442	FALSE	FALSE	:::Cys_CAM:::::::::::::::
AGKPAYIHVVGIGLGVWK	6	10.18	0.034	1283	50.1	AE003431	TRUE	TRUE	3	1866.3	2	17of 68	1.7756	FALSE	FALSE	::::::::::::::::::
EEQIVPKLDSPFHMREPHNLAA	7	5.26	0.027	2191	48.03	AE003431	TRUE	FALSE	3	2559.9	-2.3	226	1.2703	FALSE	FALSE	::::::::::::::::::::
QVMRKRYAISFDTLLLEAQDR	3	9.72	0.005	2066	56.83	AE003431	TRUE	FALSE	3	2571	-2.7	21of 80	2.3159	FALSE	FALSE	:::Oxidation_M:::::::::::::::::
GGNGIVGAQVPLGAGIGLAHSYR	9	9.85	0.161	2544	48.6	AE003432	TRUE	FALSE	2	2165.5	-2.8	7of 44	0.9613	FALSE	FALSE	::::::::::::::::::::::
ERERECRLCAVTFFAKLHPGDVCGSNGLPLTP	14	6.93	0.053	2374	73.7	AE003432	TRUE	FALSE	3	3689.1	-2.9	19of124	1.297	FALSE	FALSE	::::::Cys_CAM:::Cys_CAM::::::::::::::Cys_CAM::::::::::
MSISRISRYGNVAPRTTLGR	11	12.41	0.037	830	39.13	AE003432	TRUE	FALSE	3	2252.6	1.1	21of 76	2.0861	FALSE	FALSE	:Oxidation_M:::::::::::::::::
GDEVTQPTAKQSKINANFVCKIESDTNMDK	2	4.65	0.032	2042	40.83	AE003432	TRUE	FALSE	3	3370.7	0.1	15of116	1.2834	FALSE	FALSE	::::::::::::::::::Cys_CAM:::::::::::
YVGHSVLHKMLPWHWR	6	10.4	0.002	2119	46.43	AE003432	TRUE	FALSE	2	2047.4	1.6	4of 30	0.8251	FALSE	FALSE	::::::::::::::::
NIDIAESPMAQTRRLREQRELLE	12	4.8	0.084	2655	52.63	AE003433	TRUE	FALSE	3	2770.1	-2.2	12of 88	1.3911	FALSE	FALSE	::::::::::::::::::::
AVKPSVAPKR	11	11.64	0.075	304	13	AE003433	TRUE	FALSE	2	1053.3	2.3	11of 18	1.3608	FALSE	FALSE	::::::::::
PPSKVKGPANAEAK	5	10.32	0.021	3009	10.8	AE003433	TRUE	FALSE	2	1394.6	2.3	6of 26	0.9702	FALSE	FALSE	::::::::::::::
LLPVPLITFQAYPSFMAAGR	15	9.85	0.392	1915	74.53	AE003434	TRUE	TRUE	2	2193.7	-0.1	17of 38	3.4025	FALSE	FALSE	::::::::::::::::::
KKNNKKKNGMLKPLGKKTEKIEKK	10	10.94	0.107	1738	8.63	AE003434	TRUE	FALSE	3	2828.5	1.2	17of 92	1.6519	FALSE	FALSE	:::::::::Oxidation_M:::::::::::::
LLGKLKRMRLRLSILPRNSSAQSMVRR	3	13.01	0.043	2214	66.66	AE003434	TRUE	FALSE	3	3181.9	1.8	17of104	1.5123	FALSE	FALSE	::::::::::::::::::::::::
GDKVLYDLEERINQAVFPSLQGGPHNNAVAGIATAFK	15	5.39	0.16	1407	82.3	AE003435	TRUE	FALSE	3	3942.4	-0.4	24of144	2.7999	FALSE	FALSE	::::::::::::::::::::::::::::::::
ALPEMPSVSRR	7	10.89	0.127	3423	24.13	AE003435	TRUE	FALSE	2	1259.5	1.4	2	1.1924	FALSE	FALSE	:::::Oxidation_M:::::::
MGSPGQSLPLIFTEEQREAAR	10	4.56	0.097	1526	47.13	AE003435	TRUE	FALSE	2	2334.6	1.9	12of 40	2.1309	FALSE	FALSE	:Oxidation_M:::::::::::::::::
EMERMSSTSKSGSSST	7	7.1	0.07	1091	10.16	AE003435	TRUE	FALSE	2	1724.8	0.4	78	1.2787	FALSE	FALSE	::Oxidation_M:::Oxidation_M:::::::::::
NIQETPGPSGLIIGGGDGDGDR	7	3.51	0.07	2383	33.8	AE003435	TRUE	FALSE	3	2126.2	-1.9	4	2.2061	FALSE	FALSE	::::::::::::::::::::
GDSFGYNWNVFTFQVDFDK	6	3.6	0.069	2884	53	AE003435	TRUE	FALSE	3	2287.4	-2.9	15of 72	1.422	FALSE	FALSE	::::::::::::::::::
ALDSQLPLLALGGLIIMGLAI	3	3.1	0.058	1581	91.83	AE003435	TRUE	FALSE	2	2093.6	2.3	10of 40	1.2095	FALSE	FALSE	::::::::::::::::::
KRNKRKRGGKSGSGA	11	12.72	0.055	1150	-10	AE003435	TRUE	FALSE	2	1587.8	-1.9	11of 28	1.3076	FALSE	FALSE	::::::::::::::
VLQTKDLKLPVGIVNIGETR	10	9.89	0.046	826	52.8	AE003435	TRUE	FALSE	3	2194.6	-2.1	23of 76	2.3359	FALSE	FALSE	::::::::::::::::::
QLIVIPLLKKYLNPSMNE	5	9.63	0.023	1906	61.73	AE003435	TRUE	FALSE	2	2130.6	2.9	11of 34	2.3695	FALSE	FALSE	::::::::::::::Oxidation_M:::
ADTVARAIAQGR	11	10.89	0.021	2599	19.8	AE003435	TRUE	FALSE	2	1229.4	-1.7	8of 22	1.4339	FALSE	FALSE	::::::::::::
LELMAHSYFLAPNLVVERHR	6	7.92	0.01	1450	62.53	AE003435	TRUE	FALSE	3	2396.8	-0.9	23of 76	2.2849	FALSE	FALSE	::::::::::::::::::
QEDTPKEEDEEEDDDK	7	3.42	0.009	1587	6	AE003435	TRUE	FALSE	2	1951.9	-1.2	22	1.2138	FALSE	FALSE	::::::::::::::::
KMVHKA	10	10.6	0.003	1368	6.23	AE003435	TRUE	FALSE	1	729.9	0.1	5of 10	0.5151	FALSE	FALSE	::Oxidation_M:::::
FNFINCRRNAELLSK	8	10.11	0.001	2646	40.2	AE003435	TRUE	FALSE	2	1883.1	-2.6	8of 28	1.2131	FALSE	FALSE	::::::Cys_CAM:::::::::::
PHSAKWADDSRLGKSSLADRSLYGREMSLLR	3	10.17	0.061	2254	58.73	AE003436	TRUE	FALSE	3	3504.9	1.2	23of120	2.1291	FALSE	FALSE	::::::::::::::::::::::::::::::::
PRFNADPGRIINGTE	3	7.05	0.053	1364	28	AE003436	TRUE	FALSE	2	1657.8	-2.5	8of 28	0.9242	FALSE	FALSE	::::::::::::::
HMIDEYQR	10	5.22	0.031	2339	16.03	AE003436	TRUE	FALSE	2	1092.2	-1.3	7of 14	1.173	FALSE	FALSE	::::::::
LARDPPIITTTAATPQDSPST	15	3.89	0.009	763	39.3	AE003436	TRUE	FALSE	2	2154.4	-1.4	13of 40	1.4016	FALSE	FALSE	::::::::::::::::::::
CGSMR	11	9.01	0.001	493	7.13	AE003436	TRUE	FALSE	1	626.7	0.2	3of 8	0.4453	FALSE	FALSE	:Cys_CAM:::Oxidation_M::
ALQSVGQIVGEVLK	8	6.95	0.371	2273	39	AE003437	TRUE	TRUE	2	1441.7	0.6	18of 26	3.0821	FALSE	FALSE	::::::::::::::
PSGIITKVAAHKLSAEPK	9	10.32	0.166	2578	30.6	AE003437	TRUE	TRUE	2	1848.2	2	10of 34	1.2125	FALSE	FALSE	::::::::::::::::::
GHTSQSQESCTAAAAASTATAASGQAPGGKEQQLANQPEEGGT	10	4.25	0.149	529	35.1	AE003437	TRUE	FALSE	3	4145.2	-2.7	26of168	2.3313	FALSE	FALSE	::::::::Cys_CAM:::::::::::::::::::::::::::::
KMAIDAMEYDDEETN	2	3.38	0.125	409	28.76	AE003437	TRUE	FALSE	3	1775.9	-2.6	15of 56	1.7203	FALSE	FALSE	::::::::::::::
PPRDNNNSDAARCPNA	6	6.25	0.118	1580	11.2	AE003437	TRUE	FALSE	3	1769.8	-0.1	15of 60	1.6039	FALSE	FALSE	::::::::::::Cys_CAM::::
YLDEQRASGALMEHKM	11	5.35	0.081	508	32.96	AE003437	TRUE	FALSE	3	1896.1	-2.2	22of 60	2.7127	FALSE	FALSE	::::::::::::::Oxidation_M:
YDEDLGVGDDTRVKKK	12	4.57	0.043	752	17.8	AE003437	TRUE	FALSE	3	1839	0.5	19of 60	1.7427	FALSE	FALSE	::::::::::::::
QVTREMKMK	5	10.59	0.03	2871	12.96	AE003437	TRUE	FALSE	2	1167.4	1.2	3of 16	0.5749	FALSE	FALSE	:::::::Oxidation_M::
YFMDSEQKKEEQER	7	4.36	0.028	1311	17.73	AE003437	TRUE	FALSE	3	1848	0.7	58	2.2274	FALSE	FALSE	::::::::::::::
PGRRLTSRSPSPATGAGGGPGGSVSRKSSFSSLFRL	15	13.01	0.012	2674	50.4	AE003437	TRUE	FALSE	2	3577	0	9of 70	1.0213	FALSE	FALSE	::::::::::::::::::::::::::::::::
SDNEESSTSESDEYGR	6	3.44	0.006	1016	7.5	AE003437	TRUE	FALSE	3	1792.7	-1.4	16of 60	1.5746	FALSE	FALSE	::::::::::::::
NWSKQAMHYVHCNASLFLTSNLSHDDPFL	2	6.3	0.004	2370	71.03	AE003437	TRUE	FALSE	3	3434.8	-0.7	17of112	0.3557	FALSE	FALSE	::::::::::Cys_CAM:::::::::::::::
KAKARAEAEAKAKAEAEAKAKAAAEA	3	9.97	0.119	1653	20.3	AE003438	TRUE	FALSE	3	2584.9	-1	17of100	1.7983	FALSE	FALSE	::::::::::::::::::::::
FRGNAKALREHLRATHSIRSIVAADIRRPMEC	3	11.74	0.1	2427	63.53	AE003438	TRUE	FALSE	3	3734.3	-1	22of124	2.047	FALSE	FALSE	::::::::::::::::::::::::::::Cys_CAM:
PEKQMKVCEICGAFLIVGDAQQRIEDHLMGK	2	5.46	0.092	1445	72.86	AE003438	TRUE	FALSE	3	3619.1	1.2	21of120	1.699	FALSE	FALSE	:::::Oxidation_M:::Cys_CAM:::Cys_CAM::::::::::::::::::
RRTLQRSDIAQAIANYDQ	3	9.84	0.087	2150	31.8	AE003438	TRUE	FALSE	2	2120.3	-0.8	9of 34	1.365	FALSE	FALSE	::::::::::::::::::
TPIAPGKTSPHGKPPVKPR	3	11.73	0.078	1333	18	AE003438	TRUE	FALSE	3	1966.3	-0.8	20of 72	1.7307	FALSE	FALSE	::::::::::::::::::
TDMEEVLEQPVQHMSLMVDEK	12	3.82	0.056	1581	50.79	AE003438	TRUE	FALSE	3	2521.8	-2.4	8of 80	1.0537	FALSE	FALSE	:::Oxidation_M::::::::::Oxidation_M:::::::::
DISTLPPPQSSAVESPAVIESCLNQREPVPE	6	3.59	0.053	1770	67.6	AE003438	TRUE	FALSE	3	3348.7	-1.2	21of120	2.5798	FALSE	FALSE	::::::::::::::::::::Cys_CAM:::::::::::
GEEMRRLMWGRASISSPVK	13	11.23	0.036	1010	41.66	AE003438	TRUE	FALSE	3	2207.6	1.8	18of 72	1.7428	FALSE	FALSE	::::Oxidation_M:::::::::::::::
LRTTVGKPQETFLGFEAIIMRHARLLSGCAKEIE	1	8.94	0.032	2020	89.23	AE003438	TRUE	FALSE	3	3890.5	-1.5	13of132	1.3417	FALSE	FALSE	::::::::::::::::::Oxidation_M::::::::Cys_CAM::::::
LENWQMLRGQNLTQNKSSYPAIEVDYS	11	4.45	0.009	2029	61.73	AE003438	TRUE	FALSE	2	3202.5	1.2	9of 52	1.1218	FALSE	FALSE	:::::Oxidation_M:::::::::::::::::::
DETSGRTEMKMSSTSTSSSSK	4	7.11	0.008	2842	9.26	AE003438	TRUE	FALSE	3	2241.4	-2.4	16of 80	1.3141	FALSE	FALSE	::::::::Oxidation_M:::::::::::::
KKVLIVISFMNAFCIVASSFS	5	9.91	0.004	1732	76.13	AE003438	TRUE	FALSE	3	2378.8	-1.8	18of 80	2.6631	FALSE	FALSE	::::::::::Oxidation_M::::Cys_CAM:::::::

TSTVFGKVSKFRHLKGTPGH	9	11.73	0.002	1010	26	AE003438	TRUE	FALSE	3	2185.5	-0.5	21of 76	1.5722	FALSE	FALSE	::::::::::::::::::::
SPAAAAAT	3	6.02	0.137	2800	12.4	AE003439	TRUE	FALSE	1	659.7	-0.8	4of 14	0.6704	FALSE	FALSE	::::::::
LASNGRSNGAVSDSGSDKK	8	9.89	0.094	2733	9.9	AE003439	TRUE	FALSE	3	1850.9	-0.9	19of 72	2.102	FALSE	FALSE	::::::::::::::::
YEVMEKGYEDLQHRYDALLQMYGEK	7	4.43	0.041	1745	57.86	AE003439	TRUE	FALSE	3	3142.5	3	159	2.3357	FALSE	FALSE	::::Oxidation_M::::::::::::::::Oxidation_M:::::
NSADSDAEKDHDNGKDKEK	7	4.38	0.187	1917	-5.1	AE003440	TRUE	FALSE	2	2104.1	0.7	99	1.3702	FALSE	FALSE	::::::::::::::::::::
YTIDNYELETNFLPD	13	2.84	0.145	1820	45.3	AE003440	TRUE	FALSE	2	1848	-0.6	17of 28	3.1722	FALSE	FALSE	::::::::::::::
VTAQMGRHVQHSHGVKIYVESP	5	9.72	0.013	1571	33.33	AE003440	TRUE	FALSE	3	2461.8	2.7	9of 84	1.1323	FALSE	FALSE	::::::::::::::::::::
GGGGGGGGGSGGGGGGGGANLR	9	11.05	0.05	2511	5.5	AE003441	TRUE	FALSE	2	1473.5	-1.1	8of 40	0.8981	FALSE	FALSE	::::::::::::::::::::
TPPYLYSAPVGPNNFFFSDMLR	14	6.64	0.032	692	68.43	AE003441	TRUE	FALSE	3	2550.9	1.2	13of 84	1.1941	FALSE	FALSE	::::::::::::::::::Oxidation_M:::
LAIGYVRKR	3	11.39	0.056	1196	23.5	AE003442	TRUE	FALSE	2	1076.3	-1.8	9of 16	1.5085	FALSE	FALSE	::::::::::
LIPRKAMRLVNDFFDTGVD	11	6.99	0.052	314	56.43	AE003442	TRUE	FALSE	3	2224.6	-2.5	21of 72	1.6735	FALSE	FALSE	::::::Oxidation_M::::::::::::
ARRGLKLVLISRSLEKLNVVAK	3	12.15	0.05	1472	58.7	AE003442	TRUE	FALSE	3	2465	2.1	14of 84	1.2474	FALSE	FALSE	::::::::::::::::::::
VVYEDLLTTVWLEVLRSGNWKHWTKAMR	1	9.63	0.037	1252	86.53	AE003442	TRUE	FALSE	3	3449	-2.9	22of108	2.7727	FALSE	FALSE	::::::::::::::::::::::::Oxidation_M::
EVLENRGEIRSNTDDLMR	15	4.29	0.037	872	35.03	AE003442	TRUE	TRUE	3	2164.4	-1.1	19of 68	1.8903	FALSE	FALSE	::::::::::::::Oxidation_M::
TEHEGPMPPLFVGLRSMNISLASMI	11	5.3	0.029	1282	75.29	AE003442	TRUE	FALSE	3	2777.2	-2.1	10of 96	1.096	FALSE	FALSE	::::::Oxidation_M::::::::Oxidation_M::::::Oxidation_M::
ESGGEAKMLAADLDSK	7	4.07	0.027	3384	25.33	AE003442	TRUE	FALSE	3	1622.8	2.4	207	2.0333	FALSE	FALSE	::::::::::::::::
AVVQTLLPSSASDVSALSTGQLLCT	7	3.1	0.026	2018	66.9	AE003442	TRUE	FALSE	3	2519.8	-0.6	13	1.2952	FALSE	FALSE	::::::::::::::::::::::Cys_CAM::
SVTSFMHNNAPIMAKMNDISDTINR	3	7.82	0.025	1463	51.69	AE003442	TRUE	FALSE	3	2841.2	2	18of 96	1.8866	FALSE	FALSE	::::::::::::Oxidation_M:::Oxidation_M:::::::::
PNNNNIGNCKAITTTITTTTTTTT	11	8.97	0.106	1089	29.5	AE003443	TRUE	FALSE	3	2453.6	2.8	11of 88	1.2778	FALSE	FALSE	::::::::Cys_CAM::::::::::::
EPLAKLLCHSTAM	15	7.16	0.073	997	35.73	AE003443	TRUE	FALSE	3	1487.7	0.8	14of 48	1.8754	FALSE	FALSE	::::::::Cys_CAM::::::Oxidation_M:
SGRSMSMPPRPSAAILGSVAMMPPSR	6	12.71	0.07	1310	55.22	AE003443	TRUE	FALSE	3	2705.2	3	22of100	2.2081	FALSE	FALSE	:::::Oxidation_M::Oxidation_M:::::::::::::::::::
QEKGHDRNARMRALAAAAAVPALGA	10	11.23	0.013	2671	41.03	AE003443	TRUE	FALSE	3	2546.9	-1.6	7of 96	0.8184	FALSE	FALSE	::::::::::::::::::::::::
QPDEPHDGVLAFNKGK	9	5.28	0.011	473	21.4	AE003443	TRUE	FALSE	3	1752.9	-1.9	14of 60	1.4847	FALSE	FALSE	::::::::::::::::
SHKLREDHLDAPSTSSCSSHDSPRRI	12	7.42	0.087	1497	22.9	AE003444	TRUE	FALSE	3	2977.1	2.1	17of100	1.6541	FALSE	FALSE	::::::::::::::::Cys_CAM:::::::::
DQFHAQGTEMIITKTGR	1	7.82	0.05	2198	28.33	AE003444	TRUE	FALSE	2	1950.2	0.8	7of 32	1.187	FALSE	FALSE	::::::::Oxidation_M:::::::
ASRNIEKDVRLMRMCLGIWRR	4	11.83	0.048	2778	55.66	AE003444	TRUE	FALSE	3	2662.2	1.4	9of 80	1.0997	FALSE	FALSE	::::::::::::::Cys_CAM::::::
PGDVGTG	15	3.1	0.041	2868	7.2	AE003444	TRUE	FALSE	1	602.6	-0.9	7of 12	1.0944	FALSE	FALSE	::::::::
DSASMVNGVEEFLGEW	4	2.89	0.035	2642	44.63	AE003444	TRUE	FALSE	2	1786.9	-0.7	8of 30	1.19	FALSE	FALSE	:::::Oxidation_M:::::::::::
LKECIRNCTLETSK	14	8.29	0.03	1551	26.6	AE003444	TRUE	FALSE	2	1752.9	-2.5	4of 26	0.7887	FALSE	FALSE	::::Cys_CAM:::Cys_CAM::::::
MRCLSLGTPPVMGGGA	3	9.01	0.005	1217	39.86	AE003444	TRUE	FALSE	2	1620.9	-0.1	7of 30	0.9522	FALSE	FALSE	:::Cys_CAM::::::::Oxidation_M:::::
GNFKSSIRVSNKNNAASGSGGGGAGGGAGGGGGKSKKQTQ	6	11.86	0.049	2270	11.6	AE003445	TRUE	FALSE	3	3594.8	2.1	27of156	1.7963	FALSE	FALSE	::::::::::::::::::::::::::::::::::::
KRSSASA	4	11.49	0.035	2929	0.7	AE003445	TRUE	FALSE	1	706.8	-0.3	6of 12	1.0472	FALSE	FALSE	::::::::
LVPLKPTGELAASILLHLGAALSDPNAVVR	10	7.82	0.3	2184	90.8	AE003446	TRUE	TRUE	3	3037.6	-0.6	34of116	3.5361	FALSE	FALSE	::::::::::::::::::::::::::
ALLSLPTAIADNAGYDSAQLVSELR	1	3.71	0.296	1756	69.5	AE003446	TRUE	TRUE	2	2589.9	0.5	17of 48	2.7862	FALSE	FALSE	::::::::::::::::::::::
RIRRLTGNSGGTAATGGSASVSGGSGTGAEVAAAG	12	12.11	0.197	1532	37.6	AE003446	TRUE	FALSE	3	3063.3	-1.8	13of136	1.2489	FALSE	FALSE	::::::::::::::::::::::::::::::
NERSRMQIFSKCGHFMR	5	11.23	0.112	1771	31.16	AE003446	TRUE	FALSE	3	2185.5	-2.3	20of 64	2.369	FALSE	FALSE	::::::::::Cys_CAM::::::
DSPLLIGLAAHEEDSLNA	13	3.59	0.094	1715	47.1	AE003446	TRUE	FALSE	2	1866	-1.6	6of 34	0.9779	FALSE	FALSE	::::::::::::::::
EDGLDMQR	9	3.71	0.083	2603	14.33	AE003446	TRUE	FALSE	2	964	-1	5of 14	0.8424	FALSE	FALSE	::::::::
RRSQASKSQSHT	7	12.42	0.079	3494	-3.6	AE003446	TRUE	FALSE	2	1373.5	-0.7	114	1.1329	FALSE	FALSE	::::::::::::
SPAAAPSLDDTEVDKK	10	3.97	0.078	2272	20.8	AE003446	TRUE	FALSE	3	1644.8	2.4	15of 60	1.779	FALSE	FALSE	::::::::::::::::
VQAADTVGGSTGLESLTDSDLQTLLQNF	1	2.79	0.071	259	64.9	AE003446	TRUE	FALSE	2	2882.1	2.4	11of 54	1.2936	FALSE	FALSE	::::::::::::::::::::::::::
VEVLTESGLTETVHR	7	4.54	0.061	1837	33.2	AE003446	TRUE	FALSE	2	1670.9	-2.7	26	1.0287	FALSE	FALSE	::::::::::::::::
RKQTPTRPMSFVRALEMADSMEMQSLE	14	7.21	0.055	1516	59.62	AE003446	TRUE	FALSE	3	3203.7	0.5	17of104	1.8507	FALSE	FALSE	::::::::Oxidation_M::::::::::Oxidation_M::::::
ISSQNGESGGGSFDDNSPDVIENG	4	2.76	0.042	1973	28.9	AE003446	TRUE	FALSE	2	2383.4	-1.4	5of 46	0.67	FALSE	FALSE	::::::::::::::::::::::
FDYRQMGAIQIRRDNPVVVASKLR	12	11.22	0.04	1827	56.93	AE003446	TRUE	FALSE	3	2850.3	1.7	18of 92	1.4576	FALSE	FALSE	::::::Oxidation_M:::::::::::::::::
PMNLAKKPQRSVGDSTEK	6	10.32	0.037	2498	18.43	AE003446	TRUE	FALSE	2	1987.3	2.7	10of 34	1.219	FALSE	FALSE	::::::::::::::::::
ESRLPKPPKPPEKPILPYMRYSKR	2	10.68	0.033	1421	43.73	AE003446	TRUE	FALSE	3	2909.5	1.9	9of 92	1.0984	FALSE	FALSE	::::::::::::::::::::::
KQQVQHQQQQQK	12	10.6	0.02	1132	-1.3	AE003446	TRUE	FALSE	3	1536.7	0.5	16of 44	1.4495	FALSE	FALSE	::::::::::::
TMDKAPGQDSNHR	15	7.82	0.019	1870	4.73	AE003446	TRUE	FALSE	3	1457.6	-1.7	17of 48	1.967	FALSE	FALSE	::::::::::::
EQLHTLRIASAQVLCLGQPVASAIRNIPKKRIRR	1	12.24	0.018	114	77.8	AE003446	TRUE	FALSE	3	3895.6	-0.5	17of132	1.3011	FALSE	FALSE	::::::::::::::Cys_CAM:::::::::::::::::
LMGVKHYATLRKMLCTAPSGR	2	10.7	0.015	512	46.56	AE003446	TRUE	FALSE	3	2407.9	1.1	10of 80	1.3674	FALSE	FALSE	::Oxidation_M::::::::::::Cys_CAM::::::
GKVIDAFK	11	9.89	0.015	596	18.3	AE003446	TRUE	FALSE	1	878.1	0.9	5of 14	1.2093	FALSE	FALSE	::::::::
LPQQMQEWNITPSRAAEETR	4	4.56	0.014	2668	40.33	AE003446	TRUE	FALSE	2	2386.6	1.6	13of 38	1.4637	FALSE	FALSE	::::::::::::::::::::
LQAYAVGDVCLVGEKGVGK	5	6.36	0.005	2668	43.6	AE003446	TRUE	FALSE	2	1964.2	-2.6	9of 36	1.2328	FALSE	FALSE	::::::::::Cys_CAM:::::::::
KMKKVKKAEMATRNAEMAAKKA	5	10.91	0.003	2018	20.49	AE003446	TRUE	FALSE	2	2513.1	1.8	11of 42	2.2376	FALSE	FALSE	::Oxidation_M::::::::Oxidation_M::::::::Oxidation_M::::::
SLHDALCVLAA	9	4.94	0	1220	35.8	AE003446	TRUE	FALSE	2	1170.3	0.4	11of 20	1.7289	FALSE	FALSE	::::::::Cys_CAM::::::
SLHDALCVLAA	10	4.94	0	636	35.8	AE003446	TRUE	FALSE	2	1170.3	0.2	9of 20	1.8175	FALSE	FALSE	::::::::Cys_CAM::::::
GELLQVDLKNTDLHKLFALLDHRRSGTVSLK	6	9.76	0.161	1534	74.7	AE003447	TRUE	FALSE	3	3519.1	-3	20of120	2.5331	FALSE	FALSE	::::::::::::::::::::::::::::::
YNRNAALKHMVMRIRR	4	12.41	0.122	1825	32.26	AE003447	TRUE	FALSE	2	2046.5	2	10of 30	1.7484	FALSE	FALSE	::::::::::Oxidation_M:::::::
SDYSFEDVIVMSRAR	11	4.31	0.059	317	37.23	AE003447	TRUE	FALSE	2	1776	0.6	12of 28	1.6994	FALSE	FALSE	::::::::::::::
VERIGMDGTMRKTIINTKIYWPNG	9	10.18	0.046	2069	56.86	AE003447	TRUE	FALSE	3	2811.3	1.1	12of 92	1.3791	FALSE	FALSE	::::::::Oxidation_M:::::::::::::
AEKHTGANMVEM	9	5.3	0.028	1142	17.86	AE003447	TRUE	FALSE	2	1334.5	0.5	9of 22	1.3237	FALSE	FALSE	::::::::Oxidation_M::::
KMVYYSASNPAVIGVMDYN	3	6.58	0.024	1703	49.26	AE003447	TRUE	FALSE	2	2123.4	2.8	12of 36	1.3403	FALSE	FALSE	::::::::::::::::::::
SSGRCILDSW	2	6.1	0.023	2382	25.7	AE003447	TRUE	FALSE	2	1181.3	0.8	10of 18	1.6344	FALSE	FALSE	:::::Cys_CAM::::::
YLFLTSKPVIYLVNLSDKDFIR	13	9.47	0.479	1703	79.6	AE003448	TRUE	TRUE	3	2646.1	0.9	31of 84	5.1503	FALSE	FALSE	::::::::::::::::::::
YLFLTSKPVIYLVNLSDKDFIR	14	9.47	0.293	1698	79.6	AE003448	TRUE	TRUE	3	2646.1	0	23of 84	3.1079	FALSE	FALSE	::::::::::::::::::::
LYFLSPLFLIPLWKWGKK	2	10.45	0.208	516	83.5	AE003448	TRUE	FALSE	3	2250.8	2.1	23of 68	1.938	FALSE	FALSE	::::::::::::::::::
LKGGYPARLKKVLIVTAPLWFK	5	11.03	0.04	1245	70.4	AE003448	TRUE	FALSE	3	2500.1	1.5	21of 84	2.3887	FALSE	FALSE	::::::::::::::::::::
SFPSPSMWKTLQESCAMWRHRVALVDQ	11	8.97	0.113	2753	69.26	AE003449	TRUE	FALSE	3	3265.7	1.2	7of104	1.0585	FALSE	FALSE	::::::Oxidation_M::::::Cys_CAM::::::::::::
PRNPYQRKTSVGMGAPSAPPPPPTPPLPPPK	8	11.51	0.099	2741	47.53	AE003449	TRUE	TRUE	3	3247.8	-0.7	17of120	1.6425	FALSE	FALSE	::::::::::::Oxidation_M:::::::::::::::::
VRSVPVVR	13	12.41	0.036	675	20.6	AE003449	TRUE	FALSE	1	912.1	2.5	6of 14	1.1078	FALSE	FALSE	::::::::
SDMERSR	4	7.05	0.024	2912	5.23	AE003449	TRUE	FALSE	2	897	-2.7	4of 12	0.673	FALSE	FALSE	:::Oxidation_M:::::
IDDPQLLTIIADINR	11	3.6	0.022	2671	49.8	AE003449	TRUE	FALSE	3	1711	0.1	11of 56	1.0908	FALSE	FALSE	::::::::::::::::
FRAIKTKWAPKFAK	13	11.8	0.014	2241	32	AE003449	TRUE	FALSE	2	1693.1	0.9	7of 26	0.8782	FALSE	FALSE	::::::::::::::
PTFGTTGSGSP	10	6.02	0.007	1982	12.9	AE003449	TRUE	FALSE	2	1009.1	1.7	9of 20	0.959	FALSE	FALSE	::::::::::::
APTSPNRRSRRASRK	2	13.01	0.049	1261	2.3	AE003450	TRUE	FALSE	2	1741	-1.9	5of 28	0.9006	FALSE	FALSE	::::::::::::::::
GMSLPVGDQS	10	3.1	0.026	2684	20.03	AE003450	TRUE	FALSE	2	1007.1	-0.7	9of 18	1.4238	FALSE	FALSE	::Oxidation_M:::::::::
GQGRSISGGYVQRGASVGGSSGYGR	1	11.16	0.021	778	23.8	AE003450	TRUE	FALSE	3	2401.6	1.5	26of 96	1.6367	FALSE	FALSE	::::::::::::::::::::::
ILRRLLRLLCELIAGKGRVLQLLK	11	11.97	0.017	1261	91.4	AE003450	TRUE	TRUE	3	2846.6	1.4	20of 92	1.7286	FALSE	FALSE	::::::::::Cys_CAM:::::::::::::
ENVLLVRRNTGGR	14	12.11	0.188	1007	24.5	AE003451	TRUE	FALSE	2	1484.7	1.5	10of 24	1.6113	FALSE	FALSE	::::::::::::::
HNNHEQNQPSNISADASHHTSPSSR	15	6.49	0.158	665	4.7	AE003451	TRUE	FALSE	3	2753.8	0.9	9of 96	1.0418	FALSE	FALSE	::::::::::::::::::::::
TLSGSSMQETGSSATSLLAAGG	3	3.3	0.141	1953	36.73	AE003451	TRUE	FALSE	2	2030.2	-0.4	11of 42	1.2373	FALSE	FALSE	::::::Oxidation_M:::::::::::::::
RQVSSSNNNTSNHKNNSKRC	8	11.48	0.084	2097	-3.9	AE003451	TRUE	FALSE	3	2333.4	2.4	22of 76	2.241	FALSE	FALSE	::::::::::::::::::::Cys_CAM:

ESEADRPGSNSSSTSNNKHSPPAASTTTTTKRR	5	10.57	0.082	2669	6.3	AE003451	TRUE	FALSE	3	3461.6	1.8	13of128	1.4679	FALSE		FALSE	::::::::::::::::::::::::::::::::
RMKFPQSQIDLMYSK	8	10.18	0.059	2089	36.16	AE003451	TRUE	FALSE	2	1889.2	2.8	15of 28	1.7697	FALSE		FALSE	::::::::::Oxidation_M::::
SSYVKAVEMLNCLQAEVVSMLTPDDIR	3	4.07	0.054	1912	75.16	AE003451	TRUE	FALSE	3	3102.5	-2.8	20of104	1.6559	FALSE		FALSE	::::::::Oxidation_M:::Cys_CAM:::::::Oxidation_M::::::::
FNSNVDFKSVVSY	6	6.68	0.051	2771	32	AE003451	TRUE	FALSE	2	1506.7	-2.4	9of 24	1.2968	FALSE		FALSE	::::::::::::
EVHSRNSTVVSCPRCQKLFQNRSN	8	10.12	0.048	2504	31.5	AE003451	TRUE	FALSE	3	2905.1	0.3	19of 92	1.77	FALSE		FALSE	::::::::::Cys_CAM:::Cys_CAM:::::::::
HRHYHGQGHGHGHGNGHSS	12	9.85	0.043	915	-13	AE003451	TRUE	FALSE	2	2057.1	2.5	4of 36	0.5986	FALSE		FALSE	::::::::::::::::::
IDLSGAGVVSSGRSSSSSGATS	10	6.79	0.032	1932	27.3	AE003451	TRUE	FALSE	3	1883	1.9	17of 80	1.2667	FALSE		FALSE	::::::::::::::::::::
PQMAPVVPRTVIRTTNPTNPAQTQDRVSGGPMSTLGELL	8	10.8	0.008	2345	79.66	AE003451	TRUE	FALSE	3	4132.7	-0.6	16of152	1.6098	FALSE		FALSE	::::::::::::::::::::::::::::::::::
MLRMASLDLTPNTANMAVGNNR	5	10.89	0.006	1863	51.29	AE003451	TRUE	FALSE	3	2407.8	1.7	20of 84	2.0777	FALSE		FALSE	::::Oxidation_M:::::::::::::::::
FGAGSAGGAGGGGGGGGGGGGSSGGS	15	6.02	0.001	1243	9.9	AE003451	TRUE	FALSE	2	1697.6	0.4	13of 48	1.2874	FALSE		FALSE	::::::::::::::::::::::::
NKTDGPGGGGGGDADDF	7	3.43	0.132	1145	9.6	AE003452	TRUE	FALSE	2	1480.4	-1.6	5	1.5172	FALSE		FALSE	::::::::::::::::
RFAYNTGPLMGMATAFTLTTLVATNARGKDDK	5	10.18	0.102	2540	69.86	AE003452	TRUE	FALSE	3	3467	2	22of124	1.6183	FALSE		FALSE	::::::::::Oxidation_M::Oxidation_M:::::::::::::::::::
FRDKSAIAEQLNKKYLKCWQ	2	9.96	0.091	464	43.1	AE003452	TRUE	FALSE	3	2527.9	2.2	17of 76	2.4913	FALSE		FALSE	::::::::::::::::::Cys_CAM:::
MLISCTMAVAFILNLYSGRTIFQDVVNAVGNRR	6	9.87	0.068	1674	103.86	AE003452	TRUE	FALSE	3	3732.4	-0.4	26of128	2.694	FALSE		FALSE	:::::Cys_CAM:::::::::::::::::::::::::::
FFGLYCFHYNSK	4	8.81	0.06	2861	38.8	AE003452	TRUE	TRUE	2	1583.8	1.7	8of 22	1.2325	FALSE		FALSE	:::::Cys_CAM:::::::
PAHQAAAVSSK	13	10.1	0.018	1164	10.4	AE003452	TRUE	FALSE	1	1067.2	-0.4	12of 20	2.3595	FALSE		FALSE	::::::::::::
KKGSYPSCSGARAPGLAADMYFQ	10	9.51	0.013	1726	39.53	AE003452	TRUE	FALSE	3	2479.7	1.1	20of 88	2.3076	FALSE		FALSE	:::::::Cys_CAM::::::::::Oxidation_M::::
PLPPPSNDSGESSETSAKICK	5	4.45	0.007	1920	25.1	AE003452	TRUE	FALSE	2	2202.3	-0.3	11of 40	1.7649	FALSE		FALSE	:::::::::::::::::::Cys_CAM:::
GRGRPISLIDALFIP	9	10.89	0.14	1180	50.9	AE003453	TRUE	FALSE	3	1626	-1.2	18of 56	1.9429	FALSE		FALSE	::::::::::::::::
SITKEDYHTPLPDNR	15	5.28	0.109	573	21.1	AE003453	TRUE	FALSE	3	1786.9	1.6	18of 56	1.649	FALSE		FALSE	::::::::::::::::
FIVDQTEKFSQQLVEGMNK	11	4.45	0.106	105	45.03	AE003453	TRUE	FALSE	2	2258.6	-2.8	5of 36	0.7851	FALSE		FALSE	::::::::::::::::Oxidation_M:::
SSKENVFNDPR	11	7.02	0.09	2649	12.1	AE003453	TRUE	FALSE	2	1293.4	0.5	6of 20	0.9839	FALSE		FALSE	::::::::::::
TMPNQMRHLQMQQQLTMPRK	12	12.42	0.079	2621	37.52	AE003453	TRUE	FALSE	2	2515	0.3	8of 38	1.3819	FALSE		FALSE	::::::::::::::::Oxidation_M::::
RGVGGGGGGGGPGGRGR	11	12.71	0.062	2680	3	AE003453	TRUE	FALSE	2	1311.4	-0.7	8of 30	0.7757	FALSE		FALSE	::::::::::::::::
AMRLEGSKIMPMR	4	11.33	0.059	1570	33.49	AE003453	TRUE	FALSE	2	1552.9	2	10of 24	1.435	FALSE		FALSE	::Oxidation_M::::::::Oxidation_M::
TDLEQQNAVLEQHVDNTK	7	4.06	0.035	1057	26.6	AE003453	TRUE	TRUE	2	2083.2	2.3	179	0.892	FALSE		FALSE	::::::::::::::::
STRGAIEGAKK	2	10.59	0.033	227	7.7	AE003453	TRUE	FALSE	2	1118.3	2.6	12of 20	1.722	FALSE		FALSE	::::::::::
SPRVMLRSTPVTAASASS	14	12.41	0.021	719	32.63	AE003453	TRUE	FALSE	2	1819.1	1.8	6of 34	1	FALSE		FALSE	::::::::::::::::
SMRRLMNVIYITVRL	8	12.11	0.019	3359	54.56	AE003453	TRUE	FALSE	3	1898.3	2.3	9of 56	1.2144	FALSE		FALSE	::Oxidation_M:::Oxidation_M:::::::::
AMRLEGSKIMPMRNLLPSGR	6	12.12	0.006	2966	50.09	AE003453	TRUE	FALSE	2	2274.8	2.3	4of 38	0.5869	FALSE		FALSE	::Oxidation_M:::::::::::::::::
AQLEESNNERRAYKRKM	7	10.17	0.006	1089	18.03	AE003453	TRUE	FALSE	3	2140.4	-1.9	41	2.1472	FALSE		FALSE	::::::::::::::Oxidation_M:
LTYSITSRHVSPKLATFFGEF	1	9.72	0.002	143	58.7	AE003453	TRUE	FALSE	2	2402.8	-0.9	11of 40	1.2187	FALSE		FALSE	::::::::::::::::::
QALLSQF	13	6.02	0.002	851	26.1	AE003453	TRUE	FALSE	1	806.9	-0.1	7of 12	1.8352	FALSE		FALSE	::::::::
MAQPIPELKENEQKRI	14	7.16	0.208	1450	32.33	AE003454	TRUE	FALSE	2	1925.3	1.5	7of 30	1.2115	FALSE		FALSE	::::::::::::::::
GSNQSLTLNMGSILGGAAGTE	8	3.3	0.196	1751	40.73	AE003454	TRUE	FALSE	3	1979.2	-0.3	22of 80	1.985	FALSE		FALSE	::::::::::::::::::
FQSQHSTQETPTTSTTLPAKLAR	11	10.09	0.149	776	31.6	AE003454	TRUE	FALSE	3	2531.8	0.9	16of 88	1.5355	FALSE		FALSE	::::::::::::::::::::
ASSQPMSNDAAAILEKSQK	13	6.99	0.143	519	26.73	AE003454	TRUE	FALSE	3	1993.2	-0.9	18of 72	1.5996	FALSE		FALSE	:::::Oxidation_M:::::::::::
IALICYGQLHDSQ	13	4.94	0.107	416	37.8	AE003454	TRUE	FALSE	2	1518.7	-1.5	8of 24	1.0132	FALSE		FALSE	:::::Cys_CAM:::::::
LLIAEDFPDLELLLEEA	14	2.77	0.098	1584	74.9	AE003454	TRUE	FALSE	2	1944.2	-2.7	9of 32	1.502	FALSE		FALSE	::::::::::::::::
QHYFIDRDGGMFRHIL	3	7.92	0.079	2271	43.73	AE003454	TRUE	FALSE	2	2006.3	1.2	11of 30	1.2495	FALSE		FALSE	::::::::::::::::
EEFQDSATAAATQQR	12	3.83	0.073	821	18.9	AE003454	TRUE	FALSE	3	1653.7	-0.2	19of 56	1.9141	FALSE		FALSE	::::::::::::::
EKAYFGRSMDPRSEVKVQVIGQWVDQHR	2	9.63	0.062	2449	52.03	AE003454	TRUE	FALSE	2	3347.8	2.3	8of 54	1.3117	FALSE		FALSE	::::::::::::::::::::::::::
RKSTDLNMGVWARNAGGQNQRTVSM	12	12.12	0.051	1308	36.66	AE003454	TRUE	FALSE	3	2795.1	1	10of 96	1.1263	FALSE		FALSE	:::::::Oxidation_M:::::::::::::::::
AIGQAIKSSPTDSEELLRSDRLPVIVGG	7	4.56	0.03	1645	63	AE003454	TRUE	FALSE	3	2910.3	-2.4	174	1.687	FALSE		FALSE	::::::::::::::::::::::::::
PRDSDQSLDALDERSH	9	4.12	0.025	2663	18.2	AE003454	TRUE	FALSE	2	1841.9	-1.2	10of 30	1.3748	FALSE		FALSE	::::::::::::::::
MPSAPTHTAEEAHLLGTMPVDPMDDIELRSVQ	1	4.06	0.023	1402	72.59	AE003454	TRUE	FALSE	3	3506.9	2.2	13of124	1.1862	FALSE		FALSE	:Oxidation_M:::::::::::::::::::::::::::::
TKVKPKRQPKR	13	12.45	0.007	870	-8.882E-16	AE003454	TRUE	TRUE	3	1366.7	1.2	15of 40	1.6675	FALSE		FALSE	::::::::::::
YNRMTNACHKKCIPPRYSESELGK	6	9.5	0.004	2196	32.63	AE003454	TRUE	FALSE	3	2941.3	1.1	10of 92	1.0335	FALSE		FALSE	:::::::Cys_CAM::::Cys_CAM:::::::::::
QAASLNHSNSSAGPSPVPPSSG	7	7.85	0.164	1877	22	AE003455	TRUE	FALSE	2	2050.1	-2.4	18	1.8341	FALSE		FALSE	::::::::::::::::::::
RGRSSINNAPVDLAPSKVSFEKFVKPHESVINIGI	14	10.32	0.102	735	73.5	AE003455	TRUE	FALSE	3	3808.4	-1.2	24of136	2.5051	FALSE		FALSE	::::::::::::::::::::::::::::::::
LYEQGILQKY	11	6.81	0.087	2568	31.4	AE003455	TRUE	FALSE	2	1255.5	-1.6	6of 18	0.9532	FALSE		FALSE	::::::::::
CYQCNSTSDPNCAASPA	8	3.1	0.058	2568	21.3	AE003455	TRUE	FALSE	2	1903.9	-2.2	7of 32	0.9275	FALSE		FALSE	:Cys_CAM:::Cys_CAM::::::::Cys_CAM::::::
WKCRPFARRLKDTQEGEDR	7	9.9	0.035	1425	28	AE003455	TRUE	FALSE	3	2449.7	2.8	10	1.755	FALSE		FALSE	:::Cys_CAM:::::::::::::::
SSSCDDIAKVSSCL	15	3.89	0.196	1080	25	AE003456	TRUE	FALSE	2	1529.6	2.9	12of 26	1.2668	FALSE		FALSE	::::Cys_CAM::::::::Cys_CAM::
KLSEKDKHDKEY	1	7.7	0.113	968	4.5	AE003456	TRUE	FALSE	2	1520.7	1	12of 22	2.7045	FALSE		FALSE	::::::::::
LATPSPSSMQAPQKRGGSGSGGGGGGG	14	11.49	0.073	1055	18.53	AE003456	TRUE	FALSE	3	2360.5	-0.1	23of104	2.504	FALSE		FALSE	::::::::Oxidation_M:::::::::::::::::
IPSDDAGNSTSQFKR	11	6.9	0.058	1512	16.4	AE003456	TRUE	FALSE	3	1623.7	2.8	20of 56	1.5087	FALSE		FALSE	::::::::::::::::
LKKHKQVDFILDNAGYE	6	7.71	0.048	2279	35.5	AE003456	TRUE	FALSE	2	2019.3	2.8	12of 32	1.438	FALSE		FALSE	::::::::::::::::
ERERQLVEHVGALERD	12	4.77	0.03	1807	28.7	AE003456	TRUE	FALSE	2	1937.1	-2.2	9of 30	1.461	FALSE		FALSE	::::::::::::::::
TCTNKGNCWLYDPLSM	11	5.95	0.026	1413	39.93	AE003456	TRUE	FALSE	2	1977.1	-0.7	12of 30	1.7102	FALSE		FALSE	::Cys_CAM::::::Cys_CAM::::::::Oxidation_M:
DDQLQLKNSALDELEKQLER	4	4.07	0.008	2305	40.8	AE003456	TRUE	FALSE	2	2386.6	-1	8of 38	1.099	FALSE		FALSE	::::::::::::::::::::
SRLSCERAGTRFNVR	6	11.93	0.005	1358	23.9	AE003456	TRUE	FALSE	2	1810	1.7	11of 28	1.6428	FALSE		FALSE	:::::Cys_CAM:::::::::::
IQGHNTEQEQ	11	4.25	0	2517	7.3	AE003456	TRUE	FALSE	2	1184.2	-2.8	3of 18	0.6404	FALSE		FALSE	::::::::::
VPGSSAVASAVASTAT	10	6.02	0.12	1193	27.2	AE003457	TRUE	FALSE	2	1376.5	-1.2	11of 30	1.4344	FALSE		FALSE	::::::::::::::::
YCFAIDRGGTFTDV	10	3.89	0.112	2448	38.3	AE003457	TRUE	FALSE	3	1622.7	0.3	17of 52	1.6406	FALSE		FALSE	::Cys_CAM:::::::::::
LIILVPHLR	11	11.05	0.107	1514	43.4	AE003457	TRUE	FALSE	2	1074.4	2.6	8of 16	1.0589	FALSE		FALSE	::::::::
SNEERQKLTLIQPQTIAAASRIQGVTPSTIVR	1	11.23	0.094	227	65.1	AE003457	TRUE	FALSE	3	3508	-2.2	15of124	1.6283	FALSE		FALSE	::::::::::::::::::::::::::::
PSPQTKSPNPVASEKINKTLSVTGIRGEDVVLK	10	10.16	0.093	2527	53.8	AE003457	TRUE	FALSE	3	3492	1.5	21of128	2.0307	FALSE		FALSE	::::::::::::::::::::::::::::
ETKPEPRGRQKRR	15	11.97	0.074	2189	-1.11E-16	AE003457	TRUE	FALSE	3	1638.9	-2	7of 48	1.163	FALSE		FALSE	::::::::::::
LPADMRFFSTTGLELNNV	6	4.08	0.035	2122	55.33	AE003457	TRUE	FALSE	2	2042.3	1.1	5of 34	0.7561	FALSE		FALSE	:::::Oxidation_M:::::::::::
QEVINGEGKLVAAYK	1	7	0.027	2101	31	AE003457	TRUE	FALSE	2	1619.9	-1.3	6of 28	0.9328	FALSE		FALSE	::::::::::::::
ALLHPALRNVKTINIGGGLGRKRPLLGVPRSGMNPTK	4	12.89	0.02	1967	78.13	AE003457	TRUE	FALSE	3	3920.7	1.7	10of144	1.0909	FALSE		FALSE	:::::::::::::::::::::::::::::::Oxidation_M:::::
RNANLSEPDQDLPPNLNVNLSP	5	3.71	0.015	1388	44.9	AE003457	TRUE	FALSE	3	2418.6	-1.1	14of 84	1.394	FALSE		FALSE	::::::::::::::::::::
HYVNITFNEVAVDGSPFR	1	5.22	0.132	497	44.7	AE003458	TRUE	FALSE	3	2066.3	-1	19of 68	1.767	FALSE		FALSE	::::::::::::::::
EEPPKSVTSPKTQPPPKTTPVAVRH	12	10.32	0.11	1548	26.2	AE003458	TRUE	FALSE	2	2710.1	0.3	7of 48	0.8303	FALSE		FALSE	::::::::::::::::::::::
FFQEPWTELIMHDDFEE	1	3.44	0.108	705	59.43	AE003458	TRUE	FALSE	3	2214.4	-1	21of 64	2.4435	FALSE		FALSE	::::::::::::::::
IEIRDIEDQGNGSLTDPATDLLK	13	3.69	0.104	598	50.8	AE003458	TRUE	FALSE	3	2514.7	-0.6	23of 88	2.4635	FALSE		FALSE	::::::::::::::::::::::
SGKTRSSPLHDSKHRSESPSMHF	4	10.58	0.098	2451	14.33	AE003458	TRUE	FALSE	2	2612.8	-0.3	12of 44	1.6842	FALSE		FALSE	::::::::::::::::::Oxidation_M:::
AFYTKESHPLHKVTIMPRGPSLGHTAYIPEK	5	9.87	0.097	2142	60.63	AE003458	TRUE	FALSE	3	3508.1	-1.3	24of120	1.974	FALSE		FALSE	::::::::::::::::::::::::::::
MVSQMLNLQKHQKQR	6	11.64	0.082	2449	24.56	AE003458	TRUE	FALSE	2	1870.2	1.7	7of 28	1.1965	FALSE		FALSE	::::::::::::::
KEMYIVNR	10	9.72	0.066	885	20.23	AE003458	TRUE	FALSE	1	1069.3	0.8	8of 14	1.5754	FALSE		FALSE	:::Oxidation_M:::::::
MRDKYLSNVAELR	2	9.72	0.061	1078	30.43	AE003458	TRUE	FALSE	2	1611.9	1.5	8of 24	1.5102	FALSE		FALSE	:Oxidation_M:::::::::::
CFYRSPAAALDLC	14	5.95	0.052	311	41.4	AE003458	TRUE	FALSE	2	1544.7	0.5	8of 24	0.9693	FALSE		FALSE	:Cys_CAM::::::::::Cys_CAM:

RLVDDVLAKVTSMLPSMRDVRVTL	5	10.08	0.051	2094	69.96	AE003458	TRUE	FALSE	3	2748.3	2	19of 92	1.7476	FALSE	FALSE	::::::::::::Oxidation_M::::Oxidation_M::::::::
EAMLEKTYAVVLAVAHSVFHHMGAFKL	6	7.96	0.034	2516	77.96	AE003458	TRUE	FALSE	3	3001.6	0.8	18of104	1.6513	FALSE	FALSE	::::::::::::::::::::::::::
SKAPTMNSPEAAKENTSEKPQVK	4	9.67	0.028	1479	16.83	AE003458	TRUE	TRUE	3	2489.8	2.9	22of 88	2.7627	FALSE	FALSE	::::::Oxidation_M::::::::::::::::
FHLHPGRSRAPAFEANLSNVVLSRTLAR	6	12.41	0.028	2016	63.7	AE003458	TRUE	FALSE	3	3118.6	2.1	14of108	1.4438	FALSE	FALSE	::::::::::::::::::::::::::
IKRVIVQVDYKGVREIMKVCRDK	7	10.3	0.026	1129	50.93	AE003458	TRUE	FALSE	3	2834.4	-0.6	121	1.3009	FALSE	FALSE	::::::::::::::::::Cys_CAM::::
QGMGQGQGQGQGQGMAGMNRQQSMQKR	8	12.42	0.02	3372	18.62	AE003458	TRUE	FALSE	3	2745	-0.6	14of 96	1.3289	FALSE	FALSE	:::Oxidation_M::::::::Oxidation_M:::Oxidation_M::::::Oxidation_M::::
ELGLSLSPNEIGCTIADLIQGQYP	14	2.95	0.018	1995	69.1	AE003458	TRUE	FALSE	2	2589.9	2.1	11of 46	1.3894	FALSE	FALSE	::::::::::::Cys_CAM::::::::::::
LPVIHDGKQSPTAVTSLLARSAAITTANMIVG	14	10.09	0.017	1653	77.23	AE003458	TRUE	FALSE	3	3234.8	-0.9	9of124	1.159	FALSE	FALSE	::::::::::::::::::::::::::::::
AELMAMQLDLCNKALEKRHSNNANH	14	7.32	0.009	2116	44.86	AE003458	TRUE	FALSE	3	2910.3	-2.3	16of 96	1.6392	FALSE	FALSE	::::::::::Cys_CAM:::::::::::::::
PTTEPTPAGAAGGAER	14	4.27	0.004	1443	16.8	AE003458	TRUE	FALSE	2	1483.6	-0.4	12of 30	1.2776	FALSE	FALSE	::::::::::::::::
LHWAASAKNNMR	14	11.49	0.002	796	22.23	AE003458	TRUE	FALSE	2	1399.6	-1.9	7of 22	1.0042	FALSE	FALSE	::::::::::::
IGHASMLPIVEHFGYADHMMNSWR	10	6.31	0	2217	64.89	AE003458	TRUE	FALSE	2	2817.2	3	5of 46	0.8955	FALSE	FALSE	::::::::::::::::::Oxidation_M::::::
SSVPEAEELKIVESS	10	3.8	0.116	2538	31	AE003459	TRUE	FALSE	3	1604.8	1.7	14of 56	1.5151	FALSE	FALSE	::::::::::::::::
YNRVPTAPTPRKQHLQKRR	8	12.42	0.088	2859	17.5	AE003459	TRUE	FALSE	2	2347.7	1.2	12of 36	2.1589	FALSE	FALSE	::::::::::::::::::
PTSSPVSFGAPTTNAAK	11	10.1	0.058	378	23.4	AE003459	TRUE	FALSE	3	1633.8	2	17of 64	1.6891	FALSE	FALSE	::::::::::::::::::
SQTATYSTTLGGVQSPLLMGGG	14	5.93	0.035	1175	44.13	AE003459	TRUE	FALSE	2	2143.4	0.9	10of 42	1.2899	FALSE	FALSE	::::::::::::::::::Oxidation_M::::
GPGGVGGGGGGGGGGGMRGNDGGGMR	6	10.89	0.014	1212	13.06	AE003459	TRUE	FALSE	3	2021.1	-1.3	20of 96	1.5287	FALSE	FALSE	::::::::::::::::Oxidation_M::::::::Oxidation_M::
PEKLVYVDELLDHLEEN	7	3.82	0.013	1693	48.9	AE003459	TRUE	FALSE	2	2056.3	-1.6	424	0.9672	FALSE	FALSE	::::::::::::::::::
HTGNPYAER	9	7.77	0.004	2707	6.7	AE003459	TRUE	FALSE	2	1045.1	-2.5	8of 16	1.0492	FALSE	FALSE	::::::::::
HELGRAHTPRVPAGRPDR	5	11.93	0.002	2975	18	AE003459	TRUE	FALSE	3	2023.3	0.9	7of 68	0.8737	FALSE	FALSE	::::::::::::::::::::
AITLIPGVLETGLFVNMAHK	11	7.82	0.268	1625	65.83	AE003460	TRUE	TRUE	2	2125.6	1.2	17of 38	2.8158	FALSE	FALSE	::::::::::::::::::::::
SDTKKRYGRRMKGSPLIVLDFPQFYFGGK	3	10.68	0.06	2895	61.03	AE003460	TRUE	FALSE	2	3394	2.9	9of 56	1.173	FALSE	FALSE	::::::::::::::::::::::::::::
GGGGKPKKDKK	9	10.71	0.005	659	-9.1	AE003460	TRUE	TRUE	2	1100.3	1.6	10of 20	1.4029	FALSE	FALSE	::::::::::::
RYLKKVSLRDWLRVVSTAKDTF	2	10.87	0.002	525	55.8	AE003460	TRUE	FALSE	3	2683.2	-2.6	9of 84	1.0378	FALSE	FALSE	::::::::::::::::::::
LAYTQPNEQDEESLHK	12	4.16	0.001	1439	23.8	AE003460	TRUE	FALSE	2	1903	0.7	8of 30	1.0191	FALSE	FALSE	::::::::::::::
MAFAYFAAQMLGAFIGYGLLMV	12	5.87	0.137	2833	95.99	AE003461	TRUE	FALSE	3	2402.9	2.5	8of 84	1.17	FALSE	FALSE	:Oxidation_M::::::::::::::::::::
GAVGVGVGVGMGMALGAR	9	11.05	0.049	698	43.16	AE003461	TRUE	FALSE	3	1575.9	0	25of 68	2.0234	FALSE	FALSE	::::::::::Oxidation_M::::::::
LAYTNTNTAFSHTVAALAR	11	9.85	0.045	964	42.1	AE003461	TRUE	FALSE	3	2023.3	2.9	16of 72	1.5569	FALSE	FALSE	::::::::::::::::::
LASKLHRAHSEMSATPNSSMTDNQR	4	10.09	0.03	2563	28.06	AE003461	TRUE	FALSE	2	2787.1	2.8	5of 48	0.808	FALSE	FALSE	::::::::::Oxidation_M::::::::::::
KGEITLIEIGTTRGEAFLFDVQSCPAMVTDGGLK	14	4.29	0.028	1532	86.93	AE003461	TRUE	FALSE	3	3672.2	2.2	15of132	1.3966	FALSE	FALSE	::::::::::::::::::::Cys_CAM::Oxidation_M:::::::::
VCKEEFQSLFRCK	10	8.29	0.008	2129	31.7	AE003461	TRUE	FALSE	2	1731.9	-2.8	4of 24	0.7106	FALSE	FALSE	::Cys_CAM::::::::Cys_CAM::
PEEFAQRK	13	7.1	0.005	1903	11.6	AE003461	TRUE	FALSE	2	1005.1	2.3	4of 14	0.6236	FALSE	FALSE	::::::::
EFLEQKCNFCGRYGASINCKMNCR	5	8.3	0.231	2038	48.53	AE003462	TRUE	FALSE	3	3044.3	1	8of 92	1.2216	FALSE	FALSE	::::::Cys_CAM::Cys_CAM::::::::Cys_CAM::::Cys_CAM::
GGTKASTAPSVATAAVVSVSSGATVPAAASK	5	10.6	0.143	1410	43.4	AE003462	TRUE	FALSE	3	2703	2.6	27of120	2.0962	FALSE	FALSE	::::::::::::::::::::::::::::
FNSMASTVEQSLGQVIKTTAAQNSSRPNSLSLVSK	4	10.59	0.088	2411	62.83	AE003462	TRUE	FALSE	3	3683.1	2.4	12of136	1.2185	FALSE	FALSE	::::::::::::::::::::::::::::::
NLIFDGNLSHQ	6	4.94	0.075	2447	28.2	AE003462	TRUE	FALSE	2	1258.4	2.1	10of 20	2.0346	FALSE	FALSE	::::::::::::
IVQQPDGQSPIAAIPQLQIQPSPQHSR	4	7.85	0.074	1777	53.4	AE003462	TRUE	FALSE	3	2935.3	-1.9	19of104	2.3365	FALSE	FALSE	::::::::::::::::::::::::::
HLDSTGVILEMVTAPIKDYLRKRNDT	10	7.73	0.051	476	58.13	AE003462	TRUE	FALSE	3	3003.4	-2.4	11of100	1.3157	FALSE	FALSE	::::::::::Oxidation_M:::::::::::::::
FNNDTNQLVGHEMELNMHDG	1	4.06	0.049	2117	36.56	AE003462	TRUE	FALSE	2	2348.5	-2.3	5of 38	0.7533	FALSE	FALSE	::::::::::::Oxidation_M::::Oxidation_M::::
LAKTNNTMILPSNPGD	8	6.76	0.041	2187	32.23	AE003462	TRUE	FALSE	2	1702.9	-2	10of 30	1.461	FALSE	FALSE	::::::::Oxidation_M:::::::::
DDKNSENATDANQVAHMYQSQDQV	4	3.77	0.031	2043	22.13	AE003462	TRUE	FALSE	3	2709.8	-2.1	9of 92	1.3097	FALSE	FALSE	::::::::::::::::::::::::
EKKMNLTVKTIRKKQK	5	11.19	0.029	1333	14.53	AE003462	TRUE	FALSE	2	1974.5	1.6	10of 30	1.3033	FALSE	FALSE	::::::::::::::::
GAKLCVVKTHRKRQPMEMVGVSQI	7	10.82	0.023	2075	44.66	AE003462	TRUE	FALSE	3	2770.3	2.4	79	1.4435	FALSE	FALSE	:::::Cys_CAM::::::::::Oxidation_M:::::::::
NPFLGIDDRETLTK	1	4.31	0.019	2312	32.9	AE003462	TRUE	FALSE	2	1619.8	2.9	4of 26	0.6888	FALSE	FALSE	::::::::::::::
CLTSVRGRSGKFVLHRMGVMSQINKKR	11	12.42	0.019	1233	48.36	AE003462	TRUE	FALSE	3	3163.7	-1	16of104	1.5509	FALSE	FALSE	:Cys_CAM::::::::::::::::Oxidation_M:::::::::
TFIERRPLMDEK	14	7.14	0.016	1116	30.83	AE003462	TRUE	FALSE	2	1551.8	-1.6	8of 22	0.8338	FALSE	FALSE	::::::::Oxidation_M::::
KMFVNTTHCVRDAHQKG	8	9.91	0.011	2673	19.83	AE003462	TRUE	FALSE	2	2046.3	-0.5	9of 32	1.1885	FALSE	FALSE	::Oxidation_M::::::Cys_CAM:::::::::
EDYAWTNVAGSRRSHRK	14	10.39	0.007	1561	17	AE003462	TRUE	FALSE	3	2034.2	2.5	22of 64	1.8383	FALSE	FALSE	::::::::::::::::::
SRSRVAGGGGGGGGGGSSGGNSSS	6	12.41	0.006	2335	1.4	AE003462	TRUE	FALSE	2	1909.9	3	10of 46	1.1188	FALSE	FALSE	::::::::::::::::::::::::
EASWTMRDRLK	15	10.09	0.004	1397	22.83	AE003462	TRUE	FALSE	1	1393.6	0.5	5of 20	0.8859	FALSE	FALSE	::::::::::::
MSYDV	10	3.1	0	2407	15.03	AE003462	TRUE	FALSE	1	630.7	-1.3	4of 8	0.6776	FALSE	FALSE	:Oxidation_M:::::
YLEWAFAQHGEATPIPSIQPYPGVFVGDLSQLNR	10	4.43	0.17	1144	95.8	AE003463	TRUE	FALSE	3	3803.3	-2.4	13of132	1.5999	FALSE	FALSE	::::::::::::::::::::::::::::::
SIEPHLEPVLHPNR	14	6.03	0.162	424	31.2	AE003463	TRUE	TRUE	3	1638.9	0.1	17of 52	1.5799	FALSE	FALSE	::::::::::::::
PWPIGGFSR	14	11.05	0.11	1741	27.1	AE003463	TRUE	TRUE	2	1017.2	2.1	5of 16	0.9079	FALSE	FALSE	::::::::::
NIILKAGQRVMVLKSAK	5	11.73	0.107	2611	42.63	AE003463	TRUE	FALSE	2	1870.4	-1.3	10of 32	1.3256	FALSE	FALSE	::::::::::::::::
PASSCS	9	5.33	0.088	1456	6	AE003463	TRUE	FALSE	1	608.6	0.5	4of 10	0.5675	FALSE	FALSE	:::::Cys_CAM::
SSRMRALAEAGGI	12	10.89	0.066	1753	26.13	AE003463	TRUE	FALSE	3	1335.5	2.9	15of 48	1.1561	FALSE	FALSE	::::Oxidation_M:::::::::
AAATAAAISRRLKASSSGGDK	12	11.47	0.051	1792	23.7	AE003463	TRUE	FALSE	2	1990.2	2.5	8of 40	1.0924	FALSE	FALSE	::::::::::::::::::::
LMRYRAHVLHSLLLGFVQRRS	10	12.41	0.024	1206	63.43	AE003463	TRUE	FALSE	3	2554.1	-1.4	23of 80	2.2199	FALSE	FALSE	::::::::::::::::::::
PRVAALPLNMR	14	12.41	0.023	366	32.93	AE003463	TRUE	FALSE	2	1238.5	-2.1	9of 20	1.27	FALSE	FALSE	::::::::::
KSPNGASHSPIKTEK	5	10.32	0.018	1536	5.3	AE003463	TRUE	FALSE	2	1581.8	1.8	9of 28	1.3325	FALSE	FALSE	::::::::::::::::
SSDSTDAEFLQRLVSIRHNQTASSR	2	7.86	0.014	106	37.7	AE003463	TRUE	FALSE	2	2807	1.1	6of 48	1.0105	FALSE	FALSE	::::::::::::::::::::::
NPKERFTRAYNLMLVHAFHLSSPADQIQEGFSK	4	9.63	0.014	1374	72.43	AE003463	TRUE	TRUE	3	3850.3	1.5	24of128	2.3618	FALSE	FALSE	::::::::::Oxidation_M:::::::::::::::::::
STGGSGGNSSPDSGK	10	6.76	0.164	916	-1.9	AE003464	TRUE	FALSE	1	1295.3	-0.4	14of 28	1.921	FALSE	FALSE	::::::::::::::
MSPICMQPKKSR	4	10.59	0.155	2832	19.86	AE003464	TRUE	FALSE	2	1463.8	-2.3	5of 22	0.8239	FALSE	FALSE	:::::Cys_CAM:::::::
IRGNFTESTLIIVSVMDSDLNPLVASLLPRLL	4	4.31	0.081	2338	112.83	AE003464	TRUE	FALSE	3	3499.1	2.7	20of124	1.8323	FALSE	FALSE	::::::::::::::::::::::::::::
IVWNMIKNVSTVNH	7	10.1	0.081	2008	38.53	AE003464	TRUE	FALSE	2	1656	-3	333	1.1394	FALSE	FALSE	::::::::::::::
PLGTASLAQVHK	10	10.1	0.08	728	23.2	AE003464	TRUE	FALSE	2	1222.4	1.9	11of 22	1.2419	FALSE	FALSE	::::::::::::
TRHAMGYSRGQL	9	11.14	0.06	1285	16.83	AE003464	TRUE	FALSE	2	1377.6	0.5	4of 22	0.7368	FALSE	FALSE	::::::::::::
QTRSANTNGALKK	15	11.64	0.035	839	6.9	AE003464	TRUE	FALSE	1	1389.6	0.4	10of 24	1.7335	FALSE	FALSE	::::::::::::
RPPVKASYPKPISNWEGV	12	10.18	0.016	2112	35.8	AE003464	TRUE	FALSE	3	2026.3	0.3	17of 68	1.5949	FALSE	FALSE	::::::::::::::::
HTTVIKDMCADCGADLR	2	5.19	0.003	1592	32.03	AE003464	TRUE	FALSE	2	1980.1	-1.3	6of 32	0.8174	FALSE	FALSE	::::::Oxidation_M:Cys_CAM:::Cys_CAM::::::
CIPVR	2	9.01	0.002	2224	16.4	AE003464	TRUE	FALSE	1	644.8	-2.2	4of 8	0.4779	FALSE	FALSE	:Cys_CAM:::::
LEGNLRDAIDMNLLGTRRALNVAKEMKQLEAF	12	7.21	0.196	2191	84.26	AE003465	TRUE	FALSE	3	3632.2	0.7	25of124	2.3821	FALSE	FALSE	::::::::::::::::::::::::::::
GTQGRQSNGGGSSRRSYHG	13	12.11	0.119	274	-1.4	AE003465	TRUE	FALSE	2	1950	0.8	6of 36	1.1167	FALSE	FALSE	::::::::::::::::::
AYQGRDTLTASTFCARTGGKDS	11	8.87	0.095	2749	27.8	AE003465	TRUE	FALSE	3	2364.5	0.8	8of 84	0.9412	FALSE	FALSE	::::::::::::Cys_CAM:::::::::
GRGGSGQKTRPR	15	12.71	0.088	492	-2.3	AE003465	TRUE	FALSE	2	1257.4	0.7	9of 22	1.1105	FALSE	FALSE	::::::::::::
AKTIANKAGKPVPYAATSNCR	11	10.45	0.082	1185	26.2	AE003465	TRUE	FALSE	2	2219.5	0.5	5of 40	0.7928	FALSE	FALSE	::::::::::::::::::Cys_CAM:::
MHEFVVAMHLVYQTLQK	13	7.89	0.059	728	52.26	AE003465	TRUE	FALSE	3	2091.5	0.9	18of 64	1.5076	FALSE	FALSE	:Oxidation_M:::::::::::::::
MLEERVEANRLKQEEKRKEQL	15	7.28	0.056	1451	34.73	AE003465	TRUE	FALSE	3	2674	1.3	9of 80	1.1868	FALSE	FALSE	:Oxidation_M:::::::::::::::::
VMQEGGFQCGRFDL	11	4.08	0.054	1421	37.53	AE003465	TRUE	FALSE	2	1660.8	1.2	9of 26	1.0936	FALSE	FALSE	::Oxidation_M::::::Cys_CAM::::::
DLLRQIHNFVNGP	2	7.85	0.053	521	34.8	AE003465	TRUE	FALSE	2	1523.7	-1.3	8of 24	1.2104	FALSE	FALSE	::::::::::::
CHKEISQFQNCYK	11	8.28	0.041	2527	19.2	AE003465	TRUE	FALSE	3	1742.9	-2	6of 48	0.8615	FALSE	FALSE	:Cys_CAM::::::::Cys_CAM:::

TAMNNTTNTTSNSASTSGT	3	6.02	0.032	2301	10.33	AE003465	TRUE	FALSE	2	1861.9	-2.1	7of 36	1.0094	FALSE	FALSE	::::::::::::::::::
FVKTVNIMDDTILVPCRLMDRQIGDSTDIIPATGK	2	4.47	0.027	2441	92.76	AE003465	TRUE	TRUE	3	3967.6	3	15of136	1.5311	FALSE	FALSE	:::::::Oxidation_M::::::::Cys_CAM:::Oxidation_M::::::::::::::::
VIESAGQQGTGTFIR	4	6.98	0.021	1579	30.8	AE003465	TRUE	FALSE	2	1564.7	-0.6	11of 28	1.24	FALSE	FALSE	::::::::::::::::
IRDQCHMQEVTI	6	5.22	0.018	2892	27.13	AE003465	TRUE	FALSE	2	1546.7	1.7	5of 22	0.8244	FALSE	FALSE	:::::Cys_CAM::Oxidation_M::::::
ASSFIRK	12	11.49	0.015	1395	14.4	AE003465	TRUE	TRUE	1	809	1.4	5of 12	1.1059	FALSE	FALSE	::::::::
GTVKPNINLLNATGTAAAAAASAASAASATGGEEPKQK	4	9.76	0.008	2191	49.7	AE003465	TRUE	TRUE	3	3440.8	2.3	24of144	1.6234	FALSE	FALSE	::::::::::::::::::::::::::::::::::::
NLENFVEKKLYECKKKYVDIPKDEGQRYG	4	8.68	0.007	2532	49.8	AE003465	TRUE	FALSE	3	3593	-1.5	21of112	1.8972	FALSE	FALSE	:::::::::::::Cys_CAM::::::::::::::::
ADREKNAGEKDQYLMDLRSLQRRNQELI	4	7.16	0	2163	49.53	AE003465	TRUE	FALSE	3	3391.8	0.3	19of108	2.3729	FALSE	FALSE	::::::::::::::::::::::::::::::
TPTPAASPDDFGMLDTSMLSSTFEDECPTMVRPSK	5	3.69	0.102	1900	72.69	AE003466	TRUE	FALSE	3	3853.2	0.1	9of136	1.34	FALSE	FALSE	:::::::::::::::::::Oxidation_M::::::::Cys_CAM:::Oxidation_M::::::
EQKSMKEEGSDQPRSLN	12	4.65	0.023	776	12.93	AE003466	TRUE	FALSE	3	1964.1	-2.4	17of 64	1.8243	FALSE	FALSE	::::::::::::::::
YIMSMVNMGCYSG	7	5.32	0.001	1475	39.19	AE003466	TRUE	FALSE	2	1545.7	-2.9	5	1.2902	FALSE	FALSE	:::::Oxidation_M:::Oxidation_M::Cys_CAM::::
FRPYDLRVPMVYVPK	7	10.04	0.105	1155	48.63	AE003467	TRUE	TRUE	2	1881.3	1	17	2.5528	FALSE	FALSE	::::::::::::::::
SSSSSSYSGGES	1	3.3	0.098	2362	3.6	AE003467	TRUE	FALSE	2	1122	2	15of 22	1.9625	FALSE	FALSE	::::::::::::
LELRGNPYPSLAADHSQNRNLLHNVLLDEARK	2	7.9	0.097	2033	67.7	AE003467	TRUE	FALSE	3	3656.1	-2.5	13of124	1.2096	FALSE	FALSE	::::::::::::::::::::::::::::::
TRTQLSASASKLADIIDDER	2	4.46	0.09	64	36	AE003467	TRUE	FALSE	2	2191.4	1.8	7of 38	1.0303	FALSE	FALSE	::::::::::::::::::::
LKKIFIANEK	13	10.32	0.085	2494	27.2	AE003467	TRUE	TRUE	2	1204.5	1.6	4of 18	0.8191	FALSE	FALSE	::::::::::
GVPGSVNPPK	9	10.1	0.081	1098	12.7	AE003467	TRUE	FALSE	2	952.1	1.8	10of 18	1.5791	FALSE	FALSE	::::::::::
KKSKRALRNEVEALQDMV	8	10.32	0.075	2933	29.83	AE003467	TRUE	FALSE	2	2132.5	2.2	8of 34	1.2139	FALSE	FALSE	:::::::::::::::Oxidation_M::
SSSSSSYSGGES	4	3.3	0.073	2986	3.6	AE003467	TRUE	FALSE	2	1122	2.9	15of 22	1.7898	FALSE	FALSE	::::::::::::
RQERTYDKENYIDF	7	4.56	0.064	1715	23.8	AE003467	TRUE	FALSE	2	1878	-2.7	98	1.1354	FALSE	FALSE	::::::::::::::
VFESMSSCSGRVFFKASSSTSVSEAPKESIK	1	8.9	0.051	1613	55.63	AE003467	TRUE	FALSE	3	3358.7	-1.2	21of120	2.3512	FALSE	FALSE	:::::::Cys_CAM::::::::::::::::::::
RTSKQKRNLSLDNNRHQPAG	8	12.14	0.051	1807	10.5	AE003467	TRUE	FALSE	3	2321.6	2.7	21of 76	2.5712	FALSE	FALSE	::::::::::::::::::::
AMGAAQGGLGAAAGAGGQFGAHGGGAAK	4	10.1	0.041	2505	35.33	AE003467	TRUE	FALSE	2	2286.5	-0.5	12of 54	1.4553	FALSE	FALSE	::Oxidation_M:::::::::::::::::::::::::
EFFSLLTSSSSIKAAAAAAAN	5	6.95	0.04	2844	51.8	AE003467	TRUE	FALSE	2	2058.3	2.9	10of 40	1.0693	FALSE	FALSE	::::::::::::::::::::
PQDLVKSPTDISKKK	12	10.16	0.038	1519	16.7	AE003467	TRUE	FALSE	2	1685	2.7	6of 28	1.1002	FALSE	FALSE	::::::::::::::
YRDIEMEVTEDEKSY	8	3.82	0.015	2324	29.43	AE003467	TRUE	FALSE	2	1908	2.1	5of 28	0.9449	FALSE	FALSE	::::::::::::::
LEARRMHYHMGGSAANGNA	5	9.85	0.012	2493	25.36	AE003467	TRUE	FALSE	2	2044.3	-0.1	10of 36	1.3773	FALSE	FALSE	::::::::::::::::
REHKQTQNDLKSAGTGGLH	7	9.89	0.012	1975	10.3	AE003467	TRUE	FALSE	2	2078.3	-2.1	24	1.3846	FALSE	FALSE	::::::::::::::::
RSAPGGGQLNYGTNSVGNDLMK	9	9.72	0.168	2153	30.13	AE003468	TRUE	TRUE	2	2253.5	2.6	8of 42	1.1208	FALSE	FALSE	:::::::::::::::::::Oxidation_M::
RHMAKEAKRCGKIEKKL	10	10.7	0.117	2066	15.83	AE003468	TRUE	FALSE	2	2084.5	-1.8	10of 32	1.1656	FALSE	FALSE	:::::::::Cys_CAM::::::::
AQETALKTPTKQKHSIIKISSTVKKR	2	11.19	0.094	1773	28.9	AE003468	TRUE	FALSE	3	2923.5	1.6	20of100	2.0529	FALSE	FALSE	::::::::::::::::::::::::
EARRKRELEKRSQVIQRSLPRPTEVNTKILR	3	12.03	0.08	2247	49.2	AE003468	TRUE	FALSE	3	3789.4	2.8	20of120	2.0886	FALSE	FALSE	::::::::::::::::::::::::::
RIMASGGWVEFNRV	9	10.89	0.025	596	40.53	AE003468	TRUE	FALSE	3	1638.9	2.3	11of 52	1.5055	FALSE	FALSE	:::Oxidation_M:::::::::::
MRNENPPLCGRDHLSYR	6	8.9	0.251	1159	28.63	AE003469	TRUE	FALSE	3	2132.3	1.7	23of 64	2.8536	FALSE	FALSE	:Oxidation_M::::::::Cys_CAM::::::::::
MTDIDAVQLDRKFR	3	6.99	0.138	2116	34.03	AE003469	TRUE	FALSE	2	1709	1.2	7of 26	1.1642	FALSE	FALSE	::::::::::::::
SFDGGSNHPPGLGMSSGAEKRSER	9	7.83	0.103	2447	22.13	AE003469	TRUE	FALSE	3	2461.6	0	19of 92	1.4405	FALSE	FALSE	::::::::::::::::::::
FCLQNVGVVAGDSRDEEGR	14	4.07	0.065	643	35.8	AE003469	TRUE	FALSE	3	2109.2	1.7	21of 72	2.3609	FALSE	FALSE	::Cys_CAM:::::::::::::::
RPKMESPDDDEVQEINSAVNSPPYPL	5	3.76	0.039	2750	46.93	AE003469	TRUE	FALSE	3	2929.2	-2.6	13of100	1.5981	FALSE	FALSE	::::::::::::::::::::::
TVRVSMLGKAVYDWIRRMMYY	3	10.22	0.031	1747	67.89	AE003469	TRUE	FALSE	3	2656.2	-0.3	16of 80	1.9632	FALSE	FALSE	:::::::::::::::::Oxidation_M:::
LMATYGFMGGFGFGMIYLPAVVAVGYYFETK	9	6.73	0.014	2250	112.59	AE003469	TRUE	FALSE	3	3451.1	2	24of120	2.5464	FALSE	FALSE	::Oxidation_M::::::Oxidation_M::::::Oxidation_M:::::::::::::::
NASAPPEPPR	2	6.98	0.177	194	11.7	AE003470	TRUE	TRUE	2	1036.1	-1.2	10of 18	1.361	FALSE	FALSE	::::::::::
LEEHTHRRKLRL	10	11.23	0.157	956	19	AE003470	TRUE	FALSE	2	1588.9	2	11of 22	1.8199	FALSE	FALSE	::::::::::::
VNVNGGAIALGHPIGASGAR	10	11.05	0.449	900	37.8	AE003471	TRUE	TRUE	2	1832.1	2.7	22of 38	3.9056	FALSE	FALSE	::::::::::::::::::
LTTLLGIPLAAIACGGNHSFLISK	15	8.97	0.277	1825	76.8	AE003471	TRUE	TRUE	2	2468.9	0.6	19of 46	2.2706	FALSE	FALSE	:::::::::::::Cys_CAM::::::::::
EVFARLLDSLSDGIEVGGASASVVARVRER	14	4.73	0.182	1127	72.7	AE003471	TRUE	FALSE	3	3160.6	0.4	12of116	1.2478	FALSE	FALSE	::::::::::::::::::::::::::::
LRLQKVLEQQQLQ	10	10.09	0.121	506	35.8	AE003471	TRUE	FALSE	2	1624.9	2.8	5of 24	0.9957	FALSE	FALSE	::::::::::::::
MILLWNEPSLVNAPAHVE	8	4.25	0.098	2688	62.73	AE003471	TRUE	FALSE	2	2034.4	0.1	11of 34	1.7095	FALSE	FALSE	::::::::::::::::::
RASGAAATKSNSPDWGNHRAK	8	11.47	0.087	1636	11.9	AE003471	TRUE	FALSE	3	2183.4	-2.5	20of 80	2.4525	FALSE	FALSE	::::::::::::::::::::
VVSVESEQTSKNQR	4	7.1	0.039	1883	13.9	AE003471	TRUE	FALSE	2	1591.7	0.4	10of 26	1.1073	FALSE	FALSE	::::::::::::::
LWHDEPVTTPVPNFLR	15	5.22	0.03	1701	48.3	AE003471	TRUE	FALSE	2	1922.2	2	11of 30	1.5499	FALSE	FALSE	::::::::::::::::
CSMELALQRNPIHFA	2	7.16	0.025	997	43.43	AE003471	TRUE	FALSE	1	1788	2.9	9of 28	1.7372	FALSE	FALSE	:Cys_CAM:::::::::::::
GEIPPGRYTKDLKR	2	10.18	0.022	829	20.1	AE003471	TRUE	FALSE	2	1630.9	-1.9	13of 26	1.9584	FALSE	FALSE	::::::::::::::
ASRELHRLHSAPGRSR	10	12.41	0.018	702	15.9	AE003471	TRUE	TRUE	3	1831.1	-2.8	13of 60	1.3717	FALSE	FALSE	::::::::::::::::
LYKEILKEHPNYIDC	11	5.35	0.017	2729	40.1	AE003471	TRUE	FALSE	3	1936.2	-1.3	7of 56	1.0049	FALSE	FALSE	:::::::::::::::Cys_CAM:
RSMPKVHKFLQRPGWFEMQGYN	8	10.7	0.005	2243	50.06	AE003471	TRUE	FALSE	3	2738.2	2.6	12of 84	1.3074	FALSE	FALSE	::::::::::::::::::::
SFDIENPDWEDAMLGHIAQLPKMK	11	4.2	0.002	2784	62.46	AE003471	TRUE	FALSE	3	2803.2	1	14of 92	1.2619	FALSE	FALSE	:::::::::::Oxidation_M:::::::::::
ENFANDQSLYFK	13	4.08	0.002	550	28.6	AE003471	TRUE	TRUE	3	1476.6	-2.7	18of 44	1.9945	FALSE	FALSE	::::::::::::
RVPLSPPPNYSPHPLTPPPSYTER	3	9.59	0.145	2403	46	AE003472	TRUE	FALSE	2	2701.1	0.9	9of 46	1.3503	FALSE	FALSE	::::::::::::::::::::::
SSGFFVDLSQ	15	3.1	0.133	2160	28.7	AE003472	TRUE	FALSE	2	1087.2	0.4	7of 18	1.2394	FALSE	FALSE	::::::::::
FFMTLEKTRLLVTPFMLSFHLMNSR	8	11.33	0.129	2172	92.99	AE003472	TRUE	FALSE	2	3077.7	0.5	9of 48	1.3322	FALSE	FALSE	:::::::::::::::Oxidation_M:::::::::
AYGVYSHGKVSKLPR	12	10.34	0.119	2342	23.4	AE003472	TRUE	FALSE	3	1662.9	1.7	12of 56	1.3345	FALSE	FALSE	::::::::::::::
MGCVYLCMWLGAWGIMLGYRFR	14	9.01	0.115	1336	93.19	AE003472	TRUE	FALSE	3	2742.3	0.1	13of 84	1.69	FALSE	FALSE	:::Cys_CAM:::Cys_CAM:::::::::::::
DLLGLEGLKEVTAHALK	8	5.35	0.105	2501	45.8	AE003472	TRUE	FALSE	2	1808.1	-1.7	7of 32	1.0481	FALSE	FALSE	::::::::::::::::
SKFDEANPIVSGGASIEDFREKQCESPSIKRR	12	6.63	0.092	2704	48.7	AE003472	TRUE	FALSE	3	3640	0.8	8of124	0.8801	FALSE	FALSE	:::::::::::::::::::::::Cys_CAM:::::::::
LSRLFPNFSK	10	11.49	0.084	598	30.7	AE003472	TRUE	FALSE	2	1209.4	2.7	8of 18	1.3251	FALSE	FALSE	::::::::::
YTAIVSDKLQGKYNAKTKKY	4	10.15	0.073	1554	27.9	AE003472	TRUE	FALSE	3	2320.7	-2	19of 76	2.6045	FALSE	FALSE	::::::::::::::::
TGGGSGAAAKGATKSGATPGSSGAPR	4	11.64	0.07	2828	10.6	AE003472	TRUE	FALSE	3	2160.3	2.4	14of100	1.3506	FALSE	FALSE	::::::::::::::::::::::::
SSSSLDSSFSNGSGSGGNSLQRR	10	10.89	0.06	2094	19.3	AE003472	TRUE	FALSE	2	2275.3	-2.4	8of 44	1.1327	FALSE	FALSE	::::::::::::::::::
MDALVGKNAKRRRK	14	12.15	0.049	2887	13.93	AE003472	TRUE	FALSE	2	1660	-1.7	7of 26	0.9005	FALSE	FALSE	:Oxidation_M:::::::::::::
VQANYLYLLPIFSSKDIVAQMP	1	6.62	0.04	510	76.83	AE003472	TRUE	FALSE	3	2512	-1.3	15of 84	1.3205	FALSE	FALSE	::::::::::::::::::
KAKSKDAKKKVLAGKKPQSVLAK	2	11.06	0.034	690	16.9	AE003472	TRUE	FALSE	3	2453	-2.9	10of 88	1.1547	FALSE	FALSE	::::::::::::::::::::
PLTRTDKQAYIMWIRNP	11	10.39	0.028	1358	45.23	AE003472	TRUE	FALSE	2	2104.5	0.9	6of 32	0.851	FALSE	FALSE	::::::::::::::::
RPPVERIAVKARSGERTA	5	11.95	0.024	2355	25.3	AE003472	TRUE	FALSE	2	1994.3	2.5	11of 34	1.453	FALSE	FALSE	::::::::::::::::
KKEISPRKESRVSVK	10	10.97	0.022	1856	11.4	AE003472	TRUE	FALSE	2	1772.1	-2.9	8of 28	1.0127	FALSE	FALSE	::::::::::::::::
DVSAQYQGALLLGDVKERV	9	4.31	0.015	1874	46	AE003472	TRUE	FALSE	3	2062.3	-1.9	22of 72	1.8132	FALSE	FALSE	::::::::::::::::::
YEIAIAMPSSTASSSATKVSEVQDQRTNSPGKSK	3	9.56	0.012	2611	41.73	AE003472	TRUE	FALSE	3	3557.9	-0.8	25of132	1.9503	FALSE	FALSE	::::::::::::::::::::::::::::::::
SDTYATLEELINDIDD	8	2.7	0.011	2844	40.9	AE003472	TRUE	FALSE	3	1827.9	0.7	7of 60	0.8374	FALSE	FALSE	::::::::::::::::
ATRRGAVAVSGSQFLHDK	9	11.33	0.01	1488	26.8	AE003472	TRUE	FALSE	2	1901.1	-0.4	8of 34	1.2535	FALSE	FALSE	::::::::::::::::
QPSKEKQRSRE	13	10.58	0.006	880	-1.6	AE003472	TRUE	FALSE	3	1373.5	0.7	15of 40	1.8053	FALSE	FALSE	::::::::::::
EIAQGNMTVGDLVMVNA	3	3.01	0.001	1921	45.86	AE003472	TRUE	FALSE	2	1779	-0.4	8of 32	1.0624	FALSE	FALSE	::::::Oxidation_M:::::::::
MMIIMGVIGLVVVGIIAKRRRI	8	12.71	0	2039	86.59	AE003472	TRUE	FALSE	2	2472.2	2.2	12of 42	2.6132	FALSE	FALSE	::Oxidation_M:::Oxidation_M:::::::::::::::::
GQGFPWAHSTRGKPR	7	12.42	0.165	1816	17.3	AE003473	TRUE	FALSE	2	1682.9	2.6	234	1.2875	FALSE	FALSE	::::::::::::::::
IEVRLKHALNVSHAK	8	10.59	0.126	2545	28.9	AE003473	TRUE	FALSE	2	1716	2.8	9of 28	1.1967	FALSE	FALSE	::::::::::::::::

YDTGNVSQRVMHKHEQESKKLGK	10	9.96	0.089	1881	16.53	AE003473	TRUE	FALSE	3	2701	2.8	17of 88	1.4703	FALSE	FALSE	::::::::::::::::::::::
ELNAPFLVNQIAKSIPPTTAPVTHLVNV	12	7.82	0.08	657	77.9	AE003473	TRUE	FALSE	3	2985.5	-1.6	17of108	1.8204	FALSE	FALSE	::::::::::::::::::::::::
EVKVVGKPKPKVKWLR	14	11.1	0.059	603	30.7	AE003473	TRUE	FALSE	3	1892.4	2.5	16of 60	1.2757	FALSE	FALSE	::::::::::::::
CELKVTPLNQAEPATRAQAER	1	6.53	0.036	1722	36.4	AE003473	TRUE	FALSE	2	2383.6	2.1	14of 40	2.1289	FALSE	FALSE	:Cys_CAM:::::::::::::::
DSLFIPETQAVLCER	14	3.83	0.018	2540	45.5	AE003473	TRUE	FALSE	3	1779	1.4	10of 56	1.0536	FALSE	FALSE	:::::::::::::Cys_CAM:::
SNAMARVGQKIKLEAIVGGIPRPEVYWLHNGK	10	10.44	0.015	1809	72.63	AE003473	TRUE	FALSE	3	3534.2	2.8	20of124	1.6516	FALSE	FALSE	::::::::::::::::::::::::::
NDKCIDDSPDYVISY	2	3.43	0.009	873	31.1	AE003473	TRUE	FALSE	2	1804.9	0.8	5of 28	0.8162	FALSE	FALSE	::::Cys_CAM::::::::::::
LHGVMEAQWQQALAILTTPSQNSI	11	5.13	0.001	222	65.43	AE003473	TRUE	FALSE	3	2654	0.5	15of 92	1.3755	FALSE	FALSE	:::::Oxidation_M:::::::::::::::::::
IRRPMHRIAKEDINEEY	1	7.75	0.119	1976	33.13	AE003474	TRUE	FALSE	2	2171.5	-1.7	10of 32	1.3372	FALSE	FALSE	::::::::::::::::::
FIVLVLRER	10	10.89	0.036	2207	41.6	AE003474	TRUE	FALSE	1	1145.4	1.2	7of 16	1.5239	FALSE	FALSE	::::::::::
VPYGNGSNIALDLDLERG	15	3.71	0.028	768	44.1	AE003474	TRUE	FALSE	3	1904.1	1.3	19of 68	2.2446	FALSE	FALSE	::::::::::::::::::
DGIHVTESTAN	14	4.07	0.026	704	13.8	AE003474	TRUE	FALSE	2	1144.2	1.9	10of 20	1.1817	FALSE	FALSE	::::::::::::
PLVPGDDDALRDLLTPQKS	15	3.88	0.026	1245	43.7	AE003474	TRUE	FALSE	2	2051.3	-2.7	8of 36	0.9702	FALSE	FALSE	::::::::::::::::::
EVVRVMAEFALDLMRTMRR	12	10.73	0.015	2161	60.49	AE003474	TRUE	FALSE	3	2356.8	1.9	14of 72	1.2802	FALSE	FALSE	:::::::::::::Oxidation_M:::Oxidation_M:::
YDVRNYLEKIYK	3	9.36	0.011	995	29.9	AE003474	TRUE	TRUE	2	1604.8	-0.1	10of 22	2.0819	FALSE	FALSE	::::::::::::
PYRYKIRKELFIAPEGMHTGQFVYCGR	5	9.79	0.282	1690	65.83	AE003475	TRUE	FALSE	3	3318.8	1.5	26of104	4.1144	FALSE	FALSE	:::::::::::::::::::::::Cys_CAM:::
PGQENYFESPLGKFFMDIGVGLVQEYVQSDLLRL	1	3.93	0.169	2396	104.93	AE003475	TRUE	FALSE	3	3891.4	0.7	15of132	1.4521	FALSE	FALSE	::::::::::::::::::::::::::::::::
PLVKIKEEPVQSPAPSAAPLPQTAPLCK	3	8.9	0.089	2267	62.4	AE003475	TRUE	FALSE	3	2968.5	1.9	15of108	1.4841	FALSE	FALSE	:::::::::::::::::::::::::Cys_CAM::
NKESLKVKLMVRRPHSQLVEQG	2	10.82	0.075	1637	38.23	AE003475	TRUE	FALSE	3	2594.1	1.1	9of 84	1.3357	FALSE	FALSE	::::::::Oxidation_M::::::::::::
TRGFGMRVVGGKTGADGRLFAY	1	11.29	0.073	2186	44.63	AE003475	TRUE	FALSE	2	2317.7	-1.7	5of 42	0.9827	FALSE	FALSE	::::::::::::::::::::
TVRAGKKMAYLDCILRRKSDGKIIAKGGQVK	10	10.84	0.067	1818	52.63	AE003475	TRUE	FALSE	3	3463.1	1.2	23of120	1.906	FALSE	FALSE	:::::::::::Cys_CAM::::::::::::::::::
NAPSDAKRAAMRLAQEH	10	10.09	0.064	721	20.73	AE003475	TRUE	FALSE	3	1867.1	1.8	20of 64	1.6986	FALSE	FALSE	::::::::::::::::
RVAPITLPEIR	10	10.89	0.051	1812	34.4	AE003475	TRUE	FALSE	3	1265.5	1.7	11of 40	1.2638	FALSE	FALSE	::::::::::::
VQSPAPSAAPLPQTAPLCK	11	8.97	0.051	1791	39.9	AE003475	TRUE	FALSE	2	1934.2	1	8of 36	1.014	FALSE	FALSE	:::::::::::::::::Cys_CAM::
CPLVAMAILPNNFNVDLSSSYNLR	3	6.09	0.039	1485	75.13	AE003475	TRUE	FALSE	3	2710.1	0	18of 92	1.5506	FALSE	FALSE	:Cys_CAM:::::::::::::::::::::
PHGGGNHQHIGK	14	10.1	0.037	2856	-0.4	AE003475	TRUE	FALSE	2	1239.3	2.2	12of 22	1.8944	FALSE	FALSE	::::::::::::
HGLVGTATAYQAMAAQAAAQKAALANIQQQQAAAQ	2	9.72	0.033	2078	62.63	AE003475	TRUE	FALSE	3	3483.9	-2.4	18of136	1.4567	FALSE	FALSE	:::::::::::Oxidation_M:::::::::::::::::::::
TPTGNSTSSNIAKFR	8	11.49	0.031	1755	16.6	AE003475	TRUE	FALSE	2	1581.7	0.9	10of 28	1.309	FALSE	FALSE	::::::::::::::::
GPVGGSMGGGGPALGLGADGAGLGIPTMPR	2	6.79	0.018	1634	59.36	AE003475	TRUE	FALSE	2	2595	0	11of 58	1.4543	FALSE	FALSE	::::::Oxidation_M:::::::::::::::::::::
AQMRVSQGDECTAFVRLFR	11	9.01	0.012	1137	46.13	AE003475	TRUE	FALSE	3	2288.6	-3	19of 72	1.9989	FALSE	FALSE	:::Oxidation_M::::::::Cys_CAM::::::::
GSGSGGSTNSPAHKRQDSDSRLPTNFERGFRR	2	11.83	0.008	1840	22.4	AE003475	TRUE	FALSE	3	3463.7	2.6	25of124	2.3069	FALSE	FALSE	::::::::::::::::::::::::::::
GSQLPDIAMLQNRGALPAVPPSSIPPPMASFT	12	6.79	0	699	83.66	AE003475	TRUE	FALSE	3	3262.8	-2	20of124	1.919	FALSE	FALSE	::::::::::::::::::::::::::::
KVLAFGQLFET	1	6.95	0.208	1164	38.8	AE003476	TRUE	FALSE	1	1253.5	1.8	11of 20	1.9061	FALSE	FALSE	::::::::::::
DRQLAADFIQKHAKQGPLAPEELSR	4	7.8	0.132	1642	46.5	AE003476	TRUE	FALSE	3	2820.2	2.8	8of 96	1.1478	FALSE	FALSE	::::::::::::::::::::::
VRLDATGFTLQRESPGGSIVKEQH	3	7.83	0.072	1980	42.9	AE003476	TRUE	FALSE	2	2626.9	-0.7	14of 46	2.6874	FALSE	FALSE	::::::::::::::::::::::
HMVDNIQPSLGRK	3	10.09	0.055	1125	22.43	AE003476	TRUE	FALSE	3	1495.7	1.2	16of 48	2.0095	FALSE	FALSE	::::::::::::
ILIRAGISRPHLLSFLYNMSSGTHLPESHDDHVK	4	8.05	0.032	2345	80.23	AE003476	TRUE	FALSE	3	3843.4	1.9	9of132	0.8526	FALSE	FALSE	::::::::::::::::::::::::::::
VKFVADEAELCQYL	5	3.83	0.03	2582	45.7	AE003476	TRUE	FALSE	2	1685.9	2.4	7of 26	1.0587	FALSE	FALSE	:::::::::Cys_CAM::::
GQLTKEAAMGQGFDRHLFALRHTAQK	4	10.58	0.02	2982	46.33	AE003476	TRUE	FALSE	3	2929.3	0.2	15of100	1.6145	FALSE	FALSE	::::::::Oxidation_M:::::::::::::::
ECVEKLINEGENEYNLGKYKEEVKK	4	4.65	0.015	2551	40.2	AE003476	TRUE	FALSE	3	3044.4	1.6	15of 96	1.3955	FALSE	FALSE	::Cys_CAM:::::::::::::::::::::
KPSNISVDVSEDE	14	3.59	0.012	1426	18.7	AE003476	TRUE	FALSE	1	1419.5	-2.6	9of 24	1.621	FALSE	FALSE	::::::::::::
ENSSNLETIIADL	15	2.95	0.005	932	34.4	AE003476	TRUE	FALSE	3	1419.5	1.9	12of 48	1.6823	FALSE	FALSE	::::::::::::
AETNVDYLEGMEDYYVDQLLWWK	6	3.38	0.126	1239	74.53	AE003477	TRUE	FALSE	3	2898.2	-1.2	19of 88	1.4044	FALSE	FALSE	:::::::::Oxidation_M:::::::::::
FMLVVFDK	2	6.76	0.102	928	37.93	AE003477	TRUE	FALSE	1	999.3	0.8	9of 14	1.6269	FALSE	FALSE	::::::::
GYAPPQRPLVTKTIQIVQPALK	3	10.71	0.093	1224	53.7	AE003477	TRUE	TRUE	3	2419.9	1.8	19of 84	2.0879	FALSE	FALSE	::::::::::::::::::::
RFGMLYMGPSNNNVMPSACPME	14	6.28	0.077	1624	56.32	AE003477	TRUE	FALSE	3	2536.9	1.2	10of 84	1.5435	FALSE	FALSE	::::::Oxidation_M:::::::Oxidation_M:::Cys_CAM::::
GEMSDKSYSWRNVFSCINLLRILNKLIK	6	10.05	0.064	2711	80.13	AE003477	TRUE	FALSE	3	3386.9	-1.7	14of108	1.6501	FALSE	FALSE	:::::::::::::::Cys_CAM::::::::::::
INSVMQVLFVIPDFQQRFVGTGAERYFK	10	9.72	0.029	1476	86.73	AE003477	TRUE	FALSE	3	3291.8	-1.2	21of108	2.7078	FALSE	FALSE	::::::::::::::::::::::::::::::
PTSQAMVTPK	9	10.1	0.027	793	15.43	AE003477	TRUE	FALSE	2	1060.3	-1.3	9of 18	1.2135	FALSE	FALSE	::::::::::
GKLEGKAVASKFIRP	8	10.83	0.025	1821	28.2	AE003477	TRUE	FALSE	2	1601.9	2.3	8of 28	1.1881	FALSE	FALSE	::::::::::::::::
SVLLACPDLSNVVLLDNSSTECSFNA	13	2.88	0.021	2597	74.1	AE003477	TRUE	FALSE	2	2827	0	5of 50	0.8479	FALSE	FALSE	:::::Cys_CAM::::::::::::::Cys_CAM::::::
VFAMIVVKDESSPHPFEVHAFVCDSR	7	5.22	0.013	1987	67.93	AE003477	TRUE	TRUE	3	3021.4	1.2	245	1.7433	FALSE	FALSE	::::Oxidation_M::::::::::::::::::Cys_CAM::::
ALVAGQSLISQQHPEREQVESLC	10	4.54	0.011	2046	50.1	AE003477	TRUE	FALSE	3	2580.8	-0.9	12of 88	1.1301	FALSE	FALSE	:::::::::::::::::::::::Cys_CAM:
VIGPIVAFHCPVEKCIYHVATKGARSFTSLR	11	9.69	0.01	237	78.1	AE003477	TRUE	FALSE	3	3516.1	-1.2	13of120	1.2448	FALSE	FALSE	:::::::::Cys_CAM::::Cys_CAM:::::::::::::::::
PFGTDVIQR	5	6.79	0.006	2014	22.5	AE003477	TRUE	FALSE	1	1033.2	0.6	10of 16	1.4064	FALSE	FALSE	::::::::::
KSKKAKNVFKVGDGNKGKGK	5	11	0.001	2449	1.3	AE003477	TRUE	FALSE	2	2119.5	1.7	10of 38	1.1323	FALSE	FALSE	::::::::::::::::::
TEMMQDSPIINIMQVQHMP	8	4.07	0.001	2427	52.32	AE003477	TRUE	FALSE	2	2276.7	-2.3	10of 36	1.3159	FALSE	FALSE	::::Oxidation_M::::::::::::Oxidation_M::
DSEPSISSVSTATSSLAGSSKRK	6	9.89	0.159	2248	22.2	AE003478	TRUE	FALSE	2	2283.5	0.4	12of 44	1.7253	FALSE	FALSE	::::::::::::::::::::::
DPIVMGVMVENGIV	15	3.01	0.043	795	48.16	AE003478	TRUE	FALSE	2	1489.8	2.2	12of 26	2.1392	FALSE	FALSE	::::::::Oxidation_M:::::::
LRPGRFDKLIHVPAPDEKSRLALLK	7	10.81	0.037	1667	61.9	AE003478	TRUE	FALSE	3	2871.4	1.9	112	1.6375	FALSE	FALSE	::::::::::::::::::::::
LNERRRMLQLLKLATSAHKLSR	5	12.42	0.008	2720	50.13	AE003478	TRUE	FALSE	3	2652.2	1.8	21of 84	1.7551	FALSE	FALSE	:::::::Oxidation_M:::::::::::::::
PPRPKSEVFLNKQETHPR	9	10.58	0.002	1933	23.7	AE003478	TRUE	TRUE	2	2161.5	-1.4	10of 34	1.6829	FALSE	FALSE	::::::::::::::::
ALSFILLR	14	11.05	0.138	1342	41	AE003479	TRUE	FALSE	1	933.2	0.7	8of 14	1.7394	FALSE	FALSE	::::::::
PLVVRQDAAGNNYSLN	11	6.7	0.112	168	34.1	AE003479	TRUE	FALSE	2	1731.9	-2	6of 30	0.8348	FALSE	FALSE	::::::::::::::::
IPCPAPGAIPYR	3	8.9	0.078	2784	33.1	AE003479	TRUE	FALSE	2	1312.5	-2.6	6of 22	0.8949	FALSE	FALSE	:::Cys_CAM:::::::::
QVLLGPGS	11	6.02	0.067	809	22.6	AE003479	TRUE	FALSE	1	770.9	0.7	8of 14	1.7917	FALSE	FALSE	::::::::
VIELGTIPLPKSSNPKRIEENFNVFDFK	11	7.16	0.03	1160	73.5	AE003479	TRUE	FALSE	3	3233.7	2.4	18of108	1.558	FALSE	FALSE	::::::::::::::::::::::::
YVRRVGVVLERLSFPEMMDMYK	5	9.53	0.002	2026	69.99	AE003479	TRUE	FALSE	2	2752.3	2.4	8of 42	1.1835	FALSE	FALSE	:::::::::::::::::::Oxidation_M::Oxidation_M:::
SHHESKGLQIEPGDTIAIIDGRHE	12	5.19	0.343	2676	36	AE003480	TRUE	FALSE	2	2640.9	2.6	8of 46	1.2804	FALSE	FALSE	::::::::::::::::::::::
SQMSGNIIISGSTDR	12	6.79	0.158	1675	26.13	AE003480	TRUE	FALSE	2	1582.7	-2.8	14of 28	1.609	FALSE	FALSE	:::Oxidation_M:::::::::::
KVGAAGDVVMRSSVGNGSSSSPFGFCWGGAAAM	11	8.97	0.153	1796	64.96	AE003480	TRUE	FALSE	3	3238.5	-0.3	17of128	1.7421	FALSE	FALSE	:::::::::Oxidation_M::::::::::::::Cys_CAM::::::Oxidation_M:
RSAGPEMTPYRNGSARENGGEWDPEDRSRARRP	4	9.83	0.15	3021	31.43	AE003480	TRUE	FALSE	3	3760	2.5	8of128	0.8402	FALSE	FALSE	::::::::::::::::::::::::::::
EKKSKPDRPAPPPPSDDSR	8	9.76	0.142	2337	7.6	AE003480	TRUE	FALSE	2	2105.3	0	6of 36	0.9872	FALSE	FALSE	::::::::::::::::::
QMGRSLPGCSPCQQEVRRMRVMKER	1	11.11	0.136	1210	40.19	AE003480	TRUE	FALSE	3	3094.5	-0.3	19of 96	2.3078	FALSE	FALSE	::::::::Cys_CAM:::Cys_CAM::::::Oxidation_M:::::::
LSSTEAAQLPLDLNREAVEDSRYNLFAMYQKF	5	4.29	0.106	1448	85.43	AE003480	TRUE	FALSE	3	3738.2	-1.7	7of124	0.9307	FALSE	FALSE	:::::::::::::::::::::::::::Oxidation_M:::::
GHLRTNSLMATTGQGPPTEQQMR	2	10.89	0.092	1233	32.06	AE003480	TRUE	FALSE	2	2512.8	1.5	6of 44	0.916	FALSE	FALSE	::::::::::::::::::::::
YPEVVIGR	14	6.89	0.053	939	24.2	AE003480	TRUE	FALSE	1	933.1	1	6of 14	1.1825	FALSE	FALSE	::::::::
ELLVSLIVPIVLFVISS	6	3.3	0.049	1738	85.2	AE003480	TRUE	FALSE	2	1842.3	1.5	11of 32	1.5883	FALSE	FALSE	::::::::::::::::
HQDGDDHPLTIDEILDE	12	3.58	0.015	1475	32.4	AE003480	TRUE	FALSE	2	1963	1.9	10of 32	1.5504	FALSE	FALSE	::::::::::::::::
VGAAGDVVMRSSVGNGSSSSPF	3	6.79	0.01	1859	36.63	AE003480	TRUE	FALSE	2	2069.3	-1.7	9of 42	1.0567	FALSE	FALSE	::::::::::::::::::::
SLHDRKIYLSNGYIIKIGR	1	10.34	0.003	910	46.1	AE003480	TRUE	FALSE	2	2247.6	1.9	9of 36	1.2577	FALSE	FALSE	::::::::::::::::::
RTWLLQSVVLMMLLVELQ	15	6.98	0.13	1012	84.36	AE003481	TRUE	FALSE	3	2173.7	-1.2	21of 68	2.7813	FALSE	FALSE	::::::::::::::::::
VLPQQQLVGHTYNSR	11	9.85	0.094	736	29.6	AE003481	TRUE	FALSE	2	1741	0.6	11of 28	2.4586	FALSE	FALSE	::::::::::::::

GTKTVRLSPEMCAAVRGSGHGPGAR	6	11.23	0.073	1615	31.13	AE003481	TRUE	TRUE	3	2553.9	-2.8	12of 96	1.2037	FALSE	FALSE	::::::::::Cys_CAM::::::::::::
DDQDNPSKEDKPKKVVKNKKQTNK	8	10.11	0.061	3344	-2.3	AE003481	TRUE	FALSE	3	2813.1	-2.1	15of 92	1.5595	FALSE	FALSE	::::::::::::::::::::::
YINLGSDLASSALYHTPIN	8	4.94	0.059	2745	50.8	AE003481	TRUE	FALSE	2	2050.3	-2.9	10of 36	1.1907	FALSE	FALSE	::::::::::::::::::
PPPTKKVVYTPPPPPPPPKK	10	10.63	0.027	1673	29.3	AE003481	TRUE	FALSE	2	2163.7	1.2	12of 38	1.8094	FALSE	FALSE	::::::::::::::::::
FLIAFALVAVASADV	2	3.1	0.024	882	64.8	AE003481	TRUE	FALSE	1	1507.8	0.1	13of 28	1.4903	FALSE	FALSE	::::::::::::::
RMMDSDQEEDAMDQGNGDSIKNSEDVEE	6	3.38	0	2419	32.79	AE003481	TRUE	FALSE	3	3192.2	0.4	16of108	1.5132	FALSE	FALSE	::Oxidation_M:::::::::::::::::::::::
SARLAAYIADCRLMTVQVSKSYTITDWR	3	9.56	0.167	1789	72.63	AE003482	TRUE	FALSE	3	3293.7	2.9	21of108	1.573	FALSE	FALSE	::::::::::Cys_CAM:::Oxidation_M::::::::::::::
GTGKTETCK	2	8.94	0.159	1628	0.9	AE003482	TRUE	FALSE	1	982	0.2	4of 16	0.8319	FALSE	FALSE	:::::::Cys_CAM:::
MRDALDMSLEQGDDDLLTVNIGRIFLDFTQMLH	8	3.8	0.136	2051	102.19	AE003482	TRUE	FALSE	3	3857.4	-3	20of128	2.3202	FALSE	FALSE	:Oxidation_M::::::Oxidation_M:::::::::::::::::::::::::
DCNMPDGESSLVITDGDSMSK	4	3.37	0.086	2326	34.76	AE003482	TRUE	FALSE	2	2259.4	2.1	10of 40	1.3572	FALSE	FALSE	::Cys_CAM:::::::::::::::::
SLRDITRVFQGIVMVPPKRMPDPEKLGR	8	11.31	0.078	2093	68.06	AE003482	TRUE	FALSE	3	3237.9	2.9	23of108	3.2915	FALSE	FALSE	::::::::::::::::::::::::::::
RDYDDDDEHNDKDESHDNK	5	3.94	0.07	2662	-2.1	AE003482	TRUE	FALSE	2	2363.2	1.5	9of 36	1.1297	FALSE	FALSE	::::::::::::::::::
RKPVGSGGAGGATVVGPATVRRQVSWGP	1	12.71	0.067	309	41.3	AE003482	TRUE	FALSE	3	2706.1	-3	17of108	1.4158	FALSE	FALSE	::::::::::::::::::::::::::::
NALANIMING	15	6.02	0.043	899	30.43	AE003482	TRUE	FALSE	1	1031.2	2.9	7of 18	1.1317	FALSE	FALSE	::::::::::
GNILMVGMGGSGRRSSARL	10	12.71	0.04	470	37.66	AE003482	TRUE	FALSE	2	1920.3	2.2	10of 36	1.2586	FALSE	FALSE	::::::::::::::::::
KAAEHKIGHGLTK	12	10.32	0.033	884	10.3	AE003482	TRUE	FALSE	3	1390.6	0.8	18of 48	1.5591	FALSE	FALSE	::::::::::::
KLFTLKIQKRYQCLLKSMSIVQLATYPSHLIR	3	10.68	0.015	1999	93.93	AE003482	TRUE	FALSE	3	3879.7	-2.4	22of124	2.5347	FALSE	FALSE	::::::::::::Cys_CAM:::::::::::::::::
YQCLLKSMSIVQLATY	3	8.81	0.015	2086	53.93	AE003482	TRUE	FALSE	2	1919.3	-0.6	8of 30	0.7495	FALSE	FALSE	:::Cys_CAM:::::::::::::
TVLDDNKKLCLMSGEIMQMTK	14	6.41	0.011	2801	51.29	AE003482	TRUE	FALSE	3	2504.9	-2.9	7of 80	0.9846	FALSE	FALSE	::::::::::Cys_CAM::Oxidation_M::::::Oxidation_M::Oxidation_M:::
AFRRINPRSALLQDAY	9	11.05	0.006	1770	41.8	AE003482	TRUE	FALSE	2	1892.2	-0.6	11of 30	1.9807	FALSE	FALSE	::::::::::::::::
RYLVANRQLEAGETLIR	1	9.84	0.212	1632	45.4	AE003484	TRUE	FALSE	2	2003.3	2.7	17of 32	3.5954	FALSE	FALSE	::::::::::::::::
HKQFWRHFAGNLASGGAAGATSLCFVYPLD	3	8.88	0.04	2327	73.6	AE003484	TRUE	FALSE	3	3280.6	-2.4	22of116	1.8419	FALSE	FALSE	:::::::::::::::::::::::::::::Cys_CAM:::::::
ILNDIAALRAEATDLTR	10	4.31	0.023	2061	48	AE003484	TRUE	FALSE	2	1857.1	1.7	13of 32	1.445	FALSE	FALSE	::::::::::::::::
RYLVANRQLEAGETLIR	2	9.84	0.021	1505	45.4	AE003484	TRUE	FALSE	2	2003.3	2.2	15of 32	2.9312	FALSE	FALSE	::::::::::::::::
SQYKPSPTGVMKARK	14	10.9	0.014	1652	14.13	AE003484	TRUE	FALSE	2	1695	2.2	7of 28	1.0155	FALSE	FALSE	::::::::::Oxidation_M:::::
TTGILLR	5	11.05	0.011	2050	24	AE003484	TRUE	FALSE	1	774	0.6	7of 12	1.4425	FALSE	FALSE	::::::::
LVGDPNLEFVAMPALLPPEVK	1	3.83	0.446	1548	72.53	AE003485	TRUE	TRUE	2	2250.7	1.5	21of 40	4.9294	FALSE	FALSE	::::::::::::::::::::
LQNSRCPPCLREK	2	9.15	0.082	2262	22.4	AE003485	TRUE	FALSE	2	1658.8	1.1	5of 24	0.8848	FALSE	FALSE	::::::Cys_CAM:::Cys_CAM:::::
KPVEKRVNIQEAPPPSKSQPSSPPTGSPMD	2	9.76	0.062	2393	35.23	AE003485	TRUE	FALSE	3	3187.6	1.2	11of116	1.1656	FALSE	FALSE	::::::::::::::::::::::::::::
TSYSQDLGRGGRGRRR	11	12.23	0.06	1584	9.2	AE003485	TRUE	FALSE	2	1823	0.6	8of 30	1.0779	FALSE	FALSE	::::::::::::::::
GIGSAIAKDLVLAGMTVVGLARRVDR	2	11.23	0.027	394	68.73	AE003485	TRUE	FALSE	3	2656.2	2.8	12of100	1.0577	FALSE	FALSE	::::::::::::::Oxidation_M:::::::::::
MQQELPMPL	9	3.3	0.018	541	32.36	AE003485	TRUE	FALSE	2	1103.3	-2.3	9of 16	1.065	FALSE	FALSE	:Oxidation_M:::::::::
INSLSNSNSNSI	2	6.02	0.015	235	19.5	AE003485	TRUE	FALSE	1	1250.3	1.3	12of 22	1.6113	FALSE	FALSE	::::::::::::
EKLMGPPSANAYSMGKGAAAGAAAVGL	7	9.63	0.009	2060	51.66	AE003485	TRUE	FALSE	2	2491.9	-2.5	455	1.3847	FALSE	FALSE	::::::::::::::::::::::::
VLPSAVLEKSQAVNAIPAIVAPPVAVVPVVLAPQPVPVK	9	9.89	0.008	1837	120	AE003485	TRUE	FALSE	3	3879.7	-2.6	23of152	2.8268	FALSE	FALSE	::::::::::::::::::::::::::::::::
VMPGAMSGAMPGAMPGAMSCGMPITGAQHIVPPPVDR	15	7.16	0	64	86.08	AE003485	TRUE	FALSE	3	3727.4	-1.5	15of144	1.421	FALSE	FALSE	::::::::::Oxidation_M:::::Oxidation_M::::::Cys_CAM::Oxidation_M:::::::::::::::
FPEPSQLQPPILGVHNVTFAFPSQKPLFIK	15	9.89	0.288	1657	89.7	AE003486	TRUE	TRUE	3	3379	1	33of116	3.9336	FALSE	FALSE	::::::::::::::::::::::::::
TCDAVAPPPGC	6	3.1	0.233	2731	20.8	AE003486	TRUE	FALSE	2	1145.2	1.4	6of 20	0.7692	FALSE	FALSE	::Cys_CAM::::::::Cys_CAM:
ELISDGYCRD	11	3.71	0.06	2009	23.1	AE003486	TRUE	FALSE	2	1228.3	2.9	5of 18	0.9885	FALSE	FALSE	:::::::Cys_CAM:::
FNQMLFEQNIDGLKRSLSTKSRRMSR	12	11.97	0.058	2587	52.06	AE003486	TRUE	FALSE	2	3176.6	0.6	9of 50	1.1488	FALSE	FALSE	::::Oxidation_M::::::::::::::::::Oxidation_M:::
TFVTFVKVNMFNSTMVTFLK	12	10.6	0.046	1397	68.36	AE003486	TRUE	FALSE	3	2355.9	-0.6	19of 76	1.7178	FALSE	FALSE	::::::::::::::::::
MRHMFKPSMSEL	11	10.09	0.014	614	30.69	AE003486	TRUE	FALSE	2	1542.8	-0.4	10of 22	1.1772	FALSE	FALSE	:Oxidation_M:::Oxidation_M:::::Oxidation_M::::
QSMVVVPTKTK	3	10.6	0.006	1192	19.33	AE003486	TRUE	FALSE	2	1218.5	-1.9	7of 20	1.0282	FALSE	FALSE	::::::::::::
TSEQCVKLFAKIGM	2	8.94	0.167	1346	35.83	AE003487	TRUE	FALSE	2	1628.9	-1.5	6of 26	1.0337	FALSE	FALSE	:::::Cys_CAM::::::::Oxidation_M:
GPGAFIDVVTQAVGRQPITLGK	3	10.09	0.167	2547	51.9	AE003487	TRUE	FALSE	2	2225.6	2.6	10of 42	1.4336	FALSE	FALSE	::::::::::::::::::::::
FKNAVLDIQ	8	6.76	0.117	1915	28.1	AE003487	TRUE	FALSE	1	1048.2	0.1	12of 16	2.5464	FALSE	FALSE	::::::::::
QRLETTGSVHYCAFEPR	5	7.16	0.06	1860	32	AE003487	TRUE	FALSE	2	2052.2	1.4	8of 32	0.9371	FALSE	FALSE	::::::::::::Cys_CAM:::::::
ARAGGQKKLSIANS	9	11.64	0.039	1254	15.3	AE003487	TRUE	FALSE	3	1401.6	0.3	14of 52	1.3859	FALSE	FALSE	::::::::::::::::
GGGGGGGGGGGRPGSGSGGLRPNRRIGR	3	13.01	0.037	1397	12.5	AE003487	TRUE	FALSE	3	2364.6	-2	23of104	2.2092	FALSE	FALSE	::::::::::::::::::::::::::
EDLADLDMEGGEGER	6	3.33	0.016	1900	27.53	AE003487	TRUE	FALSE	2	1652.7	2.4	7of 28	0.9793	FALSE	FALSE	:::::::Oxidation_M:::::::
TLEDRLTITTCYPSPGINPNPIALG	2	4.08	0.004	83	64.9	AE003487	TRUE	FALSE	2	2715	2.1	5of 48	0.9259	FALSE	FALSE	::::::::::Cys_CAM:::::::::::::
RQMTLTNECLDDVSAPSFDQSVFRGSS	13	3.97	0.223	1200	54.43	AE003488	TRUE	FALSE	3	3065.3	2.2	13of104	1.5789	FALSE	FALSE	:::Oxidation_M::::::Cys_CAM:::::::::::::::::
DKPKSGEDQSKEQE	14	4.29	0.079	1295	-1.2	AE003488	TRUE	FALSE	2	1605.7	1.5	5of 26	0.8486	FALSE	FALSE	::::::::::::::
TDECLEDVTMPF	13	2.84	0.023	1267	35.13	AE003488	TRUE	FALSE	2	1457.6	0.3	8of 22	1.043	FALSE	FALSE	::::Cys_CAM:::::::::
PEDVMIDMMEGLFRDVPNLTHKEYLALADLQSR	6	4.16	0.021	1636	93.39	AE003488	TRUE	FALSE	3	3865.4	-2.6	20of128	1.5642	FALSE	FALSE	:::::Oxidation_M:::::::::::::::::::::::::::
RTTLVIAHR	9	12.41	0.101	986	20.4	AE003489	TRUE	FALSE	2	1067.3	-1.2	10of 16	1.258	FALSE	FALSE	::::::::::
GTMDDSGIEV	11	2.88	0.075	2673	19.43	AE003489	TRUE	FALSE	2	1024.1	1.4	5of 18	0.809	FALSE	FALSE	::::::::::
SDDLVRPLPPQLQRSPRKLTVAPAEHNK	8	10.57	0.032	2189	49.4	AE003489	TRUE	FALSE	3	3164.6	0.2	24of108	2.0378	FALSE	FALSE	::::::::::::::::::::::::::
YSDLLK	11	6.68	0	297	18.6	AE003489	TRUE	FALSE	1	738.9	0.2	6of 10	1.2421	FALSE	FALSE	::::::
PQPNGKAAVGGGMGDG	3	6.76	0.143	1509	14.83	AE003490	TRUE	FALSE	2	1413.5	2.5	13of 30	1.1857	FALSE	FALSE	::::::::::::::
IHLNSVPYCSLYDR	10	7.15	0.116	2635	38.7	AE003490	TRUE	FALSE	2	1737.9	3	5of 26	0.8251	FALSE	FALSE	::::::::Cys_CAM:::::::
RSGSGISVKSR	14	12.42	0.074	404	7.9	AE003490	TRUE	FALSE	2	1134.3	-0.9	9of 20	1.2097	FALSE	FALSE	::::::::::
NSQGSGGGGGGGGGGGGAGGGTGSGCGSNAAGSVSPQMPRSGSGISVK	4	10.11	0.031	24	26.23	AE003490	TRUE	FALSE	3	3897	2.1	27of184	2.1543	FALSE	FALSE	:::::::::::::::::::::::::::Cys_CAM::::::::::::Oxidation_M:::::::::::
QETQSILPPDRWKQNRRMQQK	13	11.38	0.025	1315	28.93	AE003490	TRUE	FALSE	3	2685	-0.3	18of 80	1.2793	FALSE	FALSE	:::::::::::::::::::Oxidation_M::::
KEKSLMEEAALAKEQRAAKE	3	7.22	0.018	1156	28.03	AE003490	TRUE	FALSE	3	2261.6	-0.6	21of 76	2.3378	FALSE	FALSE	::::::::::::::::::
NFEEVHQDLNIPVLPPLLVK	2	4.43	0.42	1318	65.9	AE003491	TRUE	TRUE	2	2315.7	0.8	22of 38	4.2367	FALSE	FALSE	::::::::::::::::::
ETEVEVTTGK	15	3.97	0.069	1417	12.8	AE003491	TRUE	FALSE	1	1093.2	1.4	9of 18	1.1303	FALSE	FALSE	::::::::::
YVPPISSFPEASFLGGYGLQDR	12	4.08	0.043	1216	61.3	AE003491	TRUE	FALSE	3	2401.7	-1.3	20of 84	2.1772	FALSE	FALSE	::::::::::::::::::::
GKYFMLPAHLKCHMWVHAR	3	10.19	0.034	1193	50.96	AE003491	TRUE	FALSE	3	2383.8	0.7	19of 72	1.7163	FALSE	FALSE	::::::::::Cys_CAM:::::::::
QSILRNLTTSPFSQK	3	11.49	0.023	1405	31	AE003491	TRUE	FALSE	2	1721	-0.2	5of 28	0.7337	FALSE	FALSE	::::::::::::::
SSDYSDTMTAHDDPLKQSDHSQSSNSLK	10	4.44	0.003	2195	21.83	AE003491	TRUE	FALSE	3	3083.2	-2.5	17of108	1.583	FALSE	FALSE	::::::::::::::::::::::::::
SNPSPVASRGR	9	12.41	0.129	366	8.4	AE003492	TRUE	FALSE	2	1128.2	2.1	13of 20	1.5983	FALSE	FALSE	::::::::::::
RDSETSSTTR	9	7.05	0.099	438	1.3	AE003492	TRUE	FALSE	2	1140.2	0.6	11of 18	1.4648	FALSE	FALSE	::::::::::::
ALATGNGSASASASGINLNGKAK	5	10.6	0.018	2517	28.6	AE003492	TRUE	FALSE	2	2061.3	1.8	11of 44	1.6166	FALSE	FALSE	::::::::::::::::::::
QLAGHQGNFKAGPEPGTVLKKLCPK	4	10.17	0.008	2517	39.8	AE003492	TRUE	FALSE	2	2677.1	0.7	7of 48	0.8886	FALSE	FALSE	:::::::::::::::::::::Cys_CAM:::
IKPLNGVFHIYENDDES	11	4.06	0.149	928	39.3	AE003493	TRUE	FALSE	2	1991.2	2.4	9of 32	1.3248	FALSE	FALSE	::::::::::::::::
FFDESKCVNKEPAVKHLRDR	11	8.9	0.112	2177	33.1	AE003493	TRUE	FALSE	2	2476.8	1.6	11of 38	1.2913	FALSE	FALSE	::::::Cys_CAM:::::::::::::
RLLFKGQGGVGAMGSRM	11	12.42	0.065	2075	37.86	AE003493	TRUE	FALSE	2	1766.1	2	9of 32	0.964	FALSE	FALSE	::::::::::::::::
NNALLSHLR	14	11.05	0.051	468	22.2	AE003493	TRUE	TRUE	2	1038.2	0.9	12of 16	2.3488	FALSE	FALSE	::::::::::
NMFPSNGREQTAASGGIAMGVPPAFVGAPRRVR	6	12.41	0.009	2751	64.36	AE003493	TRUE	TRUE	3	3400.9	-1.3	17of128	1.5998	FALSE	FALSE	::::::::::::::::::::::::::::::::
MTMSTNSTMSARIH	11	11.05	0.009	929	23.89	AE003493	TRUE	FALSE	2	1568.8	2.6	11of 26	1.1842	FALSE	FALSE	::::::::::::::
SAPTTPG	14	6.02	0.003	566	6.8	AE003493	TRUE	FALSE	1	630.7	1.8	5of 12	0.8015	FALSE	FALSE	::::::::
PKSDTQLDGAMFGPSFPDIFFSMLPNLTSPLDDPR	10	3.7	0.146	1598	94.96	AE003494	TRUE	FALSE	3	3856.4	-0.1	20of136	1.8677	FALSE	FALSE	::::::::::::::::::::::::::::::::

RHMQQRSASAGGGLGGDLDYR	4	9.84	0.133	2728	25.33	AE003494	TRUE	FALSE	2	2233.4	2.3	12of 40	2.0577	FALSE	FALSE	::::::::::::::::::::
VEFMYKGEVNVQYCQLSALLKTAESLKVK	2	8.75	0.026	2184	75.93	AE003494	TRUE	FALSE	3	3377.9	1.2	12of112	1.3653	FALSE	FALSE	::::::::::::Cys_CAM::::::::::::::
KLSRLKTQLNERRPKYDNLLDLPPK	7	10.62	0.007	1779	49.6	AE003494	TRUE	FALSE	3	3037.6	-1.8	74	2.673	FALSE	FALSE	::::::::::::::::::::::::
SAVLTFVFVVEVVMK	13	6.95	0.165	1292	61.23	AE003495	TRUE	FALSE	2	1685.1	1.8	14of 28	1.9426	FALSE	FALSE	::::::::::::Oxidation_M::
TRTPQFLCTMRFQRSAGL	9	12.11	0.089	1920	44.13	AE003495	TRUE	FALSE	2	2171.5	2.1	10of 34	2.0837	FALSE	FALSE	::::::::Cys_CAM::::::::::
TPMAPMAPMAPMAPMTPKPEAFSVKKPES	3	9.76	0.036	2082	63.45	AE003495	TRUE	FALSE	3	3120.7	1.7	22of112	1.7688	FALSE	FALSE	::::::Oxidation_M:::Oxidation_M:::Oxidation_M:::::::::::::::::
GSNDTFTTTSATSSFAAQQF	11	3.1	0.035	1145	31.9	AE003495	TRUE	FALSE	2	2070.1	2.2	5of 38	0.7088	FALSE	FALSE	::::::::::::::::::::
NFVHNHNMTKCIKGSAYGDT	11	8.85	0.035	2760	25.73	AE003495	TRUE	FALSE	2	2295.5	-1.5	6of 38	0.9426	FALSE	FALSE	::::::::::Cys_CAM:::::::::
PDGTDPHQLPGLDGLDVLSAQK	11	3.87	0.032	1769	41.8	AE003495	TRUE	FALSE	3	2274.5	2.5	16of 84	1.6791	FALSE	FALSE	::::::::::::::::::::
EIVELMSQLLQL	6	3.13	0.022	1843	52.33	AE003495	TRUE	FALSE	1	1432.7	-2.7	12of 22	1.8013	FALSE	FALSE	::::::Oxidation_M::::::
SPQQMSVVAMPVVIEHQLGNSDL	12	4.07	0.133	1969	58.46	AE003497	TRUE	FALSE	3	2496.9	0.3	16of 88	1.8425	FALSE	FALSE	::::::Oxidation_M:::::::::::::::::
GRIELMKPFGFTTTK	11	10.59	0.13	229	36.93	AE003497	TRUE	FALSE	2	1743.1	0.6	7of 28	1.1931	FALSE	FALSE	::::::Oxidation_M:::::::::
EELVCGGCSDVAR	15	3.83	0.08	1741	26.5	AE003497	TRUE	FALSE	2	1452.5	-0.6	9of 24	1.0828	FALSE	FALSE	:::::Cys_CAM:::Cys_CAM::::::
GNELVFKAKKTSEKISEN	6	9.67	0.061	1044	24.3	AE003497	TRUE	FALSE	2	2023.3	1.9	15of 34	2.1338	FALSE	FALSE	::::::::::::::::::
SPQQMSVVAMPVVIEHQLGNSDL	13	4.07	0.022	1738	58.46	AE003497	TRUE	FALSE	3	2496.9	-1.5	15of 88	2.0548	FALSE	FALSE	:::::Oxidation_M:::::::::::::::
GIEQAVSLLDMPAFKAIGAHLLEKRIPNCAK	14	8.91	0.015	1682	82.03	AE003497	TRUE	TRUE	2	3393	-2.9	4of 60	0.7819	FALSE	FALSE	::::::::::::::::::::::::::::::Cys_CAM:::
GIEQAV	8	3.3	0	2319	15.3	AE003497	TRUE	FALSE	1	616.7	-2.6	4of 10	0.4446	FALSE	FALSE	::::::
PPQKQDSTTKR	3	10.59	0.27	1098	0.4	AE003498	TRUE	FALSE	2	1286.4	1.2	9of 20	1.4701	FALSE	FALSE	::::::::::
HPSDSESRPEKKIPPPLTPPVKQPGVSNILARTG	9	10.32	0.158	2587	51.2	AE003498	TRUE	FALSE	3	3632.2	0.1	18of132	1.8582	FALSE	FALSE	::::::::::::::::::::::::::::::
KVPATGKNGRVLK	14	11.73	0.117	724	14.8	AE003498	TRUE	FALSE	3	1368.7	0.2	19of 48	1.8679	FALSE	FALSE	::::::::::::::
AAAANIAIAAASAPAAAGGAPSVAMGGALSSDKLELAK	5	6.99	0.1	2228	80.53	AE003498	TRUE	FALSE	3	3353.8	1.2	22of148	1.7507	FALSE	FALSE	::::::::::::::::::::::::Oxidation_M::::::::::::::
VRAEGSGDTDDTKGLDK	15	4.13	0.089	2685	12.6	AE003498	TRUE	FALSE	3	1764.8	-2.1	7of 64	1.1063	FALSE	FALSE	::::::::::::::::
VPPQVMPPPAVPPPNARGNRRWWK	8	12.71	0.078	3213	52.83	AE003498	TRUE	FALSE	2	2765.3	-1.2	6of 46	1.1703	FALSE	FALSE	::::::Oxidation_M:::::::::::::::::
RRGPHRGLGHFEH	14	12.11	0.068	1172	10.6	AE003498	TRUE	FALSE	2	1556.7	2.9	11of 24	1.8669	FALSE	FALSE	::::::::::::::
KIPPPLTPPVKQPGVSNILA	13	10.6	0.005	786	50.4	AE003498	TRUE	FALSE	3	2067.5	2	20of 76	1.7697	FALSE	FALSE	::::::::::::::::::
YHVDSALTTLLENQK	13	5.22	0.186	384	33.3	AE003499	TRUE	FALSE	2	1732.9	0.9	7of 28	1.037	FALSE	FALSE	::::::::::::::::
NPMEPGNPNGQINSMSQINPMGQINR	6	6.98	0.08	3076	42.69	AE003499	TRUE	FALSE	3	2856.2	-2	15of100	1.4218	FALSE	FALSE	::::::::::::::::::Oxidation_M:::::::
MTPEEMASDDM	14	2.84	0.073	914	23.59	AE003499	TRUE	FALSE	1	1273.4	-1.4	10of 20	1.7185	FALSE	FALSE	:Oxidation_M:::::::::::
GRQTSAEHPGPHDQPMARHQLPTTEHLL	15	6.49	0.068	1353	35.83	AE003499	TRUE	FALSE	3	3143.5	0.4	22of108	2.3112	FALSE	FALSE	::::::::::::::::::::::::::
TELTDDKPVPKTDP	12	3.97	0.065	2508	18.4	AE003499	TRUE	FALSE	3	1556.7	-0.4	8of 52	1.0663	FALSE	FALSE	::::::::::::::
VQNMKNQADMLLHNIIPKHVAEH	12	8.03	0.053	2682	47.06	AE003499	TRUE	FALSE	2	2682.1	-2.5	6of 44	0.8162	FALSE	FALSE	::::::::::::::::::::
QYEMARAATHTMR	15	9.85	0.036	2899	20.56	AE003499	TRUE	FALSE	2	1582.8	0.7	7of 24	1.0848	FALSE	FALSE	:::Oxidation_M:::::::::
RIVYIVLVVLLLIYGFGHI	7	9.59	0.03	1683	96	AE003499	TRUE	FALSE	3	2201.8	2.4	70	2.1962	FALSE	FALSE	::::::::::::::::::
LTKAYGADVVKYQYLEDLIVLNV	11	4.31	0.028	1518	74.4	AE003499	TRUE	FALSE	3	2629.1	1.5	14of 88	1.6469	FALSE	FALSE	::::::::::::::::::::
PYHGFIVQSTIKIIYSWVPTRSQLLGQGVAQAE	2	9.53	0.026	1952	91	AE003499	TRUE	FALSE	3	3689.3	2.7	24of128	1.6594	FALSE	FALSE	::::::::::::::::::::::::::::
GRIDESKTKNENK	10	9.76	0.02	1468	1.9	AE003499	TRUE	TRUE	2	1519.7	2.6	11of 24	2.3235	FALSE	FALSE	::::::::::::::
LVSGAGDIKITKDGNVLLHEMQIQHPTASMIAR	8	7.95	0.26	1879	75.06	AE003500	TRUE	FALSE	3	3546.1	-1	25of128	4.0185	FALSE	FALSE	::::::::::::::::::::::::::::
VEKLPKVVMRRFNENPN	3	10.58	0.162	2791	35.73	AE003500	TRUE	FALSE	3	2087.4	-0.1	7of 64	1.1276	FALSE	FALSE	::::::::Oxidation_M:::::::::
DALLVIPKTLAVNSGYDAQDTIVK	2	4.18	0.154	629	63.2	AE003500	TRUE	FALSE	3	2545.9	-2.7	22of 92	2.8735	FALSE	FALSE	::::::::::::::::::::
DMSSELLIAGDGDSSMD	3	2.72	0.138	1212	37.36	AE003500	TRUE	FALSE	2	1759.9	-2.4	9of 32	1.2774	FALSE	FALSE	::Oxidation_M:::::::::::::::
VRLSENEMALGALLTRSKKTR	8	11.38	0.119	2129	43.13	AE003500	TRUE	TRUE	3	2374.8	-1.2	19of 80	2.0541	FALSE	FALSE	::::::::::::::::::::
TADHLFDAAYYGQTDAINGVSERIILGMPACI	15	3.97	0.107	704	86.83	AE003500	TRUE	FALSE	3	3484.9	2.6	14of124	1.4762	FALSE	FALSE	::::::::::::::::::::::::::::::Cys_CAM::
TFVLINQKGIDPISLDALAKE	1	4.31	0.087	1273	62.5	AE003500	TRUE	FALSE	2	2286.7	1.3	10of 40	1.5313	FALSE	FALSE	::::::::::::::::::::
YDKTHQERAGVYEERSLTTETASS	8	4.77	0.085	2881	26.9	AE003500	TRUE	FALSE	3	2759.9	2	14of 92	1.5864	FALSE	FALSE	::::::::::::::::::::
DLDVSIDPNTVFPWFHPNCTKNEAVDMLVK	1	4.12	0.076	1725	79.53	AE003500	TRUE	FALSE	3	3519.9	1.4	19of116	1.9774	FALSE	FALSE	::::::::::::::::::Cys_CAM:::::::Oxidation_M::::
KLSPSSKMTKTAKRR	6	12.45	0.065	2992	8.63	AE003500	TRUE	FALSE	3	1736.1	-2.5	7of 56	0.9284	FALSE	FALSE	::::::::Oxidation_M:::::::::
KIQQIPSTKKANGVPERELTEEEKLCAKL	2	8.85	0.061	2178	49.3	AE003500	TRUE	FALSE	3	3339.8	-2.8	11of112	1.08	FALSE	FALSE	:::::::::::::::::::::::::::::Cys_CAM::::
EQASPASGNPASGDSNAGAKR	9	7.02	0.052	1461	10	AE003500	TRUE	FALSE	3	1973	-1.6	19of 80	1.6853	FALSE	FALSE	::::::::::::::::::::
VYLKANEGKLSPSSKMTKTAKRR	12	11.11	0.039	1764	26.43	AE003500	TRUE	FALSE	3	2611.1	-2.3	15of 88	1.6775	FALSE	FALSE	::::::::::::::::Oxidation_M:::::::::
EALVRIISKNLYQAQRQPVPYGVLDRRMGISTK	4	10.76	0.037	1790	77.93	AE003500	TRUE	FALSE	3	3818.5	2.6	18of128	1.4569	FALSE	FALSE	::::::::::::::::::::::::::::Oxidation_M::::::
RILFGSGGPGGPNASGNG	3	11.05	0.035	2162	26	AE003500	TRUE	FALSE	2	1615.7	-1.3	6of 34	0.8077	FALSE	FALSE	::::::::::::::::::
GEEPTNYDDDEDEENVNNDEQERKNLP	7	3.39	0.034	2127	25	AE003500	TRUE	FALSE	3	3209.1	-1.9	263	1.9799	FALSE	FALSE	::::::::::::::::::::::::::
ESSGSGSGSGSHGGGHHVASTPSPMVMVAGTGSAS	10	6.31	0.03	2138	28.26	AE003500	TRUE	FALSE	3	3145.3	0.5	16of136	1.3459	FALSE	FALSE	::::::::::::::::::::::::::Oxidation_M::Oxidation_M:::::::::
TIIMSEITEVMEGHGMS	15	3.96	0.024	2850	45.39	AE003500	TRUE	FALSE	3	1898.2	1.5	12of 64	1.2289	FALSE	FALSE	::::::::::Oxidation_M::::Oxidation_M::
LQLQGTRTIIDNLDNGYDVVPILTNYQ	7	3.6	0.023	1571	75.2	AE003500	TRUE	FALSE	3	3078.4	2.7	189	2.3365	FALSE	FALSE	::::::::::::::::::::::::::
EFLAALPLNIQSEVLMQQR	2	4.27	0.017	857	65.23	AE003500	TRUE	FALSE	3	2217.6	1.7	20of 72	2.5175	FALSE	FALSE	::::::::::::::::Oxidation_M::::
VVRTAPDGSGTVHSDE	11	4.3	0.017	1289	18.2	AE003500	TRUE	FALSE	3	1627.7	0.8	13of 60	1.5731	FALSE	FALSE	::::::::::::::::
EMALGALLTR	13	6.98	0.013	642	34.73	AE003500	TRUE	FALSE	2	1091.3	0.4	10of 18	1.2456	FALSE	FALSE	::Oxidation_M:::::::::
DDEDDDEDNDVIEDEDVDK	15	2.92	0.009	1335	21.1	AE003500	TRUE	FALSE	3	2240.1	-2.1	25of 72	2.3413	FALSE	FALSE	::::::::::::::::::
PIDAVNTTMN	3	3.1	0.101	1112	22.13	AE003501	TRUE	FALSE	2	1092.2	1.9	9of 18	1.4333	FALSE	FALSE	::::::::Oxidation_M::
AAAAGMGGLSPFCRR	10	10.9	0.084	998	32.33	AE003501	TRUE	FALSE	2	1522.7	-0.9	8of 28	1.0431	FALSE	FALSE	::::::::::::Cys_CAM:::
LGEMVPLDQLAQR	15	4.08	0.076	361	39.33	AE003501	TRUE	FALSE	3	1486.7	2.1	14of 48	1.618	FALSE	FALSE	:::::Oxidation_M:::::::::
IGIGKLGPCVALVAILQLL	13	8.97	0.03	344	78.6	AE003501	TRUE	FALSE	2	1949.4	-2.2	6of 36	0.7289	FALSE	FALSE	::::::::Cys_CAM:::::::::
GHGGYSGGGGGGGGGGGGGGSGGN	3	7.76	0.008	1236	-2.2	AE003501	TRUE	FALSE	3	1634.5	-2	15of 88	1.4354	FALSE	FALSE	::::::::::::::::::::
RYPAQNAMVMMTLYSFTDGITNKLVGCFHK	6	9.51	0.005	2262	77.29	AE003501	TRUE	FALSE	3	3496.1	2.7	21of116	1.8287	FALSE	FALSE	::::::::::::::::::::::::Cys_CAM::::
KGVTASASNQSLPTETNRK	1	10.59	0.003	1454	15.2	AE003501	TRUE	FALSE	2	1990.2	1.3	4of 36	0.5772	FALSE	FALSE	::::::::::::::::::
HNTTDAVLILD	9	3.88	0.164	861	29.5	AE003502	TRUE	FALSE	2	1212.3	-2.5	10of 20	1.3222	FALSE	FALSE	::::::::::
EAIIKSQDVIPGELIVVERDCDVPCDLVLL	5	3.63	0.099	1555	99.2	AE003502	TRUE	FALSE	3	3409.9	0.6	21of116	2.5271	FALSE	FALSE	::::::::::::::::::Cys_CAM:::Cys_CAM::::::
GQENAELQALVVQEK	1	3.97	0.079	2314	30.6	AE003502	TRUE	FALSE	2	1656.8	2.2	5of 28	0.9979	FALSE	FALSE	::::::::::::::::
ATAEANRAAGAAGGNISTQK	13	10.09	0.052	1470	19	AE003502	TRUE	FALSE	2	1860	0.3	4of 38	0.5917	FALSE	FALSE	::::::::::::::::::
HPFLRQAGPPSLLVPLMRNAR	6	12.71	0.043	1110	58.13	AE003502	TRUE	FALSE	3	2387.9	-0.1	19of 80	1.5123	FALSE	FALSE	::::::::::::::Oxidation_M:::::
ISTQKYRQVVMNAFIK	7	10.71	0.035	1717	39.93	AE003502	TRUE	FALSE	2	1927.3	2.6	138	1.3549	FALSE	FALSE	::::::::::::::::
SARDMLLLAATPED	10	3.71	0.02	2458	39.13	AE003502	TRUE	FALSE	3	1519.7	2.7	8of 52	0.7628	FALSE	FALSE	:::::Oxidation_M:::::::::
IHCGQVLEECPNGCQAFIPR	10	5.3	0.002	1494	48.3	AE003502	TRUE	FALSE	2	2386.6	0.6	11of 38	1.8437	FALSE	FALSE	:::Cys_CAM::::::Cys_CAM:::Cys_CAM::::::
QSMGIGGGHLMNVYNR	1	9.85	0.116	420	31.16	AE003503	TRUE	FALSE	2	1735	2.3	15of 30	2.167	FALSE	FALSE	::::::::::::::::
YYPEYEK	7	4.27	0.089	1112	15.6	AE003503	TRUE	FALSE	1	992.1	1.6	14	1.1753	FALSE	FALSE	::::::::
ESRDVELTFGKDWGSVAVSMGDTK	10	4.21	0.079	661	45.53	AE003503	TRUE	FALSE	3	2631.9	-2.7	24of 92	1.9539	FALSE	FALSE	::::::::::::::::::Oxidation_M:::::
SIQGRDLWVMVVSSSPY	3	6.7	0.05	2338	49.93	AE003503	TRUE	FALSE	2	1941.2	2.8	13of 32	1.7025	FALSE	FALSE	::::::::::Oxidation_M:::::::::
SEWIPTTLAMKRD	3	7.02	0.049	2880	33.43	AE003503	TRUE	FALSE	2	1548.8	-1.5	4of 24	0.8218	FALSE	FALSE	::::::::::::::
RRKDSEDDSNETDTDLHEFPD	10	3.9	0.041	1653	17.5	AE003503	TRUE	FALSE	3	2522.5	0	11of 80	1.4415	FALSE	FALSE	::::::::::::::::::::
TSTNFSLLMGLCDQGGDTTISYIGT	5	2.93	0.033	3039	61.23	AE003503	TRUE	FALSE	3	2669.9	-1.9	17of 96	1.6776	FALSE	FALSE	::::::::Oxidation_M:::Cys_CAM::::::::::::::
IFEGTDFHCIPEILEIYYDIIK	4	3.92	0.026	1866	82.2	AE003503	TRUE	FALSE	3	2730.1	-2	14of 84	1.2793	FALSE	FALSE	::::::::Cys_CAM::::::::::::
VENGKRDLEIMLTYIKQHQKELLR	6	9.56	0.003	1871	55.93	AE003503	TRUE	FALSE	3	2972.5	-1.2	18of 92	1.676	FALSE	FALSE	::::::::::Oxidation_M:::::::::::::

EFQCPYCR	11	6.14	0.311	2697	20.3	AE003504	TRUE	FALSE	2	1160.2	2.1	3of 14	0.6549	FALSE	FALSE	::::Cys_CAM:::Cys_CAM::
FDQNLKSNK	12	9.89	0.043	1631	10.8	AE003504	TRUE	FALSE	1	1094.2	1.5	9of 16	1.1125	FALSE	FALSE	::::::::
SIDNLHVESGPMLMIDCPPYAVYMIMSSARETK	13	4.54	0.027	1697	88.92	AE003504	TRUE	FALSE	3	3790.3	2.8	15of128	1.3707	FALSE	FALSE	::::::::::Oxidation_M::Oxidation_M::::Cys_CAM::::::::::::::
GQAANLRGPEISPKLAK	8	10.59	0.013	3336	28.7	AE003504	TRUE	FALSE	3	1751	-2.7	7of 64	0.8882	FALSE	FALSE	::::::::::::::
WSKKPDFYEATELC	12	4.45	0.012	1067	34.7	AE003504	TRUE	FALSE	2	1774.9	0.6	8of 26	1.2585	FALSE	FALSE	:::::::::::::Cys_CAM:
MLKSRLIDNVLDVVVPPNCMPNEHWDKTP	9	5.33	0.011	1976	75.56	AE003504	TRUE	FALSE	3	3419.9	2.8	20of112	2.0304	FALSE	FALSE	::::::::::::::::Cys_CAM::::::::::
ATLDGGVMVANASPATPGGNASSGS	12	3.1	0.009	1923	36.03	AE003504	TRUE	FALSE	3	2206.3	0.3	25of 96	2.0112	FALSE	FALSE	:::::::Oxidation_M::::::::::::::::
ATLDGGVMVANASPATPGGNASSGSSGA	6	3.1	0	1171	37.63	AE003504	TRUE	FALSE	3	2421.6	2.7	18of108	1.5812	FALSE	FALSE	:::::::Oxidation_M::::::::::::::::::
PQTIRLGDTDLVVPSLLPINMCIYASCGNR	11	6.1	0.147	186	86.23	AE003505	TRUE	FALSE	3	3391.8	2	13of116	1.208	FALSE	FALSE	::::::::::::::::::::Oxidation_M:Cys_CAM::::Cys_CAM::::
LRSQSFNR	5	12.41	0.077	2766	14	AE003505	TRUE	FALSE	2	1008.1	-2.2	7of 14	1.0319	FALSE	FALSE	::::::::
ELLNESKREAEQYQAFK	14	4.73	0.066	1156	31.6	AE003505	TRUE	FALSE	2	2084.3	0.9	9of 32	1.3983	FALSE	FALSE	::::::::::::::::
STTYKSLKIALR	7	10.71	0.059	1416	26.1	AE003505	TRUE	FALSE	2	1381.7	2.1	425	1.3012	FALSE	FALSE	::::::::::::
DEEMAWVDSC	12	2.84	0.055	697	26.33	AE003505	TRUE	FALSE	2	1242.3	-1.8	8of 18	1.0898	FALSE	FALSE	:::::::::Cys_CAM:
QYDVGGRDGR	11	6.85	0.029	2773	8.1	AE003505	TRUE	FALSE	2	1123.2	-0.3	7of 18	1.2471	FALSE	FALSE	::::::::::
QYDVGGRDGR	6	6.85	0.026	2963	8.1	AE003505	TRUE	FALSE	2	1123.2	2.4	9of 18	1.408	FALSE	FALSE	::::::::::
QCSSNTVLMLTTSGCLLRA	9	8.3	0.001	833	49.93	AE003505	TRUE	FALSE	3	2113.4	0	21of 72	1.8784	FALSE	FALSE	::Cys_CAM::::::::::::Cys_CAM:::::
LLQHMDENPLFNTSTMEMLVLDEADRCLDMGF	14	3.63	0.199	2579	99.52	AE003506	TRUE	FALSE	3	3804.3	-1.2	17of124	1.7361	FALSE	FALSE	::::::::::::::::::Oxidation_M::::::::Cys_CAM::::::
GLEVDYARLEAEYLAAH	7	4.16	0.104	1673	46.9	AE003506	TRUE	FALSE	2	1921.1	2.5	19	1.3881	FALSE	FALSE	::::::::::::::::
VSPTTSVANNATAAAKAS	2	10.1	0.085	191	21.9	AE003506	TRUE	FALSE	2	1661.8	2.7	7of 34	1.0415	FALSE	FALSE	::::::::::::::::
LARTPSAASIQVAS	11	11.05	0.042	290	29.9	AE003506	TRUE	FALSE	3	1372.6	-0.3	20of 52	1.9576	FALSE	FALSE	::::::::::::::
REEPSASTKK	13	9.89	0.033	638	1.6	AE003506	TRUE	FALSE	2	1133.2	1	11of 18	1.2987	FALSE	FALSE	::::::::::
RQFGHSALKSIVWR	9	12.42	0.029	902	33.4	AE003506	TRUE	FALSE	3	1686	0.3	17of 52	1.4415	FALSE	FALSE	::::::::::::::::
LFNVFSLDLDAFAQSLGLAVTPRV	12	3.89	0.022	2661	87	AE003506	TRUE	FALSE	2	2595	-2.8	7of 46	0.8199	FALSE	FALSE	::::::::::::::::::::::
TIREWAFEGHIDCK	13	5.35	0.017	1599	34.3	AE003506	TRUE	FALSE	2	1762.9	-2.9	6of 26	1.0249	FALSE	FALSE	:::::::::::Cys_CAM::
SRPKQLYSSVVANKQD	3	10.18	0.013	1873	20.8	AE003506	TRUE	FALSE	2	1821	0.6	5of 30	0.7177	FALSE	FALSE	::::::::::::::
TMGGPR	1	11.05	0.012	2072	7.13	AE003506	TRUE	FALSE	1	618.7	-1.7	4of 10	0.7406	FALSE	FALSE	::::::
MNKASSGQRPGSNEDVLK	9	9.89	0.009	1002	16.93	AE003506	TRUE	FALSE	3	1919.1	-1.8	22of 68	1.6359	FALSE	FALSE	::::::::::::::::
GSGLGVTPVTAGGSLPSQAASEIQEAMK	13	4.27	0.004	158	50.63	AE003506	TRUE	FALSE	3	2645	0.4	10of108	1.1323	FALSE	FALSE	::::::::::::::::::::::::::
VEAVTVSNVD	9	3.01	0.169	63	23.1	AE003507	TRUE	FALSE	2	1033.1	0.6	9of 18	1.3284	FALSE	FALSE	::::::::::
REFIAKTIFR	13	11.33	0.11	1478	31.4	AE003507	TRUE	FALSE	1	1281.5	-1	11of 18	2.1911	FALSE	FALSE	::::::::::
PADDHLAAEDLDAVQLELEQM	3	3.28	0.085	1892	54.93	AE003507	TRUE	FALSE	3	2324.5	2.7	24of 80	2.5118	FALSE	FALSE	::::::::::::::::::
NLHVVMSMSPVGDAFRR	7	10.89	0.074	1169	41.96	AE003507	TRUE	FALSE	3	1917.3	2.6	69	1.6716	FALSE	FALSE	::::::::::::::::
EFNRIDIEVLSVIAQQLITIR	7	4.45	0.068	1723	74.3	AE003507	TRUE	FALSE	3	2471.9	-1.8	369	1.2631	FALSE	FALSE	::::::::::::::::::
RVTGEDRPSSMSMDRLDSDFAAFT	10	4.13	0.068	1002	46.66	AE003507	TRUE	FALSE	3	2708.9	-1	19of 92	1.7087	FALSE	FALSE	:::::::::::Oxidation_M:::::::::::
TMNPVLR	4	11.05	0.051	2892	20.03	AE003507	TRUE	TRUE	2	831	2	9of 12	1.6086	FALSE	FALSE	::::::::
NIKLAHFSGSLGSGGFGISASSG	6	10.1	0.043	1795	44	AE003507	TRUE	FALSE	2	2152.4	1.2	11of 44	1.8623	FALSE	FALSE	::::::::::::::::::::::
SLAMMKHGVGIEQRLKKTLIENGLIDASEFAAHED	3	5.35	0.039	1413	79.46	AE003507	TRUE	FALSE	3	3886.4	0.4	26of136	2.4192	FALSE	FALSE	:::Oxidation_M:Oxidation_M:::::::::::::::::::::::::
QRRHELYIKLGKIDGTTSHAHYDNFEL	5	7.91	0.037	3076	49.1	AE003507	TRUE	FALSE	3	3243.6	-2.7	13of104	1.3739	FALSE	FALSE	::::::::::::::::::::::::::
SKVRLCCELNSAQFEAVKWSAMSEEQGK	1	6.44	0.011	111	55.73	AE003507	TRUE	FALSE	3	3290.6	-1.1	11of108	1.1036	FALSE	FALSE	::::::Cys_CAM:Cys_CAM::::::::::::Oxidation_M::::::
CYLCLMGAFQMDLGGAPAGPAGTGK	13	5.95	0.011	215	62.66	AE003507	TRUE	TRUE	3	2560.9	-2.3	8of 96	0.8651	FALSE	FALSE	:Cys_CAM:::Cys_CAM::::::Oxidation_M:::::::::::::
SEMDSLIDQSNMDIEEKNQMLAAAK	9	3.76	0.01	1754	51.49	AE003507	TRUE	FALSE	3	2829.1	-1.7	20of 96	2.4417	FALSE	FALSE	:::Oxidation_M:::::::::::::::::::::
REFIAKTIFR	14	11.33	0.009	1383	31.4	AE003507	TRUE	FALSE	1	1281.5	0.4	10of 18	1.7322	FALSE	FALSE	::::::::::
STVIHTTPGNAVQVRNK	7	11.49	0.079	1172	21.8	AE003508	TRUE	FALSE	2	1823.1	1.6	106	1.2328	FALSE	FALSE	::::::::::::::::
THTWLPLAVAALLLILGPQSSLAEEPI	6	4.25	0.078	1819	100	AE003508	TRUE	FALSE	3	2855.4	0.8	24of104	2.4756	FALSE	FALSE	::::::::::::::::::::::::::
TTTTSSTSITATTSTFYF	1	5.93	0.003	1698	34.7	AE003508	TRUE	FALSE	2	1919	-2.5	8of 34	1.2538	FALSE	FALSE	::::::::::::::::
MPSTSHEYHGGNQF	10	6.02	0.14	1362	16.23	AE003509	TRUE	FALSE	2	1608.7	2.1	5of 26	0.8721	FALSE	FALSE	:Oxidation_M:::::::::::::
LLVLLPLLYLLANWSDHHKR	1	9.72	0.064	1649	79.6	AE003509	TRUE	FALSE	3	2415.9	-1.6	12of 76	1.5267	FALSE	FALSE	::::::::::::::::::::
IFSVLEARAAASGLKLRTSDVEVYVAS	12	7.06	0.057	1913	73	AE003509	TRUE	FALSE	3	2854.3	-2.8	21of104	1.9577	FALSE	FALSE	::::::::::::::::::::::::::
REQHDIPEVLKR	14	7.83	0.033	868	19.5	AE003509	TRUE	FALSE	3	1520.7	0.8	13of 44	1.612	FALSE	FALSE	::::::::::::
LVDDFSDKENLRSQLDEYVLQFKGLVK	10	4.31	0.028	1262	71.1	AE003509	TRUE	FALSE	3	3200.6	0.7	19of104	2.574	FALSE	FALSE	::::::::::::::::::::::::
SEQPTTSRMAK	15	10.09	0.007	1661	8.73	AE003509	TRUE	FALSE	2	1252.4	-1.9	4of 20	0.8753	FALSE	FALSE	:::::::::Oxidation_M:::
SVPQSGARVQDDGAPNNNNNNI	6	3.89	0.002	2330	20.8	AE003509	TRUE	FALSE	2	2282.3	2.8	11of 42	1.4225	FALSE	FALSE	::::::::::::::::::::
LEGRPREVPKLVDGLGNFEPKDVKPRSGPGENGEAH	11	5.57	0.002	1508	52.5	AE003509	TRUE	FALSE	3	3883.3	-1.6	18of140	1.5747	FALSE	FALSE	::::::::::::::::::::::::::::::::::::
QLRYLLAAYNVGMLAMETLARR	9	10.2	0.203	2803	72.66	AE003510	TRUE	FALSE	2	2555.1	-1	8of 42	1.2711	FALSE	FALSE	::::::::::::::::::::::
APRYRIVHLLRRRGNATEAGSTKK	8	12.24	0.163	1777	32.9	AE003510	TRUE	TRUE	3	2752.2	-0.9	17of 92	1.4761	FALSE	FALSE	::::::::::::::::::::::
KHTHAPLVSPTQTPLLNPLLNA	2	10.1	0.086	1217	51.6	AE003510	TRUE	FALSE	2	2363.8	2.8	12of 42	1.6765	FALSE	FALSE	::::::::::::::::::::::
TLYILLTK	1	9.72	0.054	1169	35.3	AE003510	TRUE	FALSE	1	965.2	-0.2	10of 14	1.874	FALSE	FALSE	::::::::
SSSAAAASVAASSTPAR	2	11.05	0.038	557	19.8	AE003510	TRUE	FALSE	2	1492.6	2.7	14of 32	1.4868	FALSE	FALSE	::::::::::::::::
PDWDADERER	10	3.85	0.019	1330	14.4	AE003510	TRUE	FALSE	2	1289.3	-0.5	9of 18	1.3139	FALSE	FALSE	::::::::::
EVMDLIHWFGRVSEPWNDRGFKPR	5	7.83	0.007	2164	64.23	AE003510	TRUE	FALSE	3	2989.4	0.9	22of 92	2.1206	FALSE	FALSE	:::Oxidation_M:::::::::::::::::::
IKGELAVIDRRRKKLRRRER	8	12.29	0.005	2779	29.7	AE003510	TRUE	FALSE	3	2550.1	0.2	13of 76	1.2488	FALSE	FALSE	::::::::::::::::::
TDSEQR	14	4.08	0	2753	1.1	AE003510	TRUE	FALSE	1	735.7	2.7	6of 10	0	FALSE	FALSE	::::::
VTTEAPGTTEKITTEAPGTTEKITTEAPGTTE	5	3.96	0.091	2656	40.8	AE003511	TRUE	FALSE	3	3264.5	-2.7	20of124	1.5883	FALSE	FALSE	::::::::::::::::::::::::::::::
SKEDPPPAAVVPK	15	6.99	0.091	1328	18.9	AE003511	TRUE	FALSE	2	1335.5	1.7	12of 24	2.39	FALSE	FALSE	::::::::::::
LQPFSEYQQKGQKDHIQERQY	4	7.68	0.072	1791	29.7	AE003511	TRUE	FALSE	3	2651.9	1	7of 80	0.9946	FALSE	FALSE	::::::::::::::::::
YEMLWGKTKEAF	1	7	0.055	325	35.43	AE003511	TRUE	FALSE	2	1503.8	0.3	12of 22	1.6657	FALSE	FALSE	::::::::::::
PAGGTTELPVPR	3	6.98	0.01	1471	22.4	AE003511	TRUE	FALSE	2	1195.4	0	8of 22	0.9653	FALSE	FALSE	::::::::::::
LMRQVSSRSR	15	12.71	0.007	828	16.23	AE003511	TRUE	FALSE	2	1220.4	2.2	8of 18	1.1294	FALSE	FALSE	::::::::::
QWMTSLRRQVHHYDEGPWQQPK	4	9.72	0.006	1747	38.73	AE003511	TRUE	FALSE	3	2825.1	-2.2	7of 84	0.9003	FALSE	FALSE	:::Oxidation_M:::::::::::::::::
SEKRAGELPATYAMNTFFMPRLLQ	11	9.72	0.001	170	65.16	AE003511	TRUE	FALSE	2	2805.2	0.4	4of 46	0.7389	FALSE	FALSE	:::::::::::::Oxidation_M::::Oxidation_M::::::
RMLVGVAAK	15	11.49	0.001	453	24.73	AE003511	TRUE	FALSE	1	961.2	1.8	10of 16	1.2924	FALSE	FALSE	::Oxidation_M:::::::
KTFMMMQSPLPLRNRLPVVVSTMIRSRRAPKLKLK	3	13.01	0	1612	91.72	AE003511	TRUE	FALSE	3	4142.2	1.8	8of136	0.8591	FALSE	FALSE	:::::Oxidation_M:::::::::::::::::::::::::
KRGRPKRIQNQSSPDGGGAVTPKP	1	12.15	0.153	1726	13.3	AE003512	TRUE	FALSE	2	2532.9	-0.7	10of 46	1.2417	FALSE	FALSE	::::::::::::::::::::
SETEFRSPSRYGAMNGTSNSNNMGTNSELK	8	7.11	0.14	3229	32.76	AE003512	TRUE	FALSE	3	3284.5	1.3	23of116	1.9886	FALSE	FALSE	:::::::::::::::::::::Oxidation_M:::::::
VAPACAIMISSFE	12	3.3	0.135	2092	44.73	AE003512	TRUE	FALSE	2	1396.6	1.2	10of 24	2.0718	FALSE	FALSE	:::::Cys_CAM::::::::
MLRVVPACAIMISTFE	15	6.29	0.11	2750	61.56	AE003512	TRUE	FALSE	3	1855.2	-0.1	14of 60	1.402	FALSE	FALSE	:::::::Cys_CAM:::Oxidation_M:::::::
VPPGAVSRNSSRHR	13	12.71	0.098	1538	10.7	AE003512	TRUE	FALSE	1	1520.7	-1.8	5of 26	0.9419	FALSE	FALSE	::::::::::::::
INRSSSRQQGGSIFVAPPTKTPDAAAST	15	11.33	0.097	1132	38.6	AE003512	TRUE	FALSE	3	2846.1	-1.3	17of108	1.6819	FALSE	FALSE	::::::::::::::::::::::::::
MQSEYMTYAELWRVLRSLIRQHGI	5	9.59	0.092	2463	73.26	AE003512	TRUE	FALSE	3	2982.5	1.3	11of 92	1.2742	FALSE	FALSE	::::::::::::::::::::::::
ETAYNFSGIQGVIRMAVAANYSDGLTT	10	4.08	0.044	1669	63.83	AE003512	TRUE	FALSE	3	2851.2	1.3	15of104	1.4201	FALSE	FALSE	::::::::::::::::::::::::
SPSRYGAMNGTSNSNNMGTN	2	9.85	0.039	1945	15.76	AE003512	TRUE	FALSE	2	2093.2	-2.8	9of 38	1.0132	FALSE	FALSE	:::::::Oxidation_M::::::::Oxidation_M::::
HEVQIANLPPMQ	12	5.13	0.029	1204	30.43	AE003512	TRUE	FALSE	2	1393.6	-1.2	8of 22	1.4243	FALSE	FALSE	:::::::::::Oxidation_M::
QKDTTMMSGDGLISSKMDK	12	6.94	0.024	2031	26.59	AE003512	TRUE	FALSE	2	2074.4	2.8	10of 36	1.1177	FALSE	FALSE	::::::::::::::::::

SSSSSSSLAEMQTVPK	2	6.95	0.016	1352	20.83	AE003512	TRUE	FALSE	1	1626.8	-0.7	7of 30	1.1104	FALSE	FALSE	::::::::::::::::
TGGGGQEHVHTVIMTHDLNNAQSIPKLTIKTKS	1	9.76	0.014	183	47.23	AE003512	TRUE	FALSE	3	3531	2.4	17of128	1.5879	FALSE	FALSE	:::::::::::::Oxidation_M::::::::::::::::::
QKDTTMMSGDGLISSKMDK	6	6.94	0.008	1998	26.59	AE003512	TRUE	FALSE	2	2106.4	-2	7of 36	0.9424	FALSE	FALSE	:::::::Oxidation_M::::::::::Oxidation_M:::
TTNGNGGSPTPAAAAVASTAR	3	11.05	0.003	2816	20.6	AE003512	TRUE	FALSE	2	1873	-0.1	10of 40	1.1398	FALSE	FALSE	::::::::::::::::::::
LIGNGMER	12	6.98	0.037	2288	20.53	AE003513	TRUE	FALSE	2	906	0.7	5of 14	0.73	FALSE	FALSE	::::::Oxidation_M:::
QVIEELIAQAVQLEPTRLAQVLLPD	8	3.69	0.026	3315	83.8	AE003513	TRUE	FALSE	3	2788.3	-1.5	19of 96	1.2938	FALSE	FALSE	::::::::::::::::::::::::
DNLTPHQHSLLQSLSQSQSQSHSHAHSTDSSQS	10	6.18	0.024	1886	24.7	AE003513	TRUE	FALSE	3	3598.7	-0.5	15of128	1.0218	FALSE	FALSE	::::::::::::::::::::::::::::::
RRGGNATPSTTKRRRNNSSVGSTSPHSTTLPSGR	9	13.01	0.017	2643	13.5	AE003513	TRUE	TRUE	3	3468.8	0.9	23of128	2.107	FALSE	FALSE	::::::::::::::::::::::::::::::
QRGYYER	11	9.59	0	1685	8.7	AE003513	TRUE	FALSE	2	972	0.5	5of 12	0.808	FALSE	FALSE	::::::::
TDSYILGRSKMRFNS	1	10.39	0.102	2356	29.73	AE003514	TRUE	FALSE	3	1792	1.8	13of 56	1.7502	FALSE	FALSE	::::::::::Oxidation_M::::::
LMICVPGACTDESVF	12	3.01	0.08	1155	49.83	AE003514	TRUE	FALSE	2	1715.9	1.4	14of 28	1.5209	FALSE	FALSE	::Oxidation_M::Cys_CAM::::Cys_CAM::::::
GSLMSLNQTEPANP	13	3.3	0.072	408	27.63	AE003514	TRUE	FALSE	2	1459.6	1	8of 26	1.0768	FALSE	FALSE	::::::::::::::
FNSASLVRSLNPFLPSVTSPKKAPHKQ	9	11.73	0.069	465	51.9	AE003514	TRUE	FALSE	3	2952.4	2.2	18of104	1.3582	FALSE	FALSE	::::::::::::::::::::::::::
SQYQSPGVVC	13	5.33	0.055	942	18.5	AE003514	TRUE	FALSE	2	1125.2	3	10of 18	1.4137	FALSE	FALSE	::::::::::Cys_CAM:
DRSSRFDVAELAAMSRDMPHMAKVLVRR	6	11.1	0.043	2307	59.79	AE003514	TRUE	FALSE	3	3262.8	0	16of108	1.4798	FALSE	FALSE	::::::::::::::::Oxidation_M::::::::::
LNAAIRRQVSASSGSTPVAGSVLSLVRQR	5	12.88	0.022	2172	57.7	AE003514	TRUE	FALSE	3	2982.4	1.5	24of112	2.4593	FALSE	FALSE	::::::::::::::::::::::::::
PKVDYSNRPSGSGDTASNDKSGSAS	11	6.89	0.019	1707	10.7	AE003514	TRUE	FALSE	2	2485.5	1.1	11of 48	1.4339	FALSE	FALSE	::::::::::::::::::::::::
NFSTTQLPDPDGQK	7	3.89	0.01	3338	18.7	AE003514	TRUE	FALSE	2	1548.6	0.8	394	1.3032	FALSE	FALSE	::::::::::::::
GGRSMP	11	11.05	0	2695	6.33	AE003514	TRUE	FALSE	1	604.7	1.8	4of 10	0	FALSE	FALSE	::::::
TFNTTAVNNSVNLATDTLY	2	3.1	0.145	1886	43.4	AE003515	TRUE	FALSE	2	2060.2	-2.4	7of 36	1.0851	FALSE	FALSE	::::::::::::::::::
HQMMQLQGMGGGAGGGMGAG	15	7.85	0.08	325	30.32	AE003515	TRUE	FALSE	2	1866.1	-1.8	8of 38	1.005	FALSE	FALSE	:::Oxidation_M::::::Oxidation_M:::::::::::
KRFKEELYGMKKIRKLKKRPNQTANSIMEMYKNE	8	10.52	0.079	1993	54.99	AE003515	TRUE	FALSE	3	4120.9	-0.2	16of128	1.7514	FALSE	FALSE	::::::::::::::::::::::::::Oxidation_M:::::::
TLENFDMSFPELGEFKGLR	1	4.17	0.046	191	56.33	AE003515	TRUE	FALSE	2	2231.5	1.3	7of 36	1.0837	FALSE	FALSE	::::::::::::::::
FVVLEDALAR	8	4.08	0.029	1619	39	AE003515	TRUE	FALSE	1	1133.3	2.8	9of 18	1.4127	FALSE	FALSE	::::::::::
WPAQSVSQLGQLK	10	10.1	0.014	2082	31.3	AE003515	TRUE	FALSE	3	1442.7	-0.9	14of 48	1.4101	FALSE	FALSE	::::::::::::
LNLNIPDAIAAIRSQHKMNFR	13	11.33	0.222	1083	52.83	AE003516	TRUE	FALSE	3	2423.8	-0.7	12of 80	1.4459	FALSE	FALSE	::::::::::::::::::::
KMSTQDTESGCSEAKNRAV	6	6.48	0.147	2860	14.53	AE003516	TRUE	FALSE	3	2116.2	-2.4	9of 72	1.0846	FALSE	FALSE	::Oxidation_M::::::::Cys_CAM::::::::
MTDVAEIKGHRR	6	10.09	0.146	1542	16.23	AE003516	TRUE	FALSE	2	1429.6	3	11of 22	1.8085	FALSE	FALSE	:Oxidation_M:::::::::::
KEAIRTQVANKEASDRK	11	10.32	0.082	173	13.1	AE003516	TRUE	FALSE	2	1945.2	-2.9	10of 32	1.3816	FALSE	FALSE	::::::::::::::::
HQLFHVSLSLATILICMA	12	7.32	0.059	997	68.43	AE003516	TRUE	FALSE	3	2071.5	1	25of 68	1.9607	FALSE	FALSE	::::::::::::::Cys_CAM:Oxidation_M::
YIEQIRTLTKMFNDAAFYKSLTDDGDLA	10	4.13	0.046	1448	73.73	AE003516	TRUE	FALSE	3	3257.6	-0.2	22of108	2.5414	FALSE	FALSE	::::::::::Oxidation_M:::::::::::::::
TMEQFLTSLDMIR	11	4.08	0.044	709	44.46	AE003516	TRUE	FALSE	3	1601.9	1.8	20of 48	2.441	FALSE	FALSE	::::::::::Oxidation_M:::
APYLRVGGNNQFTMME	1	6.89	0.016	756	40.26	AE003516	TRUE	FALSE	2	1829.1	2	8of 30	1.1246	FALSE	FALSE	::::::::::::::
AEGPALPMGAVRSSDII	9	4.08	0.005	1032	43.33	AE003516	TRUE	FALSE	3	1700.9	1.9	19of 64	1.5962	FALSE	FALSE	:::::::Oxidation_M:::::::::
EETEIIEGEVVEIQIERPASGTGQKVGKVTLKT	8	4.38	0.073	2439	63.9	AE003517	TRUE	FALSE	3	3570	-1.8	21of128	1.7375	FALSE	FALSE	::::::::::::::::::::::::::
GSYTVQMWWHYMR	3	9.59	0.042	1932	40.16	AE003517	TRUE	TRUE	2	1762	-0.2	4of 24	0.9289	FALSE	FALSE	::::::::::Oxidation_M::
AGTTNRAPKVIAAPQEVEAFADR	3	7.14	0.026	2637	41	AE003517	TRUE	FALSE	2	2413.7	-0.2	11of 44	1.3607	FALSE	FALSE	::::::::::::::::::::
PHTVKDSIANFK	6	9.89	0	2780	18.2	AE003517	TRUE	FALSE	2	1357.6	-2.7	4of 22	0.244	FALSE	FALSE	::::::::::::
GYITFMALEAVAMVYSNVLRDHVNKGK	11	9.47	0.112	2831	70.96	AE003518	TRUE	FALSE	3	3060.6	-1.5	14of104	1.2766	FALSE	FALSE	::::::Oxidation_M::::::Oxidation_M:::::::::::::
KRNFIELARPESK	6	10.58	0.086	1562	23.6	AE003518	TRUE	FALSE	2	1588.9	1.1	11of 24	1.327	FALSE	FALSE	::::::::::::::
RTRSAQSLSARSSS	3	12.71	0.056	1488	9.7	AE003518	TRUE	FALSE	2	1494.6	-1.5	11of 26	1.5111	FALSE	FALSE	::::::::::::::
VVGQSRLAAIK	7	11.49	0.043	1207	26.4	AE003518	TRUE	FALSE	2	1142.4	2.3	145	2.8257	FALSE	FALSE	::::::::::::
PVLAIPILAEQEVMAKRLQ	3	7.1	0.037	1145	64.13	AE003518	TRUE	FALSE	2	2120.6	1.4	11of 36	1.6838	FALSE	FALSE	::::::::::::::::::::
PVVIDADGLFLLNDNLNLICGQP	5	2.82	0.012	1788	80.4	AE003518	TRUE	FALSE	3	2511.8	-0.8	15of 88	1.1123	FALSE	FALSE	::::::::::::::::::Cys_CAM::::
FLQRLPVPPVAITMAHSAQDDYCP	7	5.1	0.001	2079	66.43	AE003518	TRUE	FALSE	3	2744.1	-1.4	194	1.4227	FALSE	FALSE	:::::::::::::Oxidation_M::::::::Cys_CAM::
AMLLEKAPR	9	10.09	0.193	524	26.13	AE003519	TRUE	FALSE	2	1029.3	-0.1	10of 16	1.4656	FALSE	FALSE	::::::::::
ITFQTAGFFDGKNV	14	6.76	0.084	1739	37	AE003519	TRUE	FALSE	2	1545.7	1.3	12of 26	2.3717	FALSE	FALSE	::::::::::::::
PNGSTTSNHLYLTPSGMTLLPRSKQP	5	10.4	0.049	1284	45.63	AE003519	TRUE	FALSE	2	2799.2	-0.1	7of 50	0.8667	FALSE	FALSE	::::::::::::::::::::::::
ELELQLANSKVLRNDKIIR	5	9.88	0.006	2176	49.8	AE003519	TRUE	TRUE	2	2253.7	3	5of 36	0.7114	FALSE	FALSE	::::::::::::::::::
GDERRNGGDRGNYRSRQY	12	10.19	0.003	2114	5.3	AE003519	TRUE	FALSE	2	2157.2	1.5	12of 34	1.4242	FALSE	FALSE	::::::::::::::::::
GRQSERLLGGNGKGGAQRGALTK	9	12.14	0.051	2756	21.8	AE003520	TRUE	TRUE	3	2312.6	1.8	20of 88	1.8825	FALSE	FALSE	::::::::::::::::::::
KLKAMHRIETTYDLQPK	7	10.05	0.032	2126	31.13	AE003520	TRUE	FALSE	2	2073.5	1.5	43	1.2997	FALSE	FALSE	::::::::::::::::
LSCLLVALPKGNCHSISGLNSTLNLPEIR	5	8.3	0.025	2012	81.6	AE003520	TRUE	FALSE	3	3178.6	0.1	22of112	3.1297	FALSE	FALSE	:::Cys_CAM::::::::Cys_CAM:::::::::::::::
NSHSNSSNSSAASATPTNGGKENGKY	6	9.63	0.017	1818	3.5	AE003520	TRUE	FALSE	3	2568.6	2.8	8of100	0.9383	FALSE	FALSE	::::::::::::::::::::::::
RHSRLRQR	9	12.88	0.077	492	3.4	AE003522	TRUE	FALSE	2	1109.3	2.1	10of 14	1.3143	FALSE	FALSE	::::::::
LGFHIKENGIISTAHATAAYLK	8	9.63	0.051	2505	51.7	AE003522	TRUE	FALSE	2	2356.7	-1.3	12of 42	1.3766	FALSE	FALSE	::::::::::::::::::::
GAMFGLCSSMMGAMFPLPRIVFAMSNDGLLFK	5	8.97	0.033	2645	112.95	AE003522	TRUE	FALSE	3	3531.2	-0.6	20of124	1.8559	FALSE	FALSE	:::Oxidation_M::::Cys_CAM::::Oxidation_M:::::::::::::::::::::
IPDVYLPKLGDLLPSIVNSLTDLK	5	4.18	0.026	1342	79.7	AE003522	TRUE	FALSE	3	2625.1	2.5	19of 92	2.2478	FALSE	FALSE	::::::::::::::::::::::::
ARQDSSGTLKTTISLGK	7	10.59	0.011	1365	21.8	AE003522	TRUE	FALSE	2	1764	0.6	77	1.3695	FALSE	FALSE	::::::::::::::::
PTFNISDYGVDKFTILLS	10	3.89	0.004	592	57	AE003522	TRUE	FALSE	3	2031.3	2.6	20of 68	1.5847	FALSE	FALSE	::::::::::::::::
YYSDPPESQYSCCSRGSTACDRSM	12	4.31	0.097	1616	32.33	AE003523	TRUE	FALSE	3	2881.9	-2.4	9of 92	1.1789	FALSE	FALSE	::::::::::Cys_CAM:Cys_CAM::::::Cys_CAM:::Oxidation_M:
LIGVHNWLHWVAWFVKSYIML	5	9.72	0.062	2643	93.33	AE003523	TRUE	FALSE	3	2614.2	-0.2	14of 80	1.3962	FALSE	FALSE	::::::::::::::::::
EKNRSEEGNRDLRNQSK	7	9.88	0.05	1073	3.2	AE003523	TRUE	TRUE	3	2061.2	-0.3	333	2.1573	FALSE	FALSE	::::::::::::::::
RKDVPLLVYK	12	10.18	0.037	1907	28.1	AE003523	TRUE	FALSE	2	1231.5	-0.2	6of 18	0.9347	FALSE	FALSE	::::::::::
LWRKLWYGANVVSLPHWSNVR	14	11.39	0.02	2893	67	AE003523	TRUE	TRUE	2	2583	2.3	8of 40	1.0651	FALSE	FALSE	::::::::::::::::::
NNNGILAQIAMQYR	11	9.85	0.016	2765	34.33	AE003523	TRUE	FALSE	2	1606.8	-2.2	7of 26	0.9628	FALSE	FALSE	::::::::::::
VQNADILIGVTSYGK	13	6.68	0.007	655	36.9	AE003523	TRUE	FALSE	3	1578.8	2.4	16of 56	1.9127	FALSE	FALSE	::::::::::::::
PTRPPTTYLPPPTVRTTR	13	12.11	0.276	2577	31.4	AE003524	TRUE	FALSE	2	2052.4	-1.7	6of 34	0.9142	FALSE	FALSE	::::::::::::::::
EHISLEEISSDSDIGGQESRK	2	4.13	0.138	2244	28.9	AE003524	TRUE	FALSE	2	2317.4	-1.8	4of 40	0.8188	FALSE	FALSE	::::::::::::::::::
FTNAPYSATVPENTPAGVSILTVK	13	6.87	0.082	526	54.7	AE003524	TRUE	FALSE	3	2478.8	0.1	9of 92	1.0852	FALSE	FALSE	::::::::::::::::::
AMQPVGNGKPLSKK	5	10.85	0.068	2442	17.13	AE003524	TRUE	FALSE	2	1471.8	2.1	10of 26	1.2005	FALSE	FALSE	::Oxidation_M:::::::::::
SRIENDNDKMRKNKYQTKVISMQTKKSK	5	10.69	0.067	2339	19.76	AE003524	TRUE	FALSE	3	3432.9	-1.9	16of108	1.663	FALSE	FALSE	::::::::Oxidation_M::::::::::Oxidation_M::::::
KCLQFDSVNNESNSRSANDIKEMETNR	8	4.73	0.018	2886	33.83	AE003524	TRUE	FALSE	3	3188.4	1.8	17of104	1.5278	FALSE	FALSE	::Cys_CAM:::::::::::::::::::::
RWWM	13	11.05	0	2512	22.53	AE003524	TRUE	FALSE	1	678.8	1.1	2of 6	0	FALSE	FALSE	:::::
LVHIVSDQSKTMTPPTRGRAPTR	1	12.12	0.175	2308	35.03	AE003525	TRUE	FALSE	3	2550	0.8	9of 88	1.1712	FALSE	FALSE	::::::::::::::::::::::
QALREGGIIIQRLKVRRGGIAIAGPGG	14	12.41	0.149	1579	61.4	AE003525	TRUE	FALSE	3	2758.3	2.5	29of104	2.8253	FALSE	FALSE	::::::::::::::::::::::::
DELPELPKPKRVLNKSPIPLRPAPPKPQA	1	10.55	0.078	2390	58.8	AE003525	TRUE	FALSE	2	3227.9	2.6	9of 56	1.0757	FALSE	FALSE	::::::::::::::::::::::::
RYKPIKPHHEKKHRFK	5	11.11	0.075	2204	7.1	AE003525	TRUE	FALSE	2	2130.6	1.9	8of 30	1.106	FALSE	FALSE	::::::::::::::::
PEIHGSGELDSGFSDK	9	4.06	0.034	885	22.8	AE003525	TRUE	FALSE	2	1675.7	2.1	12of 30	1.709	FALSE	FALSE	::::::::::::::::
LSLGSSNSAGG	14	6.02	0.01	903	16.2	AE003525	TRUE	FALSE	2	950	-0.3	9of 20	1.2382	FALSE	FALSE	::::::::::::
LLLQPALELRPGTNIVGGSVK	15	10.09	0.233	1363	61.5	AE003526	TRUE	TRUE	2	2176.6	1.1	15of 40	3.0955	FALSE	FALSE	::::::::::::::::::
SMHFTMVNGEGGPPKKPK	4	10.32	0.178	1417	22.06	AE003526	TRUE	FALSE	2	1943.3	-0.9	8of 34	1.2865	FALSE	FALSE	::::::::::::::::::
EEITTNFDNPPTEPGLSRTPLAPHELDSD	13	3.68	0.144	324	54.7	AE003526	TRUE	FALSE	2	3194.4	-3	5of 56	0.8143	FALSE	FALSE	::::::::::::::::::::::::::

RREKPSLSMAEILKS	13	10.58	0.117	2085	29.33	AE003526	TRUE	FALSE	3	1762.1	0.3	7of 56	0.7961	FALSE	FALSE	:::::::::Oxidation_M:::::::
FIPPLLDLLEPALQSPEPVLR	2	3.83	0.089	1849	82.7	AE003526	TRUE	TRUE	2	2358.8	2.9	19of 40	2.0985	FALSE	FALSE	::::::::::::::::::::
SLPRTADMSELSLNGGGGFSFGSASLAAEGQDESFAP	10	3.51	0.042	2334	76.73	AE003526	TRUE	FALSE	3	3662.9	-2.4	25of144	1.8989	FALSE	FALSE	::::::::::::::::::::::::::::::::::
PNGTFKLAVLGATVGAATGSVY	10	9.72	0.024	2655	51.9	AE003526	TRUE	FALSE	3	2095.4	-1.1	18of 84	1.5255	FALSE	FALSE	::::::::::::::::::::
TVPSEL	8	3.3	0	3401	16.6	AE003526	TRUE	FALSE	1	645.7	-2.6	3of 10	0.4582	FALSE	FALSE	::::::::
NKYNQVLSRLKLVENFDGSDPGK	13	9.56	0.18	308	40.9	AE003527	TRUE	FALSE	3	2622.9	-0.3	14of 88	1.4575	FALSE	FALSE	::::::::::::::::::::::
SVALIVLTTLLAMESGRQMELLQRR	11	10.8	0.082	1374	82.06	AE003527	TRUE	FALSE	3	2830.4	0.2	6of 96	0.8964	FALSE	FALSE	::::::::::::::::::::::::
DSNQDMASSSTHLSANLSETLRK	8	5.28	0.076	3412	29.33	AE003527	TRUE	FALSE	3	2493.7	0.2	7of 88	0.9578	FALSE	FALSE	::::::::::::::::::::::
TGSFFKTSGIKEVPAYVNKRR	9	10.89	0.072	1149	35.5	AE003527	TRUE	FALSE	3	2386.8	0.4	10of 80	0.9347	FALSE	FALSE	::::::::::::::::::::
RLEMSRKDLENVLWGDFYYNS	8	4.56	0.019	2335	58.23	AE003527	TRUE	FALSE	3	2652.9	-2.1	10of 80	1.0473	FALSE	FALSE	::::Oxidation_M:::::::::::::::
PTDKTPATMLSLLHGKSVEPHL	11	7.95	0.01	210	45.03	AE003527	TRUE	FALSE	2	2389.8	-0.5	7of 42	0.8235	FALSE	FALSE	:::::::::Oxidation_M:::::::::::::
KVLVERILRLQQ	2	11.33	0.006	816	39.5	AE003527	TRUE	FALSE	1	1495.9	0.1	8of 22	1.6249	FALSE	FALSE	::::::::::::
LLVGQNGILSTPAVSSLIR	6	11.05	0.308	1990	59.6	AE003528	TRUE	TRUE	2	1939.3	2.3	14of 36	2.1033	FALSE	FALSE	::::::::::::::::::
LTRELEARDFPTPEVSKQPLK	13	7.18	0.193	1346	44.5	AE003528	TRUE	FALSE	2	2455.8	-2	8of 40	1.1464	FALSE	FALSE	::::::::::::::::::::
REESTSERWIKFLQRDAHKHYVKS	9	10.05	0.188	2261	35.1	AE003528	TRUE	FALSE	3	3032.4	0.4	8of 92	1.3945	FALSE	FALSE	::::::::::::::::::::::
SYAPLGYAGNSAGWYEPGIWGVSSYPSIYLK	13	6.7	0.156	1322	84.5	AE003528	TRUE	FALSE	3	3355.7	2.2	11of120	1.2193	FALSE	FALSE	::::::::::::::::::::::::::::
DYAQFEERAKVAQLTNSIAVFTKGILMMKTT	6	9.56	0.129	2364	77.66	AE003528	TRUE	FALSE	3	3539.1	1.4	14of120	1.6012	FALSE	FALSE	:::::::::::::::::::::::::::::Oxidation_M:Oxidation_M::::
MEDQKSTTEEVKANAKEKPQPLR	1	7.19	0.111	962	22.63	AE003528	TRUE	FALSE	3	2659	-1.9	10of 88	0.9966	FALSE	FALSE	::::::::::::::::::::::
IARLPLGVLEQRIPNIIL	6	10.89	0.059	1322	72.1	AE003528	TRUE	FALSE	2	2029.5	1.9	14of 34	2.3043	FALSE	FALSE	::::::::::::::::::
KAKPQKADESVEIIDLDNSNPAATPKKLAPLFVR	1	9.6	0.057	2094	65.9	AE003528	TRUE	FALSE	3	3706.3	-2.4	14of132	1.4883	FALSE	FALSE	::::::::::::::::::::::::::::::::
PINQSALKHADVLIMTGLTQA	13	7.82	0.057	227	53.83	AE003528	TRUE	FALSE	2	2238.6	-1.5	6of 40	1.094	FALSE	FALSE	:::::::::::::::Oxidation_M:::::::
LRHLMTSSQWPETRDGECDIKIN	8	5.39	0.044	2351	47.13	AE003528	TRUE	FALSE	3	2788.1	2.3	21of 88	2.5188	FALSE	FALSE	:::::::::::::::::::::Cys_CAM:::::::
DPKELVSNSKSKK	9	10.16	0.018	2181	6.8	AE003528	TRUE	FALSE	2	1460.7	1.7	10of 24	1.2781	FALSE	FALSE	::::::::::::::
KLCDCKFNDPNAKEMHMKGR	11	9.05	0.01	2839	25.46	AE003528	TRUE	FALSE	2	2512.8	0.7	6of 38	0.8114	FALSE	FALSE	:::Cys_CAM::Cys_CAM::::::::::Oxidation_M::Oxidation_M::::
AKKLDDRGAYF	10	9.63	0.003	466	20.1	AE003528	TRUE	FALSE	1	1284.5	-2.9	5of 20	0.7658	FALSE	FALSE	::::::::::
ELVESGWDVNQPDSETVTLLHW	2	3.51	0.079	1882	60.5	AE003529	TRUE	FALSE	2	2555.8	-3	6of 42	0.9728	FALSE	FALSE	::::::::::::::::::::
ISLPKKISLQKGKYINLSDNSR	11	10.63	0.031	868	42	AE003529	TRUE	FALSE	3	2503.9	1.9	21of 84	2.1759	FALSE	FALSE	::::::::::::::::::::
ERTMLEPRRKSKK	10	11.47	0	360	10.13	AE003529	TRUE	FALSE	2	1660	1.2	4of 24	0.5393	FALSE	FALSE	::::::::::::
SGMGSGSGSSG	14	6.02	0.072	446	3.73	AE003530	TRUE	FALSE	1	783.8	2	9of 18	1.2238	FALSE	FALSE	::::::::::
VGIIYKRDELEAQMAPNRNPSLQVQKNFKRVVD	9	10.05	0.056	2252	69.43	AE003530	TRUE	FALSE	3	3858.5	-1.9	11of128	1.3003	FALSE	FALSE	::::::::::::::::::::::::::::
KLISRNYRRVAEIWLDEYK	1	9.94	0.045	1705	51.4	AE003530	TRUE	TRUE	2	2453.8	-2.4	6of 36	0.7292	FALSE	FALSE	::::::::::::::::::
PCSRVGHLQPKDEDYLKR	8	8.85	0.042	2192	25.9	AE003530	TRUE	FALSE	2	2199.4	0.3	5of 34	0.8087	FALSE	FALSE	::Cys_CAM:::::::::::::::
SPGSTLPTLQTAVNANTKKAGFAR	2	11.64	0.019	758	36.9	AE003530	TRUE	FALSE	3	2431.8	0.1	14of 92	1.354	FALSE	FALSE	::::::::::::::::::::
LKSSTHR	9	11.49	0.002	566	3.5	AE003530	TRUE	TRUE	2	828.9	1.7	9of 12	1.1918	FALSE	FALSE	::::::::
VLHLNHSRIEVLHNRTFY	4	9.85	0.136	2249	47.1	AE003531	TRUE	FALSE	2	2249.6	0.1	10of 34	2.0602	FALSE	FALSE	::::::::::::::::
LRFALPDVSSSQRSNVAGQ	2	10.89	0.034	2100	37.7	AE003531	TRUE	FALSE	2	2033.3	-0.3	9of 36	1.1978	FALSE	FALSE	::::::::::::::::::
DLSANKISRLEAHIFRPLASLQILK	3	10.58	0.03	1365	71.4	AE003531	TRUE	FALSE	3	2835.4	2.3	18of 96	1.4505	FALSE	FALSE	::::::::::::::::::::::
SLPTAMLSALGRLTHLNMAK	3	11.49	0.021	2776	54.76	AE003531	TRUE	FALSE	3	2142.6	-2.3	12of 76	1.1614	FALSE	FALSE	::::::Oxidation_M:::::::::::::
TGPHIYSIHPHGSSDKLPYATMGSGSLAAMTVFESR	10	7.93	0.461	1506	68.26	AE003532	TRUE	TRUE	3	3805.3	1.4	39of140	4.993	FALSE	FALSE	::::::::::::::::::::::::::::::
PPLVAPIK	12	10.1	0.264	2071	26.4	AE003532	TRUE	FALSE	1	835.1	-0.1	9of 14	1.6702	FALSE	FALSE	::::::::
VQPDSKCGDRRIRAHSVQRSVLAQSRGP	12	11.83	0.188	1933	33.1	AE003532	TRUE	FALSE	3	3162.5	1.4	15of108	1.7263	FALSE	FALSE	::::::Cys_CAM:::::::::::::::::::
PPLVAPIK	13	10.1	0.166	1543	26.4	AE003532	TRUE	FALSE	1	835.1	0.3	11of 14	2.3192	FALSE	FALSE	::::::::
HILLAGSDSGEVFVFR	15	5.22	0.1	653	49.6	AE003532	TRUE	FALSE	3	1748	-2	16of 60	1.3345	FALSE	FALSE	::::::::::::::::
CNKNQFFGGCFKKSEPFR	11	9.81	0.076	1020	32	AE003532	TRUE	FALSE	3	2252.5	1.2	19of 68	1.9871	FALSE	FALSE	:Cys_CAM::::::::Cys_CAM::::::::
GSGSLAAMTVFESRWKPDLSEEEGK	12	4.36	0.028	1120	48.63	AE003532	TRUE	FALSE	3	2729	1.3	15of 96	1.65	FALSE	FALSE	:::::::Oxidation_M:::::::::::::::
SVDDVNKMFENSPSFFANITV	7	3.71	0.026	1355	53.83	AE003532	TRUE	FALSE	2	2362.6	2	30 1.2913	FALSE	FALSE	::::::::::::::::::
ENFCLAHVSLVPLPKATGEPKT	1	7.16	0.022	1989	51.1	AE003532	TRUE	FALSE	2	2409.8	2.7	11of 42	1.55	FALSE	FALSE	::::Cys_CAM:::::::::::::::::
LRALNAKRKNE	8	11.47	0.021	2188	14.7	AE003532	TRUE	FALSE	2	1313.5	2.4	7of 20	0.9729	FALSE	FALSE	::::::::::::
DINGACGDR	15	3.89	0.011	395	10.8	AE003532	TRUE	FALSE	1	978	1	7of 16	1.0023	FALSE	FALSE	::::::Cys_CAM::::
LQREKSDLMMQVREFQDK	10	7.14	0.009	2185	37.36	AE003532	TRUE	FALSE	3	2282.6	-3	17of 68	1.9724	FALSE	FALSE	::::::::::::::::::
PPREGKRGASAKDEVEAPK	11	9.76	0.152	620	12.4	AE003533	TRUE	TRUE	2	2023.3	1.3	10of 36	1.3472	FALSE	FALSE	::::::::::::::::::
VTLQSCRWDSVSDPECQRDFESRLLR	12	4.65	0.09	1803	58.6	AE003533	TRUE	FALSE	3	3241.5	2.3	20of100	1.7514	FALSE	FALSE	::::::Cys_CAM::::::::::Cys_CAM:::::::::::
PLPPPLNANPSLPLR	9	11.05	0.071	862	44.4	AE003533	TRUE	FALSE	3	1596.9	-2	19of 56	1.9179	FALSE	FALSE	::::::::::::::::
SPGQSQAQAGVAGSGTGGK	3	10.1	0.046	1019	9.7	AE003533	TRUE	FALSE	2	1645.7	-2.9	8of 36	1.1553	FALSE	FALSE	::::::::::::::::::
FVLRAFSQKF	10	11.49	0.034	618	36.5	AE003533	TRUE	FALSE	2	1243.5	2.7	9of 18	1.4735	FALSE	FALSE	::::::::::
DPTKRAVYEALIEDK	11	4.56	0.025	2579	29.4	AE003533	TRUE	FALSE	3	1749	-1.8	9of 56	1.2366	FALSE	FALSE	::::::::::::::::
AAPTAAPTAPPTTNHFNPFK	5	10.1	0.021	3068	33.2	AE003533	TRUE	FALSE	2	2052.3	-3	8of 38	1.0059	FALSE	FALSE	::::::::::::::::::::
MKRSISPKLQGVQILNARSPVEADTL	1	10.58	0.015	1357	57.73	AE003533	TRUE	FALSE	3	2869.4	-2.2	25of100	2.5643	FALSE	FALSE	:Oxidation_M:::::::::::::::::::::::
NRGGGR	4	12.41	0.005	2712	-2.4	AE003533	TRUE	TRUE	1	616.7	-2	5of 10	0.9112	FALSE	FALSE	::::::
EAAQAMECEAIMPLALANDSTRIILLCENYR	6	4.01	0.001	2108	91.96	AE003533	TRUE	FALSE	3	3585	2.9	7of120	0.8344	FALSE	FALSE	:::::::Cys_CAM:::Oxidation_M::::::::::::::Cys_CAM::::
HWDNCLDLVVECANV	5	3.7	0.098	2327	45.4	AE003534	TRUE	FALSE	2	1845	1	8of 28	1.1318	FALSE	FALSE	::::::Cys_CAM::::::Cys_CAM::::
WGNLREGDEIVSIDGRDVR	14	4.21	0.064	1190	41.3	AE003534	TRUE	FALSE	2	2187.4	-1.3	7of 36	0.8058	FALSE	FALSE	::::::::::::::::::
QTIPGYANNFREAVPKMLK	14	10.18	0.03	2620	42.13	AE003534	TRUE	FALSE	3	2194.6	0.5	18of 72	1.7708	FALSE	FALSE	::::::::::::::Oxidation_M:::
VSGGKPVEIM	14	6.95	0.001	1114	23.33	AE003534	TRUE	FALSE	1	1033.2	0.6	5of 18	0.9789	FALSE	FALSE	:::::::::Oxidation_M:
GAAGGSAGGGSGGATAADFRR	2	10.89	0.034	438	17.7	AE003535	TRUE	FALSE	2	1751.8	-2.4	9of 40	1.1795	FALSE	FALSE	::::::::::::::::::
APSNAMTRSVMESVSENLLLNISIKNR	2	10.09	0.25	155	62.26	AE003536	TRUE	FALSE	2	3008.4	-2.4	5of 52	0.8024	FALSE	FALSE	::::::Oxidation_M::::::Oxidation_M:::::::::::::::
HVTQPLVNNCSTKVASLPFYNTIYGK	1	9.51	0.174	67	57.4	AE003536	TRUE	FALSE	3	2953.3	1.8	9of100	1.2007	FALSE	FALSE	:::::::::Cys_CAM:::::::::::::::
CWFTKEAGACIINALIIKLDR	3	8.29	0.165	1232	70.2	AE003536	TRUE	FALSE	3	2493.9	-2	21of 80	1.7351	FALSE	FALSE	:Cys_CAM::::::::Cys_CAM:::::::::::
SPERFQAAIR	10	10.89	0.148	2345	21.2	AE003536	TRUE	FALSE	2	1175.3	1.4	5of 18	0.9865	FALSE	FALSE	::::::::::
SLMSSWFQQAEQQHA	8	5.13	0.138	1691	32.93	AE003536	TRUE	FALSE	2	1778.9	0.7	7of 28	0.9762	FALSE	FALSE	::::::::::::::
NAMLKLGLEDDPDRF	10	3.97	0.093	302	40.13	AE003536	TRUE	FALSE	2	1751	0.8	6of 28	0.9032	FALSE	FALSE	:::Oxidation_M:::::::::::
FMPAPDGAMTIK	15	6.76	0.079	875	33.06	AE003536	TRUE	FALSE	1	1279.6	0.7	10of 22	1.4012	FALSE	FALSE	::::::::::::
ALIGAGMIVVGLARRHERVEKLRSG	6	11.95	0.065	1571	60.23	AE003536	TRUE	FALSE	3	2706.2	-2.9	24of 96	2.8193	FALSE	FALSE	::::::Oxidation_M:::::::::::::::
ILKSMGWKPGQGVGPR	10	11.64	0.061	1668	33.03	AE003536	TRUE	TRUE	2	1728.1	-2.8	10of 30	1.3472	FALSE	FALSE	:::::Oxidation_M:::::::::::
NSGGRQSGKLTHSQSMGNGLK	10	11.64	0.06	2692	12.43	AE003536	TRUE	FALSE	2	2161.4	-0.7	6of 40	0.8703	FALSE	FALSE	::::::::::::::Oxidation_M:::::::
SRTITSADVDADEQLQHPHSHAHHHSMRNGHQHN	13	6.49	0.045	272	16.73	AE003536	TRUE	FALSE	3	3890.1	-2.2	9of132	1.1656	FALSE	FALSE	::::::::::::::::::::::::::::::
TQSSSSVPTGGSAGLSGHHLR	5	11.05	0.03	2536	19.6	AE003536	TRUE	FALSE	2	2024.2	1.8	11of 40	1.562	FALSE	FALSE	::::::::::::::::::::
NLDFSQNGAGNDSGVGTGSVAGAPAMLQLEIG	11	2.88	0.023	1863	63.63	AE003536	TRUE	FALSE	3	3065.3	0.2	20of124	1.6748	FALSE	FALSE	:::::::::::::::::::::::::::Oxidation_M:::::::
GMPQFICVECAEAVR	9	4.27	0.015	2793	43.63	AE003536	TRUE	FALSE	2	1768	-0.3	6of 28	0.9043	FALSE	FALSE	::::::Cys_CAM:::Cys_CAM:::::::
SSGAPGPSSFEAEDIGMAF	15	2.95	0.004	1341	40.13	AE003536	TRUE	FALSE	2	1858	-2.1	6of 36	1.082	FALSE	FALSE	::::::::::::::::::
VLLAIIMSCTGLASQRARLKKPVQEMR	11	11.38	0.002	188	73.96	AE003536	TRUE	FALSE	2	3071.7	-1.1	5of 52	0.7303	FALSE	FALSE	:::::::::Cys_CAM:::::::::::::::::
LPYMGEITLDNYKPR	11	6.89	0.131	2413	40.53	AE003537	TRUE	FALSE	2	1811.1	0.2	9of 28	1.4921	FALSE	FALSE	::::::::::::::::
LVISTTKLQPAHVPIKTSP	11	10.6	0.091	716	44.1	AE003537	TRUE	FALSE	2	2031.4	-1.3	9of 36	1.4988	FALSE	FALSE	::::::::::::::::::

PSNASTHSRLRAQSSNANASSSSL	11	12.41	0.068	946	19.9	AE003537	TRUE	FALSE	3	2431.5	0.3	20of 92	2.3281	FALSE	FALSE	::::::::::::::::::::::
GLELLSPED	13	2.95	0.011	666	28.3	AE003537	TRUE	FALSE	2	973.1	-2.7	8of 16	0.9697	FALSE	FALSE	::::::::
SISSDPSTGSSSSTTATPTATTPK	5	6.76	0.163	2376	17.9	AE003538	TRUE	FALSE	2	2270.4	-2.1	11of 46	1.5002	FALSE	FALSE	::::::::::::::::::::::
CDFAKNVNCTIDAVARNILPYSRTPLRR	8	9.77	0.143	2221	63.9	AE003538	TRUE	FALSE	3	3322.7	0.1	24of108	2.357	FALSE	FALSE	:Cys_CAM::::::Cys_CAM::::::::::::::::
DDDFHNDR	14	3.87	0.135	1134	5.6	AE003538	TRUE	FALSE	2	1034	1.1	8of 14	2.034	FALSE	FALSE	::::::::
TTRTRTTAQPRISESPLNQ	5	12.11	0.123	1938	22.8	AE003538	TRUE	FALSE	2	2158.4	1.4	8of 36	2.1799	FALSE	FALSE	::::::::::::::::::
AEKIPEVEVPAVVSEKETLAVEPMK	6	4.26	0.118	1896	58.73	AE003538	TRUE	FALSE	2	2740.2	-0.7	6of 48	1.0684	FALSE	FALSE	:::::::::::::::::::::::Oxidation_M::
PPPGGGGVH	1	7.85	0.034	2286	8.1	AE003538	TRUE	FALSE	1	774.9	-0.5	6of 16	0.8285	FALSE	FALSE	::::::::::
TIDTGGKKGRLLLWSKEFWARALIVMM	2	10.82	0	108	87.16	AE003538	TRUE	FALSE	2	3138.8	2.6	9of 52	0.9844	FALSE	FALSE	:::::::::::::::::::::::Oxidation_M::
HANCGQDGGPFGRAEK	8	7.16	0.124	2308	11.8	AE003539	TRUE	FALSE	2	1701.8	0.9	6of 30	0.9659	FALSE	FALSE	::::Cys_CAM::::::::::::
LMVPGLIDVK	2	6.76	0.086	929	39.03	AE003539	TRUE	TRUE	1	1101.4	0.3	11of 18	1.6804	FALSE	FALSE	::Oxidation_M:::::::::
YIICQDIGAQLSWVSWTKEDLK	9	4.31	0.036	1245	67.4	AE003539	TRUE	FALSE	3	2655	1.9	18of 84	1.9825	FALSE	FALSE	::::Cys_CAM:::::::::::::::::
YSSDDAPPSRCSGGRGLK	11	8.87	0.035	2832	16.9	AE003539	TRUE	FALSE	2	1911	0.1	9of 34	0.9965	FALSE	FALSE	::::::::::Cys_CAM::::::::
ELFRRQAELMYLRR	13	10.98	0.033	1275	44.23	AE003539	TRUE	FALSE	2	1898.2	-1.2	8of 26	1.1242	FALSE	FALSE	::::::::::Oxidation_M:::::
HGEALEF	9	4.25	0.028	2036	18.1	AE003539	TRUE	FALSE	1	802.9	-1.2	8of 12	1.5966	FALSE	FALSE	::::::::
EALNHVFGFMVVQDIVARDWNVPLGG	14	4.3	0.016	1496	82.13	AE003539	TRUE	FALSE	3	2901.3	-2.6	21of100	2.3512	FALSE	FALSE	::::::::::Oxidation_M:::::::::::::::
QDNGGGNGGNRFQRSNSRRRSRSRRLS	6	12.88	0.004	2931	7.2	AE003539	TRUE	FALSE	3	3077.3	-2.3	19of104	0.372	FALSE	FALSE	::::::::::::::::::::::::::
KLDESEKHSENISCA	4	4.63	0.183	1829	16.1	AE003540	TRUE	FALSE	2	1747.8	2.7	8of 28	1.2941	FALSE	FALSE	::::::::::::Cys_CAM::
LPVELHETKKALGLTLI	14	7.8	0.144	1512	53.8	AE003540	TRUE	FALSE	2	1876.3	-0.6	13of 32	1.7844	FALSE	FALSE	::::::::::::::::
LFQYLLNNETK	13	6.87	0.094	1032	35.3	AE003540	TRUE	FALSE	2	1383.6	1.5	11of 20	1.6031	FALSE	FALSE	::::::::::::
AREKDNQTNLEVNGKIVDACTTLMECVKA	1	4.73	0.077	2393	51.93	AE003540	TRUE	FALSE	3	3309.6	-2.5	15of112	1.3502	FALSE	FALSE	::::::::::::::::::Cys_CAM:::::Cys_CAM::::
QKTITDIQTKLRDIEKLIEKIKASF	8	10.05	0.074	2373	56.4	AE003540	TRUE	FALSE	3	2961.5	-2.7	14of 96	1.3759	FALSE	FALSE	::::::::::::::::::::::
DNQTNLEVNGKIVDACTTLM	15	3.71	0.061	2831	42.93	AE003540	TRUE	FALSE	3	2237.5	0.1	23of 76	1.5472	FALSE	FALSE	::::::::::::::Cys_CAM:::::
SSAPGADGSSTSGATVTGFQR	8	6.79	0.05	2727	20.7	AE003540	TRUE	FALSE	2	1942	-1.1	8of 40	1.0583	FALSE	FALSE	::::::::::::::::::
RVEPKKFVKIGRPGYRVTK	10	11.55	0.046	2666	30.1	AE003540	TRUE	FALSE	3	2259.7	-0.1	17of 72	1.5599	FALSE	FALSE	::::::::::::::::::
VKIQSLRILKSGFFCSK	4	10.84	0.045	2449	47.1	AE003540	TRUE	FALSE	2	2012.4	1.7	7of 32	1.3424	FALSE	FALSE	::::::::::::Cys_CAM:::
NLTDLQIDNPLGISLWQL	9	2.93	0.035	2260	65.5	AE003540	TRUE	FALSE	2	2054.4	2	9of 34	1.0489	FALSE	FALSE	::::::::::::::::
NKEKQVNSQLLLETK	15	9.76	0.034	2751	24.4	AE003540	TRUE	FALSE	3	1773	-2.3	7of 56	0.7813	FALSE	FALSE	::::::::::::::
PERQKTITDIQTK	2	9.89	0.004	605	15.1	AE003540	TRUE	FALSE	2	1558.8	-1	9of 24	1.288	FALSE	FALSE	::::::::::::
KQLSNFGLDYIDLYLMHMPVGYK	10	7.63	0.423	1880	72.36	AE003541	TRUE	TRUE	3	2747.2	1.6	37of 88	5.3963	FALSE	FALSE	::::::::::::::::::::
DATGTSVLHKATVPI	15	7.82	0.225	1759	28.9	AE003541	TRUE	FALSE	2	1510.7	2.3	9of 28	1.8716	FALSE	FALSE	::::::::::::::
GVSNFNSEQLARVLANCEIKPVTNQVECSPALNQK	7	6.38	0.148	1075	70.3	AE003541	TRUE	FALSE	3	3917.3	1.9	37	3.0755	FALSE	FALSE	::::::::::::::::Cys_CAM::::::::::Cys_CAM::::::::
IVLRYLVGLGVIPIPKSSNTNR	15	11.39	0.11	513	65.3	AE003541	TRUE	FALSE	3	2410.9	-1.6	12of 84	1.342	FALSE	FALSE	::::::::::::::::::::
SIIHHAPKAGRQR	12	12.42	0.108	1492	12.9	AE003541	TRUE	FALSE	2	1471.7	0.2	12of 24	1.4476	FALSE	FALSE	::::::::::::::
FLGVGNGSGVAPTGYGNGGSAVAANRHHPRSHR	5	12.11	0.107	1291	36.2	AE003541	TRUE	FALSE	3	3259.5	-2	24of128	1.752	FALSE	FALSE	::::::::::::::::::::::::::::
AHLTRHKMVHG	9	11.49	0.062	1524	12.03	AE003541	TRUE	FALSE	2	1303.5	0.7	9of 20	1.2297	FALSE	FALSE	::::::::Oxidation_M::::
PYGCDSVRAAAEYFTKS	8	6.35	0.022	2475	31.3	AE003541	TRUE	FALSE	2	1923.1	-0.1	11of 32	1.7353	FALSE	FALSE	::::Cys_CAM:::::::::::::
PLDYSRQRSSVSASTCSKIKARKKH	11	11	0.02	1860	20.9	AE003541	TRUE	FALSE	2	2892.3	-2.5	6of 48	0.9772	FALSE	FALSE	::::::::::::::Cys_CAM::::::::
SISSKLLGARKR	2	12.43	0.015	442	19.4	AE003541	TRUE	FALSE	2	1316.6	0.2	11of 22	1.2866	FALSE	FALSE	::::::::::::
EYGGTVPIADMI	4	3.01	0.013	3016	35.33	AE003541	TRUE	FALSE	2	1282.5	1.1	11of 22	1.8086	FALSE	FALSE	:::::::::::Oxidation_M::
ANRIIELGVSMLSDKLKKRIIVHKNVDILK	4	10.7	0.008	2429	77.83	AE003541	TRUE	FALSE	3	3446.2	-0.1	24of116	2.0584	FALSE	FALSE	::::::::::::::::::::::::::
SGHRMTVSKKRL	1	12.43	0.001	1058	11.13	AE003541	TRUE	FALSE	2	1416.7	1.7	6of 22	0.7792	FALSE	FALSE	:::::Oxidation_M::::::::
NYHDAMFK	9	7.74	0.198	1012	15.53	AE003542	TRUE	TRUE	2	1026.2	1.7	12of 14	2.1033	FALSE	FALSE	::::::::
EQTAAEEADFAKWL	7	3.69	0.02	1595	35	AE003542	TRUE	FALSE	2	1609.7	-0.2	344	0.8594	FALSE	FALSE	::::::::::::::
RMLFYGRGVLRRVSTTR	2	12.58	0.003	762	41.93	AE003542	TRUE	FALSE	3	2085.5	2.6	20of 64	1.7804	FALSE	FALSE	::Oxidation_M:::::::::::::::
AELQQHEGGPGPGPNSPSLLR	2	5.3	0.002	2021	32	AE003542	TRUE	FALSE	2	2142.3	2.7	7of 40	0.9154	FALSE	FALSE	::::::::::::::::::::
GNVFNANLSVCEVDADNTCC	12	2.88	0.137	1295	42.3	AE003543	TRUE	FALSE	3	2260.3	-1.4	19of 76	1.7517	FALSE	FALSE	::::::::::Cys_CAM:::::::Cys_CAM:Cys_CAM:
MDIFEPEPPAPIINPPP	1	2.95	0.134	472	53.63	AE003543	TRUE	FALSE	2	1891.2	1.1	9of 32	1.3394	FALSE	FALSE	:Oxidation_M:::::::::::::::
QQQMEEHIKGQQERINM	9	5.4	0.125	1073	23.56	AE003543	TRUE	FALSE	3	2144.4	2.4	20of 64	1.9174	FALSE	FALSE	::::::::::::::::Oxidation_M:
LHSETMSSQDK	13	5.22	0.086	688	10.73	AE003543	TRUE	FALSE	2	1279.4	-1.2	8of 20	1.3541	FALSE	FALSE	::::::Oxidation_M:::::::
NEIPSRIPSFGNVLHLK	3	10.09	0.069	2226	42.6	AE003543	TRUE	FALSE	2	1922.2	1.8	9of 32	1.2938	FALSE	FALSE	::::::::::::::::
KQADNVLMDN	4	3.89	0.056	2557	17.73	AE003543	TRUE	FALSE	2	1148.3	1.2	6of 18	0.8702	FALSE	FALSE	::::::::::
DELGQATGAYR	11	4.08	0.053	526	17.5	AE003543	TRUE	FALSE	2	1181.2	1.7	9of 20	1.2891	FALSE	FALSE	::::::::::::
KASDTASSVSGS	13	6.76	0.053	1146	6.5	AE003543	TRUE	FALSE	2	1097.1	-2.8	9of 22	1.3652	FALSE	FALSE	::::::::::::::
WTWADANVTSASPSACVR	1	6.1	0.035	140	39.8	AE003543	TRUE	FALSE	2	1980.1	0.7	9of 34	0.853	FALSE	FALSE	::::::::::::::Cys_CAM:::
QDIVDAHRR	15	7.85	0.022	265	11.5	AE003543	TRUE	FALSE	2	1110.2	-2.6	8of 16	1.1263	FALSE	FALSE	::::::::::
YDPRNPLNK	6	9.72	0.02	1530	12.9	AE003543	TRUE	FALSE	1	1117.2	1.5	8of 16	1.5379	FALSE	FALSE	::::::::::
GLDAKSPTSLGSTTGAGATGKAKGKASRKANAGPDGGQKGR	14	11.17	0.014	1474	19.8	AE003543	TRUE	FALSE	3	3814.2	2.7	23of160	2.63	FALSE	FALSE	::
SSDDGESEPKDIDDR	10	3.58	0.009	2309	9.1	AE003543	TRUE	FALSE	3	1665.6	1.3	21of 56	1.6564	FALSE	FALSE	::::::::::::::::
YYGGTNG	6	5.87	0.008	2814	8.4	AE003543	TRUE	FALSE	1	731.7	2.1	5of 12	0.8681	FALSE	FALSE	::::::::
GNNDEDIPGTAMRR	12	4.31	0.002	2825	16.23	AE003543	TRUE	FALSE	3	1546.7	-1.3	7of 52	0.9291	FALSE	FALSE	::::::::::::::
DTPEAEQRPSTSKQSSHSPQK	10	7.8	0.256	1777	3.7	AE003544	TRUE	FALSE	2	2326.4	-2.4	5of 40	0.836	FALSE	FALSE	::::::::::::::::::
AAWDTRHGKLPVMISER	2	10.09	0.124	618	36.93	AE003544	TRUE	FALSE	3	1984.3	2.9	19of 64	2.2663	FALSE	FALSE	::::::::::Oxidation_M:::::
LAFPDP	1	3.1	0.098	2200	22.4	AE003544	TRUE	FALSE	1	659.8	-1.7	5of 10	0.7288	FALSE	FALSE	::::::
HLYAAHFREIALLGLHTHLNLTFAHLTALHR	2	9.85	0.073	2381	91.2	AE003544	TRUE	FALSE	3	3589.2	-0.8	14of120	1.4914	FALSE	FALSE	::::::::::::::::::::::::::::
DSNSKPLLLATLKYLMTLQ	11	9.63	0.023	456	58.83	AE003544	TRUE	FALSE	2	2166.6	2.9	9of 36	1.3066	FALSE	FALSE	::::::::::::::Oxidation_M::::
SHLNMLRK	13	11.49	0	1002	16.13	AE003544	TRUE	FALSE	1	1015.2	-2.8	2of 14	0.4834	FALSE	FALSE	:::::Oxidation_M::::
RRGYGLPMR	12	12.11	0.062	944	17.93	AE003545	TRUE	FALSE	2	1106.3	0.1	9of 16	1.4577	FALSE	FALSE	::::::::::
GWMLMHPGRLTHYHEGLLVTNGTRYIMIS	7	9.59	0.029	2011	82.39	AE003545	TRUE	FALSE	3	3402	-1.4	84	2.3666	FALSE	FALSE	::::::::::::::::::::::::Oxidation_M:::
ELIGMFNVPHVTSIYLVK	11	7.74	0.008	1356	62.63	AE003545	TRUE	TRUE	2	2077.5	1.9	14of 34	1.8725	FALSE	FALSE	:::::Oxidation_M:::::::::::
AMKTVHSSGCKSLR	1	10.59	0.006	2221	16.13	AE003545	TRUE	FALSE	2	1578.8	0	8of 26	1.1049	FALSE	FALSE	::Oxidation_M:::::::Cys_CAM:::::
KRTSVPPK	12	11.64	0.002	769	4.6	AE003545	TRUE	FALSE	2	913.1	1.4	8of 14	1.1817	FALSE	FALSE	::::::::
EFAFQRTCMATVGRL	14	9.01	0.179	356	42.33	AE003546	TRUE	FALSE	3	1788	-1.2	16of 56	1.5785	FALSE	FALSE	:::::::Cys_CAM::::::::
RYENMLMSY	4	6.83	0.171	2227	27.86	AE003546	TRUE	FALSE	1	1207.4	0.7	3of 16	0.7293	FALSE	FALSE	::::::::
IRRRILAGSGGNSYAAH	14	12.11	0.119	2381	27.9	AE003546	TRUE	FALSE	2	1800	-2.6	6of 32	1.0275	FALSE	FALSE	::::::::::::::::
RLLSKSGGKRDFQR	7	12.14	0.099	1755	17.7	AE003546	TRUE	FALSE	2	1648.9	2.2	13	1.2747	FALSE	FALSE	::::::::::::::
LQKQNYEILSGTSTSR	5	9.72	0.068	2845	26.3	AE003546	TRUE	TRUE	3	1826	0.4	10of 60	1.217	FALSE	FALSE	::::::::::::::::
NISSSSSSGNNNTSGNMR	12	11.05	0.067	881	8.13	AE003546	TRUE	FALSE	3	1830.8	0	21of 68	1.6185	FALSE	FALSE	::::::::::::::Oxidation_M::
MRRHHQQQHQQMATNTLKKSSS	8	12.43	0.041	2253	9.46	AE003546	TRUE	FALSE	3	2680	-1.5	12of 84	1.3532	FALSE	FALSE	:Oxidation_M:::::::::::::::::::
ENFKKPQRIKFDE	15	9.76	0.025	2816	20.5	AE003546	TRUE	FALSE	2	1679.9	1.2	6of 24	0.9624	FALSE	FALSE	::::::::::::::
GPTGGPVMGPMGPGGMTAGGMGPGPGCMSQQR	14	9.01	0.102	426	47.25	AE003547	TRUE	FALSE	2	3006.4	0.3	6of 62	1.2195	FALSE	FALSE	:::::::Oxidation_M:::Oxidation_M::::::::::::::Cys_CAM::::::
PDRQCLMFSATFKKRIERLAR	3	11.31	0.045	1596	49.03	AE003547	TRUE	TRUE	3	2641.1	-2.3	10of 80	1.1716	FALSE	FALSE	:::::Cys_CAM::Oxidation_M:::::::::::::
EYFKIEKMLTHAPSALPPK	11	9.56	0.008	1616	45.93	AE003547	TRUE	TRUE	3	2217.6	-2.6	17of 72	1.636	FALSE	FALSE	:::::::Oxidation_M:::::::::::

ELQIGQEVSNLFVNSTADK	10	3.83	0.187	2093	42.8	AE003548	TRUE	FALSE	2	2093.3	1	8of 36	1.1531	FALSE	FALSE	::::::::::::::::::
MAYFREYLLGLHNGYR	7	9.44	0.062	2000	50.23	AE003549	TRUE	FALSE	2	2004.3	-0.7	4	1.1339	FALSE	FALSE	::::::::::::::
ATFLRLGHKNHSQWTALGSASFILIS	15	11.49	0	1688	70.7	AE003549	TRUE	FALSE	3	2857.3	-0.6	24of100	1.9771	FALSE	FALSE	::::::::::::::::::::::
QRQLAALSSLPSTIQSTLDAVTK	5	10.09	0.104	1916	51.3	AE003550	TRUE	FALSE	2	2429.8	-0.8	11of 44	1.3632	FALSE	FALSE	::::::::::::::::::::
DGNAALHIAIE	14	4.07	0.103	574	27.3	AE003550	TRUE	FALSE	2	1124.2	-2.8	10of 20	1.51	FALSE	FALSE	::::::::::
GTMSMRGG	14	11.05	0.088	132	10.26	AE003550	TRUE	FALSE	1	796.9	2.3	4of 14	0.5761	FALSE	FALSE	::::::::
IAANTQPSTESIEDDGSSG	4	2.84	0.07	2251	22.8	AE003550	TRUE	FALSE	2	1879.9	0	9of 36	1.1277	FALSE	FALSE	::::::::::::::::::
SNKSPLELAEAKLRLLRN	5	10.58	0.044	2395	41.7	AE003550	TRUE	FALSE	2	2053.4	2.2	13of 34	1.3229	FALSE	FALSE	::::::::::::::::::
PLGALTPYVGVVDGPEVKKSKKIHGGDSAILGTYKMQSR	14	10.04	0.041	1814	71.33	AE003550	TRUE	FALSE	3	4099.8	-1.9	24of152	2.0528	FALSE	FALSE	::::::::::::::::::::::::::::::::::::
TPVPPPLPSPIMRSK	10	11.49	0.014	1978	35.53	AE003550	TRUE	FALSE	2	1634	-0.1	7of 28	1.0142	FALSE	FALSE	:::::::::::Oxidation_M::::
HQRDGSMGPPKRMMRSV	11	12.12	0.014	938	18.99	AE003550	TRUE	FALSE	2	1987.3	-2.6	9of 32	1.2021	FALSE	FALSE	:::::::::::Oxidation_M::::
PAPAPVQRVTRQSKAIAEEK	9	10.58	0.125	1614	28.6	AE003551	TRUE	FALSE	3	2177.5	-2.4	18of 76	1.7701	FALSE	FALSE	::::::::::::::::::::
SAMGSASPQALYKLVVP	5	9.72	0.113	2887	43.33	AE003551	TRUE	FALSE	3	1736	0.8	13of 64	1.3201	FALSE	FALSE	:::Oxidation_M:::::::::::::
DTYIDTFVTDIMMPK	15	3.6	0.073	1347	45.76	AE003551	TRUE	TRUE	2	1823.1	1.7	6of 28	0.9181	FALSE	FALSE	:::::::::::Oxidation_M:Oxidation_M:::
VGVPGQLDVLLDFMQDLR	7	3.6	0.072	1640	62.63	AE003551	TRUE	FALSE	2	2016.4	-2	275	0.9777	FALSE	FALSE	::::::::::::::::::
KKAKAKKLAGGGDNELTIK	5	10.54	0.061	3077	17.7	AE003551	TRUE	FALSE	2	1971.4	2.3	9of 36	1.3368	FALSE	FALSE	::::::::::::::::::
TQRVIKVTMKPPTTTVAPNKARVVCMSDTHS	9	10.82	0.061	2439	49.26	AE003551	TRUE	FALSE	3	3456	-2.9	21of120	2.1591	FALSE	FALSE	:::::::::::::::::::::::Cys_CAM::::::
YLATQSIVMNHPPWIGGMEVDLPRLYHTVQE	5	5.18	0.059	2702	88.56	AE003551	TRUE	FALSE	3	3629.1	-0.1	22of120	2.9288	FALSE	FALSE	:::::::::Oxidation_M::::::::::Oxidation_M:::::::::::::
FGHVTNQLRKLVKALKACEETYAR	5	10.05	0.015	2657	48.5	AE003551	TRUE	TRUE	3	2834.3	-2	15of 92	1.7105	FALSE	FALSE	:::::::::::::::::Cys_CAM::::::
NFRGVLPDVCDEDLGGAMPTRSSFEFILVRL	10	4.21	0.003	2104	93.23	AE003551	TRUE	FALSE	3	3513	-0.4	23of120	1.9082	FALSE	FALSE	:::::::::Cys_CAM:::::::::::::::::::::
SRAPISAKLVANMLSVAGADHI	5	10.09	0.001	3045	52.53	AE003551	TRUE	FALSE	3	2222.6	1.1	10of 84	1.2286	FALSE	FALSE	::::::::::::::::::::::
SASSGSGMGLGMGLGGGMSGGSLGKAN	4	10.1	0.146	2442	38.79	AE003552	TRUE	FALSE	2	2334.6	0.7	13of 52	1.7049	FALSE	FALSE	:::::::Oxidation_M::::Oxidation_M::::::Oxidation_M:::::::::::
DNNNNSIGITFLGTFR	14	6.79	0.115	2601	36.9	AE003552	TRUE	TRUE	3	1783.9	-2.1	7of 60	0.9078	FALSE	FALSE	::::::::::::::::
RNMLDKLVVIKLNGGLGTSMGCHGPKSVIPVR	5	10.82	0.109	1762	73.46	AE003552	TRUE	FALSE	3	3449.1	-1.4	21of124	2.5501	FALSE	FALSE	:::::::::::::::::::Cys_CAM:::::::::::
SRDSRSASSGSGMGLGMGLGGGMSGGSLGKANGSM	15	11.33	0.085	2954	42.52	AE003552	TRUE	FALSE	3	3195.5	-0.8	13of136	1.5181	FALSE	FALSE	:::::::::::::::::::::Oxidation_M::::::::::::Oxidation_M:
PSEVEQQAAASATTSTLNPTAPTPTP	8	3.13	0.075	2160	37.7	AE003552	TRUE	FALSE	3	2568.8	-2.1	15of100	1.4423	FALSE	FALSE	::::::::::::::::::::::::
QILNGNLAVATPTSPAGGATQGIGSI	13	6.02	0.075	390	54.6	AE003552	TRUE	FALSE	2	2409.7	2.7	7of 50	1.0196	FALSE	FALSE	::::::::::::::::::::::
GSPIDWFMQR	14	6.79	0.04	183	31.03	AE003552	TRUE	FALSE	3	1253.4	-2.8	10of 36	1.4151	FALSE	FALSE	:::::::Oxidation_M:::
NNQRIFSDDEDDAYGAATQVMNI	2	3.37	0.004	92	43.63	AE003552	TRUE	FALSE	3	2588.7	-2.6	13of 88	1.0924	FALSE	FALSE	::::::::::::::::::::::
AGGLLALTGAKPALEGTPGMIGYGMAK	15	9.63	0.329	1463	66.06	AE003553	TRUE	TRUE	2	2547	0.4	19of 52	3.5274	FALSE	FALSE	::::::::::::::::::::::
ADEISMEKK	3	4.45	0.107	1153	12.93	AE003553	TRUE	FALSE	2	1067.2	-1.6	8of 16	1.0861	FALSE	FALSE	:::::Oxidation_M::::
PVNPMIYVGR	9	9.85	0.068	1565	30.03	AE003553	TRUE	FALSE	1	1162.4	0.5	10of 18	1.5547	FALSE	FALSE	:::::Oxidation_M:::::::
SHTMQLPICSRSKDVIEYMILPQWFL	13	7.16	0.022	1475	87.06	AE003553	TRUE	FALSE	3	3194.7	-2.9	7of100	1.0548	FALSE	FALSE	:::::::::Cys_CAM:::::::::::::::
MAFSLSQRACRPSRLLSTEDRVR	8	11.81	0.021	1776	49.63	AE003553	TRUE	FALSE	3	2738.1	2.2	20of 88	1.7892	FALSE	FALSE	:::::::::Cys_CAM:::::::::::::
PPTPPPRIIKH	14	11.49	0.292	2772	20.6	AE003554	TRUE	FALSE	2	1253.5	2	5of 20	0.9167	FALSE	FALSE	::::::::::
PPTGPSTPSGPSNP	6	6.02	0.205	1308	11.6	AE003554	TRUE	FALSE	1	1293.4	-1.7	6of 26	1.0202	FALSE	FALSE	::::::::::::::
QLEGKDAVEAKEKQDTLK	15	4.73	0.117	113	20.9	AE003554	TRUE	FALSE	2	2031.3	2.4	6of 34	1.1197	FALSE	FALSE	::::::::::::::::
MLHKVVGSEADTGR	3	7.82	0.086	1028	22.13	AE003554	TRUE	FALSE	2	1500.7	0.4	11of 26	2.2499	FALSE	FALSE	::::::::::::::
FNMKALQLEGKDAVEAKEK	13	7.14	0.072	326	35.13	AE003554	TRUE	FALSE	2	2150.5	2.8	10of 36	1.1511	FALSE	FALSE	::::::::::::::::
MLHKVVGSEADTGR	2	7.82	0.016	468	22.13	AE003554	TRUE	FALSE	2	1500.7	0.7	12of 26	1.9478	FALSE	FALSE	::::::::::::::
LWNFYSKAVRAGGR	12	11.39	0.001	935	34	AE003554	TRUE	FALSE	3	1625.9	1.5	16of 52	1.3691	FALSE	FALSE	::::::::::::::
INAVTRRDYQETFEFINTLAK	14	7.06	0.15	1100	52.3	AE003555	TRUE	FALSE	3	2530.8	-2.7	11of 80	1.4794	FALSE	FALSE	::::::::::::::::::
NASLMASPLSKMYAPQPGQR	5	10.4	0.147	2992	39.66	AE003555	TRUE	FALSE	3	2164.5	-1	16of 76	1.3582	FALSE	FALSE	:::::Oxidation_M:::::::::::::
GACSLGSTQPDSQVMVIN	9	3.1	0.085	2228	36.83	AE003555	TRUE	FALSE	2	1881	2	11of 34	1.6499	FALSE	FALSE	:::Cys_CAM::::::::::Oxidation_M::::
NILGGTVFR	14	11.05	0.077	923	27.6	AE003555	TRUE	TRUE	2	977.2	1.5	12of 16	1.9892	FALSE	FALSE	::::::::::
SLTDMLEHVKLSSREHANRTST	15	7.97	0.063	1292	32.13	AE003555	TRUE	FALSE	3	2513.8	-1.1	13of 84	1.2069	FALSE	FALSE	::::::::::::::::::::
FPDTLSMRSGPSLRRISAGNSKTDLYC	6	9.74	0.052	1535	54.13	AE003555	TRUE	FALSE	3	3047.4	-1	21of104	1.8345	FALSE	FALSE	:::::::Oxidation_M::::::::::::::::::Cys_CAM:
LSKESHVAPILNGYYIR	7	9.53	0.038	2124	44.1	AE003555	TRUE	FALSE	2	1961.3	2.3	2	1.3164	FALSE	FALSE	::::::::::::::::
NYQPDFDS	7	2.93	0.015	2205	14.2	AE003555	TRUE	FALSE	1	986	0.1	67	0.6893	FALSE	FALSE	::::::::
YNKQYKKEYEAAGIWYEHR	1	9.24	0	2113	31.7	AE003555	TRUE	FALSE	2	2477.7	-3	9of 36	1.7145	FALSE	FALSE	::::::::::::::::::
PLSALEDSQNGLNRLENGQAK	4	4.45	0.153	2510	35.5	AE003556	TRUE	FALSE	2	2255.4	-1.6	11of 40	1.6963	FALSE	FALSE	::::::::::::::::::::
PPNYQDHINPPARFSDANDKTK	10	7.72	0.15	2559	24.3	AE003556	TRUE	FALSE	3	2526.7	1	10of 84	1.0839	FALSE	FALSE	::::::::::::::::::::
TGHQRRAKQFRAR	11	12.88	0.145	1898	5.9	AE003556	TRUE	TRUE	2	1612.8	2.3	5of 24	0.6999	FALSE	FALSE	::::::::::::::
VLSEVAGKIVPALILLFDGLKR	15	9.89	0.145	1950	80.3	AE003556	TRUE	FALSE	3	2352.9	-2.7	21of 84	2.2677	FALSE	FALSE	::::::::::::::::::::
AMAIALQIR	14	11.05	0.082	115	33.83	AE003556	TRUE	FALSE	2	987.2	1	10of 16	1.9197	FALSE	FALSE	::::::::::
EDYATPVPAAQSLLHSMCKKRK	9	9.59	0.068	2795	36.33	AE003556	TRUE	FALSE	3	2547.9	-2.5	10of 84	1.133	FALSE	FALSE	:::::::::::::::Oxidation_M:Cys_CAM:::::
QAQQQLILTNYLHL	9	7.76	0.049	2556	44.2	AE003556	TRUE	FALSE	2	1683.9	0.7	5of 26	0.9454	FALSE	FALSE	::::::::::::::
GSPSNVVSEKYQK	9	9.63	0.042	525	12	AE003556	TRUE	FALSE	3	1423.6	-2.4	14of 48	1.559	FALSE	FALSE	::::::::::::::
HSRCRIILGGQYQFVSREHANIIVSEKG	9	9.74	0.035	1925	57.2	AE003556	TRUE	FALSE	2	3256.7	0	12of 54	2.6714	FALSE	FALSE	::::Cys_CAM:::::::::::::::::::::
GAGFVGSHLVDDLMVQGHEVIVVDNFFTGRKR	10	6.04	0.023	1626	78.43	AE003556	TRUE	FALSE	3	3518	-1.9	20of124	1.6804	FALSE	FALSE	:::::::::::::Oxidation_M:::::::::::::::
AAINGVFPPTLQELVK	1	6.95	0.022	409	48.5	AE003556	TRUE	FALSE	2	1698	-1.3	8of 30	1.393	FALSE	FALSE	::::::::::::::::
VWRTVVDAGHLPVR	11	10.89	0.015	1196	38.2	AE003556	TRUE	FALSE	2	1605.9	-1.6	10of 26	1.2012	FALSE	FALSE	::::::::::::::
SCEACKAFFK	2	8.29	0.012	990	22.1	AE003556	TRUE	FALSE	2	1248.4	0.4	5of 18	0.8224	FALSE	FALSE	::Cys_CAM:::Cys_CAM::::::
LRGVSAEVKVKDK	7	10.32	0.001	3420	19.1	AE003556	TRUE	TRUE	2	1429.7	0.8	26	0.9619	FALSE	FALSE	::::::::::::
MFGNEEHKLVMVGLDNAGKTTILYQFL	1	5.35	0	2032	79.06	AE003556	TRUE	FALSE	3	3070.6	2.7	12of104	1.1939	FALSE	FALSE	::::::::::::::::::::::
LSSTLMNGNQR	10	11.05	0.079	1062	19.93	AE003557	TRUE	FALSE	2	1221.4	-2.5	10of 20	1.2135	FALSE	FALSE	::::::::::
ILRCPVTTNCGHTFCR	6	8.59	0.029	2427	36.1	AE003557	TRUE	FALSE	2	1993.2	-1.3	9of 30	1.0734	FALSE	FALSE	:::Cys_CAM:::::Cys_CAM:::::Cys_CAM::
ALRQADKAGSCSDKLVKIA	5	9.79	0.104	1778	32.1	AE003558	TRUE	FALSE	2	2032.3	2.9	14of 36	2.1607	FALSE	FALSE	:::::::::Cys_CAM:::::::::
GEAVVEDASETLTTTL	14	2.89	0.059	2061	35.7	AE003558	TRUE	FALSE	3	1636.8	-0.3	16of 60	1.3831	FALSE	FALSE	::::::::::::::::
LRPEVPKSLWVNQLQPR	6	11.33	0.057	2858	46.1	AE003558	TRUE	FALSE	3	2061.4	-1.4	9of 64	1.0785	FALSE	FALSE	::::::::::::::::
AKRRSDDVRLQLALSQSEQDFKDPNGRPIPAPKK	1	10.54	0.054	2110	48.5	AE003558	TRUE	FALSE	3	3863.4	1.8	9of132	1.097	FALSE	FALSE	::::::::::::::::::::::::::::::
LSNKTESRRSVTSSTSTTTSSASATSRVISEIHF	6	11.23	0.053	2179	42.6	AE003558	TRUE	FALSE	3	3617.9	2.3	25of132	2.5996	FALSE	FALSE	::::::::::::::::::::::::::::::
EANEVDLGGQS	13	2.95	0.042	2229	16.3	AE003558	TRUE	FALSE	2	1119.1	2.3	7of 20	1.3706	FALSE	FALSE	::::::::::::
EEFSMAELHGLR	2	4.54	0.034	2202	32.03	AE003558	TRUE	FALSE	2	1419.6	2.3	6of 22	1.2343	FALSE	FALSE	::::::::::::
FLLQNGANVDAATSIG	3	3.1	0.022	1511	41.7	AE003558	TRUE	FALSE	2	1591.8	1.4	13of 30	1.6376	FALSE	FALSE	::::::::::::::::
NREVRLAEMS	14	7.13	0.001	1026	20.83	AE003558	TRUE	FALSE	1	1221.4	-0.5	7of 18	1.1603	FALSE	FALSE	:::::::::Oxidation_M::
RLLVVPKLTVCALHVTQTAR	13	11.33	0.095	1063	57.4	AE003559	TRUE	FALSE	3	2276.7	-2.9	20of 76	2.1179	FALSE	FALSE	:::::::::::Cys_CAM:::::::::
RFIWKTVLGEMSRQMETGDETDKPTHFHKR	1	9.76	0.079	1889	51.76	AE003559	TRUE	FALSE	3	3695.2	1.7	22of116	2.5725	FALSE	FALSE	:::::::::::Oxidation_M:::Oxidation_M:::::::::::::::
HKGTEIKRYCVLMSDIFMYCKMIK	1	9.46	0.076	860	64.59	AE003559	TRUE	FALSE	3	3101.6	-2	20of 92	2.2595	FALSE	FALSE	:::::::::::Cys_CAM:::Oxidation_M::::Oxidation_M::Cys_CAM::Oxidation_M:::
QNMLTVRNASIKSKAAN	9	11.64	0.074	1525	25.63	AE003559	TRUE	FALSE	2	1847.1	2.4	7of 32	0.9796	FALSE	FALSE	::::::::::::::::::
LKRHMVIHTGEKKYQCDICK	1	9.57	0.069	805	31.63	AE003559	TRUE	TRUE	3	2561.9	0.4	17of 76	1.6955	FALSE	FALSE	:::::Oxidation_M::::::::::Cys_CAM:::Cys_CAM::
VATLLAIASVFSVVR	13	11.05	0.057	536	57.3	AE003559	TRUE	FALSE	3	1546.9	-3	18of 56	1.7046	FALSE	FALSE	::::::::::::::::
IIYKQYDAMVGEEVYSR	6	4.45	0.051	2343	45.13	AE003559	TRUE	FALSE	2	2081.3	0.8	10of 32	1.1177	FALSE	FALSE	:::::::::Oxidation_M:::::::::

TEIKRYCVLMSDIFMYCK	14	8.26	0.041	1891	58.16	AE003559	TRUE	FALSE	2	2358.7	2.9	11of 34	1.555	FALSE	FALSE	::::::Cys_CAM::::::::Cys_CAM::
SMSYRRDAWPTMPEQN	10	6.96	0.03	2204	30.06	AE003559	TRUE	FALSE	2	1970.2	1.4	7of 30	1.0248	FALSE	FALSE	::::::::::::::
RRCNPFGQAGSNAGP	2	10.9	0.026	769	15.5	AE003559	TRUE	FALSE	2	1589.7	1.7	10of 28	1.531	FALSE	FALSE	:::Cys_CAM::::::::::::
TPSQVRNEDLYWTRHWQKNIGY	1	9.53	0.002	989	44.6	AE003559	TRUE	FALSE	3	2793.1	2	14of 84	1.2638	FALSE	FALSE	::::::::::::::::::::
GQMYLTLHSYGSLILYP	12	7.65	0	1056	58.53	AE003559	TRUE	FALSE	3	1957.3	-2.6	16of 64	1.5968	FALSE	FALSE	::::::::::::::::
RDLYDLASITKDTGDRIK	4	6.95	0.103	1918	33.7	AE003560	TRUE	TRUE	2	2081.3	-0.8	6of 34	1.02	FALSE	FALSE	::::::::::::::
SVMKLPVNGNSEVIVSGPTTNVAP	15	6.95	0.092	1460	51.43	AE003560	TRUE	FALSE	2	2427.8	2.6	14of 46	2.2332	FALSE	FALSE	:::Oxidation_M:::::::::::::::::
STENLHYLSSEQALEDLASFVTAMKVK	15	4.63	0.042	67	63.53	AE003560	TRUE	FALSE	3	3029.4	1.2	14of104	1.2712	FALSE	FALSE	:::::::::::::::::::::::Oxidation_M::::
PPPHEVQMIPATMLRR	9	10.89	0.132	2552	39.96	AE003561	TRUE	FALSE	3	1874.3	-0.9	14of 60	1.6511	FALSE	FALSE	::::::::::::::::
QCRNQRNVLGTPPPVKGRK	14	12.14	0.083	1603	19.7	AE003561	TRUE	FALSE	2	2206.5	0.5	10of 36	1.3838	FALSE	FALSE	::Cys_CAM:::::::::::::::
SRMKLRVSFAGKEGGGKLKESVV	7	10.97	0.047	1165	38.03	AE003561	TRUE	FALSE	3	2464.9	-2.2	440	1.3497	FALSE	FALSE	::::::::::::::::::::
MFPDKIYKSVQPKGE	9	9.56	0.045	1194	29.13	AE003561	TRUE	FALSE	3	1784.1	0.3	14of 56	1.3084	FALSE	FALSE	:Oxidation_M:::::::::::::
KITPTQHAGALPPGTRIMQPQR	5	12.42	0.036	1480	36.43	AE003561	TRUE	FALSE	2	2415.8	1.7	11of 42	1.3987	FALSE	FALSE	:::::::::::::::::Oxidation_M:::::
AQAQQVKAKANVMRTIDRLQPGKAK	6	11.63	0.01	1870	33.43	AE003561	TRUE	FALSE	3	2752.3	-2.8	14of 96	1.3453	FALSE	FALSE	::::::::::::::::::::::::
SDKASKADTEKHSEKSKK	5	9.97	0.004	2799	-8.3	AE003561	TRUE	TRUE	3	2005.2	-2.4	12of 68	1.2649	FALSE	FALSE	::::::::::::::::
AAMVSAFRLFLRP	11	12.41	0.138	445	49.53	AE003562	TRUE	FALSE	3	1479.8	-2.1	16of 48	2.0463	FALSE	FALSE	::::::::::::
RPVRVLPSSSSDSSFSRGKMSR	7	12.41	0.087	1892	29.63	AE003562	TRUE	FALSE	2	2424.7	0.1	3	1.7807	FALSE	FALSE	::::::::::::::::::::
RTWCMGA	3	9.01	0.067	2408	18.73	AE003562	TRUE	FALSE	1	882	-0.5	4of 12	0.9326	FALSE	FALSE	::::Cys_CAM::::
DNKWRSKSLVTWKKIDRR	15	11.53	0.044	901	27.9	AE003562	TRUE	FALSE	3	2317.7	2.8	22of 68	2.2915	FALSE	FALSE	::::::::::::::::::::
TQVVTLVLYTYFIAALLGRQMLPNVLDR	3	9.59	0.044	1727	104.63	AE003563	TRUE	FALSE	3	3209.9	1.8	21of108	2.6104	FALSE	FALSE	::::::::::::::::::::::::::::
FREDCLPVVLPILK	14	6.36	0.022	2648	55	AE003563	TRUE	FALSE	3	1700	2.2	12of 52	1.278	FALSE	FALSE	:::::Cys_CAM:::::::::
RKRIPIEE	1	10.09	0.012	1100	15.7	AE003563	TRUE	FALSE	1	1041.2	1.7	7of 14	1.3317	FALSE	FALSE	::::::::
AQLAPRNIDR	13	10.89	0.066	2505	19.9	AE003564	TRUE	FALSE	2	1154.3	-2.5	5of 18	1.0114	FALSE	FALSE	::::::::::
SGFGGEIGSGR	14	6.98	0.064	2805	14.6	AE003564	TRUE	FALSE	2	1024.1	-0.1	11of 20	1.3759	FALSE	FALSE	::::::::::
PMMSAVMLLCA	11	5.33	0	746	46.19	AE003564	TRUE	FALSE	2	1240.5	0.3	6of 20	1.0337	FALSE	FALSE	::Oxidation_M::::::::Cys_CAM::
VNKTLKAVIGLCVVDASVR	7	9.91	0.208	1296	50.2	AE003565	TRUE	FALSE	3	2043.4	-0.9	2	2.7083	FALSE	FALSE	:::::::::::Cys_CAM::::::::
QMLVSAFTVPVAVCGTAF	14	5.33	0.179	1458	61.23	AE003565	TRUE	FALSE	2	1899.2	2.7	10of 34	1.5723	FALSE	FALSE	:::::::::::Cys_CAM:::::
NPANLASPTEECGCVR	13	4.27	0.075	1597	26.9	AE003565	TRUE	FALSE	2	1775.8	1.9	13of 30	1.8563	FALSE	FALSE	:::::::::::Cys_CAM::Cys_CAM:::
TIETILKAKLNLPAY	11	9.63	0.073	706	47.1	AE003565	TRUE	FALSE	2	1689	2.4	7of 28	1.0458	FALSE	FALSE	::::::::::::::
ESKLPSETKSTEPLIENNRSR	4	7.22	0.065	2770	25.8	AE003565	TRUE	TRUE	3	2416.7	2.7	11of 80	1.1565	FALSE	FALSE	::::::::::::::::::::
KPINEIPEYLDFLDDVQD	11	3.32	0.059	492	52.9	AE003565	TRUE	FALSE	3	2164.4	0.3	18of 68	2.2421	FALSE	FALSE	::::::::::::::::::
ADKRNRKFKEAERLFSKSSITSMAI	1	10.95	0.058	116	42.03	AE003565	TRUE	FALSE	3	2931.4	-2.7	11of 96	1.3063	FALSE	FALSE	:::::::::::::::::::::Oxidation_M:::
IVQHFGQGIVSDDGRIDRSK	3	7.82	0.043	2607	34.5	AE003565	TRUE	TRUE	2	2228.5	3	11of 38	1.349	FALSE	FALSE	::::::::::::::::::
NGAQHGVPFFLDDFKNK	13	7.79	0.024	1919	33.9	AE003565	TRUE	FALSE	2	1935.1	0.1	10of 32	1.5536	FALSE	FALSE	::::::::::::::::
YFAMKVLKKASIVTNQKDTAHT	11	10.3	0.023	1264	40.33	AE003565	TRUE	FALSE	3	2495.9	2.9	14of 84	1.4948	FALSE	FALSE	::::::::::::::::::
ATHYVADAHGYRTVEPE	10	5.18	0.015	2137	25.6	AE003565	TRUE	FALSE	2	1917	-3	12of 32	1.2995	FALSE	FALSE	::::::::::::::::
NCHEVWSMIVPPDEAVRRIIERNK	11	7.17	0.013	204	56.23	AE003565	TRUE	FALSE	3	2966.4	2.4	10of 92	1.0181	FALSE	FALSE	::Cys_CAM::::::Oxidation_M:::::::::::::::
VICMVTLQEESAKAFTYAVK	9	6.43	0.011	850	56.23	AE003565	TRUE	FALSE	3	2289.7	-1.7	16of 76	1.532	FALSE	FALSE	:::Cys_CAM:::::::::::::::
AVACIFLQCVYSAK	15	8.28	0.004	1562	47	AE003565	TRUE	FALSE	2	1630.9	-1.6	4of 26	0.7975	FALSE	FALSE	::::Cys_CAM::::::Cys_CAM::::::
TNKFSFILTQKCQSIVLMQLHPK	10	10.33	0.111	2663	62.23	AE003566	TRUE	FALSE	3	2779.3	2.9	14of 88	1.3851	FALSE	FALSE	:::::::::::Cys_CAM::::::Oxidation_M::::::
EPGTTNPEASTTEKPADGICEGK	5	4.01	0.027	1499	21.4	AE003566	TRUE	FALSE	3	2390.5	1	23of 88	1.9465	FALSE	FALSE	:::::::::::::::::::Cys_CAM::::
KPPCVKKIETSDLHVDMDTV	8	5.33	0.022	1680	36.93	AE003566	TRUE	FALSE	3	2313.6	-0.3	20of 76	1.8179	FALSE	FALSE	:::::Cys_CAM:::::::::::::::
DGTIFAYIGNCSEYL	15	3.01	0.021	2213	45.3	AE003566	TRUE	FALSE	2	1723.8	-2.9	5of 28	0.8652	FALSE	FALSE	:::::::::::Cys_CAM:::::
YMERPEYDGTYCATALWTK	13	4.45	0.014	356	45.83	AE003566	TRUE	FALSE	2	2372.6	2	6of 36	0.8774	FALSE	FALSE	::Oxidation_M::::::::::Cys_CAM::::::::
ILLFSYAITLMILGTEILYSK	2	6.81	0.01	1705	94.33	AE003566	TRUE	FALSE	2	2420	0.2	5of 40	0.6803	FALSE	FALSE	:::::::::::Oxidation_M:::::::::::
VHPIRADYSAIDLDIDSADRAMLSSEVQ	6	3.93	0.009	1584	66.43	AE003566	TRUE	FALSE	3	3105.4	-1.5	18of108	1.5208	FALSE	FALSE	:::::::::::::::::::::Oxidation_M:::::::
KMVPLVARVMAANRISQNRQTWA	12	12.71	0.003	2829	55.66	AE003566	TRUE	FALSE	3	2674.2	1.6	9of 88	0.9957	FALSE	FALSE	::Oxidation_M::::::::Oxidation_M::::::::::::::
EVIDKIAPSAARK	15	9.89	0.088	2827	24.1	AE003567	TRUE	TRUE	2	1398.6	3	8of 24	1.1303	FALSE	FALSE	::::::::::::::
KLQSKVKSVGKTKP	2	11.13	0.146	182	9.6	AE003568	TRUE	FALSE	3	1528.9	-1.6	11of 52	1.7954	FALSE	FALSE	::::::::::::::
IGKLSSGSMKL	9	10.6	0.11	838	23.93	AE003568	TRUE	FALSE	2	1137.4	2.6	11of 20	1.456	FALSE	FALSE	:::::::::Oxidation_M:::
SGSGLVGLGTGTGTGSGCGPAIR	14	9.01	0.053	1966	34	AE003568	TRUE	FALSE	3	2020.2	1.4	22of 88	1.7993	FALSE	FALSE	:::::::::::::::::Cys_CAM::::::
YNVKGNPFTPHLVIGWAPK	6	10.18	0.028	1284	47.6	AE003568	TRUE	FALSE	2	2139.5	-2.4	8of 36	0.9437	FALSE	FALSE	::::::::::::::::::
QQAHHQNYSKTLQRPPMMLPPQMKAIP	5	10.71	0.02	2549	49.49	AE003568	TRUE	FALSE	3	3188.8	-1.7	19of104	1.703	FALSE	FALSE	:::::::::::::::::Oxidation_M:::::::::::
SQVFFLKANAGTFFVAHDIFR	5	10.09	0.352	1970	67	AE003569	TRUE	FALSE	3	2416.8	-1.4	22of 80	2.8685	FALSE	FALSE	::::::::::::::::::::
STPAAALKAQQQRKLSSMEPSMDDALAIGTQMTR	4	9.88	0.159	1639	61.19	AE003569	TRUE	FALSE	3	3651.2	2.4	22of132	2.948	FALSE	FALSE	:::::::::::::::::::::::::::::::::::Oxidation_M:::
PKNIYYISGGDEAEEEEQ	15	3.51	0.104	784	30.2	AE003569	TRUE	FALSE	3	2072.1	0.3	18of 68	2.3578	FALSE	FALSE	::::::::::::::::::
RQQLKNARMKYKASERAMERRLKRSN	7	12.14	0.09	2173	26.36	AE003569	TRUE	FALSE	3	3266.8	-1.5	406	1.7687	FALSE	FALSE	:::::::::::::::::Oxidation_M:::::::::
ERLLKAGQAFNPGEPVIKI	7	9.89	0.031	3286	48.5	AE003569	TRUE	FALSE	3	2081.5	-1.7	143	1.0289	FALSE	FALSE	::::::::::::::::::
ARKTHRKRREHSRESQEQEQEH	6	10.55	0.018	2399	-5.8	AE003569	TRUE	FALSE	3	2844	2.6	14of 84	1.3423	FALSE	FALSE	::::::::::::::::::::
CEQCPQLFRHKSAISRHVRV	1	10.12	0.01	195	35.4	AE003569	TRUE	FALSE	2	2509.8	2	7of 38	1.1068	FALSE	FALSE	:Cys_CAM:::Cys_CAM:::::::::::::::
PMLILKKSVD	2	9.89	0	1986	31.93	AE003569	TRUE	FALSE	1	1144.5	-2.4	3of 18	0.4151	FALSE	FALSE	::::::::::
LSHCLMHHEHIITMEMK	14	6.48	0.01	822	42.29	AE003570	TRUE	FALSE	3	2164.5	-1.8	18of 64	2.1327	FALSE	FALSE	::::Cys_CAM::::::::::Oxidation_M::
KAAREKGGTKSAAKQGKKSTK	12	11.26	0.121	2796	-6	AE003571	TRUE	FALSE	3	2161.5	0	10of 80	1.2937	FALSE	FALSE	::::::::::::::::::::
KQNRSIKRR	9	12.71	0.092	1457	0.6	AE003571	TRUE	FALSE	2	1186.4	-2.6	5of 16	0.9614	FALSE	FALSE	::::::::::
SGKRSSCSSDSIIK	9	9.91	0.09	1305	11.4	AE003571	TRUE	FALSE	3	1512.6	1.7	17of 52	1.8866	FALSE	FALSE	::::::Cys_CAM::::::::
QQHNIMAGGGVTHPGDLTL	10	6.01	0.025	1666	33.93	AE003571	TRUE	FALSE	3	1947.2	-2.8	20of 72	1.6945	FALSE	FALSE	::::::::::::::::
YFDDGGGAGAGDV	1	2.82	0.024	2046	21.2	AE003571	TRUE	FALSE	2	1201.2	-2.8	6of 24	0.9012	FALSE	FALSE	::::::::::::
QEQNNMEPLR	5	4.27	0.001	2964	16.03	AE003571	TRUE	FALSE	2	1275.4	-1.2	6of 18	1.0062	FALSE	FALSE	::::::Oxidation_M:::::
LKETYGSLER	13	7.02	0.082	2489	20.4	AE003572	TRUE	FALSE	2	1196.3	-0.5	4of 18	0.7622	FALSE	FALSE	::::::::::
MEPDVAAMVQHMHQDDEA	12	3.84	0.06	1016	33.19	AE003572	TRUE	FALSE	3	2087.3	-0.5	19of 68	2.2819	FALSE	FALSE	:Oxidation_M::::::::::Oxidation_M:::::::
TAASPPLDVASGSDDLVIIDSDASADAAANMINIMDAQR	2	3.15	0.008	1740	87.86	AE003572	TRUE	FALSE	3	3936.3	0.3	27of152	2.5352	FALSE	FALSE	:::::::::::::::::::::::::::::::Oxidation_M::::Oxidation_M:::::
CSSSGLGLQLRQR	14	10.9	0.082	646	24.7	AE003574	TRUE	FALSE	2	1462.6	1.4	10of 24	1.0856	FALSE	FALSE	:Cys_CAM:::::::::::
MQITSSGCSS	15	5.33	0.082	248	15.13	AE003574	TRUE	FALSE	2	1074.1	0.2	9of 18	0.9662	FALSE	FALSE	:Oxidation_M::::::Cys_CAM:::
VIAPRRSSTSAAGSGSLYGTSAVGT	14	11.14	0.058	1678	38.6	AE003574	TRUE	FALSE	2	2354.6	-0.5	13of 48	1.9056	FALSE	FALSE	::::::::::::::::::::::
INPLATETINRR	11	10.89	0.034	2655	26.8	AE003574	TRUE	FALSE	2	1398.6	3	9of 22	1.0694	FALSE	FALSE	::::::::::::
NYKRDLEHR	7	9.72	0.032	1131	7.9	AE003574	TRUE	FALSE	2	1231.4	-2.6	220	1.5083	FALSE	FALSE	::::::::::
RPYNLNQAKLPFKFR	10	11.51	0.004	1724	36.3	AE003574	TRUE	FALSE	2	1893.2	1.3	4of 28	0.9396	FALSE	FALSE	::::::::::::::::
LGMPENLSPEAQSLLRALFK	1	7.1	0.003	1718	60.43	AE003574	TRUE	TRUE	2	2231.6	1.2	5of 38	0.8532	FALSE	FALSE	:::Oxidation_M:::::::::::::::
LTDMILGLLKKILRK	13	10.83	0.172	540	54.53	AE003575	TRUE	FALSE	3	1756.3	-1.8	11of 56	1.51	FALSE	FALSE	::::::::::::::::
LGKLPRDQLDEQQLERLQKAEEYIVAHKAML	1	5.52	0.112	1616	74.03	AE003575	TRUE	FALSE	3	3665.2	2.7	10of120	1.1745	FALSE	FALSE	::::::::::::::::::::::::::::
ATILCEVKGEP	1	4.27	0.054	1985	27.6	AE003575	TRUE	FALSE	1	1217.4	1.9	4of 20	0.9702	FALSE	FALSE	:::::Cys_CAM::::::
STTTTCTSGPTTTTPRSTTKT	8	10.11	0.041	2972	10.3	AE003575	TRUE	FALSE	2	2189.3	2.7	8of 40	1.0106	FALSE	FALSE	::::::Cys_CAM:::::::::::::::
QQVMEEAERLMTST	7	3.97	0.031	1743	29.86	AE003575	TRUE	FALSE	2	1653.9	1.8	79	1.0384	FALSE	FALSE	::::::::::::::

KPMYLNFTHIAIMNR	6	10.4	0.02	2140	45.16	AE003575	TRUE	FALSE	2	1866.3	-0.6	8of 28	1.1335	FALSE	FALSE		::::::::::::Oxidation_M::::
DRYERARRSPSPVPSSAAAMIRE	13	10.93	0.019	2242	35.03	AE003575	TRUE	FALSE	3	2603.9	-0.7	11of 88	1.2804	FALSE	FALSE		::::::::::::::::::::::
QRERLPIR	10	12.11	0.004	881	16.8	AE003575	TRUE	FALSE	1	1068.3	-0.2	8of 14	1.7986	FALSE	FALSE		::::::::
MNRIRIIK	13	12.42	0	2286	23.83	AE003575	TRUE	FALSE	2	1060.3	-2.1	4of 14	0.5404	FALSE	FALSE		:Oxidation_M::::::::
GERNRIINIATPSRLCANK	14	11.23	0.176	2625	34.5	AE003576	TRUE	FALSE	3	2184.5	1.4	14of 72	1.6169	FALSE	FALSE		::::::::::::::::Cys_CAM::::
DSTRSKPGFLSVPMAGQDSRR	9	11.23	0.118	2201	28.63	AE003576	TRUE	FALSE	2	2293.6	-2.1	10of 40	1.4165	FALSE	FALSE		::::::::::::::::::::::
PGVINIPSVTHPEYPTSQVPV	1	5.13	0.105	1005	48.3	AE003576	TRUE	FALSE	2	2232.5	1	10of 40	1.3089	FALSE	FALSE		::::::::::::::::::::::
YQGDAYNGLCALAQR	3	6.09	0.076	2818	32.4	AE003576	TRUE	FALSE	2	1700.8	-2.9	6of 28	1.2719	FALSE	FALSE		::::::::::Cys_CAM::::::
NPPIQDVTYPAPQPSPPVPGIVNIPSLP	6	3.1	0.037	2359	70.8	AE003576	TRUE	FALSE	3	2906.4	-0.4	20of108	1.8033	FALSE	FALSE		::::::::::::::::::::::::::::
PPTIYNQQRYLLV	12	9.59	0.034	2513	41	AE003576	TRUE	FALSE	3	1605.9	2.4	9of 48	1.479	FALSE	FALSE		::::::::::::::
ACMRNRCVDP	2	8.3	0.029	2373	18.13	AE003576	TRUE	FALSE	2	1295.4	3	7of 18	1.2122	FALSE	FALSE		::Cys_CAM:Oxidation_M::::Cys_CAM::::
ESNLKSHDCAHTR	15	7.32	0.017	121	6.7	AE003576	TRUE	FALSE	2	1555.6	0.6	7of 24	1.0526	FALSE	FALSE		::::::::Cys_CAM:::::
LHLVENHPEFGRASVNL	4	6.03	0.008	2933	42.2	AE003576	TRUE	FALSE	2	1933.2	0.1	4of 32	0.8256	FALSE	FALSE		::::::::::::::::
LPKYVEKSFRSGLLNFSAVALALNDLGYHALGIR	10	9.94	0.119	2431	100.7	AE003577	TRUE	FALSE	3	3735.4	-1.1	26of132	3.34	FALSE	FALSE		::::::::::::::::::::::::::::::
MALVDTYDVKRSGLLNFSAVALALNDLGYHALGIR	5	7.69	0.099	2847	105.33	AE003577	TRUE	FALSE	3	3795.4	-1.5	24of136	2.7383	FALSE	FALSE		:Oxidation_M:::::::::::::::::::::::::::::::
NAARYRMVAGKHVK	3	11.51	0.093	1484	17.73	AE003577	TRUE	FALSE	2	1617.9	2.7	5of 26	1.154	FALSE	FALSE		:::::::Oxidation_M:::::::
EEQLIPDCATLANSNSA	11	2.95	0.093	1409	35.6	AE003577	TRUE	FALSE	2	1833.9	1.3	8of 32	0.9268	FALSE	FALSE		:::::::Cys_CAM::::::::
IAKSENQKSESAPFIDDPDIVLATEVLASGLDEP	11	3.58	0.004	2796	78.6	AE003577	TRUE	FALSE	3	3601	-2.5	11of132	0.4517	FALSE	FALSE		::::::::::::::::::::::::::::::
RVEGVGNSTVALLVRH	10	10.89	0.132	909	35.4	AE003578	TRUE	FALSE	3	1708	2.5	15of 60	1.7428	FALSE	FALSE		::::::::::::::::
TNGLQNGKKLTK	11	10.85	0.108	778	9.5	AE003578	TRUE	FALSE	2	1302.5	0.6	9of 22	1.2199	FALSE	FALSE		::::::::::::
IKKPTGSSKITSPEQSISGTMDNGSSPSKMK	4	10.39	0.098	2968	29.06	AE003578	TRUE	FALSE	3	3242.6	-1.4	14of120	1.4867	FALSE	FALSE		::::::::::::::::::::Oxidation_M::::::::Oxidation_M::
DKQTTLTKAQLKSPIGSVAELTRKSP	9	10.55	0.061	1994	38.6	AE003578	TRUE	FALSE	3	2799.2	2.6	10of100	0.9834	FALSE	FALSE		::::::::::::::::::::::::
SISINAFFEYLTNKYGKQK	14	9.87	0.048	2765	43.7	AE003578	TRUE	FALSE	3	2252.6	1.6	12of 72	1.06	FALSE	FALSE		::::::::::::::::::
EKTHAGSSFESASSLYSMR	3	7.75	0.025	2796	26.83	AE003578	TRUE	FALSE	3	2076.2	-2.8	9of 72	0.9599	FALSE	FALSE		::::::::::::::::::
RKMAAQKQQQMHQEQLK	1	10.83	0.013	1765	15.26	AE003578	TRUE	FALSE	2	2128.5	1.4	11of 32	2.7899	FALSE	FALSE		:::Oxidation_M:::::::::::::
PIWVNITGNSFNGSQQND	5	3.1	0.007	2591	36.3	AE003578	TRUE	FALSE	2	1992.1	1.7	8of 34	1.069	FALSE	FALSE		::::::::::::::::::
YIAWQANKNNEVWVSTRRAARNMTYQGFTAVEG	2	10.04	0.133	2150	69.73	AE003579	TRUE	FALSE	3	3834.3	0.4	21of128	1.9541	FALSE	FALSE		::::::::::::::::::::::::::::
RQAITQALPMITR	9	12.41	0.108	806	34.43	AE003579	TRUE	FALSE	3	1515.8	0.5	16of 48	2.1068	FALSE	FALSE		::::::::Oxidation_M::::
LYTFIEWVKEMLENR	12	4.56	0.108	1557	56.13	AE003579	TRUE	TRUE	2	1972.3	-2.5	7of 28	1.1215	FALSE	FALSE		::::::::::::::
PFMLQEADKKLRSEINVMIQKTLG	11	9.76	0.106	1488	62.36	AE003579	TRUE	FALSE	3	2791.3	-1.5	21of 92	1.855	FALSE	FALSE		::::::::::::::::::::::
LFWSHGGLLGTTE	11	5.13	0.065	1265	40.6	AE003579	TRUE	FALSE	2	1418.6	0.8	9of 24	1.2721	FALSE	FALSE		::::::::::::
RLERDLFGDIDDLFHESYEDPMVKKARTE	7	4.35	0.055	2109	64.43	AE003579	TRUE	FALSE	3	3526.9	2.6	36	1.5674	FALSE	FALSE		::::::::::::::::::::::::::
HIYSMTNQGGTGIVGSGSAGIAHLTSGGSHRPSLI	8	9.85	0.044	2525	58.33	AE003579	TRUE	FALSE	3	3438.8	-1.5	26of136	2.2798	FALSE	FALSE		:::::Oxidation_M:::::::::::::::::::::::::::
PDEFNAYDGPSTSK	10	3.71	0.042	2069	17.4	AE003579	TRUE	FALSE	2	1528.6	-1	9of 26	1.4348	FALSE	FALSE		::::::::::::::
GTPVKAKNDGVTPQMNIQEDENE	11	3.93	0.038	272	27.43	AE003579	TRUE	FALSE	3	2531.7	-0.4	14of 88	1.3452	FALSE	FALSE		::::::::::::::Oxidation_M:::::::::
PTIHPLPPIPALPPLPTARVPIPRSR	1	12.71	0.025	317	72.6	AE003579	TRUE	FALSE	2	2805.4	1.3	5of 50	0.8136	FALSE	FALSE		::::::::::::::::::::::
CFTFNYSGCHGNNNLFHKKLECEEKCK	3	7.86	0.02	2171	43.7	AE003579	TRUE	FALSE	3	3423.6	-1	21of104	1.9654	FALSE	FALSE		:Cys_CAM:::::::Cys_CAM::::::::::::Cys_CAM::::Cys_CAM::
PVVRFKNNQEYVCKHER	10	9.66	0.014	2502	25.7	AE003579	TRUE	FALSE	2	2204.5	-1.8	6of 32	0.9689	FALSE	FALSE		::::::::::Cys_CAM:::::
VVLLLVVIVTVSLVTTLVVERRMKNAAELTEQLD	8	4.65	0.013	1650	120.43	AE003579	TRUE	FALSE	3	3782.6	1.7	24of132	2.2243	FALSE	FALSE		:::::::::::::::::::::Oxidation_M:::::::::::
AAKNADSFSGGAGSSHGESR	10	7.82	0.012	2703	10.2	AE003579	TRUE	FALSE	2	1893.9	-1.6	7of 38	0.9854	FALSE	FALSE		::::::::::::::::::
SLASASSGSGSLESK	9	6.95	0.224	1153	17.4	AE003580	TRUE	FALSE	2	1368.4	-2.5	7of 28	1.2519	FALSE	FALSE		::::::::::::::
IGRKMVLFFIA	9	11.49	0.068	482	48.73	AE003580	TRUE	FALSE	2	1295.7	-2	10of 20	1.4226	FALSE	FALSE		::::::::::::
TIEMPQEDSTAHMNGIR	9	4.43	0.049	294	29.76	AE003580	TRUE	FALSE	2	1947.1	-2.8	8of 32	1.1926	FALSE	FALSE		::::::::::::Oxidation_M:::::
ATPKGFEGVMKLGL	11	9.89	0.02	2562	35.73	AE003580	TRUE	FALSE	2	1464.8	-2.6	9of 26	1.1766	FALSE	FALSE		::::::::::Oxidation_M:::::
AANAAEFTKEKATAAAAAATEAATSAASTVRE	5	4.73	0.001	2544	44.7	AE003580	TRUE	FALSE	3	3054.3	0.9	23of124	1.7475	FALSE	FALSE		::::::::::::::::::::::::::::
YYLAK	12	9.53	0	1201	17	AE003580	TRUE	FALSE	1	657.8	0	6of 8	1.1204	FALSE	FALSE		::::::
VICAILETHQTETGIKVPEPLKK	11	7.17	0.286	997	53.5	AE003581	TRUE	TRUE	2	2606	0.2	19of 44	3.0084	FALSE	FALSE		:::Cys_CAM:::::::::::::::::::
FQDEIPFVKPAPIDLELAAAEK	2	3.93	0.265	1252	65.7	AE003581	TRUE	TRUE	2	2442.8	1.6	17of 42	2.9203	FALSE	FALSE		::::::::::::::::::::
LIKSAEHNAIMAQDYGLK	15	7.73	0.164	1838	41.03	AE003581	TRUE	FALSE	3	2003.3	-2.2	9of 68	1.1459	FALSE	FALSE		::::::::::::::::::
GKMAAVGLSWEQIGS	6	6.95	0.149	2078	36.83	AE003581	TRUE	FALSE	2	1550.8	-1	10of 28	1.185	FALSE	FALSE		:::Oxidation_M:::::::::::
SNSVGSQGSGSNTPPGR	6	11.05	0.139	1340	6	AE003581	TRUE	FALSE	2	1589.6	2.8	10of 32	1.8629	FALSE	FALSE		::::::::::::::::::
ADSLFVITSCNWTEDELVDSFAEKFVK	10	3.76	0.124	1546	78	AE003581	TRUE	FALSE	3	3152.4	1.7	7of104	0.9429	FALSE	FALSE		::::::::Cys_CAM:::::::::::::::
LRSITEPGLLR	9	10.89	0.096	2510	33.8	AE003581	TRUE	FALSE	2	1255.5	2.5	4of 20	0.6825	FALSE	FALSE		::::::::::::
ELVHLMQSFEAIFAGSYLRGDDK	12	4.54	0.076	1851	63.93	AE003581	TRUE	FALSE	3	2628	0.7	10of 88	1.0599	FALSE	FALSE		::::::::::::::::::::::
KASSRPMSINLQTTKEENGHIA	7	9.89	0.054	2116	28.93	AE003581	TRUE	FALSE	3	2429.7	-2.8	49	2.2936	FALSE	FALSE		:::::::Oxidation_M:::::::::::::::
DRKAQRATFRDV	2	11.23	0.043	2228	14.2	AE003581	TRUE	FALSE	2	1463.6	-0.4	8of 22	1.2797	FALSE	FALSE		::::::::::::
IAKDTEWRQCRHRADNLNKVKNVCSKVIGEKMK	3	10.27	0.042	2625	45.93	AE003581	TRUE	FALSE	3	4014.6	-0.7	16of128	1.5743	FALSE	FALSE		::::::::::Cys_CAM::::::::::::::Cys_CAM:::::::::::
PQVFGDQTK	15	6.76	0.025	1433	13.6	AE003581	TRUE	FALSE	1	1020.1	2.8	7of 16	0.8209	FALSE	FALSE		::::::::::
GNTSKIVRRAGSLRSNN	11	12.71	0.017	930	16.4	AE003581	TRUE	FALSE	3	1831	-0.5	21of 64	1.9091	FALSE	FALSE		::::::::::::::::
FIMENLRAFLHAHNFR	1	10.89	0.013	226	51.93	AE003581	TRUE	FALSE	2	2033.4	-2.2	9of 30	1.035	FALSE	FALSE		:::Oxidation_M:::::::::::::
QLRVLIDDAMTENQKSLELAEQTR	11	4.29	0.009	1158	55.13	AE003581	TRUE	TRUE	3	2803.2	-1.1	17of 92	1.4065	FALSE	FALSE		::::::::::::::::::::::::
AFMEIDDTQQKETSQL	11	3.59	0.005	810	32.63	AE003581	TRUE	FALSE	3	1901.1	-1.1	18of 60	1.9088	FALSE	FALSE		:::Oxidation_M:::::::::::::
DIMDQKHIDDQMKDEAAFLQRKYPTL	11	4.63	0.16	205	54.36	AE003582	TRUE	FALSE	3	3167.6	-1.6	13of100	1.5013	FALSE	FALSE		::::::::::::Oxidation_M:::::::::::::
VPLFNNPVPSVMKMLSPERLFLLGDPR	3	10.09	0.138	2217	88.96	AE003582	TRUE	TRUE	2	3100.7	1.8	12of 52	1.7408	FALSE	FALSE		::::::::::::Oxidation_M::Oxidation_M:::::::::::::
KLQDLRKEINEERDREELRRLG	2	7.3	0.095	1530	37.7	AE003582	TRUE	FALSE	3	2797.1	2	6of 84	0.9128	FALSE	FALSE		::::::::::::::::::::
CMLETPYHLSVAHEDTDK	5	4.53	0.093	2429	35.13	AE003582	TRUE	FALSE	2	2163.3	1.2	11of 34	2.275	FALSE	FALSE		:Cys_CAM:Oxidation_M:::::::::::::::
RETLATHSMTGKPSPAFKDQDK	1	9.76	0.078	204	23.43	AE003582	TRUE	FALSE	2	2446.7	3	6of 42	0.5932	FALSE	FALSE		::::::::::::::::::::
MTSFNIEPMQD	9	3.01	0.039	864	29.66	AE003582	TRUE	FALSE	2	1329.5	2.7	9of 20	1.1733	FALSE	FALSE		:Oxidation_M:::::::::
MNSINLESLRGD	11	4.08	0.019	2647	28.03	AE003582	TRUE	FALSE	2	1349.5	-1	6of 22	0.8849	FALSE	FALSE		::::::::::::
RIFNIQTSKAQEARRREL	1	11.95	0.012	950	32.5	AE003582	TRUE	FALSE	3	2217.5	0.7	19of 68	2.1839	FALSE	FALSE		::::::::::::::::
VTVISNVLVTSQERLT	3	6.98	0.01	1380	44.9	AE003582	TRUE	FALSE	2	1760	-2.1	7of 30	0.9313	FALSE	FALSE		::::::::::::::::
ESHNCYAFVLAFLQALGHAHLSEAARSK	10	7.41	0.227	1505	64.5	AE003583	TRUE	FALSE	3	3129.5	-1	21of108	2.8071	FALSE	FALSE		:::::Cys_CAM:::::::::::::::::::::
MLLKGILLLVSIAQIAADFK	4	9.89	0.156	2601	82.93	AE003583	TRUE	FALSE	2	2158.7	2.6	11of 38	1.4686	FALSE	FALSE		::::::::::::::::::::
KITKDMICAAAPGKDACSGDSGGPLVSGNKL	8	8.28	0.145	2706	49.33	AE003583	TRUE	FALSE	3	3136.5	1.2	25of120	1.963	FALSE	FALSE		::::::Oxidation_M::Cys_CAM::::::::Cys_CAM:::::::::::::
AVLGMANKVQQDLGATSAGGVLSVPVN	2	6.76	0.133	856	61.13	AE003583	TRUE	FALSE	3	2598	-2.9	22of104	2.2673	FALSE	FALSE		::::::::::::::::::::::::::
DYRKSRTFGAAVMDMGIGLFVVTMGLVSHRAR	4	11.22	0.085	1389	80.69	AE003583	TRUE	FALSE	2	3576.2	2.5	11of 62	1.0078	FALSE	FALSE		::::::::::::Oxidation_M::Oxidation_M:::::::::::::::
RTTTAGKYISLYRKIRR	7	11.98	0.065	1839	28.7	AE003583	TRUE	FALSE	2	2084.5	-1.4	168	1.1861	FALSE	FALSE		::::::::::::::::::
PDSSAGSNSGGSGAGLSLFSLQG	13	3.1	0.062	1699	35.4	AE003583	TRUE	FALSE	2	2084.2	-0.4	8of 44	1.1076	FALSE	FALSE		::::::::::::::::::::
PLAMNTFGMVKLPQGLGVTFRKN	9	11.64	0.027	310	62.16	AE003583	TRUE	FALSE	3	2537.1	-2.9	14of 88	1.2797	FALSE	FALSE		::::::::Oxidation_M:::::::::::::
GGKNSSAGADQQAKVQ	4	9.89	0.025	1494	5.4	AE003583	TRUE	FALSE	2	1546.6	1.7	11of 30	1.8106	FALSE	FALSE		::::::::::::::::
TTPSFRGNSYLILPPPR	12	11.14	0.004	1035	43	AE003583	TRUE	FALSE	3	1917.2	0.2	17of 64	1.6277	FALSE	FALSE		::::::::::::::::
GQIDADRVSIRPNSQK	3	10.09	0.124	1449	19.7	AE003584	TRUE	FALSE	2	1785	1.7	7of 30	1.167	FALSE	FALSE		::::::::::::::::
RSRFIRPASTVICCAGA	10	10.82	0.064	1286	39.3	AE003584	TRUE	FALSE	3	1923.2	0.5	16of 64	1.6349	FALSE	FALSE		::::::::::::Cys_CAM:Cys_CAM::::

SQRLEELEAQQRKREKTSRRGGEER	1	10.54	0.045	1800	16.8	AE003584	TRUE	TRUE	3	3058.3	-1.4	11of 96	1.1946	FALSE	FALSE	::::::::::::::::::::::::
LRSGHAPLPRPLAPISPPDGIVLESPTSEIEQ	1	4.63	0.034	1932	77.2	AE003584	TRUE	FALSE	3	3375.8	-2.2	11of124	1.1306	FALSE	FALSE	::::::::::::::::::::::::::::::
SIKFVGAGLNFQMISCGADKSIMFR	6	9.91	0.031	1936	70.86	AE003584	TRUE	FALSE	3	2779.3	-1.3	12of 96	1.35	FALSE	FALSE	::::::::::::::Cys_CAM:::::::::
QMISCGADKSIMFR	6	8.97	0.015	1991	35.46	AE003584	TRUE	FALSE	2	1676.9	2.4	7of 26	1.0987	FALSE	FALSE	::Oxidation_M:::Cys_CAM::::::::Oxidation_M:::
KTAHKMVMVMVT	13	10.6	0.01	2528	28.49	AE003584	TRUE	FALSE	2	1392.8	-1.1	5of 22	0.7797	FALSE	FALSE	:::::::::Oxidation_M:::
KALFMKKLQEAS	3	10.32	0.001	1777	28.43	AE003584	TRUE	FALSE	2	1394.7	1.6	6of 22	1.0909	FALSE	FALSE	::::::::::::
YEMMNPMEQTSST	7	3.13	0	3729	25.49	AE003584	TRUE	FALSE	2	1565.7	2.2	44	0.7108	FALSE	FALSE	:::Oxidation_M:::::::::::
GPIVTYELGQIR	14	6.89	0.123	840	35.1	AE003585	TRUE	FALSE	1	1346.6	-0.4	8of 22	1.2812	FALSE	FALSE	::::::::::::
RLMDQMKDLSETVRDIKLYMASNKEATNGMMTR	13	9.56	0.099	362	67.55	AE003585	TRUE	FALSE	3	3927.5	-0.4	10of128	1.2877	FALSE	FALSE	:::Oxidation_M:::Oxidation_M::::::::::::Oxidation_M::::::::::::::
LHMSEAEPDIQAEAIYDHMPNTPTSPPHIIPPNDTPT	15	4.06	0.092	1725	73.66	AE003585	TRUE	FALSE	3	4111.5	1.1	29of144	2.4867	FALSE	FALSE	:::Oxidation_M::::::::::::::Oxidation_M::::::::::::::::::
LPRLPLRRLR	2	12.88	0.024	776	34	AE003585	TRUE	FALSE	2	1290.6	1.8	6of 18	0.9794	FALSE	FALSE	::::::::::::
PMPDVLWLRTASGGNMPLDRVSVLEDR	12	4.46	0.101	1836	74.36	AE003586	TRUE	FALSE	3	3042.5	-2.2	20of104	1.9179	FALSE	FALSE	::::::::::::::Oxidation_M:::::::::::
LSVVILASCKSGGDAHVRVKRIVGGKQSK	10	10.97	0.045	2727	49.5	AE003586	TRUE	FALSE	2	3051.6	1.3	10of 56	1.1567	FALSE	FALSE	:::::::::Cys_CAM::::::::::::::::::::
KINITENKMDQ	2	6.99	0.031	782	16.83	AE003586	TRUE	FALSE	2	1350.5	-0.4	10of 20	1.3089	FALSE	FALSE	:::::::::Oxidation_M:::
EGVLMYVLDTDYVNFAIR	2	3.71	0.007	418	63.93	AE003586	TRUE	FALSE	2	2135.4	-2.5	7of 34	0.9798	FALSE	FALSE	:::::Oxidation_M:::::::::::::
SVKSVPL	4	10.1	0.005	2981	17.6	AE003586	TRUE	FALSE	1	729.9	0.2	5of 12	0.685	FALSE	FALSE	::::::::
KKAYRKLALRYHPDKNKAANAEDKFK	10	10.52	0.133	1855	27.6	AE003587	TRUE	FALSE	3	3105.6	-0.4	12of100	1.4392	FALSE	FALSE	::::::::::::::::::::::::::
RQRLYTELLRAAHAAVEHSVAVRGMRA	3	11.82	0.129	2264	56.53	AE003587	TRUE	FALSE	3	3063.6	-2.4	20of104	1.7358	FALSE	FALSE	::::::::::::::::::::::::::::
ADIMSELIKVNMEPACIRIIRKQGTDSSRG	11	8.93	0.104	125	65.36	AE003587	TRUE	FALSE	3	3406.9	-2.3	10of116	1.209	FALSE	FALSE	::::Oxidation_M::::::::::Cys_CAM::::::::::::::
AKKGAGPKKDDDLDNRPQPPN	14	9.67	0.078	899	10.3	AE003587	TRUE	FALSE	2	2262.5	2.9	11of 40	1.9777	FALSE	FALSE	::::::::::::::::::::
LVLPPPPKVDYRA	8	9.72	0.066	1877	38.2	AE003587	TRUE	FALSE	2	1465.8	-2.7	9of 24	1.2925	FALSE	FALSE	::::::::::::::
DRPMLFFGKDEYTK	2	6.98	0.057	2045	33.43	AE003587	TRUE	FALSE	2	1748	0.3	5of 26	0.9601	FALSE	FALSE	::::::::::::::
MSVAGFEDIVAGPLSQYLTLSAK	6	4.08	0.049	2312	66.63	AE003587	TRUE	FALSE	2	2414.8	2.2	10of 44	2.3779	FALSE	FALSE	:Oxidation_M:::::::::::::::::::
QPTQAEAASKSSPANPALAPK	1	9.89	0.03	2030	24.4	AE003587	TRUE	FALSE	2	2065.3	-1.5	6of 40	1.013	FALSE	FALSE	::::::::::::::::::::
MGNDEEDKVSVVSDLE	14	3.38	0.019	2711	29.23	AE003587	TRUE	FALSE	3	1782.9	2.2	11of 60	1.3772	FALSE	FALSE	:Oxidation_M:::::::::::::
VLSRLKKNQ	4	11.64	0.016	1999	15.6	AE003587	TRUE	FALSE	1	1086.3	0.7	4of 16	0.6669	FALSE	FALSE	::::::::::
DLITFKYGFPDGDGLLITDMDR	14	3.7	0.015	1367	66.23	AE003587	TRUE	TRUE	2	2519.8	0	11of 42	2.0992	FALSE	FALSE	:::::::::::::::::Oxidation_M:::
PLSQYLTLSAK	1	9.72	0.01	2077	30.9	AE003587	TRUE	FALSE	1	1221.4	1.6	10of 20	1.7243	FALSE	FALSE	::::::::::::
SAAIVRDLNTLRAQVR	2	12.11	0.008	2285	37.8	AE003587	TRUE	FALSE	2	1784.1	1.9	8of 30	1.1431	FALSE	FALSE	::::::::::::::::
PTIRHTDQK	13	10.09	0.005	987	6	AE003587	TRUE	FALSE	1	1096.2	-2.9	2of 16	0.4805	FALSE	FALSE	::::::::::
KKVMKQQHSAEDHAP	9	9.76	0	450	7.13	AE003587	TRUE	FALSE	3	1735	-2.5	18of 56	1.9025	FALSE	FALSE	::::::::::::::
RLARFFEGRHVSSERDF	6	10.73	0.156	1116	36.7	AE003588	TRUE	FALSE	3	2110.3	-0.9	14of 64	1.2533	FALSE	FALSE	::::::::::::::::
PGMEQRSPDPTDMMRSKHLGKKGEFR	2	10.31	0.125	1884	30.79	AE003588	TRUE	FALSE	3	3049.5	2.7	14of100	1.409	FALSE	FALSE	:::Oxidation_M::::::::::Oxidation_M:::::::::::
MITQQRGATPTQSGGGGASSMAMMMSKT	3	11.49	0.069	1656	40.95	AE003588	TRUE	FALSE	3	2837.2	2.1	23of108	1.9578	FALSE	FALSE	:Oxidation_M::::::::::::::::::Oxidation_M:::::::
KRYYLEPASPLKSLANAVNLKSSAPA	7	10.21	0.059	1237	54.6	AE003588	TRUE	FALSE	3	2790.2	2.4	255	2.3591	FALSE	FALSE	::::::::::::::::::::::::
AGKFYSEPLMGSDSQDMDGTLSNK	10	3.97	0.057	2097	39.96	AE003588	TRUE	FALSE	2	2579.8	-0.8	11of 46	1.143	FALSE	FALSE	::::::::::::::::::::::
FVRNIPDSSASSQQYP	5	6.7	0.049	2927	29.2	AE003588	TRUE	FALSE	2	1796.9	2.8	6of 30	0.9925	FALSE	FALSE	::::::::::::::::
PPRSDWKYKRTKVK	12	11.02	0.036	1507	13.3	AE003588	TRUE	FALSE	2	1790.1	2.7	5of 26	0.8195	FALSE	FALSE	::::::::::::::
AVLQRCFEIYVNDQLYGSFEFVKFPK	1	6.47	0.012	994	83.2	AE003588	TRUE	FALSE	3	3199.6	-1.5	19of100	2.5353	FALSE	FALSE	::::::Cys_CAM:::::::::::::::::
MYYNDFYEDLVTTK	10	3.71	0.186	484	40.23	AE003589	TRUE	FALSE	3	1819	-0.2	15of 52	1.569	FALSE	FALSE	:Oxidation_M:::::::::::::
FMDNQPKGQNLPFMK	5	9.89	0.096	2088	33.96	AE003589	TRUE	TRUE	2	1828.1	1.5	14of 28	2.3538	FALSE	FALSE	::Oxidation_M::::::::::Oxidation_M:::
FMDNQPKGQNLPFMK	6	9.89	0.087	1994	33.96	AE003589	TRUE	TRUE	2	1828.1	2.6	15of 28	2.406	FALSE	FALSE	::Oxidation_M::::::::::Oxidation_M:::
YTAPMGLGMGGMGIGM	11	5.93	0.076	2636	45.52	AE003589	TRUE	FALSE	2	1576.9	1.9	11of 30	1.4159	FALSE	FALSE	::::::::::Oxidation_M::::Oxidation_M:
NIAEGIYKLYGDVNLISAVGNDQMGQTLLQMMPKAL	1	4.31	0.044	127	101.39	AE003589	TRUE	FALSE	3	3911.6	1.4	23of140	1.887	FALSE	FALSE	::::::::::::::::::::::::::::::::::
DKANGVNRHVSLANNNT	5	10.09	0.044	1360	14.7	AE003589	TRUE	FALSE	3	1825	-2.4	16of 64	2.3551	FALSE	FALSE	::::::::::::::::::
QTGSGVSGPEGVSQSGKDKEKGR	3	9.76	0.037	1381	6.1	AE003589	TRUE	FALSE	3	2276.4	1.8	19of 88	1.414	FALSE	FALSE	::::::::::::::::::::::
SSTSNGDLPAPK	12	6.76	0.016	925	11.4	AE003589	TRUE	FALSE	2	1174.3	-0.1	12of 22	1.6066	FALSE	FALSE	::::::::::::
IEANGAIQKAQQPKPAETKST	6	9.76	0.01	2952	22.9	AE003589	TRUE	FALSE	2	2211.5	1.9	5of 40	0.8125	FALSE	FALSE	::::::::::::::::::::
CLQLCLTSDAQNGAALNNL	5	3.1	0.009	1763	50.3	AE003589	TRUE	FALSE	3	2077.2	3	16of 72	2.401	FALSE	FALSE	:Cys_CAM::::Cys_CAM:::::::::::::
SNLLQSLNQQRPGQQQMQPMSNIR	5	12.41	0.002	2380	42.96	AE003589	TRUE	FALSE	3	2830.2	-1.3	20of 92	1.5063	FALSE	FALSE	::::::::::::::::Oxidation_M:::Oxidation_M::::
PISPKMQSIMAEEKLREKREYLRRMRHR	2	11.33	0	2388	50.09	AE003589	TRUE	FALSE	3	3603.3	1.5	11of108	0.403	FALSE	FALSE	:::::::::Oxidation_M::::::::::::::Oxidation_M::::
NSEVRLVEIQEKLCSEGEVIN	8	4.09	0.185	2108	49.6	AE003590	TRUE	FALSE	3	2446.7	-2.4	21of 80	2.1345	FALSE	FALSE	::::::::::::::Cys_CAM:::::::
MLSILNTTDVNQLANLDINK	15	3.89	0.153	752	56.63	AE003590	TRUE	FALSE	3	2247.6	-2.1	21of 76	2.1109	FALSE	FALSE	:Oxidation_M:::::::::::::::::
NATSLSSLLPGMSLSAATGSSAGGVSGLSVPSAGSGVGKK	1	10.6	0.124	1385	67.63	AE003590	TRUE	FALSE	3	3566	2.6	24of156	1.755	FALSE	FALSE	::::::::::Oxidation_M:::::::::::::::::::::::::::
FFEIKYAPSICDSNNRKDMIKIAQNYCTK	8	8.93	0.065	2148	62.43	AE003590	TRUE	FALSE	3	3557	-2.6	22of112	2.6277	FALSE	FALSE	:::::::::Cys_CAM::::::::::::::Cys_CAM:::
SLRECMSTVPRKRS	5	11.23	0.051	2132	20.43	AE003590	TRUE	FALSE	2	1708	-1.7	6of 26	1.0242	FALSE	FALSE	:::::Cys_CAM:::::::::
PPPTTTQRPLVK	9	11.49	0.049	500	20.2	AE003590	TRUE	FALSE	2	1335.6	0.1	13of 22	1.9463	FALSE	FALSE	::::::::::::
PLGNVTPSISASGNASTTK	15	10.1	0.023	2747	25.8	AE003590	TRUE	FALSE	3	1803	0	14of 72	1.4027	FALSE	FALSE	::::::::::::::::
VQLHPCPSSFIR	8	9.02	0.019	2664	32.1	AE003590	TRUE	FALSE	3	1441.6	-0.6	8of 44	0.9708	FALSE	FALSE	:::::Cys_CAM::::::
TSTVPEDICDPKAR	12	4.31	0.019	1509	20.8	AE003590	TRUE	FALSE	2	1589.7	2.8	9of 26	1.2195	FALSE	FALSE	:::::::Cys_CAM:::::
EHDVVDGTGSLEAEAAPASISPSNFST	14	3.51	0.015	2885	46.4	AE003590	TRUE	FALSE	2	2689.8	-2.9	5of 52	0.7408	FALSE	FALSE	::::::::::::::::::::::::::
QQKMMQFLPPAQRKAYENMLAEMEQAMK	12	9.56	0.009	672	64.25	AE003590	TRUE	FALSE	3	3437	-2.2	18of108	1.4961	FALSE	FALSE	:::Oxidation_M:Oxidation_M::::::::::::::::Oxidation_M:::Oxidation_M::
DVNQLANLDINK	14	3.89	0.008	886	27.1	AE003590	TRUE	FALSE	2	1357.5	0.8	13of 22	1.5639	FALSE	FALSE	::::::::::::
PLVGESEYFYDQYVDATEAPDTT	3	2.73	0.122	1468	53	AE003591	TRUE	FALSE	3	2611.7	-2.2	15of 88	1.4527	FALSE	FALSE	::::::::::::::::::::
QDIIFVNDTLEDVSKLGTMDVLAEIMK	6	3.69	0.068	1312	81.66	AE003591	TRUE	FALSE	2	3055.5	-0.9	11of 52	1.2831	FALSE	FALSE	:::::::::::::::::::::::Oxidation_M::
EAGVDCVTLGQYMQPTNKHLKVIEYVT	11	5.35	0.051	1000	61.63	AE003591	TRUE	FALSE	3	3095.5	1.7	22of104	1.8896	FALSE	FALSE	:::::Cys_CAM:::::::::::::::::
VIDPTTAEIFKCDIVEMPK	6	4.07	0.05	1204	54.03	AE003591	TRUE	FALSE	3	2207.6	1.1	19of 72	1.8024	FALSE	FALSE	::::::::::Cys_CAM:::::::
PKVESVIPITKVVK	2	10.32	0.041	817	34	AE003591	TRUE	FALSE	2	1537.9	1.2	11of 26	1.6042	FALSE	FALSE	::::::::::::::
DRTLGVREAITAINYVRK	2	10.39	0.04	2130	39.2	AE003591	TRUE	FALSE	2	2076.4	2.9	5of 34	0.8809	FALSE	FALSE	::::::::::::::::
LTMGSTPPEPTPMDTYS	9	3.01	0.024	2010	34.76	AE003591	TRUE	FALSE	2	1858	-0.8	6of 32	0.8891	FALSE	FALSE	:::Oxidation_M::::::::Oxidation_M::::
EERSRSYELVSATFAASLVIAPAMGNLIMDRYG	12	4.65	0.022	1305	89.76	AE003591	TRUE	FALSE	3	3636.1	-1.7	19of128	1.6251	FALSE	FALSE	:::::::::::::::::::::::Oxidation_M:::::::::
WFEKGVPIPSRMLPPQDAVDYYTDPKN	6	4.46	0.002	1263	65.43	AE003591	TRUE	FALSE	3	3165.6	1.8	24of104	2.9735	FALSE	FALSE	::::::::::::::::::::::::::
FGPSGTIDMTFGDVECR	5	3.71	0.17	1471	40.03	AE003592	TRUE	TRUE	2	1890	2.9	6of 32	1.0769	FALSE	FALSE	::::::::::::::Cys_CAM:::
ELVPTSLQTAKGRMQNSRQEAQQHLK	5	10.58	0.074	2863	35.53	AE003592	TRUE	FALSE	3	2996.4	2.6	13of100	1.3669	FALSE	FALSE	::::::::::::Oxidation_M:::::::::::
TTTTTTTTTFKAKSKDKDK	2	10.39	0.046	2414	4.6	AE003592	TRUE	FALSE	2	2004.2	1.3	6of 34	0.8902	FALSE	FALSE	::::::::::::::::::
LFLMGERLFATELLESNSFVDKIC	5	4.17	0.043	2066	87.53	AE003592	TRUE	FALSE	3	2850.3	1.9	12of 92	1.0497	FALSE	FALSE	::::Oxidation_M::::::::::::::::Cys_CAM:
KTARKASLIIHMRQH	2	12.43	0.019	2134	23.23	AE003592	TRUE	FALSE	2	1791.2	1.3	9of 28	1.0269	FALSE	FALSE	::::::::::::::::
GEVSNKPLMRK	14	10.59	0.011	1722	15.93	AE003592	TRUE	FALSE	2	1275.5	-1.2	9of 20	1.0836	FALSE	FALSE	:::::::::Oxidation_M:::
HNLLAVDLIKSN	8	7.82	0.006	2683	33.3	AE003592	TRUE	FALSE	2	1337.6	-1.9	9of 22	1.2749	FALSE	FALSE	::::::::::::
GLVGMSMTNTSPLMAPTRAK	8	11.49	0.137	2347	43.49	AE003593	TRUE	FALSE	2	2080.5	-0.6	11of 38	1.7102	FALSE	FALSE	::::::::::::::Oxidation_M::::::::
PRTPPAPQNSPIGFGQNA	11	11.05	0.121	1428	27.7	AE003593	TRUE	FALSE	2	1850	0.8	11of 34	1.4318	FALSE	FALSE	::::::::::::::::::
KENESVLRVPTTSGSVSMSE	12	4.56	0.095	2085	30.63	AE003593	TRUE	FALSE	2	2154.4	-1.1	9of 38	1.1742	FALSE	FALSE	::::::::::::::::Oxidation_M:::
AMSRERSAVQSEFEQTHMR	2	7.86	0.08	466	27.56	AE003593	TRUE	FALSE	3	2281.5	-0.8	16of 72	1.374	FALSE	FALSE	::::::::::::::::::

SSVKTNPMSEE	15	4.27	0.064	2709	12.03	AE003593	TRUE	FALSE	2	1209.3	-0.8	9of 20	1.1364	FALSE	FALSE	::::::::::
LVGMSMTNTSPLMAPTR	6	11.05	0.048	2461	43.79	AE003593	TRUE	FALSE	2	1840.2	2.2	7of 32	1.0248	FALSE	FALSE	::::::Oxidation_M::::::Oxidation_M::::
KLQQLQLQNQQQQQAAAAAAAAASGGVGHQK	5	10.6	0.043	1543	39.6	AE003593	TRUE	FALSE	3	3144.5	-2.8	26of120	2.224	FALSE	FALSE	::::::::::::::::::::::::::::
GYVTDLVKGYTAKPVKYLEIVEPISDFRELRKLL	15	9.29	0.037	69	97.6	AE003593	TRUE	FALSE	3	3955.7	-2.5	15of132	1.2717	FALSE	FALSE	::::::::::::::::::::::::::::::
DQFYKDVFLVQPVEDV	7	3.51	0.024	1720	50.4	AE003593	TRUE	FALSE	2	1942.2	0.5	142	1.1085	FALSE	FALSE	::::::::::::::
CRTPTERDGGCMHMVCT	1	6.92	0.021	1562	25.26	AE003593	TRUE	FALSE	3	2085.2	-0.4	14of 64	1.4637	FALSE	FALSE	:Cys_CAM::::::::Cys_CAM:::Oxidation_M::Cys_CAM::
MYHPTNYVLVTDLDDMEHMEFV	13	3.84	0.018	2117	66.09	AE003593	TRUE	FALSE	3	2733.1	0.8	12of 84	1.3094	FALSE	FALSE	:Oxidation_M::::::::::::::Oxidation_M:::::::
WSSHKSRAATLAKAAAAQQQQHQK	14	11.73	0.017	1166	19.8	AE003593	TRUE	FALSE	3	2633.9	1.1	21of 92	2.3495	FALSE	FALSE	::::::::::::::::::::::
ICETFNLAELQALNKAM	9	4.27	0.006	2213	53.43	AE003593	TRUE	FALSE	2	1967.3	-0.7	6of 32	0.9541	FALSE	FALSE	::Cys_CAM:::::::::::::::
QAVSFALDVARGMAFLHSLER	11	7.85	0.005	1302	61.43	AE003593	TRUE	FALSE	3	2319.7	-2.5	21of 80	2.1471	FALSE	FALSE	::::::::::::::::::::
NPSARKISRFSVSR	8	12.71	0.166	1732	19.2	AE003594	TRUE	FALSE	2	1605.8	-1.2	10of 26	1.304	FALSE	FALSE	::::::::::::::
TCPYLFIK	2	8.88	0.149	2266	31.2	AE003594	TRUE	FALSE	2	1042.2	-1.5	5of 14	0.8216	FALSE	FALSE	::Cys_CAM:::::::
DEGASNSQHSIPHMRK	9	7.97	0.06	2580	9.93	AE003594	TRUE	FALSE	2	1810.9	-2.2	8of 30	1.4067	FALSE	FALSE	:::::::::::::Oxidation_M:::
PGVSWAEVVGGPSSLNK	4	6.95	0.049	1745	35.1	AE003594	TRUE	FALSE	2	1684.9	-1.6	9of 32	1.1111	FALSE	FALSE	::::::::::::::::
GAQMNGEMIRTTGQTNLSAAMVLQEYS	13	4.27	0.04	992	56.89	AE003594	TRUE	FALSE	3	2919.3	1.8	20of104	1.3543	FALSE	FALSE	:::::::::::::::::::Oxidation_M:::::::
RPNTNSNYYGESSLETANSALGSNLQVTV	11	4.27	0.038	1522	48.3	AE003594	TRUE	FALSE	3	3088.3	2.6	15of112	1.2629	FALSE	FALSE	::::::::::::::::::::::::::::
VEPTASEQFLS	15	3.13	0.028	1828	27.6	AE003594	TRUE	FALSE	2	1208.3	-2.4	5of 20	0.9727	FALSE	FALSE	::::::::::::
LDAKPDKEGYDNYR	9	4.46	0.021	1252	17.2	AE003594	TRUE	TRUE	2	1684.8	1.4	7of 26	1.1474	FALSE	FALSE	::::::::::::::
RLKEERQRLQ	5	11.23	0.019	2302	14.5	AE003594	TRUE	FALSE	2	1356.6	2.1	13of 18	1.8114	FALSE	FALSE	::::::::::
INSIIKELPEPQPKRPHLYKPAQK	3	10.3	0.013	2081	45.2	AE003594	TRUE	FALSE	3	2826.4	0.5	13of 92	1.3688	FALSE	FALSE	::::::::::::::::::::::::
SSSTASRDAPNSSNDVTIGSGSVSRK	6	10.09	0.011	1208	18.3	AE003594	TRUE	FALSE	3	2568.7	-2.4	11of100	1.1775	FALSE	FALSE	::::::::::::::::::::::::::
ISGIKPAALAK	6	10.6	0.01	1499	26.3	AE003594	TRUE	FALSE	1	1069.3	0.8	10of 20	1.4516	FALSE	FALSE	::::::::::
TSATVFLVMFMPK	13	10.1	0.161	514	48.26	AE003595	TRUE	FALSE	3	1504.8	1.8	19of 48	1.7668	FALSE	FALSE	::::::::Oxidation_M::Oxidation_M:::
FYLNNSPMDYHPKE	10	5.22	0.103	545	30.43	AE003595	TRUE	FALSE	3	1755.9	1.9	16of 52	1.6029	FALSE	FALSE	::::::::::::::
VANRTAHGRFK	10	12.42	0.097	1104	11.5	AE003595	TRUE	TRUE	2	1257.4	2.8	7of 20	1.1665	FALSE	FALSE	::::::::::
GPVDQAPAADPVPAGLIQPRNER	4	4.31	0.096	2573	42.8	AE003595	TRUE	FALSE	2	2369.6	-1.8	12of 44	1.5879	FALSE	FALSE	::::::::::::::::::::::
GGGGRGGGGFGGRGGRGGGGRGGGFGNKS	11	12.88	0.055	2769	6.9	AE003595	TRUE	FALSE	2	2408.5	1.4	7of 56	0.9184	FALSE	FALSE	::::::::::::::::::::::::::
AAISAVNCAAQAPLRRTLRLRPVAFAR	5	12.58	0.045	2055	69.2	AE003595	TRUE	FALSE	3	2951.5	-0.3	9of104	0.9967	FALSE	FALSE	::::::Cys_CAM:::::::::::::::::
LVDVKDTVFDLRLPVLMRDRLMQ	13	7.05	0.034	1342	79.16	AE003595	TRUE	FALSE	3	2806.4	-2.6	12of 88	1.4209	FALSE	FALSE	::::::::::::::Oxidation_M::::Oxidation_M::
DIVGFAVDGYYMPL	8	2.93	0.033	2766	52.13	AE003595	TRUE	FALSE	1	1576.8	-1.6	12of 26	1.259	FALSE	FALSE	::::::::::Oxidation_M:::
RSLADAFAASTSAAAAIAGLINLK	3	10.09	0.028	2134	61.9	AE003595	TRUE	FALSE	2	2304.7	2.3	12of 46	1.4226	FALSE	FALSE	::::::::::::::::::::
SATAGVASGGGISPASVAAAVAALK	3	10.1	0.021	1376	47.4	AE003595	TRUE	FALSE	3	2085.4	-2.4	20of 96	1.6265	FALSE	FALSE	::::::::::::::::::::
AKSSSEDSSSEEE	9	3.59	0.008	1157	3.3	AE003595	TRUE	FALSE	2	1372.3	-0.8	11of 24	1.3929	FALSE	FALSE	::::::::::::
ADHLKGCVAR	10	8.97	0.001	412	14.9	AE003595	TRUE	FALSE	2	1127.3	2.1	8of 18	1.454	FALSE	FALSE	::::::Cys_CAM::::
NLGGNKYTNFMLNGFIQIPGLLLPLVIMDR	3	9.72	0.134	2090	106.46	AE003596	TRUE	FALSE	3	3396	-1.3	29of116	2.8137	FALSE	FALSE	:::::::::Oxidation_M::::::::::::::Oxidation_M:::
NPLASLAALGLAGMNPASTGGINHTGELSASA	8	5.13	0.082	2453	68.03	AE003596	TRUE	FALSE	3	2965.3	2.9	15of124	1.1368	FALSE	FALSE	::::::::::::::::::::::::::::
DLDLVVTATQAQ	11	2.93	0.004	585	31.8	AE003596	TRUE	FALSE	2	1274.4	-0.4	11of 22	1.4381	FALSE	FALSE	::::::::::::
GLTAGILGPAASIDLGSSPLSHR	5	7.85	0.164	2126	53.7	AE003597	TRUE	FALSE	2	2191.5	0.4	15of 44	2.577	FALSE	FALSE	::::::::::::::::::::
ILWQIINQDITFEIQARTLGYVGFGF	13	4.08	0.094	1595	98.5	AE003597	TRUE	FALSE	3	3044.5	-2.6	21of100	1.7637	FALSE	FALSE	::::::::::::::::::::
MSKRIMLSFPLK	7	11.64	0.042	1228	39.56	AE003597	TRUE	FALSE	2	1467.9	1.3	6	1.9532	FALSE	FALSE	::::::Oxidation_M:::::::
GSLAEKMMR	9	10.09	0.07	669	19.16	AE003598	TRUE	FALSE	2	1039.3	0.2	8of 16	1.2465	FALSE	FALSE	:::::::Oxidation_M::
LQAFGNLTKTHN	11	10.1	0.008	273	21.9	AE003598	TRUE	FALSE	3	1344.5	0.5	17of 44	2.1554	FALSE	FALSE	::::::::::::
HGVAHRIESRAYRG	10	11.05	0.007	960	15.4	AE003598	TRUE	FALSE	3	1609.8	1.7	17of 52	1.7995	FALSE	FALSE	::::::::::::::
FLDMYLR	14	6.7	0.001	1139	33.93	AE003598	TRUE	FALSE	1	974.2	-0.1	8of 12	1.5281	FALSE	FALSE	::::Oxidation_M::::
GLILFAFIFVSQQW	6	6.02	0.207	1696	70.7	AE003599	TRUE	FALSE	1	1670	2.9	8of 26	1.4607	FALSE	FALSE	::::::::::::::
LQFIMTLRFPYSSMSHNIRGRTVYISVKK	11	11.44	0.15	149	78.16	AE003599	TRUE	FALSE	3	3491.2	2.2	11of112	1.2097	FALSE	FALSE	:::::Oxidation_M::::::::::::::::::::::
YDRTEEELLGNMPRA	12	4.17	0.017	1621	32.33	AE003599	TRUE	FALSE	2	1811	1.9	14of 28	2.08	FALSE	FALSE	::::::::::Oxidation_M::::
RSGANSLGVDP	12	6.79	0.136	1101	15.3	AE003600	TRUE	FALSE	2	1073.2	-1.6	11of 20	1.3186	FALSE	FALSE	::::::::::::
PPEEDWQPLINATKFPTR	9	4.45	0.096	1494	42.7	AE003600	TRUE	FALSE	3	2140.4	0.8	14of 68	1.515	FALSE	FALSE	::::::::::::::::
LAFFLAILVGGSRLLGGFGNKFG	11	11.49	0.037	1042	84.6	AE003600	TRUE	FALSE	3	2355.8	2.2	20of 88	1.9919	FALSE	FALSE	::::::::::::::::::::
FKNSQSMSGSFSAGAGGGAPGMTK	5	10.6	0.019	2364	28.86	AE003600	TRUE	FALSE	2	2279.5	1.2	14of 46	1.8824	FALSE	FALSE	::::::Oxidation_M:::::::::::::::
EEVPCLMRCLAREKGWF	9	6.38	0.008	816	52.63	AE003600	TRUE	FALSE	2	2182.5	-2.7	4of 32	0.5739	FALSE	FALSE	:::::Cys_CAM::::Cys_CAM::::::::
MMGMMMMGMAMKMMGMI	14	10.1	0.005	1644	67.53	AE003600	TRUE	FALSE	3	2009.7	-2	19of 64	2.2528	FALSE	FALSE	::::Oxidation_M::Oxidation_M::::::Oxidation_M:::Oxidation_M::
SSPTGKILVKEAPEMLAIAHWTGQ	1	7.8	0.124	1778	56.63	AE003601	TRUE	FALSE	2	2582	2.1	10of 46	1.6933	FALSE	FALSE	::::::::::::::Oxidation_M:::::::::
SAPTGGDASSPLGNRPSGLFAGGGGGG	13	6.79	0.11	516	33.1	AE003601	TRUE	FALSE	3	2302.4	2.7	25of104	2.2469	FALSE	FALSE	::::::::::::::::::::::::::
EMVREAREALKLNPLQ	14	7.18	0.1	1399	40.23	AE003601	TRUE	FALSE	3	1914.2	-1	18of 60	2.2484	FALSE	FALSE	::Oxidation_M:::::::::::::
LAATQFVLSRIIGPTVMAATTTGLA	1	11.05	0.07	108	76.53	AE003601	TRUE	FALSE	2	2521	-2.8	5of 48	0.5469	FALSE	FALSE	::::::::::::::::Oxidation_M:::::::::
VRDLYQNKVKDVRVMI	9	10.18	0.058	1861	39.93	AE003601	TRUE	FALSE	3	1977.4	-2.7	18of 60	2.1212	FALSE	FALSE	::::::::::::::::
VPFVVTNTDEAISAGSNQISENIVPIFCVS	8	2.95	0.053	1781	82.2	AE003601	TRUE	FALSE	3	3209.5	-1.3	14of116	1.1564	FALSE	FALSE	:::::::::::::::::::::::::::Cys_CAM:::
IVAQYCISNCQHIMES	14	5.13	0.051	504	42.43	AE003601	TRUE	FALSE	3	1970.1	0.4	21of 60	2.1631	FALSE	FALSE	:::::Cys_CAM::::Cys_CAM:::Oxidation_M:::
HLAQALVDYVLKVFHK	6	9.63	0.039	2595	47.7	AE003601	TRUE	FALSE	2	1882.3	2.5	7of 30	1.1869	FALSE	FALSE	::::::::::::::::
WISSLIAVGALVAPFVAGPMADRIGR	6	10.89	0.028	2976	87.83	AE003601	TRUE	FALSE	3	2669.2	-2.6	13of100	1.4347	FALSE	FALSE	::::::::::::::::::::::
AEDVADAVSYYIQTPP	8	2.88	0.004	1991	38.3	AE003601	TRUE	FALSE	2	1739.9	-0.1	4of 30	0.707	FALSE	FALSE	::::::::::::::::
RRKRLAANDILATVAAASTSASLSSPPASSAASLAATATA	14	12.12	0.003	1495	73.3	AE003601	TRUE	FALSE	3	3800.3	-0.1	23of156	2.404	FALSE	FALSE	::::::::::::::::::::::::::::::::::::
SAPTGGDASSPLGNRPSG	8	6.79	0	1689	16.1	AE003601	TRUE	FALSE	2	1628.7	1.1	8of 34	1.1141	FALSE	FALSE	::::::::::::::::
DNKPDGSPAKSSKQRMRR	13	11.47	0	1220	2.43	AE003601	TRUE	FALSE	2	2059.3	-1.1	3of 34	0.3012	FALSE	FALSE	::::::::::::::::
NGVEDRMSLVWEK	7	4.45	0.173	1223	31.13	AE003602	TRUE	FALSE	2	1579.8	2.5	19	2.1249	FALSE	FALSE	::::::Oxidation_M:::::::
TGNSNAKLSDAV	7	6.76	0.104	1447	14	AE003602	TRUE	FALSE	2	1177.3	2.1	172	1.2666	FALSE	FALSE	::::::::::::
RNVENLKK	9	10.59	0.071	1053	8.2	AE003602	TRUE	FALSE	2	1001.2	2.5	11of 14	1.6293	FALSE	FALSE	::::::::
GIGLPSCAGCFLVPMCT	13	5.1	0.059	1704	55.83	AE003602	TRUE	FALSE	2	1857.1	1.7	5of 32	0.941	FALSE	FALSE	::::::Cys_CAM::::Cys_CAM::::Oxidation_M:Cys_CAM::
SRRSRSHTPNRINGDGNRSSLYMGSPHYTPRISR	15	12.28	0.048	2960	32.63	AE003602	TRUE	FALSE	3	3931.3	-0.9	10of132	1.149	FALSE	FALSE	:::::::::::::::::::::Oxidation_M:::::::::::
AARQSAYAINAMLVKQEF	3	9.72	0.038	2452	46.23	AE003602	TRUE	FALSE	2	2012.3	1.6	10of 34	1.2518	FALSE	FALSE	::::::::::::::::::
HIKEQGGYASLPH	9	7.89	0.031	1482	18.2	AE003602	TRUE	FALSE	2	1437.6	0.9	14of 24	1.9285	FALSE	FALSE	::::::::::::::
DKCRLEEELSQEKSRRQEMESSVAAMRSSAY	8	4.99	0.02	2967	44.36	AE003602	TRUE	FALSE	3	3709	2.8	22of120	1.7478	FALSE	FALSE	:::Cys_CAM::::::::::::::Oxidation_M:::::::::::::
FGMSQDDFDGKRLRK	8	9.88	0.015	2717	24.43	AE003602	TRUE	FALSE	2	1801	-0.3	6of 28	0.9481	FALSE	FALSE	::::::::::::::::
VKNLSGDMMK	9	9.89	0.004	1022	19.16	AE003602	TRUE	FALSE	2	1139.4	0.7	8of 18	1.1098	FALSE	FALSE	:::::::Oxidation_M:::
VNLLYQDMM	2	3.1	0.001	664	36.36	AE003602	TRUE	FALSE	1	1159.4	-0.3	8of 16	1.5235	FALSE	FALSE	:::::::Oxidation_M:Oxidation_M:
RHPPQPNHPHEKDQ	10	8.06	0.12	1318	-0.3	AE003603	TRUE	FALSE	2	1717.8	1.4	5of 26	0.7719	FALSE	FALSE	::::::::::::::
LLRADSAIYA	15	6.7	0.056	937	33.5	AE003603	TRUE	FALSE	1	1093.3	-2.3	8of 18	1.6126	FALSE	FALSE	::::::::::
GKALMDDNVMKKYTTRSDEARHY	13	9.43	0.052	2210	29.46	AE003603	TRUE	FALSE	3	2731.1	2.4	17of 88	1.4528	FALSE	FALSE	::::::::::::::::::::::
QPRRQIGTLDVAFK	12	11.33	0.051	1324	29.9	AE003603	TRUE	TRUE	3	1629.9	-2.5	13of 52	1.4764	FALSE	FALSE	::::::::::::::
KQILFLTDIPGEAAAARCAGLQAIILK	5	8.93	0.02	2080	83.4	AE003603	TRUE	FALSE	3	2883.4	0.8	25of104	3.0705	FALSE	FALSE	::::::::::::::::Cys_CAM:::::::::
LTRAQLELHRMNTGFRK	8	12.12	0.02	2707	35.43	AE003603	TRUE	FALSE	2	2072.4	-1.6	8of 32	1.1104	FALSE	FALSE	::::::::::::::::

GNQKQIVESVNPTPQLKPH	3	9.89	0.004	1512	25.3	AE003603	TRUE	FALSE	2	2115.4	1	10of 36	1.2309	FALSE	FALSE	::::::::::::::::::
PGGRMTHSLSTPSGVDGTPSTPRHRGGKK	9	12.14	0.181	2160	17.03	AE003604	TRUE	FALSE	3	2976.3	-2.4	17of112	1.9395	FALSE	FALSE	:::::Oxidation_M::::::::::::::::::::::
SGCMFTPIPVELTSYEPETFGLK	2	3.97	0.266	1457	65.63	AE003605	TRUE	TRUE	2	2604.9	2.2	13of 44	2.1468	FALSE	FALSE	:::Cys_CAM::::::::::::::::::
YEKSKEMTSQLKSNEESLLAERKQMMDNL	2	4.91	0.12	1930	50.79	AE003605	TRUE	FALSE	3	3494.9	1.7	9of112	1.0514	FALSE	FALSE	::::::::::::::::::::::::Oxidation_M:Oxidation_M:::::
QAIESAVEAYTK	9	4.27	0.074	729	23.4	AE003605	TRUE	FALSE	3	1310.4	-1.2	18of 44	1.8656	FALSE	FALSE	::::::::::::
VELDQLAKHSKPNSDAKE	14	5.39	0.062	2712	20.4	AE003605	TRUE	FALSE	3	2010.2	2.1	11of 68	1.3571	FALSE	FALSE	::::::::::::::::::
SDSELDSSKGIDLTFRRRRRK	3	10.56	0.059	1345	26.4	AE003605	TRUE	FALSE	3	2367.6	1.6	8of 76	0.8389	FALSE	FALSE	::::::::::::::::::::
KKTELWHEGIAPVVISALKPFLSSSLPA	10	9.76	0.046	1365	79.5	AE003605	TRUE	FALSE	3	3020.6	2.9	23of108	2.4512	FALSE	FALSE	::::::::::::::::::::::::::
MIEDTFGIPVGLPNKI	14	4.08	0.04	1362	51.73	AE003605	TRUE	FALSE	2	1745.1	0.7	9of 30	1.033	FALSE	FALSE	::::::::::::::::
VVHMHSKARIASQALYIL	4	10.4	0.038	2274	49.73	AE003605	TRUE	FALSE	2	2054.5	-1.7	8of 34	0.966	FALSE	FALSE	::::Oxidation_M::::::::::::::
SIPAEDTTANRNGSAGSGSSSKSGVIPKNR	1	10.58	0.034	988	22.9	AE003605	TRUE	FALSE	2	2947.1	0.4	15of 58	2.4828	FALSE	FALSE	::::::::::::::::::::::::::
TSEDAAVGAQAASGAD	15	2.88	0.031	2781	18.3	AE003605	TRUE	FALSE	2	1421.4	1.6	9of 30	1.1378	FALSE	FALSE	::::::::::::::::
GPSTGTSETATATAAVAS	8	3.3	0.027	2249	20.1	AE003605	TRUE	FALSE	1	1580.6	-0.3	9of 34	1.0723	FALSE	FALSE	::::::::::::::::
LSLSPPIPTHR	8	11.05	0.006	3327	27.1	AE003605	TRUE	FALSE	2	1218.4	-1	6of 20	1.0728	FALSE	FALSE	::::::::::::
CTKVVEAQSATGTRMLTIVK	9	9.91	0.006	1186	40.93	AE003605	TRUE	FALSE	3	2210.6	-1.6	18of 76	1.7283	FALSE	FALSE	:Cys_CAM::::::::::::Oxidation_M:::::
NCQHGEDMVIMHLPKDRVR	11	7.32	0.174	2128	34.36	AE003606	TRUE	TRUE	2	2368.7	-2.5	10of 36	1.4095	FALSE	FALSE	::Cys_CAM:::::Oxidation_M:::Oxidation_M:::::::::
QAVKANGYANGSASNGHSKHLGEGDALI	10	7.88	0.124	1869	32.6	AE003606	TRUE	FALSE	2	2768	-0.1	10of 54	1.0877	FALSE	FALSE	::::::::::::::::::::::::::
SLNDLSLTITTGGETAPAAAAGEGGEKAESAETATPVQTK	2	3.89	0.123	930	60.2	AE003606	TRUE	TRUE	3	3847.1	0.8	30of156	2.628	FALSE	FALSE	::::::::::::::::::::::::::::::::::::::
VLAYSNGGDGRMSSPTLHFQMGKT	4	9.72	0.093	1485	43.46	AE003606	TRUE	FALSE	3	2571.9	1.5	20of 92	1.5493	FALSE	FALSE	:::::::::::Oxidation_M::::::::::::
IPLLHDTTRSPK	7	10.09	0.077	2175	24	AE003606	TRUE	FALSE	2	1378.6	2.8	7	1.0224	FALSE	FALSE	::::::::::::
QQQQQHHQHPQQPHHDR	6	8.2	0.072	1647	-6.9	AE003606	TRUE	FALSE	2	2195.3	-0.5	10of 32	1.151	FALSE	FALSE	::::::::::::::::::
ITHVKEPRLPSLSRGRLTE	15	11.23	0.063	581	37.5	AE003606	TRUE	FALSE	3	2190.6	1.4	20of 72	2.1377	FALSE	FALSE	::::::::::::::::::
NLTPHSQIPK	13	10.1	0.041	1172	15.1	AE003606	TRUE	FALSE	1	1135.3	0.3	8of 18	1.4262	FALSE	FALSE	::::::::::
HTGVLTGLSKATTTVPHPATAFR	14	11.49	0.034	2023	40.4	AE003606	TRUE	FALSE	3	2364.7	-1.6	22of 88	1.7925	FALSE	FALSE	::::::::::::::::::::::
NLTPHSQIPK	11	10.1	0.031	1045	15.1	AE003606	TRUE	FALSE	1	1135.3	0.3	9of 18	1.5056	FALSE	FALSE	::::::::::
NLTPHSQIPK	12	10.1	0.025	1399	15.1	AE003606	TRUE	FALSE	1	1135.3	0.6	8of 18	1.5259	FALSE	FALSE	::::::::::
EKPAAKRDQAQEK	5	9.76	0.02	1748	3.5	AE003606	TRUE	FALSE	2	1499.7	2.9	13of 24	1.6455	FALSE	FALSE	::::::::::::
YAIEPRGLIDIKGKGMMNTFWLLGK	5	10.05	0.016	1487	76.56	AE003606	TRUE	FALSE	3	2869.5	0.4	21of 96	2.2423	FALSE	FALSE	::::::::::::::::Oxidation_M:::::::::
RVPVRGMQFLVPANA	13	12.41	0.014	1356	42.73	AE003606	TRUE	FALSE	2	1656	-0.2	8of 28	1.0971	FALSE	FALSE	::::::::::::::
LMVEERQCSLNEGN	12	3.97	0.006	1089	30.43	AE003606	TRUE	FALSE	2	1695.8	-2.2	6of 26	0.9786	FALSE	FALSE	::Oxidation_M:::::Cys_CAM::::::
ESKVLYSSDNVNIKLDDKR	4	7	0.004	2906	31.1	AE003606	TRUE	FALSE	3	2224.5	0.7	11of 72	1.3918	FALSE	FALSE	::::::::::::::::
MQHQSRSGMGLMQRPPR	7	12.71	0.004	1527	23.99	AE003606	TRUE	FALSE	3	2014.3	-0.3	383	1.6555	FALSE	FALSE	:Oxidation_M:::::::::::::::
FEQRVGEVLQSFGI	4	4.27	0.003	2869	42.7	AE003606	TRUE	FALSE	2	1609.8	-1.3	4of 26	0.7574	FALSE	FALSE	::::::::::::::
GIGRKTRKKRRK	15	12.89	0.002	473	-3.2	AE003606	TRUE	FALSE	3	1484.8	-1.2	18of 44	1.7078	FALSE	FALSE	::::::::::::
IINANYMLPPDPQYQCFSDIIRGCLK	2	6.09	0.032	2446	77.73	AE003607	TRUE	TRUE	2	3144.5	-1.2	7of 50	0.9528	FALSE	FALSE	::::::Oxidation_M::::::::Cys_CAM::::::::Cys_CAM:::
VQVFAVKRHTINLR	5	12.42	0.012	1396	35.2	AE003607	TRUE	FALSE	3	1682	-0.7	16of 52	1.8233	FALSE	FALSE	::::::::::::::
EPMNFSDSEEEPVPESQTEVTPLAPFKDVAVDK	9	3.58	0.119	2314	66.83	AE003608	TRUE	FALSE	3	3680	2.7	19of128	1.7717	FALSE	FALSE	:::Oxidation_M:::::::::::::::::::::::::
AIMQLTTKYNALLTLAKEVMR	10	10.18	0.106	1353	63.86	AE003608	TRUE	FALSE	3	2442	-2.7	21of 80	2.4591	FALSE	FALSE	:::Oxidation_M::::::::::::::Oxidation_M::
LHRAVMRGHLEVCRILLAK	6	11.23	0.105	1872	54.73	AE003608	TRUE	FALSE	2	2289.8	0.9	8of 36	1.3689	FALSE	FALSE	::::::Oxidation_M::::::Cys_CAM::::::
LRLLNAAGTDE	6	4.08	0.076	1275	28.8	AE003608	TRUE	FALSE	2	1173.3	0.1	4of 20	0.7773	FALSE	FALSE	::::::::::::
RPPQQQKPVESSQQPSIEIQLE	12	4.56	0.056	1024	35.9	AE003608	TRUE	FALSE	3	2547.8	-2.5	8of 84	1.0458	FALSE	FALSE	::::::::::::::::::::
PISLEEAVAMQQNAQQF	2	3.13	0.051	1017	43.53	AE003608	TRUE	FALSE	3	1905.1	0.9	14of 64	1.4149	FALSE	FALSE	::::::::::::::::
FTSKTTQPGRQVEK	10	10.59	0.051	1276	12.8	AE003608	TRUE	FALSE	2	1607.8	1.7	7of 26	1.1109	FALSE	FALSE	::::::::::::::
LDTVNSLASRLPEGQHLLALVQDAYSKASN	1	5.28	0.045	1608	68.2	AE003608	TRUE	FALSE	3	3212.6	1.9	20of116	1.8519	FALSE	FALSE	::::::::::::::::::::::::::::
RFRENQPTQIGVLFDGIEGTL	8	4.45	0.028	2644	55.4	AE003608	TRUE	FALSE	2	2391.7	1.1	10of 40	1.1199	FALSE	FALSE	::::::::::::::::::::
EVVLRGPNSRT	15	10.89	0.026	1570	19.6	AE003608	TRUE	FALSE	2	1228.4	2.4	6of 20	0.8551	FALSE	FALSE	::::::::::::
VVNYQNLETNMLQKK	14	9.63	0.018	2622	31.93	AE003608	TRUE	FALSE	3	1839.1	1.1	7of 56	1.0188	FALSE	FALSE	::::::::::Oxidation_M:::::
PGQQGPPGEAGEGGINSKGT	15	4.27	0.004	555	13.9	AE003608	TRUE	FALSE	3	1838.9	-0.3	16of 76	1.5704	FALSE	FALSE	::::::::::::::::::
ETVVLDPALVWTNA	4	3.01	0.002	1762	47.9	AE003608	TRUE	FALSE	2	1528.7	-1.8	9of 26	1.4417	FALSE	FALSE	::::::::::::::
LRLTRLK	9	12.42	0	1260	21.6	AE003608	TRUE	FALSE	1	900.2	-0.4	7of 12	1.1327	FALSE	FALSE	::::::::
VRAPIAPVR	12	12.41	0	2102	24.2	AE003608	TRUE	FALSE	2	979.2	-1.5	5of 16	0.8563	FALSE	FALSE	::::::::::
ACSPSYEHMLSSTTSSTLSSASSS	5	5.13	0.141	1980	33.43	AE003609	TRUE	FALSE	2	2482.6	-0.6	10of 46	1.5051	FALSE	FALSE	::Cys_CAM::::::Oxidation_M:::::::::::::::
PMGISSDQERSRDSLASNKSATSR	14	10.08	0.083	1822	23.03	AE003609	TRUE	FALSE	3	2581.8	1.3	10of 92	1.1945	FALSE	FALSE	::::::::::::::::::::::
AQAQAQAQSLNDPQLIV	9	3.1	0.079	2292	38	AE003609	TRUE	FALSE	3	1796	2.9	23of 64	1.9261	FALSE	FALSE	::::::::::::::::::
HGQVLDVLKSTNSLRINSK	1	10.59	0.078	1660	33.6	AE003609	TRUE	FALSE	2	2110.4	1.4	13of 36	2.0319	FALSE	FALSE	::::::::::::::::::
CSSPSALKEELKRLKFFELSLKEQI	7	8.88	0.067	1404	65.3	AE003609	TRUE	FALSE	3	2982.5	2.3	115	1.9892	FALSE	FALSE	:Cys_CAM:::::::::::::::::::::::::
LEKYVANVGEDGNHIPLAGVHDMNTGMTPLMYA	8	4.53	0.027	1623	77.19	AE003609	TRUE	FALSE	3	3576.1	0.2	21of128	1.6576	FALSE	FALSE	::::::::::::::::::::::::::::Oxidation_M:::
WTVVASDDFR	5	3.89	0.273	2899	29.1	AE003610	TRUE	FALSE	2	1196.3	-2.6	6of 18	1.0328	FALSE	FALSE	::::::::::
PLYSIFCQAYSYGGTTTQGHDAEKVEHMKK	4	7.31	0.109	2502	48.93	AE003610	TRUE	FALSE	3	3464.8	-1.9	21of116	2.013	FALSE	FALSE	::::::Cys_CAM::::::::::::::::::Oxidation_M:::
VCLTSLGSPLWYDEH	13	4.07	0.092	1094	46.4	AE003610	TRUE	FALSE	2	1777.9	2.4	8of 28	1.0826	FALSE	FALSE	::Cys_CAM:::::::::::::
DRNLFVQPVNAALLECMLIQATEAEQLGLN	3	3.69	0.042	2097	93.73	AE003610	TRUE	FALSE	3	3372.8	1.7	23of116	2.493	FALSE	FALSE	::::::::::::::Cys_CAM:::::::::::::
KQKNLLAAKQER	12	10.83	0.012	791	13.8	AE003610	TRUE	FALSE	2	1427.7	0.6	12of 22	1.8849	FALSE	FALSE	::::::::::::
LKMRHRDPRLFYLSMEVAVRRAGV	3	11.84	0.223	2393	62.66	AE003611	TRUE	FALSE	3	2918.5	2.7	21of 92	2.6611	FALSE	FALSE	:::Oxidation_M:::::::::::::::::::::
FVLCLIGIR	15	9.01	0.093	428	45.9	AE003611	TRUE	FALSE	2	1091.3	0.8	11of 16	1.8476	FALSE	FALSE	::::Cys_CAM:::::::
PLTPANHILPEAEDAPYGGHTNGGQTDAERSASKRRRGR	4	9.72	0.06	2174	39.7	AE003611	TRUE	FALSE	3	4185.5	-1	23of152	2.4178	FALSE	FALSE	::::::::::::::::::::::::::::::::
VYDVSDNDPTMHTIVAPVDIVGDDHILQ	13	3.58	0.058	1355	68.53	AE003611	TRUE	FALSE	3	3096.4	2.1	22of108	1.5615	FALSE	FALSE	::::::::::Oxidation_M:::::::::::::::
GAHLAGLLAVAATLMASDGERYLRLGTLKVNFK	5	10.18	0.053	2791	90.23	AE003611	TRUE	FALSE	3	3459.1	-0.7	25of128	1.746	FALSE	FALSE	::::::::::::::::::::::::::::
STSMSINSSSASINTSDGSQFSSFGS	8	3.1	0.05	2191	35.93	AE003611	TRUE	FALSE	3	2574.6	1.9	22of100	2.5587	FALSE	FALSE	::::::::::::::::::::::::
LLIFGAGNHELE	11	4.25	0.042	641	40.9	AE003611	TRUE	FALSE	2	1313.5	1.2	18of 22	2.7384	FALSE	FALSE	::::::::::::
SRESALRGDGSKKRK	1	11.47	0.006	748	2.3	AE003611	TRUE	FALSE	2	1675.9	2.3	9of 28	1.1114	FALSE	FALSE	::::::::::::::
KLHPDDLPLRTQMERMKRGEG	11	9.88	0.002	2596	34.06	AE003611	TRUE	FALSE	3	2540.9	2.1	14of 80	1.4769	FALSE	FALSE	:::::::::::Oxidation_M:::Oxidation_M:::::
TIPAWIAIVFLIVMIFAV	7	6.02	0.181	1865	99.23	AE003612	TRUE	FALSE	2	2018.6	1.4	372	1.2807	FALSE	FALSE	::::::::::::::::
VYLIMQLAENGTLLDYVRERKFLDEPQS	15	4.29	0.159	964	84.53	AE003612	TRUE	FALSE	3	3358.8	3	21of108	1.6436	FALSE	FALSE	:::::Oxidation_M:::::::::::::::::::::
DVTIKLHHRVGKYLKINLYF	11	10.21	0.154	1461	55.1	AE003612	TRUE	FALSE	2	2459	0.3	6of 38	1.0568	FALSE	FALSE	::::::::::::::::::
GLNIPIQLEELSRMQGHLNSAHQWKDNTACAF	1	6.03	0.086	1993	73.73	AE003612	TRUE	FALSE	3	3681.1	-0.1	11of124	1.2314	FALSE	FALSE	:::::::::::::::::::::::::::::::Cys_CAM:::
AHSFERWLSRCRDIVDAHTPTSVTLQELQELCK	10	6.05	0.074	2477	74.7	AE003612	TRUE	TRUE	3	3985.4	-0.8	14of128	1.4072	FALSE	FALSE	::::::::::Cys_CAM::::::::::::::::::::Cys_CAM::
ELRESLPRELQANFIPRRCDVSKED	8	4.85	0.072	2008	52.7	AE003612	TRUE	FALSE	3	3059.4	0.7	12of 96	1.4224	FALSE	FALSE	:::::::::::::::::::Cys_CAM::::::
ISKDAQGLVWDLASGQLQHK	15	7.79	0.062	2718	42.8	AE003612	TRUE	FALSE	3	2195.5	-1.5	18of 76	1.5914	FALSE	FALSE	::::::::::::::::::
RHSLFSGIKMLTYDYMREKMIVPDEDGR	5	7.68	0.034	2391	66.19	AE003612	TRUE	FALSE	3	3405.9	2.7	14of108	1.4097	FALSE	FALSE	::::::::::Oxidation_M:::::::::::::::::
DGQEVANALRTILSYNASVNLYM	14	4.08	0.031	1039	61.13	AE003612	TRUE	FALSE	3	2543.9	-2.6	21of 88	2.0403	FALSE	FALSE	::::::::::::::::::::
KLAVVTGASGGIGAACARAMIGAGLR	5	11.33	0.009	1927	59.03	AE003612	TRUE	FALSE	3	2429.9	2.4	22of100	2.009	FALSE	FALSE	::::::::::::::Cys_CAM:::::::::::
VWRSRAKAKEFNIP	4	11.47	0.006	2498	30.2	AE003612	TRUE	FALSE	2	1703	-1.3	4of 26	0.9915	FALSE	FALSE	::::::::::::::
DEQEQRSNSPSQAQDVHDETNGSEYQANRNK	4	4.22	0	2597	12.3	AE003612	TRUE	FALSE	3	3563.6	1.2	22of120	2.2086	FALSE	FALSE	::::::::::::::::::::::::::::

NASSNNVVTVTVNSPPDDGN	14	2.93	0.161	912	23.8	AE003613	TRUE	FALSE	3	2002.1	-0.9	20of 76	1.9039	FALSE	FALSE	::::::::::::::::::::
YHGAPHIQSPVVHM	12	8	0.124	2810	26.73	AE003613	TRUE	FALSE	2	1589.8	2.3	11of 26	1.5094	FALSE	FALSE	:::::::::::::Oxidation_M:
HQRRQMHNNGPKFGTASPQAVK	10	12.43	0.123	2716	15.83	AE003613	TRUE	FALSE	2	2506.8	2.6	7of 42	1.0501	FALSE	FALSE	::::::Oxidation_M::::::::::::::::
KQRYLPSMAEGKLIGAFGLTEPNHGSDPAGMETRAK	15	9.56	0.105	1299	62.46	AE003613	TRUE	FALSE	3	3860.4	-0.9	23of140	3.155	FALSE	FALSE	::::::::::::::::::::::::::::::::::
TAMSSGPYYLMRLNIIVVPHGL	7	9.59	0.068	1663	71.66	AE003613	TRUE	FALSE	3	2433.9	-2.4	270	1.6549	FALSE	FALSE	::::::::::::::::::::::
ADFVAVSPLETVSFLKDMDTILQSK	15	3.97	0.037	1745	72.53	AE003613	TRUE	FALSE	3	2772.2	1.5	9of 96	1.2305	FALSE	FALSE	::::::::::::::::Oxidation_M:::::::
MPVPLKYEN	8	6.87	0.035	2850	25.53	AE003613	TRUE	FALSE	2	1107.3	2	6of 16	1.222	FALSE	FALSE	:Oxidation_M::::::::
PRYASLDQLAAANAMATSQGRHMAR	9	11.05	0.032	1406	43.46	AE003613	TRUE	TRUE	3	2705	0.7	21of 96	1.6801	FALSE	FALSE	::::::::::::::::::::::Oxidation_M:::
SDSTTDELSSVSASNRAHMVRLS	4	5.28	0.024	2704	33.13	AE003613	TRUE	FALSE	2	2451.6	1.7	13of 44	1.3616	FALSE	FALSE	::::::::::::::::::::::
QSAMSQAAAAAA	9	6.02	0.021	1693	19.13	AE003613	TRUE	FALSE	2	1078.2	-2.1	13of 22	1.23	FALSE	FALSE	::::::::::::
SMDRQSPPMSGRSTPNS	10	10.89	0.098	2695	14.86	AE003614	TRUE	FALSE	3	1852	-0.4	13of 64	1.2417	FALSE	FALSE	:::::::::Oxidation_M::::::::
FVKDLDRLDMVM	10	4.18	0.087	1606	43.26	AE003614	TRUE	FALSE	1	1498.8	-1	6of 22	1.0867	FALSE	FALSE	::::::::::Oxidation_M:
MQELLQKWIQMG	9	6.95	0.06	2772	42.26	AE003614	TRUE	FALSE	2	1521.8	-0.3	6of 22	1.0849	FALSE	FALSE	::::::::::Oxidation_M::
YKNKTNRDSRLPKNNMWSL	7	10.89	0.055	1279	27.53	AE003614	TRUE	FALSE	2	2382.7	-1.8	7	2.6816	FALSE	FALSE	::::::::::::::Oxidation_M::::
VSEAHATISEADDSSNV	10	3.59	0.028	1070	23.1	AE003614	TRUE	FALSE	3	1732.8	-2.1	21of 64	2.0522	FALSE	FALSE	::::::::::::::::::
GVRPTKIPAPLFLGPSASSRIYSSLMPER	6	11.29	0.007	1439	72.63	AE003614	TRUE	FALSE	3	3145.7	2.7	23of112	1.8065	FALSE	FALSE	::::::::::::::::::::::::Oxidation_M::::
PPLFEKK	9	9.89	0.004	924	17.1	AE003614	TRUE	FALSE	2	859.1	1.2	9of 12	1.9457	FALSE	FALSE	::::::::
SMLRAHAETCLLTSEEGEERLTAEK	11	4.55	0.001	1425	48.93	AE003614	TRUE	FALSE	3	2863.1	-0.9	12of 96	1.3494	FALSE	FALSE	::::::::::Cys_CAM:::::::::::::::
IDSILDSILTTGTTNTQQPNTSMGSQSQI	8	2.93	0.181	1743	54.73	AE003615	TRUE	FALSE	3	3069.3	-1.1	13of112	1.7391	FALSE	FALSE	::::::::::::::::::::::::Oxidation_M::::::::
RHLPVTKGH	10	11.49	0.138	2266	8.6	AE003615	TRUE	FALSE	2	1045.2	-1.9	5of 16	0.874	FALSE	FALSE	::::::::::
STLKTSSENESDN	6	3.83	0.116	2911	7.6	AE003615	TRUE	FALSE	2	1412.4	0.3	8of 24	1.1194	FALSE	FALSE	::::::::::::
IIFSDKLAR	9	10.09	0.11	381	30.3	AE003615	TRUE	FALSE	2	1063.3	-2.3	9of 16	1.453	FALSE	FALSE	::::::::::
SDHERNGSGAVDSPPPPK	15	5.28	0.108	971	10.1	AE003615	TRUE	FALSE	2	1847.9	2.8	12of 34	1.5699	FALSE	FALSE	::::::::::::::::::
SCNECPSNMR	9	6.14	0.064	1370	11.63	AE003615	TRUE	FALSE	2	1255.3	0.7	8of 18	1.1205	FALSE	FALSE	::Cys_CAM::::Cys_CAM::::::
PFLMRIWGSPNGVENESGVAIDTKSDIH	11	4.54	0.06	1469	64.73	AE003615	TRUE	FALSE	3	3087.4	2.7	19of108	1.5789	FALSE	FALSE	:::::Oxidation_M:::::::::::::::::::::::
RMRCAATGAPNGGAGC	5	9.2	0.059	3036	18.73	AE003615	TRUE	FALSE	2	1623.7	-1.2	6of 30	0.7383	FALSE	FALSE	::Oxidation_M::Cys_CAM::::::::::Cys_CAM:
FKGYKLIGSNIMR	11	10.71	0.034	1085	35.03	AE003615	TRUE	FALSE	2	1527.9	-2.6	10of 24	1.3805	FALSE	FALSE	::::::::::::
GSVAIRFGRLLHLKRKEVY	5	11.41	0.019	2441	48.7	AE003615	TRUE	FALSE	3	2243.7	-1.8	20of 72	1.8119	FALSE	FALSE	::::::::::::::::::
MERAGSDQR	15	7.05	0.019	2207	7.23	AE003615	TRUE	FALSE	2	1050.1	-0.1	5of 16	0.6985	FALSE	FALSE	::::::::::
PFRDNVTITCGSPGRQLRATASSGFR	3	11.93	0.011	1524	45.1	AE003615	TRUE	FALSE	3	2853.1	-0.4	25of100	1.6626	FALSE	FALSE	::::::::::Cys_CAM:::::::::::::::
GIFFTLYGVQSARMTQQRRM	1	12.11	0.005	238	53.06	AE003615	TRUE	FALSE	2	2391.8	0.4	10of 38	1.3772	FALSE	FALSE	::::::::::::::::::
TPDSIMSTGSSGM	11	3.1	0.15	497	20.66	AE003616	TRUE	FALSE	2	1303.4	-0.2	11of 24	1.4263	FALSE	FALSE	::::::Oxidation_M::::::Oxidation_M:
RTETNPTWDVEIR	7	4.45	0.128	1113	25.6	AE003616	TRUE	FALSE	3	1617.8	2.6	7	2.4604	FALSE	FALSE	::::::::::::
NLMATEGPKALFRG	7	10.09	0.023	1184	33.83	AE003616	TRUE	FALSE	2	1505.8	0.1	4	1.4669	FALSE	FALSE	::::::::::::
YRKRIPPSIYMN	10	10.56	0.019	401	29.23	AE003616	TRUE	FALSE	2	1554.9	-1.9	7of 22	1.3209	FALSE	FALSE	::::::::::Oxidation_M::
SNKYPSVANPHDK	12	9.63	0.001	1939	7.8	AE003616	TRUE	FALSE	2	1457.6	-2.1	8of 24	1.0963	FALSE	FALSE	::::::::::::
IFAILLISLLNRKELLKLLATFDR	15	10.58	0.118	1718	102.9	AE003617	TRUE	FALSE	3	2815.5	-2	18of 92	1.8012	FALSE	FALSE	::::::::::::::::::::
MLTVTLSADHRVVDGAVAAR	3	7.85	0.083	1500	47.63	AE003617	TRUE	FALSE	2	2099.4	2.4	11of 38	1.3554	FALSE	FALSE	:Oxidation_M:::::::::::::::::
EKFAKLEQRTRTSLLQNLCEELREK	2	8.9	0.079	70	51	AE003617	TRUE	FALSE	3	3121.5	-2.6	10of 96	1.0275	FALSE	FALSE	::::::::::::::::Cys_CAM:::::::
VCEKSVKGSPDSSPLLEKGRK	3	9.7	0.06	2133	25	AE003617	TRUE	FALSE	2	2302.6	-0.3	12of 40	1.601	FALSE	FALSE	::Cys_CAM:::::::::::::::::
VHLQVIISVSQM	13	7.85	0.032	784	40.93	AE003617	TRUE	FALSE	2	1354.7	2.6	10of 22	1.9293	FALSE	FALSE	::::::::::::
HSSNSA	12	7.85	0.114	2717	-1.3	AE003618	TRUE	FALSE	1	602.6	-2.4	5of 10	0.9367	FALSE	FALSE	::::::::
YFSYFRDNNVTTV	9	6.64	0.077	2462	34.6	AE003618	TRUE	FALSE	2	1626.8	-2	5of 24	0.8872	FALSE	FALSE	::::::::::::
GFVNFRDSKEIMMTSDSETKFKYSQRANRTSV	6	10.05	0.05	1579	53.16	AE003618	TRUE	FALSE	3	3762.2	2.3	16of124	1.6439	FALSE	FALSE	::::::::::::::::::::::::::::::
QQMLSVTTSFCGNGSASR	6	9.01	0.029	2324	30.13	AE003618	TRUE	FALSE	2	1932.1	-0.8	8of 34	1.0871	FALSE	FALSE	::::::::::Cys_CAM:::::::
RRRKSPSGANKPTVIATSLRRLVNPNANR	10	13.01	0.024	1350	35.8	AE003618	TRUE	FALSE	3	3231.7	-1.3	21of112	1.6232	FALSE	FALSE	::::::::::::::::::::::::::::
LSSFQSISSPIDEGVEDV	10	2.84	0.007	1728	44.4	AE003618	TRUE	FALSE	2	1910	2.8	4of 34	0.6911	FALSE	FALSE	::::::::::::::::::
AGVSDQQMLLMANIIKDFD	6	3.6	0.04	1523	56.66	AE003619	TRUE	FALSE	3	2126.4	-1.7	20of 72	2.6263	FALSE	FALSE	::::::::::Oxidation_M:::::::::
NGGLPLSGIGNILLAILSGQRHPPHKDH	9	10.1	0.036	2068	59.3	AE003619	TRUE	FALSE	3	2913.4	-2.7	9of108	1.0037	FALSE	FALSE	::::::::::::::::::::::::::::
LSMCGIAALYNAVLTSIATSVL	5	5.33	0.027	987	77.63	AE003619	TRUE	FALSE	3	2269.7	0	15of 84	1.3601	FALSE	FALSE	::::Cys_CAM:::::::::::::::
YWSMMAYNNAKLCNVLFAQEL	15	6.28	0.027	1285	71.86	AE003619	TRUE	FALSE	3	2583.9	1.4	14of 80	1.4032	FALSE	FALSE	::::Oxidation_M::::::::Cys_CAM:::::::::
ASVLRPLNAFGVNSSAATAPVAQL	1	11.05	0.024	2274	61.4	AE003619	TRUE	FALSE	3	2355.7	-2.4	21of 92	1.5293	FALSE	FALSE	::::::::::::::::::::::::::
WLLVWMTVLLLVVPPHLVDGRYLPTRSH	9	9.85	0.022	2205	110.93	AE003619	TRUE	FALSE	3	3329	1.6	8of108	1.0879	FALSE	FALSE	::::::Oxidation_M:::::::::::::::::::
KFFKMVQVGVPAPAVKQKMQSEGLEPRILDT	1	10.16	0.011	1689	74.26	AE003619	TRUE	FALSE	3	3490.2	-1.2	19of120	1.2121	FALSE	FALSE	::::::Oxidation_M:::::::::::::::::::::
LGLDFHLPTCPGFYNIFHPFDPVAYR	9	6.01	0.276	2354	85.9	AE003620	TRUE	TRUE	3	3095.5	0.3	27of100	2.9052	FALSE	FALSE	::::::::::Cys_CAM:::::::::::::::
FTIAPKSEVTSKIHLPSVPK	14	10.32	0.136	410	42.3	AE003620	TRUE	FALSE	2	2180.6	0.1	5of 38	0.8234	FALSE	FALSE	::::::::::::::::::::
RMLEEMVNALEPYIEYAE	5	3.68	0.122	1634	58.96	AE003620	TRUE	FALSE	2	2217.5	0	9of 34	1.1838	FALSE	FALSE	::Oxidation_M:::::::::::::::
IRIKAPSIER	9	11.33	0.115	1721	23.8	AE003620	TRUE	FALSE	2	1183.4	-2.1	9of 18	1.4006	FALSE	FALSE	::::::::::
SENLPHPQMLEEYTVAFCAVGEDGR	6	4	0.098	2376	56.23	AE003620	TRUE	FALSE	3	2867.1	1.8	17of 96	1.6173	FALSE	FALSE	::::::::Oxidation_M::::::::Cys_CAM::::::::
TILMHGFHFLVWLFAVRSIR	12	12.41	0.09	1267	84.53	AE003620	TRUE	TRUE	3	2445	0	18of 76	1.7474	FALSE	FALSE	::::::::::::::::::::
LEYCQQFKPPVDPKISDSL	1	4.31	0.064	330	46.7	AE003620	TRUE	FALSE	2	2265.5	-1.9	5of 36	0.7146	FALSE	FALSE	::::Cys_CAM:::::::::::::::
GTHDIDAGWLTDVRRK	15	7.82	0.052	944	27.3	AE003620	TRUE	FALSE	2	1841	-2.8	8of 30	1.1131	FALSE	FALSE	::::::::::::::
NKVLVAMGIQDAFEK	1	6.99	0.046	2354	39.43	AE003620	TRUE	FALSE	2	1664	-2.2	4of 28	0.6072	FALSE	FALSE	::::::::::::::
FNADHPFAYVIRDR	6	7.76	0.046	2259	35.6	AE003620	TRUE	FALSE	2	1721.9	-1.6	14of 26	1.7488	FALSE	FALSE	::::::::::::::
HSRDADGVSLCHGGLEINCMLK	1	6.02	0.044	1798	42.43	AE003620	TRUE	FALSE	2	2486.7	-3	10of 42	1.0538	FALSE	FALSE	::::::::::Cys_CAM::::::::Cys_CAM:Oxidation_M:::
KFFALGSPIGMFVTI	2	10.1	0.027	518	59.63	AE003620	TRUE	FALSE	2	1645	-2.4	7of 28	0.9291	FALSE	FALSE	::::::::::Oxidation_M:::::
PLDKQTHFDEHGYPLPAPTV	14	5.12	0.022	1629	40	AE003620	TRUE	FALSE	3	2263.5	3	19of 76	1.7003	FALSE	FALSE	::::::::::::::::::
FACAPPTFQQ	10	5.33	0.019	745	27.4	AE003620	TRUE	FALSE	2	1167.3	-1.1	9of 18	1.1831	FALSE	FALSE	::::Cys_CAM:::::::
PELVPPPIGFFAPKSESEVLSQPPLAPSP	1	3.97	0.015	909	80.1	AE003620	TRUE	FALSE	3	3029.5	-1.1	16of112	1.5104	FALSE	FALSE	::::::::::::::::::::::::::
DGELNRGCVKVPEKHSG	13	7.17	0.012	1798	16.8	AE003620	TRUE	FALSE	2	1883	2.2	11of 32	1.652	FALSE	FALSE	:::::::Cys_CAM:::::::::
VATTMIPEY	5	3.3	0.002	2677	28.73	AE003620	TRUE	FALSE	2	1041.2	1	5of 16	0.8451	FALSE	FALSE	:::::Oxidation_M:::::
ILALKDNYQ	13	6.68	0.002	1370	27.6	AE003620	TRUE	FALSE	1	1078.3	1.4	7of 16	1.2821	FALSE	FALSE	::::::::::
YVARSLWASHLRYMR	15	11.16	0.196	2855	44.23	AE003621	TRUE	FALSE	3	1910.2	-1.6	10of 56	1.2591	FALSE	FALSE	::::::::::::::
RTMDLPPLESA	6	4.08	0.154	2448	28.83	AE003621	TRUE	FALSE	2	1230.4	2.1	5of 20	0.8053	FALSE	FALSE	::::::::::::
NAYLDFFK	5	6.68	0.153	1731	28.3	AE003621	TRUE	TRUE	1	1018.2	0.5	9of 14	2.1693	FALSE	FALSE	::::::::
VHSEDSLAVHAAASGSGDDEIGSTDK	1	3.99	0.099	1730	29.2	AE003621	TRUE	FALSE	2	2556.6	-2.4	7of 50	0.9771	FALSE	FALSE	::::::::::::::::::::::::::
MLYPHNAMHIIRGYDVV	13	7.85	0.088	1326	51.56	AE003621	TRUE	FALSE	2	2046.4	0	11of 32	2.327	FALSE	FALSE	:Oxidation_M:::::::::::::::::
PFFGIGAWLWGTLYIDR	3	6.7	0.071	2268	72.9	AE003621	TRUE	FALSE	2	2013.3	0.6	8of 32	1.1587	FALSE	FALSE	::::::::::::::::::
PHPPHEQETAVPAPPLAA	5	5.13	0.07	2683	31.7	AE003621	TRUE	FALSE	2	1860.1	-0.5	9of 34	1.2607	FALSE	FALSE	::::::::::::::::::
MATTIINLLFEDKPVASDKPRTHQK	9	9.76	0.064	1534	51.13	AE003621	TRUE	FALSE	3	2855.3	1.9	26of 96	3.3575	FALSE	FALSE	::::::::::::::::::::::::::
KREIAELR	9	10.09	0.053	1465	16.4	AE003621	TRUE	FALSE	2	1015.2	-1.6	10of 14	1.5129	FALSE	FALSE	::::::::
HLKDTMCSEFSQIFTLCSFVLENSMNAALIH	4	5.18	0.044	2042	92.06	AE003621	TRUE	FALSE	3	3678.1	-0.8	20of120	2.2609	FALSE	FALSE	::::::Oxidation_M:Cys_CAM::::::::::Cys_CAM::::::::Oxidation_M::::::
QAAPYPSADELK	10	4.08	0.034	774	21.6	AE003621	TRUE	FALSE	2	1290.4	1.2	11of 22	1.312	FALSE	FALSE	::::::::::::

MLNGSIMHQVDLDDSFDV	12	3.43	0.018	2274	50.26	AE003621	TRUE	FALSE	2	2053.3	-0.4	9of 34	1.239	FALSE	FALSE	::::::Oxidation_M::::::::::
FKQFNARYRMLAPFR	9	12.13	0.015	663	43.93	AE003621	TRUE	TRUE	3	1946.3	2	13of 56	1.4479	FALSE	FALSE	::::::::::::
QLGPELAKVLLKMFDHGLDIEKFHIVGHS	5	6.32	0.014	1988	80.23	AE003621	TRUE	FALSE	3	3289.9	1.7	17of112	1.5281	FALSE	FALSE	::::::::::::Oxidation_M::::::::::::::
MLYPHNAMHIIRGYDVV	14	7.85	0.008	1212	51.56	AE003621	TRUE	FALSE	2	2046.4	2.8	12of 32	2.6549	FALSE	FALSE	:Oxidation_M::::::::::::::
YKSDESLAKQMSMSKYFDIKTNLNPVSPSHLSQTS	1	9.39	0.007	2104	60.26	AE003621	TRUE	FALSE	3	3980.5	-2.5	23of136	2.4311	FALSE	FALSE	::::::::::::Oxidation_M::::::::::::::::::::
SPAPPSSSPSPQESPK	12	6.95	0.004	1088	11.8	AE003621	TRUE	FALSE	2	1580.7	-1.5	10of 30	1.4844	FALSE	FALSE	::::::::::::::::
IGMTSTVISNLFLAFFFYCLVK	14	8.88	0.004	1456	94.03	AE003621	TRUE	FALSE	3	2589.1	-2.2	11of 84	1.154	FALSE	FALSE	:::Oxidation_M::::::::::::::Cys_CAM::::
ADESIKSKSKKDK	15	10.05	0.003	1925	-0.2	AE003621	TRUE	FALSE	2	1464.7	0.9	8of 24	0.9657	FALSE	FALSE	::::::::::::
LADHARTITIALADGGTPDNTGRGYVLR	5	7.77	0.002	1612	56.3	AE003621	TRUE	FALSE	3	2926.3	2.9	24of108	1.8793	FALSE	FALSE	::::::::::::::::::::::::::::::
LKFHHDGSGPSHSVPEYFTSLHKPLAADKTQDASEF	3	6.03	0.131	1752	58	AE003622	TRUE	FALSE	3	3983.3	-0.7	25of140	2.5238	FALSE	FALSE	::::::::::::::::::::::::::::::::::::
DYELVIISVLGIRSEVDMRISPAVQYLSLLGIR	11	4.56	0.031	841	115.63	AE003623	TRUE	FALSE	3	3720.4	0.5	11of128	1.2028	FALSE	FALSE	::::::::::::::::::::::::::::::
LGFSGVTANSMHAVGDRDFVVDFIY	14	4.17	0.007	906	70.73	AE003623	TRUE	FALSE	3	2735	-0.1	20of 96	2.4872	FALSE	FALSE	::::::::::Oxidation_M:::::::::::::
YVNDHVAQLKLRSMK	5	10.18	0.002	2693	30.73	AE003623	TRUE	FALSE	2	1819.1	-0.3	7of 28	0.9541	FALSE	FALSE	::::::::::::Oxidation_M::
LGPALATGNTIVLKPAEQTSLTALYIAQLVK	15	9.63	0.46	1844	90	AE003624	TRUE	TRUE	3	3196.8	0.8	40of120	6.7196	FALSE	FALSE	::::::::::::::::::::::::::::::
LIVSYILAGMNAGLNNIGSLLNTTGAPNVSLSRTN	5	9.85	0.147	1983	94.83	AE003624	TRUE	FALSE	3	3561.1	2.8	13of136	1.4123	FALSE	FALSE	::::::::::::::::::::::::::::::
GSFSGIGWQMMMQLMQKDIKMMGIMHRMENVK	4	10.32	0.057	2754	86.94	AE003624	TRUE	FALSE	3	3808.6	-0.9	19of124	1.9059	FALSE	FALSE	::::::::::Oxidation_M:Oxidation_M:::::::::::::::::::::
LGPALATGNTIVLKPAEQTSLTALYIAQLVK	14	9.63	0.057	1757	90	AE003624	TRUE	TRUE	3	3196.8	0.4	25of120	2.1953	FALSE	FALSE	::::::::::::::::::::::::::::::
KMDSALEKIDEMSKR	5	7.12	0.034	2134	23.86	AE003624	TRUE	FALSE	2	1798.1	1.6	14of 28	2.2131	FALSE	FALSE	::Oxidation_M:::::::::::::
PSTPAPNTEEQRKEAERKELISRLVAK	11	9.76	0.015	2788	38.2	AE003624	TRUE	FALSE	3	3079.5	-2.4	7of104	0.3849	FALSE	FALSE	::::::::::::::::::::::::::::
KNGIKQHDVDLSFETK	15	7.77	0.013	1388	21.3	AE003625	TRUE	FALSE	2	1860.1	2.5	11of 30	1.9081	FALSE	FALSE	::::::::::::::::
SKTKLGLPEVMLGLLPGGGGTVRLPK	3	10.83	0.009	1975	64.13	AE003625	TRUE	FALSE	3	2636.2	-1.6	21of100	1.862	FALSE	FALSE	:::::::::Oxidation_M:::::::::::::
LTGSSMDLDYCMLPDLPCLMRWK	12	4.18	0.14	2226	77.49	AE003626	TRUE	FALSE	2	2820.2	-2.6	7of 44	1.0891	FALSE	FALSE	:::::::::Cys_CAM:Oxidation_M:::::Cys_CAM::::::
VHADNVGCCSSYRYTHTILK	6	8.28	0.118	1330	35	AE003626	TRUE	TRUE	3	2382.6	-0.5	21of 76	2.6236	FALSE	FALSE	::::::::Cys_CAM:Cys_CAM::::::::::::
SHGTGGGGSGNGKRSR	8	12.42	0.111	3174	-7.4	AE003626	TRUE	TRUE	2	1472.5	2.4	11of 30	1.4049	FALSE	FALSE	::::::::::::::::
EVAEEDVLELRGHQMEKPPGPRK	2	4.87	0.076	1265	37.53	AE003626	TRUE	FALSE	3	2662	-0.2	8of 88	0.999	FALSE	FALSE	::::::::::::::Oxidation_M:::::::::
RRLNLRHILAKATPVQHKA	12	12.71	0.061	1864	34.5	AE003626	TRUE	FALSE	2	2223.7	0	9of 36	1.2717	FALSE	FALSE	::::::::::::::::::::
KFLFFVNQPAVQKGLGIYLEGLK	4	10.05	0.046	1387	76.2	AE003626	TRUE	FALSE	3	2611.1	2.6	14of 88	1.5007	FALSE	FALSE	::::::::::::::::::::::
LLGPDAKVYNVFSK	5	9.63	0.03	1447	37.8	AE003626	TRUE	FALSE	2	1551.8	-2	10of 26	1.3892	FALSE	FALSE	::::::::::::::
ITGHLVHELQRKKLKYGIGSA	5	10.45	0.026	2386	40.4	AE003626	TRUE	FALSE	2	2349.8	-1.8	10of 40	1.7249	FALSE	FALSE	::::::::::::::::::::
KPIKLLKSTDSDSVEK	9	9.67	0.069	1372	23.7	AE003627	TRUE	FALSE	3	1789.1	-0.6	17of 60	1.7504	FALSE	FALSE	::::::::::::::::
VPIIIAARVSTRRLER	13	12.41	0.062	614	45.4	AE003627	TRUE	FALSE	3	1851.2	1.4	19of 60	2.2165	FALSE	FALSE	::::::::::::::::
PSGPSNAKRGKR	2	12.43	0.06	1148	-0.8	AE003627	TRUE	FALSE	1	1255.4	-3	5of 22	0.7828	FALSE	FALSE	::::::::::::
GSPPAPAR	9	11.05	0.059	1044	9	AE003627	TRUE	FALSE	1	752.8	1.9	7of 14	1.3707	FALSE	FALSE	::::::::
MKSIVKTSFRIYEKVYEK	4	10.11	0.051	2966	40.83	AE003627	TRUE	FALSE	2	2250.7	-2.2	8of 34	1.2456	FALSE	FALSE	::::::::::::::::::
FGDFLEAALYGGLKFNVTLRSSALKAR	2	10.18	0.05	809	77.2	AE003627	TRUE	FALSE	3	2946.4	2.1	9of104	1.3135	FALSE	FALSE	::::::::::::::::::::::::
RRFMSLLAHMFKPCMIYNGS	3	10.4	0.046	1461	60.89	AE003627	TRUE	FALSE	3	2460.9	-0.8	12of 76	1.2085	FALSE	FALSE	::::::::::::Cys_CAM::::::
LIPPMGLGLEKAINDS	11	4.08	0.03	2628	48.63	AE003627	TRUE	FALSE	3	1669	0.1	15of 60	1.4726	FALSE	FALSE	::::::::::::::::
DSSASPVTSPAVTTKAAGKR	8	10.59	0.02	1984	18.2	AE003627	TRUE	FALSE	2	1932.1	1.5	13of 38	1.6094	FALSE	FALSE	::::::::::::::::::
LTNDDVVLICDKNYDCPTK	1	3.88	0.004	2365	41.9	AE003627	TRUE	FALSE	2	2284.5	-2.7	4of 36	0.6546	FALSE	FALSE	::::::::Cys_CAM:::::Cys_CAM::::
VLVVGNPANTNALVCSSYAPSIPR	15	8.9	0.561	1263	60.1	AE003628	TRUE	TRUE	2	2500.8	1.1	26of 46	5.378	FALSE	FALSE	::::::::::::::Cys_CAM::::::::::
VLVVGNPANTNALVCSSYAPSIPR	14	8.9	0.399	1187	60.1	AE003628	TRUE	TRUE	2	2500.8	1.4	21of 46	3.3793	FALSE	FALSE	::::::::::::::Cys_CAM::::::::::
TYIQCLASICR	14	8.29	0.341	978	34.4	AE003628	TRUE	TRUE	2	1385.5	2.8	12of 20	1.7602	FALSE	FALSE	:::::Cys_CAM:::::Cys_CAM::
AAASHALGAVSVGSLQTYLPLILHEIEVQPK	9	6.03	0.301	2359	84.3	AE003628	TRUE	TRUE	3	3214.7	0.5	33of120	3.9752	FALSE	FALSE	::::::::::::::::::::::::::::
ILKSLYGCEHGK	7	8.85	0.117	1643	24.9	AE003628	TRUE	FALSE	2	1405.6	2.3	201	1.6804	FALSE	FALSE	::::::::Cys_CAM:::::
DVDHNLSYLRELIR	15	5.28	0.102	2810	38.6	AE003628	TRUE	TRUE	3	1744	1.3	10of 52	1.2151	FALSE	FALSE	::::::::::::::
KNNSNSSKRKASSVPATPSSPQGDLAQIR	4	11.57	0.083	2957	22.4	AE003628	TRUE	FALSE	3	3027.3	-0.9	22of112	1.5657	FALSE	FALSE	::::::::::::::::::::::::::::
EEDENAADMQELKNELQPLLGGQAA	6	3.38	0.08	1460	50.13	AE003628	TRUE	FALSE	3	2714.9	-0.5	13of 96	1.3754	FALSE	FALSE	::::::::::::::::::::::::
RMSVAFRACGATTRNALNQLTVQSKDNVKDTSA	3	10.57	0.075	2163	51.63	AE003628	TRUE	FALSE	3	3629	-1.1	25of128	2.6038	FALSE	FALSE	::Oxidation_M::::::Cys_CAM::::::::::::::::::::::
DPIFEFKPDHPEGCGYQNPNGVGFKITG	8	4.54	0.059	3470	53.9	AE003628	TRUE	FALSE	3	3122.4	-2.3	13of108	1.2834	FALSE	FALSE	::::::::::::Cys_CAM::::::::::::
KNPSSPMFTSLGVITKGTVIEVNISE	15	7.07	0.055	1994	60.33	AE003628	TRUE	FALSE	3	2766.2	-2.2	19of100	1.8089	FALSE	FALSE	::::::Oxidation_M:::::::::::::::::::
FKPLSQEEMIAFKSQKRQR	6	10.82	0.037	2024	35.53	AE003628	TRUE	FALSE	2	2352.8	-2.3	10of 36	1.2915	FALSE	FALSE	::::::::::::::::::::
LLVLMELFSK	2	6.95	0.034	544	49.83	AE003628	TRUE	FALSE	1	1193.5	1	12of 18	1.782	FALSE	FALSE	::::::::::
LLKERIICLMGNITDDISSTVVAQLLFLQSE	1	4.07	0.008	1425	106.13	AE003628	TRUE	FALSE	3	3522.1	2.1	24of120	2.1063	FALSE	FALSE	::::::::Cys_CAM::::::::::::::::::::::
SSNSLAPNVCQR	12	9.01	0.007	2059	17.3	AE003628	TRUE	FALSE	2	1333.4	-1.2	8of 22	1.0653	FALSE	FALSE	::::::::::Cys_CAM:::
IELSFEEQHMAPNGNWETTLTDALMK	15	4	0.003	1428	66.26	AE003628	TRUE	FALSE	3	3023.4	-2.2	19of100	2.2909	FALSE	FALSE	::::::::::Oxidation_M:::::::::::::::
TNGNISTSNMNAVR	7	11.05	0.001	1396	17.53	AE003628	TRUE	FALSE	2	1479.6	2.8	2	2.0144	FALSE	FALSE	::::::::::::::
MKSGHFRKFDRGYLRNQLEYNR	15	10.76	0.164	2466	37.73	AE003629	TRUE	FALSE	2	2817.2	1.3	5of 42	0.9115	FALSE	FALSE	::::::::::::::::::::::
STVEVKGRLLLTLLLHCLVALEVCGRAGAF	10	8.3	0.102	437	101.3	AE003629	TRUE	FALSE	3	3297.9	-2.3	11of116	1.0853	FALSE	FALSE	::::::::::::::::Cys_CAM::::::Cys_CAM:::::::
AEVTKMPFVKANYYNRPKK	7	10.39	0.095	1568	32.13	AE003629	TRUE	FALSE	3	2285.7	-1.4	24	2.3754	FALSE	FALSE	::::::::::::::::::
MGPKSGLGYMLSDLGYDVWMGNSRGNRYSK	6	9.78	0.031	2106	61.99	AE003629	TRUE	FALSE	3	3373.8	-2.8	8of116	0.9828	FALSE	FALSE	:Oxidation_M::::::::Oxidation_M::::::::::::::::::
PNKYWDFSFHEIGKFDV	14	5.28	0.017	498	46.2	AE003629	TRUE	FALSE	2	2130.4	-3	5of 32	0.8519	FALSE	FALSE	::::::::::::::::
FHIPNAVWLPSLE	12	5.13	0.013	1215	49.7	AE003629	TRUE	FALSE	2	1523.8	2.2	11of 24	1.3789	FALSE	FALSE	::::::::::::
VVQPKFITVKNLT	6	10.6	0.009	3044	37	AE003629	TRUE	FALSE	2	1487.8	2.7	6of 24	0.9283	FALSE	FALSE	::::::::::::
MGLKLPLPERPPCPMHGR	9	10.11	0.002	997	43.26	AE003629	TRUE	FALSE	3	2103.5	-1.5	16of 68	1.3298	FALSE	FALSE	:Oxidation_M::::::::::Cys_CAM::::::
GPRVPPDLHRV	4	10.89	0.091	3030	20.8	AE003630	TRUE	FALSE	2	1243.5	2.2	4of 20	0.699	FALSE	FALSE	::::::::::
KELWTMADEPDSSR	4	4.07	0.074	3001	26.53	AE003630	TRUE	FALSE	3	1681.8	-1.4	11of 52	1.2828	FALSE	FALSE	:::::Oxidation_M::::::::
QVVTLKVIAPRQQKPTGLMSIATKVVIQMNAK	1	11.8	0.045	1958	76.26	AE003630	TRUE	FALSE	3	3509.3	-0.8	17of124	1.6774	FALSE	FALSE	::::::::::::::::Oxidation_M:::::::::::::
EEEAGQEGKRT	12	4.26	0.018	744	3.9	AE003630	TRUE	FALSE	2	1234.3	2.4	11of 20	1.8938	FALSE	FALSE	::::::::::
FVVEYME	15	3.13	0.007	852	30.33	AE003630	TRUE	FALSE	1	933.1	0	6of 12	0.9641	FALSE	FALSE	::::::Oxidation_M::
MLVGVYR	9	9.85	0.152	1536	27.33	AE003631	TRUE	FALSE	1	854.1	-0.1	9of 12	1.9143	FALSE	FALSE	:Oxidation_M:::::::
MLVGVYR	10	9.85	0.096	974	27.33	AE003631	TRUE	FALSE	1	854.1	-0.3	9of 12	1.9754	FALSE	FALSE	:Oxidation_M:::::::
EGHMLSIAPEQEDIA	13	3.69	0.086	1653	35.43	AE003631	TRUE	FALSE	2	1640.8	0.7	6of 28	1.228	FALSE	FALSE	::::::::::::::
MLVGVYR	11	9.85	0.078	752	27.33	AE003631	TRUE	FALSE	1	854.1	-0.1	10of 12	1.9322	FALSE	FALSE	:Oxidation_M:::::::
SNTHSPAVSFK	9	10.1	0.065	522	12.3	AE003631	TRUE	FALSE	2	1175.3	1.9	7of 20	1.103	FALSE	FALSE	::::::::::::
AFKKDLNMHLCMGSRRTADVLLEYMK	15	9.59	0.064	1491	64.69	AE003631	TRUE	FALSE	3	3177.7	-2.3	20of100	2.3332	FALSE	FALSE	::::::::Oxidation_M:::Cys_CAM:Oxidation_M::::::::::::Oxidation_M::
HKEGGHIK	8	9.89	0.059	2804	-0.3	AE003631	TRUE	TRUE	2	906	-0.6	7of 14	0.9679	FALSE	FALSE	::::::::
LAEASTQQSKMED	13	3.83	0.056	967	18.13	AE003631	TRUE	FALSE	2	1454.5	-0.5	7of 24	1.0559	FALSE	FALSE	::::::::::Oxidation_M:::
LHHCARVQAKCNLWQR	9	10.12	0.055	1410	31.1	AE003631	TRUE	FALSE	3	2078.3	2.5	18of 60	1.9795	FALSE	FALSE	::::Cys_CAM::::::Cys_CAM:::::::
ERETLNLTISDLRLH	10	5.35	0.05	2133	39.3	AE003631	TRUE	FALSE	2	1811	-2.8	7of 28	1.0094	FALSE	FALSE	::::::::::::::::
MLVGVYR	1	9.85	0.048	677	27.33	AE003631	TRUE	FALSE	1	854.1	0.3	8of 12	1.7123	FALSE	FALSE	:Oxidation_M:::::::
NSKEGHMLSIAP	3	7.82	0.048	1337	20.73	AE003631	TRUE	FALSE	2	1300.5	-0.4	10of 22	1.4074	FALSE	FALSE	::::::Oxidation_M:::::::
QQFIKNSPKNSQFSNVR	12	11.64	0.042	1444	23.4	AE003631	TRUE	FALSE	2	2023.3	2.3	10of 32	1.3122	FALSE	FALSE	::::::::::::::::
QVGGKLEVKIRVRNPILTKQMEHIT	10	10.82	0.031	1490	53.73	AE003631	TRUE	FALSE	3	2889.5	-0.9	10of 96	1.0481	FALSE	FALSE	::::::::::::::::::::::::

VTIYQITPEQREYYNK	3	6.92	0.026	2389	35.4	AE003631	TRUE	FALSE	2	2046.3	-2.3	9of 30	1.3327	FALSE	FALSE	::::::::::::::::
EEQLRAKKVEIDRR	12	9.88	0.02	2728	20	AE003631	TRUE	FALSE	2	1771	2.3	4of 26	0.7349	FALSE	FALSE	::::::::::::::
KQQVYDVFHPPPLPKNSSGSNMFMPLHPTRGSHP	8	10.18	0.092	2783	59.26	AE003632	TRUE	FALSE	3	3830.4	2.6	21of132	2.0194	FALSE	FALSE	::::::::::::::::::::::::::::::
GRGGGSFGGLFGGWRKYKKPSSSGGGRR	15	12.42	0.059	459	27.9	AE003632	TRUE	TRUE	3	2858.2	-1.5	20of108	1.6789	FALSE	FALSE	::::::::::::::::::::::::::
SSQDAEEAKRVRDWAISQREKIVQ	5	7.21	0.011	2751	36.7	AE003632	TRUE	FALSE	3	2831.1	0.2	13of 92	1.35	FALSE	FALSE	::::::::::::::::::::::
LLNHVRQHTGESPHR	9	10.89	0.165	1428	16.4	AE003633	TRUE	FALSE	2	1782	2.5	9of 28	1.4079	FALSE	FALSE	::::::::::::::
NSTVQDSSPQVPQNGMVTYG	3	3.1	0.066	1607	28.23	AE003633	TRUE	FALSE	2	2110.3	0.8	7of 38	1.105	FALSE	FALSE	::::::::::::::::::::
RVRFVDEDVRMLQRVFPNLKSLKLRGCQITGK	1	11.35	0.04	1878	77.73	AE003633	TRUE	TRUE	3	3861.6	2.2	10of124	1.0561	FALSE	FALSE	:::::::::::::::::::::::::::Cys_CAM::::::
AMVLAPTNPALIVHQAIMVLQWR	12	11.05	0.041	1931	83.26	AE003634	TRUE	TRUE	3	2574.2	-0.1	10of 88	1.3523	FALSE	FALSE	::::::::::::::::::::::
LLALIMIILSGLYYMAT	9	5.87	0	324	86.96	AE003634	TRUE	FALSE	2	1916.4	2.9	4of 32	0.8206	FALSE	FALSE	::::::Oxidation_M:::::::::::
LLLIGVASRIFR	9	12.41	0.114	1246	52.6	AE003635	TRUE	FALSE	3	1358.7	2.9	15of 44	1.583	FALSE	FALSE	::::::::::::
HISAAHSCAAYSMGRRGTQPSFPGKESAK	6	10.18	0.029	2556	32.63	AE003635	TRUE	FALSE	3	3091.4	-2.9	23of112	1.8387	FALSE	FALSE	:::::::Cys_CAM::::::::::::::::::::
KLPSSGVRPTGK	10	11.64	0.029	613	12.1	AE003635	TRUE	FALSE	2	1227.4	0	11of 22	1.3088	FALSE	FALSE	::::::::::::
MSEADCDAGDTMNKKIR	10	4.46	0.006	1705	21.56	AE003635	TRUE	FALSE	3	1943.1	-2.4	20of 64	1.9958	FALSE	FALSE	::::::Cys_CAM:::::::::::
RRSYSRSRSPGSHSPERR	5	12.41	0.082	2987	2.5	AE003636	TRUE	TRUE	3	2159.3	-2.1	12of 68	1.449	FALSE	FALSE	::::::::::::::
IVGPISIMGMVVGLIGSGMVLSKKK	2	10.85	0.045	2261	76.49	AE003636	TRUE	FALSE	3	2548.2	-1.5	15of 96	1.5684	FALSE	FALSE	:::::::Oxidation_M::Oxidation_M:::::::::::::::
ISIMGMVVGLIGSGMVLSKKK	7	10.85	0.045	1179	62.29	AE003636	TRUE	FALSE	3	2149.8	-0.4	26	3.0843	FALSE	FALSE	::::::::::::::::::::
KCQMVHIEWVTRRLATGSFIKLNPEVPEGY	4	8.85	0.016	2361	77.33	AE003636	TRUE	FALSE	3	3577.1	1.5	18of116	1.5649	FALSE	FALSE	::Cys_CAM::Oxidation_M:::::::::::::::::::::::::
APAQTAVVEYPGDIVVKPGQVLTPTQVKDEPCVK	4	4.56	0.431	1634	71.3	AE003637	TRUE	TRUE	3	3636.1	-0.2	35of132	5.8627	FALSE	FALSE	:::::::::::::::::::::::::::::Cys_CAM:::
AFADALEVIPSTLAENAGLNPIATVTELR	1	3.69	0.304	1904	84.4	AE003637	TRUE	TRUE	2	2998.4	0.8	21of 56	3.5402	FALSE	FALSE	::::::::::::::::::::::::::
RNIPYPVAPVC	14	8.9	0.064	2572	31.3	AE003637	TRUE	FALSE	2	1286.5	-0.1	6of 20	0.941	FALSE	FALSE	::::::::::Cys_CAM:
KESTVGEIVNLMAVDAQRFMELTTYLNMIWS	4	4.17	0.06	2732	96.89	AE003637	TRUE	FALSE	3	3608.2	-1.7	18of120	1.9502	FALSE	FALSE	:::::::::::::::::::Oxidation_M:::::::::::
TLLYYNLR	5	9.59	0.04	1874	32.7	AE003637	TRUE	FALSE	1	1056.2	-0.7	4of 14	0.8136	FALSE	FALSE	::::::::
ARDNHEGLCFAISQDDVGPDS	3	3.77	0.034	2196	35	AE003637	TRUE	FALSE	2	2304.4	-2	11of 40	1.4807	FALSE	FALSE	::::::::Cys_CAM:::::::::::::
RSNFIEGNDNFRDQN	5	4.31	0.032	2408	21.1	AE003637	TRUE	FALSE	2	1826.9	1	10of 28	0.98	FALSE	FALSE	::::::::::::::
PSRASSSAGWAIAIPIDGKPNSSFILNCLIAGFTSFF	8	8.97	0.031	1917	107.9	AE003637	TRUE	FALSE	3	3902.4	-1	21of144	2.0998	FALSE	FALSE	:::::::::::::::::::::::::Cys_CAM:::::::::
ANLLNLQKLYL	2	9.72	0.008	1646	43.7	AE003637	TRUE	FALSE	1	1303.6	-0.4	4of 20	0.82	FALSE	FALSE	::::::::::
IMNDTMVRSSFLDRYQFI	15	6.85	0.076	700	58.46	AE003638	TRUE	FALSE	3	2253.6	1.3	20of 68	2.1168	FALSE	FALSE	::Oxidation_M:::::::::::::::
RFDMAASTFKVQR	7	11.33	0.066	3470	28.03	AE003638	TRUE	FALSE	2	1557.8	-1	2	1.2897	FALSE	FALSE	::::::::::::
NSLQDTLR	13	6.79	0.029	750	15.6	AE003638	TRUE	FALSE	1	947	2.7	6of 14	0.9562	FALSE	FALSE	::::::::
AMLINFPMNLPSLR	6	11.05	0.018	1622	54.86	AE003638	TRUE	FALSE	2	1634	-1.7	10of 26	1.4562	FALSE	FALSE	::Oxidation_M:::::::::::
IYRGMTFVKGRGDIPTYFVGIDENLK	2	9.47	0.013	1012	68.93	AE003638	TRUE	FALSE	3	2991.5	2	20of100	2.37	FALSE	FALSE	::::::::::::::::::::::::
ALNVANQYWRDIYGIMLPETRQFWQPLMLR	1	9.59	0.243	1509	104.66	AE003639	TRUE	FALSE	3	3725.4	1.6	20of116	1.9994	FALSE	FALSE	::::::::::::::::::::::::::
KQRLQEMQD	6	7.02	0.147	2964	12.23	AE003639	TRUE	FALSE	2	1176.3	1.5	4of 16	0.8352	FALSE	FALSE	::::::::::
DIIVSVFETNIRMVGGLLSAHILAEYLQK	5	5.35	0.098	1266	95.93	AE003639	TRUE	FALSE	3	3231.8	-1.4	20of112	1.7978	FALSE	FALSE	::::::::::::::::::::::::
RPVSGTSSEGLPL	2	6.98	0.086	197	25.3	AE003639	TRUE	FALSE	2	1300.5	2.1	9of 24	1.4513	FALSE	FALSE	::::::::::::::
VVSFEGLIYIVGGCTTTTR	9	6.28	0.081	1006	55.2	AE003639	TRUE	FALSE	3	2074.3	0.1	20of 72	2.0091	FALSE	FALSE	:::::::::::::Cys_CAM::::::
HNVLDFMRTCPSSNRLFPEK	7	8.97	0.077	1152	44.43	AE003639	TRUE	FALSE	3	2449.8	-2.1	202	1.8392	FALSE	FALSE	::::::::::Cys_CAM:::::::::::
DGGNDVSMIQQADAGVGIEGR	2	3.51	0.071	138	33.63	AE003639	TRUE	FALSE	2	2106.2	-0.3	11of 40	1.386	FALSE	FALSE	:::::::Oxidation_M:::::::::::::
LVKAMDPPLEAD	15	3.71	0.06	371	34.13	AE003639	TRUE	FALSE	2	1315.5	2	13of 22	1.7468	FALSE	FALSE	:::::Oxidation_M:::::::
DMEAEKDEDMRELM	3	3.69	0.026	2583	28.99	AE003639	TRUE	FALSE	2	1758.9	-1.6	8of 26	1.0573	FALSE	FALSE	::Oxidation_M:::::::::::
HYRVCEFGGNDCIK	5	7.01	0.021	2744	25.7	AE003639	TRUE	FALSE	2	1755.9	-2.6	8of 26	1.1772	FALSE	FALSE	:::::Cys_CAM::::::Cys_CAM:::
NIPETKPPR	2	10.09	0.017	221	11.8	AE003639	TRUE	FALSE	2	1052.2	1.2	9of 16	1.3677	FALSE	FALSE	::::::::::
VNGSNEPLPNSSPGQKR	4	10.09	0.016	1638	14.7	AE003639	TRUE	FALSE	2	1781.9	0.6	6of 32	0.9024	FALSE	FALSE	::::::::::::::::
TPEQPQPKRRFFRPWM	2	12.12	0.006	1777	36.33	AE003639	TRUE	FALSE	2	2102.5	-0.3	5of 30	0.7969	FALSE	FALSE	::::::::::::::
SECKQEKKMA	2	8.9	0	1841	5.83	AE003639	TRUE	FALSE	1	1255.4	3	2of 18	0.2313	FALSE	FALSE	:::Cys_CAM::::::Oxidation_M:::
PGISTGATPKTTTTTTTPTITA	15	10.1	0.146	1834	28.7	AE003640	TRUE	FALSE	3	2120.4	-1.6	21of 84	1.7226	FALSE	FALSE	::::::::::::::::::::
AIVGASLAEILAKRNMKP	8	10.59	0.126	2136	46.83	AE003640	TRUE	FALSE	3	1883.3	2.7	18of 68	2.5439	FALSE	FALSE	::::::::::::::::::
KEVLARRKLAPERSNAVF	13	11.38	0.119	403	37.7	AE003640	TRUE	FALSE	2	2085.5	-2.4	7of 34	1.0376	FALSE	FALSE	::::::::::::::::::
NEINKGRILVSSLLMLPRFYR	2	11.29	0.077	2180	67.73	AE003640	TRUE	FALSE	2	2521	2.6	10of 40	2.3315	FALSE	FALSE	::::::::::::::::::::
IMTGVAAFGPA	15	6.02	0.037	909	34.23	AE003640	TRUE	FALSE	1	1051.2	2	10of 20	1.5639	FALSE	FALSE	::Oxidation_M:::::::::
HYTGINATYMRHFVKRVKK	11	10.94	0.025	1362	30.73	AE003640	TRUE	FALSE	3	2350.8	-0.1	17of 72	1.7183	FALSE	FALSE	::::::::::::::::::::
ERPLLIIAKNFGSDLLKILVLNNLQ	7	9.89	0.02	2016	90.3	AE003640	TRUE	FALSE	3	2836.4	-0.3	94	1.7638	FALSE	FALSE	::::::::::::::::::::::::
ACQGMHVLR	13	9.02	0.014	2281	20.33	AE003640	TRUE	FALSE	2	1088.2	-1.4	6of 16	1.2552	FALSE	FALSE	::Cys_CAM::::Oxidation_M:::::
QETGGPLAENSGQ	12	3.13	0.006	836	13.5	AE003640	TRUE	FALSE	2	1288.3	-2.3	10of 24	1.2176	FALSE	FALSE	::::::::::::
LQYTRDLQRGT	3	9.85	0.122	984	20.7	AE003641	TRUE	FALSE	2	1351.5	-0.2	7of 20	1.1848	FALSE	FALSE	::::::::::::
MRIGYGYPTPRVNFSDSPFSGARFSNHNYGPISSTTE	4	9.44	0.107	2593	68.53	AE003641	TRUE	FALSE	3	4128.5	-1.4	9of144	1.1685	FALSE	FALSE	:Oxidation_M:::::::::::::::::::::::::::::::::
SLELKGQETMNLLDRIMHGLRPLFLQ	3	7.83	0.061	1952	81.66	AE003641	TRUE	FALSE	3	3054.6	1.4	22of100	2.2792	FALSE	FALSE	::::::::::::::::::::::::
SRLHMAAYLCVASNGVPPSISK	2	9.75	0.037	556	49.83	AE003641	TRUE	FALSE	2	2359.7	-0.6	10of 42	1.5421	FALSE	FALSE	::::::::Cys_CAM:::::::::::::
AEDEKAAAPAEEKKAEPEA	8	4.08	0.03	1969	18.5	AE003641	TRUE	FALSE	2	1985.1	-2.8	9of 36	1.0959	FALSE	FALSE	::::::::::::::::::
GGGVGGVVYSDNEDVVIEEEK	11	3.44	0.022	825	37.8	AE003641	TRUE	FALSE	3	2152.3	-1.1	21of 80	2.2423	FALSE	FALSE	::::::::::::::::::
PCLAIVLLAGVVLVADSF	11	3.1	0.017	1177	78.3	AE003641	TRUE	FALSE	2	1858.2	-0.8	12of 34	1.7238	FALSE	FALSE	::Cys_CAM:::::::::::::::
SPRIVVTALDCLQ	13	6.1	0.015	823	40.2	AE003641	TRUE	FALSE	3	1472.7	0.7	17of 48	2.021	FALSE	FALSE	::::::::::Cys_CAM:::
SREMSDFGDDEFPNMLCVE	6	3.38	0.006	2896	47.06	AE003641	TRUE	FALSE	2	2279.4	-2.6	5of 36	0.6255	FALSE	FALSE	:::::::::::::::Cys_CAM:::
LAAGDNEEPIVELAFQTTGKIIGDLYK	4	3.93	0.002	1561	71.6	AE003641	TRUE	FALSE	3	2907.3	1.9	23of104	2.3329	FALSE	FALSE	::::::::::::::::::::::::
TKPCGEVIRE	12	6.44	0.246	2336	16.9	AE003642	TRUE	FALSE	2	1189.3	-2.8	5of 18	0.9909	FALSE	FALSE	:::::Cys_CAM:::::::
GGGAAAGAGGGAGGAGGLLGDVVSGLGGGLVNESEAYAGLMK	1	3.83	0.125	1712	77.43	AE003642	TRUE	FALSE	3	3504.9	2.3	29of164	2.9384	FALSE	FALSE	::
TTTTAPTTARHNLIFESSTSHVNAASLIR	4	10.89	0.047	1550	52	AE003642	TRUE	FALSE	3	3099.4	-0.9	8of112	0.8972	FALSE	FALSE	::::::::::::::::::::::::::
TSPHRCSPTCRPGCGQNSRCAAPDTCACDVG	3	7.64	0.04	2334	31.1	AE003642	TRUE	FALSE	3	3494.5	2	22of120	2.0606	FALSE	FALSE	::::::Cys_CAM::::Cys_CAM::::Cys_CAM::::::Cys_CAM::::::Cys_CAM::Cys_CAM::::
RTYRKVACVEEFFDIIYNVHME	1	5.43	0.008	1118	63.23	AE003642	TRUE	FALSE	3	2837.2	-0.7	19of 84	1.8819	FALSE	FALSE	:::::::Cys_CAM::::::::::::Oxidation_M::
CSWAMSYERSTLASV	3	6.28	0.102	1983	38.83	AE003643	TRUE	FALSE	2	1764.9	-2.2	6of 28	1.0331	FALSE	FALSE	:Cys_CAM::::Oxidation_M:::::::::
GPSHVR	13	11.05	0.068	962	3.9	AE003643	TRUE	FALSE	1	652.7	1	5of 10	0.6248	FALSE	FALSE	::::::
YFGMNAVAYRMDDLAALR	14	6.78	0.064	2745	55.76	AE003643	TRUE	FALSE	3	2078.4	2.2	12of 68	1.3323	FALSE	FALSE	::::::::::::::::::
NATHATRTTTVASVSATATTLLPK	6	11.49	0.061	1915	37.2	AE003643	TRUE	TRUE	2	2414.7	1.1	10of 46	1.9522	FALSE	FALSE	::::::::::::::::::::::
LQKSGGGAGGGALRLLK	12	11.64	0.033	1443	30.2	AE003643	TRUE	TRUE	2	1583.9	0.9	11of 32	1.2782	FALSE	FALSE	::::::::::::::::::
MPMFQ	15	6.02	0.015	1037	21.16	AE003643	TRUE	FALSE	1	685.8	1.3	6of 8	1.0717	FALSE	FALSE	:Oxidation_M::Oxidation_M:::
KKSKSLLSNMVTSSEIVDKK	11	10.39	0.007	1166	28.93	AE003644	TRUE	FALSE	3	2239.6	-2.7	20of 76	1.8833	FALSE	FALSE	::::::::::Oxidation_M:::::::::::
RKLNSSAIGAAKK	1	11.73	0.168	685	13.4	AE003645	TRUE	FALSE	2	1344.6	-2.1	10of 24	1.5872	FALSE	FALSE	::::::::::::
LRPFRELAVDQLNAESGEQKTKPSQKR	10	10.31	0.125	1870	40.2	AE003645	TRUE	FALSE	3	3127.5	-1.6	17of104	1.5607	FALSE	FALSE	::::::::::::::::::::::::::
QFRKSLDALMKTLSSCQPFFIR	9	10.58	0.168	2780	62.93	AE003646	TRUE	FALSE	3	2675.1	-1.2	10of 84	1.4562	FALSE	FALSE	:::::::::::::::Cys_CAM:::::::
ARANTCHDPTSGRHLPIL	6	9.02	0.102	2540	29.2	AE003646	TRUE	FALSE	3	2017.2	1.4	15of 68	1.3431	FALSE	FALSE	::::::Cys_CAM:::::::::::::
NTYFHMTIGNLVRGSK	3	10.4	0.087	2863	33.23	AE003646	TRUE	FALSE	2	1839.1	-2.1	7of 30	1.3252	FALSE	FALSE	::::::::::::::::
SIDKRDGAGSHNWG	14	7.82	0.072	407	12.2	AE003646	TRUE	FALSE	2	1500.6	-2.6	10of 26	1.1329	FALSE	FALSE	::::::::::::::

KRYRNMRVGYMRLQALIRSRVLS	7	12.41	0.069	2038	56.86	AE003646	TRUE	FALSE	3	2884.5	-2.9	31	1.8749	FALSE	FALSE	::::::::::Oxidation_M::::::::::::
YGASSPALSDR	15	6.7	0.066	2971	17.4	AE003646	TRUE	FALSE	2	1124.2	0.9	11of 20	1.1748	FALSE	FALSE	::::::::::
LKKEDLMLSEMAMSALARATRGLAKSYDAFSK	4	9.95	0.134	2718	74.29	AE003647	TRUE	FALSE	2	3551.2	-2.7	6of 62	0.9942	FALSE	FALSE	::::::::::Oxidation_M::::::::::::::::::
MKNDMRVTMMFLNDLEIADYGSSDDETGFYRKRR	12	4.78	0.039	663	73.72	AE003647	TRUE	FALSE	3	4107.6	-0.8	8of132	1.0271	FALSE	FALSE	::::::::::::::::::::::::::::::::
ADYGSSDDETGFYR	8	3.51	0.005	3404	20	AE003647	TRUE	FALSE	2	1583.6	-1.9	7of 26	1.2765	FALSE	FALSE	::::::::::::::
GPGELPHGKTESPAKSKMPRQQQK	12	10.55	0.004	1679	14.33	AE003647	TRUE	FALSE	2	2618	-1.4	11of 46	2.0475	FALSE	FALSE	::::::::::::::::::::::
SNMLF	13	6.02	0	1541	20.93	AE003647	TRUE	FALSE	1	611.7	2	3of 8	0.5827	FALSE	FALSE	::::::
YFARVKGVEMCVEK	10	8.85	0.069	2662	34.93	AE003648	TRUE	FALSE	2	1717	1.7	6of 26	0.9322	FALSE	FALSE	::::::::::Cys_CAM::::
TRNAQDRNIKYYLDDLLTTADEYNCFCK	9	4.56	0.024	2229	59	AE003649	TRUE	TRUE	3	3502.8	0.5	20of108	1.8471	FALSE	FALSE	::::::::::::::::::::::Cys_CAM::Cys_CAM::
RSSSCQLMQPLPSGAHSSANGRKSLCR	15	11.23	0.017	991	34.63	AE003649	TRUE	FALSE	3	2974.3	1.5	21of104	2.3927	FALSE	FALSE	:::::Cys_CAM::::::::::::::::::Cys_CAM::
MVGGSLMAVLSWTLARQLVSPLQAMMTK	10	11.49	0	1410	91.92	AE003649	TRUE	FALSE	3	3069.7	1	10of108	1.2184	FALSE	FALSE	:Oxidation_M::::::Oxidation_M::::::::::::::::::Oxidation_M:::
RQRLLSLQM	10	12.41	0	2620	28.43	AE003649	TRUE	FALSE	2	1161.4	0.8	4of 16	0.6358	FALSE	FALSE	::::::::Oxidation_M:
AGIVTLAILIGRTASHVLYAMLL	5	9.85	0.116	1928	88.63	AE003650	TRUE	FALSE	2	2414	-2.5	6of 44	0.8477	FALSE	FALSE	::::::::::::::::::::Oxidation_M:::
KYPTMVKQADLTGHTSR	13	10.18	0.091	1358	21.83	AE003650	TRUE	FALSE	2	1934.2	0.7	6of 32	0.9339	FALSE	FALSE	::::::::::::::::
TSLKRSYTIWQTDYAQRFIK	1	10.34	0.062	572	47	AE003650	TRUE	FALSE	2	2506.9	0.8	11of 38	2.023	FALSE	FALSE	::::::::::::::::::::
AGRLCDDNPVLMQLARLYV	10	6.24	0.055	2160	59.43	AE003650	TRUE	FALSE	2	2221.5	-2.7	9of 36	1.1812	FALSE	FALSE	:::::Cys_CAM::::::Oxidation_M:::::::
AESFVYSVKYYD	9	4.08	0.048	1338	32.4	AE003650	TRUE	FALSE	2	1471.6	-2.9	10of 22	1.2309	FALSE	FALSE	::::::::::::
SMSGTNTSKGGGGGGGSGALSDGDGSGK	3	6.88	0.035	2089	9.03	AE003650	TRUE	FALSE	2	2287.3	2.6	12of 52	1.3774	FALSE	FALSE	::::::::::::::::::::::::::
EDSDTPRKRHDTQPNYNHMNRRSHR	11	10.38	0.026	1272	3.33	AE003650	TRUE	FALSE	3	3165.3	2	11of 96	1.2587	FALSE	FALSE	::::::::::::::::::Oxidation_M:::::::
STHPIVDENINRVNIMGNLIKGLR	3	10.09	0.021	1675	56.83	AE003650	TRUE	FALSE	3	2721.2	1.7	16of 92	1.46	FALSE	FALSE	::::::::::::::::Oxidation_M:::::::::
MAAMAHMLAPPPPPPPTPSEGRYTMLHHTAAQR	4	9.85	0.004	2519	65.82	AE003650	TRUE	FALSE	3	3613.2	2.7	23of128	2.3221	FALSE	FALSE	::::Oxidation_M:::Oxidation_M::::::::::::::::::Oxidation_M:::::::::
QIYIPPALR	2	9.85	0	960	32.8	AE003650	TRUE	FALSE	1	1071.3	0.9	9of 16	1.621	FALSE	FALSE	::::::::::
TQKMLAQSSKGHSEEQNIL	3	7.8	0.112	2179	26.23	AE003651	TRUE	FALSE	2	2130.4	2.2	14of 36	1.3071	FALSE	FALSE	::::::::::::::::::::
AKQLQQSSLPSGNMSSVTTTTTTTA	8	10.1	0.071	2544	32.43	AE003651	TRUE	FALSE	3	2440.7	1.4	24of 92	2.4144	FALSE	FALSE	::::::::::::::::::::::::
LAGLTLGMGYARIIDYDNLRIIEHV	9	5.28	0.071	2210	83.13	AE003651	TRUE	FALSE	3	2834.3	-3	20of 96	2.6292	FALSE	FALSE	::::::::Oxidation_M:::::::::::::::::
TQRIIAEKLISEVLYY	10	6.96	0.062	858	54.3	AE003651	TRUE	FALSE	3	1940.3	-0.1	18of 60	1.5675	FALSE	FALSE	::::::::::::::::
WMSEQLAYIGIRSNISYLSK	12	9.53	0.049	70	60.53	AE003651	TRUE	FALSE	2	2376.7	-2	5of 38	0.7755	FALSE	FALSE	::Oxidation_M:::::::::::::::::
FFEILIGSSAAPELQVLVR	12	4.27	0.021	876	72.3	AE003651	TRUE	TRUE	3	2090.5	1.6	25of 72	2.1438	FALSE	FALSE	::::::::::::::::::
CGEQCIWQDLADNMQCSGPWMHEIASE	9	3.51	0.131	273	65.56	AE003652	TRUE	FALSE	3	3270.4	0.7	11of104	1.4983	FALSE	FALSE	:Cys_CAM::::Cys_CAM::::::::::Cys_CAM::::Oxidation_M:::::::
MPPPMMMMK	3	10.1	0.1	2764	31.55	AE003652	TRUE	FALSE	2	1142.5	2.9	4of 16	0.7888	FALSE	FALSE	:Oxidation_M::::::Oxidation_M:Oxidation_M::
IHLIVVPMKEEQERIMEDQMTEMAGQK	12	4.49	0.075	1515	65.62	AE003652	TRUE	FALSE	3	3231.8	0.1	25of104	2.0037	FALSE	FALSE	:::::::::::::::::::::Oxidation_M:::::
VFREVPRCLK	11	10.11	0.043	2657	28.6	AE003652	TRUE	FALSE	2	1304.5	-2.6	5of 18	1.0138	FALSE	FALSE	:::::::Cys_CAM:::
EVVVTSKPKVKPTMPATKYLMGTTKPHQPQPSVGF	3	10.47	0.031	2616	61.46	AE003652	TRUE	FALSE	3	3827.5	-2.1	22of136	2.0891	FALSE	FALSE	::::::::::::::::::Oxidation_M:::::::::::::::
QKNGGKS	3	10.6	0.028	2767	-5.4	AE003652	TRUE	FALSE	1	718.8	-2.5	8of 12	1.1113	FALSE	FALSE	::::::::
NEIPGETEPQAPLK	11	3.97	0.024	1757	24.5	AE003652	TRUE	FALSE	2	1523.7	2	14of 26	1.6577	FALSE	FALSE	::::::::::::::
LYFMDEIDAALDFKNVSIVGHYIK	1	4.44	0.018	881	77.53	AE003652	TRUE	FALSE	3	2803.2	-2.7	8of 92	1.0715	FALSE	FALSE	::::::::::::::::::::
NNKFLQLKDGYGQTQLMIED	8	4.31	0.016	1848	46.13	AE003652	TRUE	FALSE	3	2356.7	-1.6	18of 76	1.5858	FALSE	FALSE	::::::::::::::::::
AQQHMPPTHLMPPPMMMMK	10	10.1	0.007	712	47.58	AE003652	TRUE	FALSE	3	2283.8	1.3	19of 72	1.7759	FALSE	FALSE	::::::::::Oxidation_M:::Oxidation_M::Oxidation_M:::
INKRFHIKEEAGMEPYHTMGLSFM	11	7.88	0.159	564	57.89	AE003653	TRUE	FALSE	3	2884.4	-1.8	24of 92	2.7988	FALSE	FALSE	:::::::::::::::::::::Oxidation_M:
GLLSIGAVNIDIPQHPVALHGMMTR	11	8	0.154	50	70.16	AE003653	TRUE	FALSE	2	2642.2	0.5	8of 48	1.3464	FALSE	FALSE	::::::::::::::::::::::
CEVSGEAPSFQTVSGHEDMIVVVTPKHGPQIT	13	4.61	0.118	358	61.83	AE003653	TRUE	FALSE	3	3454.8	-3	12of124	0.9827	FALSE	FALSE	:Cys_CAM::::::::::::::::Oxidation_M::::::::::::::
TRLLATLSG	13	11.05	0.056	754	26.5	AE003653	TRUE	FALSE	1	932.1	2.4	8of 16	1.5826	FALSE	FALSE	::::::::::
HKQRKVAGSLNAYVVLEKP	8	10.45	0.048	1783	32.8	AE003653	TRUE	FALSE	3	2138.5	-0.2	18of 72	1.4081	FALSE	FALSE	::::::::::::::::::
FGFEMNKKY	6	9.63	0.002	1675	22.33	AE003653	TRUE	FALSE	2	1164.4	-2.8	5of 16	0.9513	FALSE	FALSE	::::::::::
RDSPTMSLHEHNILK	10	7.97	0	2390	25.13	AE003653	TRUE	FALSE	2	1779	-0.4	5of 28	0.7692	FALSE	FALSE	::::::::::::::::
KRQQQLATVGQMLLKAK	1	11.73	0.273	2298	32.33	AE003654	TRUE	FALSE	2	1958.4	2.8	10of 32	1.3143	FALSE	FALSE	::::::::::Oxidation_M:::::
VTLQSSGLYRCEVSGEAPAFNTVSESETM	4	3.8	0.061	1357	61.53	AE003654	TRUE	FALSE	2	3151.4	2.9	9of 56	1.0014	FALSE	FALSE	::::::::::Cys_CAM:::::::::::::::::
AQTLGWSKATKVADRATAHGLIGVLIRGNR	4	12.14	0.122	2369	60.2	AE003655	TRUE	FALSE	3	3162.7	-2.8	23of116	2.6568	FALSE	FALSE	::::::::::::::::::::::::::::::
RIRRNSTDQQKAYME	15	10.39	0.107	1602	16.63	AE003655	TRUE	FALSE	2	1897.1	1.3	9of 28	1.3526	FALSE	FALSE	::::::::::::::::
VIQKGLNAYLEKK	11	10.05	0.015	2720	29.1	AE003655	TRUE	FALSE	2	1504.8	0.2	5of 24	0.6155	FALSE	FALSE	::::::::::::::
REYLETLICSYEGSYVGT	11	3.97	0.004	1517	47.8	AE003655	TRUE	FALSE	3	2141.3	-1.1	19of 68	1.3665	FALSE	FALSE	::::::::Cys_CAM:::::::::
CRDHHPPKKYECHCPMGFTGM	9	8.03	0.071	1928	27.86	AE003656	TRUE	FALSE	3	2646.9	2.7	9of 80	1.2552	FALSE	FALSE	:Cys_CAM::::::::::Cys_CAM::Cys_CAM::::::::
DKIRKDRKKGLLVTDPTQLPPEFAAMIPPV	9	10.16	0.124	2005	69.83	AE003657	TRUE	FALSE	3	3392	0.5	24of116	2.5668	FALSE	FALSE	::::::::::::::::::::::::::Oxidation_M:::::
EGGATHMTHTAGQWLFDG	12	5.05	0.025	1615	32.63	AE003657	TRUE	FALSE	2	1917.1	-1.4	6of 34	0.8642	FALSE	FALSE	::::::::::::::::
EKRQLANEALEMISFTMRNANEQK	3	7.22	0.011	1649	46.36	AE003657	TRUE	FALSE	3	2869.2	-1.3	14of 92	1.1876	FALSE	FALSE	::::::::::::Oxidation_M:::::::::::::
TAATGGGSSGAGGGKTGK	7	10.6	0.025	1088	1.6	AE003658	TRUE	FALSE	2	1422.5	-0.6	20	1.6025	FALSE	FALSE	::::::::::::::::::
SYVGKIHVNLMRSRQTQDFIR	1	11.29	0.009	2236	44.63	AE003658	TRUE	FALSE	3	2550	-1.6	13of 80	1.3996	FALSE	FALSE	::::::::::::::::::::
AKAKRAKEKARLRKTQQKEAAEAAN	4	11.14	0.177	2564	13	AE003659	TRUE	FALSE	3	2797.2	2.1	16of 96	1.9304	FALSE	FALSE	::::::::::::::::::::
KKAAKQVDKLSAQLADAR	9	10.55	0.096	1833	22.4	AE003659	TRUE	FALSE	2	1942.3	-1.5	11of 34	1.5508	FALSE	FALSE	::::::::::::::::::
QPVTTNGSSKESPVEAAAETVK	4	4.56	0.059	2606	24.5	AE003659	TRUE	FALSE	2	2231.4	-1.4	10of 42	1.5563	FALSE	FALSE	::::::::::::::::::::
MVCMSATR	11	9.01	0.056	330	20.46	AE003659	TRUE	TRUE	2	988.1	-0.3	8of 14	1.174	FALSE	FALSE	:Oxidation_M::Cys_CAM:Oxidation_M:::::
TALVDLFEGSSLTDPIQM	11	2.88	0.044	554	56.43	AE003659	TRUE	FALSE	2	1938.2	1.4	12of 34	2.0593	FALSE	FALSE	::::::::::::::::
TMGVGMTGLVPGPNMQK	6	10.1	0.034	2094	36.39	AE003659	TRUE	FALSE	2	1735.1	-2.6	8of 32	1.0806	FALSE	FALSE	::::::::::::Oxidation_M:::
PSMPGLIDVGGAHIQ	15	4.94	0.007	685	36.73	AE003659	TRUE	FALSE	3	1508.7	1.3	19of 56	1.8036	FALSE	FALSE	:::Oxidation_M::::::::::::
SKRYETASPVGDHPCPR	14	8.88	0.001	1939	16	AE003659	TRUE	FALSE	2	1958.1	-2.5	9of 32	0.9952	FALSE	FALSE	::::::::::::::Cys_CAM:::
RRRLISK	12	12.71	0	2152	11.4	AE003659	TRUE	FALSE	1	929.2	1.5	6of 12	1.0881	FALSE	FALSE	::::::::
RSAGSFFTAPAEDNLMLHR	13	7.85	0.083	1615	43.33	AE003660	TRUE	TRUE	2	2137.4	1.8	10of 36	1.3123	FALSE	FALSE	::::::::::::::Oxidation_M::::
EEVPSEEERSTK	10	4.09	0.071	760	10	AE003660	TRUE	TRUE	3	1420.5	-2	12of 44	1.3781	FALSE	FALSE	::::::::::::
QTLNHHAKGKR	9	11.64	0.062	608	0.9	AE003660	TRUE	FALSE	2	1290.5	0	8of 20	1.0665	FALSE	FALSE	::::::::::::
LQRNGPLKDRSNISGDGK	3	10.58	0.052	1110	18.4	AE003660	TRUE	FALSE	2	1956.2	0.4	9of 34	1.1333	FALSE	FALSE	::::::::::::::::
VPESLIIETVYDSLADTTMKLDDIPK	1	3.69	0.015	1812	72.73	AE003660	TRUE	FALSE	3	2924.3	1	18of100	1.644	FALSE	FALSE	::::::::::::::::Oxidation_M:::::::
QNKRCKDKKK	2	10.71	0.015	2005	-8.9	AE003660	TRUE	FALSE	1	1333.5	0.7	4of 18	0.6463	FALSE	FALSE	:::::Cys_CAM::::::
VPLRGD	5	6.79	0.002	2928	14.5	AE003660	TRUE	FALSE	1	656.8	1.3	4of 10	0.7281	FALSE	FALSE	::::::
LLGIGLNCVNPLFVTPLLSSLTK	15	8.97	0.501	2228	85.9	AE003661	TRUE	TRUE	2	2471	1.5	23of 44	5.1902	FALSE	FALSE	:::::::Cys_CAM:::::::::::::
ERYLTECYQAQLSVQEGY	10	3.97	0.109	1561	42.2	AE003661	TRUE	FALSE	2	2238.4	1.5	10of 34	1.9213	FALSE	FALSE	::::::Cys_CAM:::::::::::
AEQQKLASIISAEGDAEAAGLLAK	1	4.17	0.054	401	51.6	AE003661	TRUE	TRUE	3	2385.7	-1.3	17of 92	1.65	FALSE	FALSE	::::::::::::::::::::
FLGEGLTWVMVYR	14	6.89	0.031	1018	53.83	AE003661	TRUE	FALSE	3	1571.9	3	19of 48	1.9061	FALSE	FALSE	::::::::::::::
MVEHLSKLGTVHRITD	13	7.97	0.029	2592	34.33	AE003661	TRUE	FALSE	2	1837.1	-0.4	6of 30	0.7832	FALSE	FALSE	::::::::::::::::
EDLEGLCDHTIVTFEKEMAEFNAMK	13	4.02	0.024	1302	62.46	AE003661	TRUE	FALSE	3	2991.3	-1.1	20of 96	2.3983	FALSE	FALSE	::::::Cys_CAM::::::::::Oxidation_M::::::Oxidation_M::
TIDPSGIFIRR	4	10.89	0.02	2794	31.5	AE003661	TRUE	FALSE	2	1275.5	-1.2	4of 20	0.5742	FALSE	FALSE	::::::::::::
DEEHLKTTSDVLDIQTEEVDE	8	3.53	0.02	1979	37.3	AE003661	TRUE	FALSE	3	2446.5	1.7	8of 80	0.9651	FALSE	FALSE	::::::::::::::::::::
LLPLKDKTILGDRGASLSGGQKARISLARSVYR	4	11.42	0.005	2418	71.6	AE003661	TRUE	FALSE	3	3542.2	-2.5	21of128	1.8052	FALSE	FALSE	::::::::::::::::::::::::::::::::
WTTNSPDYTLSGVNLQVHAGALVAIVG	14	4.94	0.001	1538	70.7	AE003661	TRUE	FALSE	3	2785.1	-1.5	18of104	1.4414	FALSE	FALSE	::::::::::::::::::::::::::

GLKMVA	2	10.1	0	1585	18.33	AE003661	TRUE	FALSE	1	618.8	-2.4	4of 10	0.8508	FALSE	FALSE	::::::
FIPDLPSGGPLAVYRKR	6	10.39	0.14	1303	45.5	AE003662	TRUE	FALSE	2	1887.2	1.5	12of 32	1.94	FALSE	FALSE	::::::::::::::::
LESSYDSVGATESAEGASAG	4	2.89	0.046	2245	28.1	AE003662	TRUE	FALSE	2	1888.9	-1.3	11of 38	1.119	FALSE	FALSE	::::::::::::::::::
SKLLKVVILGDGGVGKSALLTR	5	10.83	0.036	2324	57.6	AE003662	TRUE	TRUE	2	2225.7	0.2	11of 42	1.9342	FALSE	FALSE	::::::::::::::::::::
RANFDWKRLRLIFEKEQGL	8	10.57	0.017	2484	54.3	AE003662	TRUE	FALSE	2	2420.8	2.2	12of 36	2.1474	FALSE	FALSE	::::::::::::::::::
YMVPTYE	14	3.3	0.011	1047	23.23	AE003662	TRUE	FALSE	1	903	0.7	10of 12	1.1271	FALSE	FALSE	::::::::
RKLKLCMTALR	14	11.48	0.165	634	29.63	AE003663	TRUE	FALSE	1	1390.7	0.3	9of 20	1.1848	FALSE	FALSE	::::::Cys_CAM::::::
DDWSISVTLHARLGFAAFVLCLI	2	5.1	0.117	1926	88.5	AE003663	TRUE	FALSE	3	2606	2.2	14of 88	1.429	FALSE	FALSE	::::::::::::::::::Cys_CAM:::
ICEGDDCKSK	8	4.31	0.108	3283	9.5	AE003663	TRUE	FALSE	2	1212.2	-3	6of 18	1.0666	FALSE	FALSE	::Cys_CAM::::Cys_CAM::::
YTYGCK	15	8.81	0.085	2812	9.9	AE003663	TRUE	FALSE	1	791.8	-2.2	5of 10	0.9956	FALSE	FALSE	:::::Cys_CAM::
TPKEELLSNGSPP	2	4.27	0.081	1418	21.7	AE003663	TRUE	FALSE	2	1369.5	2.9	10of 24	1.6871	FALSE	FALSE	::::::::::::::
HSVVGTADMVGGKAKLTMDLKDFASYLPHK	6	9.51	0.077	2954	59.16	AE003663	TRUE	FALSE	3	3234.8	1.4	14of116	1.5	FALSE	FALSE	::::::::Oxidation_M::::::::::::::::::::
ILQIVGGSMVLLGSLGKFSSKEVHFNTWHGR	8	10.59	0.026	2459	83.03	AE003663	TRUE	FALSE	3	3400	2.9	20of120	2.498	FALSE	FALSE	::::::::::::::::::::::::::::::
VGAGGIGIK	12	10.1	0.024	1175	18.9	AE003663	TRUE	FALSE	1	771.9	0	9of 16	2.1599	FALSE	FALSE	::::::::::
ANEAAGASFLIR	15	6.98	0.02	429	31.1	AE003663	TRUE	FALSE	2	1220.4	2	9of 22	1.3624	FALSE	FALSE	::::::::::::
FAAARLNKAAARDLVQQQ	1	11.33	0.18	478	37.6	AE003664	TRUE	FALSE	3	1972.3	2.9	19of 68	1.8416	FALSE	FALSE	::::::::::::::::
FINEKAMR	10	10.09	0.054	298	20.83	AE003664	TRUE	FALSE	2	1025.2	1.4	10of 14	1.4114	FALSE	FALSE	::::::Oxidation_M::
LEALSSASQLESLKEMMNKMRAEMM	15	4.73	0.024	1536	64.25	AE003664	TRUE	FALSE	3	2876.4	-1.5	22of 96	2.162	FALSE	FALSE	::::::::::::::::Oxidation_M:::::::::
YQKEKSDQMNSLT	15	6.92	0.012	2815	14.83	AE003664	TRUE	FALSE	2	1572.7	-2.5	10of 24	1.4229	FALSE	FALSE	::::::::::::::
MDGSPHHRPGSRNGRDNWSKMPEPLNGQKVE	4	9.88	0.004	2571	30.16	AE003664	TRUE	FALSE	3	3531.9	-0.6	18of120	2.0662	FALSE	FALSE	::::::::::::::::::::Oxidation_M::::::::::
DSPLQFSDDGGISVDEMMR	3	3.37	0.057	2352	41.96	AE003665	TRUE	FALSE	2	2100.3	1.9	9of 36	1.2172	FALSE	FALSE	::::::::::::::::::
AMPSVYKFVRQPGWFEMQGYNK	3	9.94	0.041	1981	56.16	AE003665	TRUE	TRUE	3	2665.1	-2.2	15of 84	1.3096	FALSE	FALSE	::::::::::::::::::::
QTEFIEDLRPVDGNSKLEYSYRPMD	11	4.07	0.036	2614	55.23	AE003665	TRUE	FALSE	2	3004.3	-1.4	5of 48	0.9478	FALSE	FALSE	::::::::::::::::::::::
YPHLVNGALAASAPVLQFPGITDCDIFYR	5	5.1	0.306	2238	88	AE003666	TRUE	TRUE	3	3207.6	0	32of112	4.1526	FALSE	FALSE	::::::::::::::::::::::Cys_CAM::::::
HHGAAHLQSPLVHM	10	8.16	0.135	2302	23.93	AE003666	TRUE	FALSE	3	1551.8	-2.5	11of 52	1.2279	FALSE	FALSE	::::::::::::Oxidation_M:
LNMSGQMDSMLRKMADVLKDQRVK	10	10.32	0.054	1146	50.32	AE003666	TRUE	FALSE	3	2844.4	0.7	8of 92	1.0465	FALSE	FALSE	::::::Oxidation_M::::Oxidation_M:::Oxidation_M:::::::::::
WKAKYVKRMISLAGVWAGSFK	10	11.03	0.021	2116	57.43	AE003666	TRUE	FALSE	3	2444	1.2	8of 80	1.1248	FALSE	FALSE	::::::::Oxidation_M::::::::::::
GDDRLSVTLAEIVHIRSVMTKAELEGLPMDVR	7	4.76	0.005	1887	82.56	AE003666	TRUE	TRUE	3	3569.1	-2.5	6	1.8883	FALSE	FALSE	::::::::::::::::::::::::::::Oxidation_M::::
QRLAVVTLHR	8	12.41	0.153	1601	25.5	AE003667	TRUE	FALSE	2	1193.4	0.3	7of 18	1.3102	FALSE	FALSE	::::::::::
EHAPGEDEVTARR	9	4.63	0.118	1681	11.6	AE003667	TRUE	TRUE	2	1467.5	0.5	10of 24	1.4008	FALSE	FALSE	::::::::::::
PLEYLTVGVGIKKKNRRK	6	11.02	0.058	2875	31.2	AE003667	TRUE	FALSE	2	2100.6	0.8	10of 34	1.2958	FALSE	FALSE	::::::::::::::::
DLVEKYEALVEVKRTSNAVKSNFTSNPDGKTMTES	10	4.85	0.043	1244	55.73	AE003667	TRUE	FALSE	3	3906.3	-0.4	24of136	2.5406	FALSE	FALSE	::::::::::::::::::::::::::::::Oxidation_M::::
NYFKEILRTMRNGGR	4	11.29	0.02	1695	29.83	AE003667	TRUE	FALSE	2	1856.2	0.3	5of 28	1.0385	FALSE	FALSE	::::::::::::::
YFVRPIFILDPGILDWMQVGAN	13	3.89	0.014	1239	88.23	AE003667	TRUE	FALSE	3	2566	0.7	10of 84	1.0479	FALSE	FALSE	::::::::::::::::::
YAIEQQLVSGNLKATSK	10	9.63	0.066	804	33.4	AE003668	TRUE	FALSE	3	1851.1	-1.8	22of 64	2.3299	FALSE	FALSE	::::::::::::::::
DKAELLLYEEVTRMPPFRRK	12	9.63	0.05	875	51.53	AE003668	TRUE	FALSE	3	2492.9	-0.6	9of 76	1.0431	FALSE	FALSE	::::::::::::::::::
VKPGENSSSSESGSER	2	4.56	0.011	1214	5.4	AE003668	TRUE	FALSE	2	1637.7	0.4	4of 30	0.6876	FALSE	FALSE	::::::::::::::::
KSKPRLSRGVLDMKFMQRTKVK	11	12.17	0.134	142	35.26	AE003669	TRUE	FALSE	2	2651.3	2.2	8of 42	1.2562	FALSE	FALSE	::::::::::::::Oxidation_M::::::
DLSTQVNYKMQMNFRRMF	11	10.39	0.04	722	46.49	AE003669	TRUE	FALSE	3	2326.7	0.4	20of 68	2.3154	FALSE	FALSE	::::::::::Oxidation_M::::::
PDNYLK	15	6.68	0.03	735	12.1	AE003669	TRUE	FALSE	1	749.8	1.3	8of 10	1.8215	FALSE	FALSE	::::::
EMDEVAGAGNLGRGKDISTI	6	4.07	0.004	2960	36.33	AE003669	TRUE	FALSE	2	2034.2	2.2	6of 38	0.8425	FALSE	FALSE	::::::::::::::::::
VGPITKTTKRLYIK	11	10.9	0.001	905	29.1	AE003669	TRUE	FALSE	2	1619	1.6	5of 26	0.8008	FALSE	FALSE	::::::::::::::
MEPQSPTSVLGSDLFPLTDSNDT	5	2.79	0.091	1451	50.83	AE003670	TRUE	FALSE	3	2452.6	-2.2	13of 88	1.1927	FALSE	FALSE	::::::::::::::::::::
ERMRMHSLNDAFQSLREVIPHVE	14	6.05	0.09	1592	53.26	AE003670	TRUE	FALSE	3	2828.2	0.1	19of 88	1.8376	FALSE	FALSE	:::Oxidation_M::Oxidation_M::::::::::::::::::
QLYDIYVRYNTM	7	6.59	0.048	3467	39.13	AE003670	TRUE	FALSE	2	1595.8	0.6	464	0.9436	FALSE	FALSE	::::::::::Oxidation_M:
ASQIIIEDKPVTKIKLIN	5	9.76	0.038	1419	48.9	AE003670	TRUE	FALSE	2	2024.5	3	5of 34	0.7635	FALSE	FALSE	::::::::::::::::::
KGALNAKERNMRRLESNER	12	11.31	0.034	1268	20.23	AE003670	TRUE	TRUE	3	2289.6	-1.5	17of 72	1.4937	FALSE	FALSE	::::::::::Oxidation_M:::::::::
LNPNAKLSKAAMLQKGADHIKQLRQERNVLK	9	11.08	0.017	2044	53.73	AE003670	TRUE	FALSE	3	3515.2	-3	23of120	1.9236	FALSE	FALSE	::::::::::::::::::::::::::::::
SSMEYQTIQRLVGMWVAFARNDNPNCPQIGPTT	7	6.36	0.069	1783	77.26	AE003671	TRUE	FALSE	3	3816.2	2.8	248	2.1829	FALSE	FALSE	:::Oxidation_M::::::::::Oxidation_M::::::::::Cys_CAM::::::::
NTWVIRRRNFLNVTLIGSTVVGCLPNTSPR	6	12.41	0.02	2191	79.4	AE003671	TRUE	TRUE	3	3443	-0.2	23of116	2.8305	FALSE	FALSE	::::::::::::::::::::::Cys_CAM::::::::
QYRLSTGHTVILDTKYGQVRGLQR	5	10.55	0.019	1364	45.9	AE003671	TRUE	FALSE	3	2791.2	2.4	21of 92	1.5097	FALSE	FALSE	::::::::::::::::::::::
SGKVVGSEDCLYLNVYTKHFNESEP	8	4.63	0.014	2532	48.5	AE003671	TRUE	FALSE	3	2874.1	-2.9	7of 96	0.8459	FALSE	FALSE	::::::::Cys_CAM:::::::::::::::
ILLLLLDVMVHSVISVISMVGITVLIAAIGHR	1	8	0.013	2373	133.06	AE003671	TRUE	FALSE	3	3430.3	-1.7	22of124	1.6852	FALSE	FALSE	::::::::Oxidation_M::::::::Oxidation_M:::::::::::::
QERPIPLQMDRRRSGKVVGSEDC	9	6.51	0.003	2458	35.53	AE003671	TRUE	FALSE	2	2558.8	-1.3	4of 42	0.6994	FALSE	FALSE	::::::::::::::::::::Cys_CAM:
DTFEAENSVDESYGHIDTRNVVMK	6	4.06	0.218	2464	41.03	AE003672	TRUE	FALSE	3	2773.9	-1.6	25of 92	2.1222	FALSE	FALSE	::::::::::::::::::::::Oxidation_M::
RLSVMMMNDAYSTTQPKRARL	1	11.29	0.112	626	44.79	AE003672	TRUE	FALSE	3	2486.9	-2	18of 80	1.9146	FALSE	FALSE	::::::Oxidation_M:::::::::::::::
IDAGSQGSSPQQQHGDDDLDLDND	14	3.15	0.106	2888	25.1	AE003672	TRUE	FALSE	3	2528.5	-0.3	11of 92	1.3768	FALSE	FALSE	::::::::::::::::::::
YTTCTAIGGKQDAAKSANV	14	8.85	0.057	1786	24.1	AE003672	TRUE	FALSE	2	1957.1	-1.3	6of 36	1.0992	FALSE	FALSE	::::Cys_CAM:::::::::::::::
VYMLRRRRDGRVMVCIDGHLYYLAG	8	9.48	0.017	2889	71.16	AE003672	TRUE	FALSE	3	2931.4	-2.7	8of 92	1.1049	FALSE	FALSE	:::Oxidation_M::::::::Cys_CAM:::::::::
DIKEMIRNIIMERGVDNINRDQLA	13	4.65	0.015	1590	60.06	AE003672	TRUE	FALSE	3	2874.3	-2.4	16of 92	1.3972	FALSE	FALSE	:::::Oxidation_M:::::::::::::::::
TCSMIIKKVDKKK	15	10.39	0.232	1702	18.03	AE003673	TRUE	TRUE	2	1595.9	0.4	9of 24	1.6495	FALSE	FALSE	::Cys_CAM::Oxidation_M:::::::::
GDVNSAWKHDMYDGPKRGAVGGGSGPTRLI	11	9.63	0.199	958	43.63	AE003673	TRUE	FALSE	3	3100.4	-1.2	8of116	1.184	FALSE	FALSE	::::::::::::::::::::::::::::
TLRKGQAKFVDVSIHDPQHIRSALVSPMQRKFL	2	11.47	0.058	2353	71.73	AE003673	TRUE	FALSE	3	3805.5	-2	19of128	1.7308	FALSE	FALSE	::::::::::::::::::::::::::::
EITMQANDGDV	4	2.88	0.058	1974	21.23	AE003673	TRUE	FALSE	1	1209.3	-1.3	6of 20	1.0109	FALSE	FALSE	::::Oxidation_M:::::::
IGVQEKIFYSLLDEIAPAGQVTSKQAN	3	4.45	0.045	952	66.4	AE003673	TRUE	FALSE	3	2921.3	2.9	20of104	2.2208	FALSE	FALSE	::::::::::::::::::::::::
MQANDGDVTKICKELAQKEKMDK	2	6.54	0.039	889	30.26	AE003673	TRUE	FALSE	3	2714	0.2	21of 88	2.7045	FALSE	FALSE	:Oxidation_M::::::::::Cys_CAM::::::::Oxidation_M:::
LHAMYKQNEVVKEQVEELR	13	5.48	0.127	1997	40.13	AE003674	TRUE	FALSE	3	2344.7	-2.6	16of 72	1.6933	FALSE	FALSE	::::::::::::::::::
GRPKGSTNRKQ	9	12.43	0.104	914	-4	AE003675	TRUE	FALSE	2	1229.4	-1.1	11of 20	1.3543	FALSE	FALSE	::::::::::::
HYKDTTLMPAPK	4	9.63	0.043	1703	19.23	AE003675	TRUE	FALSE	2	1402.7	1.4	8of 22	1.2314	FALSE	FALSE	::::::::::::
SENTKAAQAAALEKEAKKAAEEKR	14	9.6	0.007	1202	18.3	AE003675	TRUE	FALSE	2	2573.9	0.5	13of 46	2.4575	FALSE	FALSE	::::::::::::::::::::
RCKMTANKGSEFCGAHA	3	9.11	0.006	1684	18.43	AE003675	TRUE	FALSE	2	1942.1	-2	7of 32	0.9742	FALSE	FALSE	::Cys_CAM::Oxidation_M::::::::Cys_CAM:::::
NSLDISKSMPTT	12	6.76	0.006	1743	21.13	AE003675	TRUE	FALSE	2	1310.5	2.5	8of 22	0.9587	FALSE	FALSE	::::::::Oxidation_M::::
MNEPDPVPTPEQ	14	2.95	0.003	983	20.93	AE003675	TRUE	FALSE	2	1370.5	2.3	12of 22	1.8394	FALSE	FALSE	:Oxidation_M:::::::::::
RSKQHPAGAINPAQSLPNNLHNII	15	11.49	0.003	1899	40.5	AE003675	TRUE	FALSE	3	2591.9	-1	8of 92	1.0002	FALSE	FALSE	::::::::::::::::::::
RFDCALSCM	13	5.95	0	811	28.33	AE003675	TRUE	FALSE	1	1160.3	-0.5	7of 16	1.1082	FALSE	FALSE	:::Cys_CAM:::Cys_CAM::
TKMQAQRQTYAQMLQFVRSVVALQ	1	11.39	0.127	1101	58.56	AE003676	TRUE	FALSE	3	2827.3	-2.3	21of 92	2.5031	FALSE	FALSE	::::::::::::::::::::
EIDALALSKHCERERIKLLKGPKRKK	11	10.53	0.093	1498	42.4	AE003676	TRUE	TRUE	3	3118.7	-0.7	21of100	2.3487	FALSE	FALSE	::::::::::Cys_CAM:::::::::::::::
RQFCCHPGLMIGMLR	4	9.2	0.066	2925	46.26	AE003676	TRUE	FALSE	2	1893.2	1.4	6of 28	0.8307	FALSE	FALSE	::::Cys_CAM:Cys_CAM::::Oxidation_M::::::
HSGFNPNQLTLDPEHA	7	5.05	0.062	1353	26.4	AE003676	TRUE	FALSE	3	1777.9	-1.5	449	1.8686	FALSE	FALSE	::::::::::::::::
KKIEGTLAIPAVPPSSRTEGII	8	9.89	0.045	2456	50.5	AE003676	TRUE	FALSE	2	2278.7	0.1	13of 42	1.5183	FALSE	FALSE	::::::::::::::::::::
IMLVKRECGPVAHNAQRTYTETL	2	8.88	0.042	753	50.03	AE003676	TRUE	FALSE	2	2705.1	0.5	9of 44	0.9569	FALSE	FALSE	::Oxidation_M::::::Cys_CAM:::::::::::::::
RLPREILMKAYEVGKMRKHFG	3	10.87	0.03	1411	47.86	AE003676	TRUE	FALSE	3	2593.1	-2.7	20of 80	2.1383	FALSE	FALSE	::::::::Oxidation_M::::::::Oxidation_M:::::::
LQDNTLTDDTTTLCSEHAGPPKPPR	5	4.44	0.029	2131	35.8	AE003676	TRUE	FALSE	3	2766	0.8	15of 96	1.2344	FALSE	FALSE	::::::::::::::Cys_CAM:::::::::::

GMLSGEKAGRTRVRFR	10	12.41	0.018	577	25.13	AE003676	TRUE	FALSE	2	1838.1	1.6	11of 30	2.0806	FALSE	FALSE	::Oxidation_M::::::::::::::
ATLALIR	1	11.05	0.007	428	27.6	AE003676	TRUE	FALSE	1	758	2.9	9of 12	1.1846	FALSE	FALSE	::::::::
KARIERQAESFSRLSKVD	15	10.57	0.154	1789	28.4	AE003677	TRUE	FALSE	2	2121.4	-2.1	7of 34	0.9829	FALSE	FALSE	::::::::::::::::::
LAADCPHRRASSPMETSSKDAILYSPMPPMPLSPKV	3	8.85	0.063	2645	75.79	AE003677	TRUE	FALSE	3	3972.5	0.9	25of140	2.506	FALSE	FALSE	:::::Cys_CAM::::::::Oxidation_M:::::::::::::::Oxidation_M::::::::
AAMYNFLIAAGVAAFVAVCFILGPFVRPLLWAFLMG	12	8.9	0.061	1974	160.96	AE003677	TRUE	FALSE	3	3935.8	-0.3	23of140	2.1643	FALSE	FALSE	:::Oxidation_M:::::::::::::::Cys_CAM::::::::::::::::::
WAADGLAYLTLDAE	14	2.88	0.047	752	47.5	AE003677	TRUE	FALSE	2	1509.7	2.4	12of 26	1.4487	FALSE	FALSE	::::::::::::::
PLLGLPVTIKESCALEGMTFAVGSLSRK	11	8.93	0.022	672	79.53	AE003677	TRUE	TRUE	3	2992.5	3	23of108	2.5703	FALSE	FALSE	:::::::::::::Cys_CAM::::::Oxidation_M:::::::::::
AALMSDHHGDGDNSVSSSSSGGAPCDFKMNGK	11	5.1	0.096	1924	31.86	AE003678	TRUE	FALSE	3	3154.3	-1.8	14of120	1.6038	FALSE	FALSE	:::::::::::::::::::::::Cys_CAM::::Oxidation_M::::
FDKYRVHKAWGLLLAKNK	2	10.63	0.091	1213	43	AE003678	TRUE	TRUE	2	2188.6	0	5of 34	0.8207	FALSE	FALSE	::::::::::::::::::
DYSNDVIAFNSKFVGKKYMATIKK	10	10.04	0.065	1560	48.23	AE003678	TRUE	FALSE	3	2785.2	-0.1	20of 92	2.2421	FALSE	FALSE	:::::::::::::::::::Oxidation_M::::::
TFSDKKATK	12	10.32	0.041	1191	5	AE003678	TRUE	TRUE	1	1026.2	2.6	7of 16	1.3059	FALSE	FALSE	::::::::::
AHALEMERQHAAIPTAAATAMPAATGSVINLALPGQSS	1	6.03	0.026	2008	80.76	AE003678	TRUE	FALSE	3	3757.3	1.1	24of148	1.9931	FALSE	FALSE	::::::::::::::::::::::::::::::::::::::
SSMHGDMPQKERDEIMKEFRAGQSR	5	7.8	0.004	2670	30.69	AE003678	TRUE	FALSE	3	2968.3	1.6	12of 96	1.2828	FALSE	FALSE	:::::::::::::::Oxidation_M:::::::::::
QPTMHEGVLTNSCSTQ	5	5.13	0	2810	22.83	AE003678	TRUE	FALSE	3	1790.9	-2.7	12of 60	1.2335	FALSE	FALSE	:::::::::::::Cys_CAM::::
IKRKEPHYHHHV	7	10.18	0	3570	6.8	AE003678	TRUE	FALSE	3	1581.8	1.8	2	0.7538	FALSE	FALSE	::::::::::::
ARREARR	13	12.41	0	1744	2.7	AE003678	TRUE	FALSE	2	915	2.8	4of 12	0.7178	FALSE	FALSE	::::::::
KDGKRCLYTK	6	10.06	0.035	1472	8.9	AE003679	TRUE	FALSE	2	1269.5	2.6	12of 18	2.1328	FALSE	FALSE	::::::Cys_CAM::::::
NSKTKKGNLSKAKKASAT	5	11.22	0.033	2160	0.7	AE003679	TRUE	FALSE	2	1863.2	-2.1	10of 34	1.158	FALSE	FALSE	::::::::::::::::::
ALMYLYRAGLHRTVAK	8	10.56	0.023	1792	44.83	AE003679	TRUE	FALSE	2	1880.3	-2.8	8of 30	1.0884	FALSE	FALSE	:::Oxidation_M::::::::::::
RGGGGGRFEDNYNGG	11	6.96	0.013	1277	10.3	AE003679	TRUE	FALSE	2	1456.5	-1.8	10of 26	1.3874	FALSE	FALSE	::::::::::::::
TVAFVSTFATFFTR	14	11.05	0.435	1785	48	AE003680	TRUE	TRUE	2	1595.8	0.5	16of 26	3.2233	FALSE	FALSE	::::::::::::::
INALTAAAEAACMILSVDETIKS	7	3.83	0.138	2502	64.03	AE003680	TRUE	FALSE	3	2409.7	2.4	1	3.1417	FALSE	FALSE	:::::::::::Cys_CAM:Oxidation_M:::::::::::
LPIGDVATQYFADRDIFCAGR	2	4.18	0.1	1269	58.8	AE003680	TRUE	TRUE	3	2386.6	1.7	25of 80	2.5204	FALSE	FALSE	:::::::::::::::::Cys_CAM::::
IMNSAFIKSGVKVVNRR	10	12.43	0.062	1446	38.23	AE003680	TRUE	TRUE	2	1936.3	2.8	5of 32	0.9338	FALSE	FALSE	::Oxidation_M:::::::::::::::
LEIILSALMITLQ	11	3.3	0.048	1597	63.63	AE003680	TRUE	FALSE	2	1458.8	2.1	7of 24	0.7936	FALSE	FALSE	::::::::::::
APFHISNILKRTAPPPSSPIG	8	11.49	0.021	2116	46.8	AE003680	TRUE	FALSE	2	2201.6	-0.6	11of 40	1.7309	FALSE	FALSE	::::::::::::::::::
SIKAQTVVADKTKFR	11	10.83	0.011	956	23.8	AE003680	TRUE	FALSE	2	1693	-1.9	5of 28	0.5602	FALSE	FALSE	::::::::::::::
HKVVATTEDGHQVPFNILQEIYEAYVCFLR	1	5.26	0.003	806	81.8	AE003680	TRUE	FALSE	3	3579	-2.6	18of116	1.6369	FALSE	FALSE	:::::::::::::::::::::::::Cys_CAM::::
GHAVMVDDRP	2	5.1	0.146	1077	17.03	AE003681	TRUE	FALSE	1	1097.2	-2.9	3of 18	0.5658	FALSE	FALSE	::::::::::
DADDEFVMLDAFGPEMAADGSNSERR	7	3.53	0.112	1208	52.06	AE003681	TRUE	FALSE	3	2847	2.6	7	1.8403	FALSE	FALSE	::::::::::::::::::::::::
KNVMLQHSVYVR	2	10.4	0.106	1184	27.53	AE003681	TRUE	FALSE	1	1474.8	0.5	4of 22	0.8148	FALSE	FALSE	::::::::::::
KKREDQIKAKQSDDEDQEKEATTMGGTSADG	11	4.36	0.065	233	14.03	AE003681	TRUE	FALSE	3	3414.6	-0.4	16of120	1.5873	FALSE	FALSE	:::::::::::::::::::::Oxidation_M:::::::
TASVEDSTKVPQKFRYPFFTEMLWYVLARY	8	9.36	0.04	2348	89.73	AE003681	TRUE	FALSE	3	3675.2	0.3	20of116	2.6512	FALSE	FALSE	::::::::::::::::::::::::::
LSGLLGKEK	9	9.89	0.04	1133	20.6	AE003681	TRUE	FALSE	1	945.1	1.8	9of 16	1.6829	FALSE	FALSE	::::::::::
MERILRGIMR	14	12.11	0.002	1853	33.06	AE003681	TRUE	FALSE	1	1291.6	1.7	9of 18	1.7984	FALSE	FALSE	:Oxidation_M:::::::::
IFGFGDSDIIGKIGFPAAQAAPAISSTFPFIFGNR	13	6.9	0.117	1927	105.1	AE003682	TRUE	FALSE	3	3632.2	1.8	22of136	2.649	FALSE	FALSE	::::::::::::::::::::::::::::::
IFGFGDSDIIGKIGFPAAQAAPAISSTFPFIFGNR	14	6.9	0.071	1981	105.1	AE003682	TRUE	FALSE	3	3632.2	2.6	25of136	2.6147	FALSE	FALSE	::::::::::::::::::::::::::::::
FGLTATTGTATTAQLGGLSK	2	10.1	0.008	482	38.9	AE003682	TRUE	FALSE	3	1897.1	0.6	25of 76	2.2083	FALSE	FALSE	::::::::::::::::::
AVGKKVKKSSKKTRRSGKKSKK	3	12.49	0.085	1688	-10.8	AE003683	TRUE	FALSE	3	2446	0.2	12of 84	1.562	FALSE	FALSE	::::::::::::::::::
RTFPPHRRIPRFWTANHGHRHVLPPQSLA	15	13.01	0.079	1120	56.4	AE003683	TRUE	FALSE	3	3484	2.9	20of112	1.8285	FALSE	FALSE	::::::::::::::::::::::::::
LAENILGTGIV	9	3.3	0.056	821	38.7	AE003683	TRUE	FALSE	2	1100.3	1.8	10of 20	1.2769	FALSE	FALSE	::::::::::::
NVPNLDSNTDEEEQ	6	2.8	0.054	2899	17.4	AE003683	TRUE	FALSE	2	1604.6	-0.9	4of 26	0.7734	FALSE	FALSE	::::::::::::::
IDNKININQGMMVQFSPKMVTQFLSGK	7	10.32	0.048	1976	66.99	AE003683	TRUE	FALSE	3	3102.7	-0.2	469	1.7168	FALSE	FALSE	:::::::::Oxidation_M:Oxidation_M:::::::::::::::
YACGNYRNVKPDR	1	9.56	0.043	1668	16.1	AE003683	TRUE	FALSE	1	1613.7	-0.7	8of 24	1.2694	FALSE	FALSE	:::Cys_CAM:::::::::::
FTDADGNGNGAGSQGGGVAARDR	12	4.18	0.043	820	18.3	AE003683	TRUE	TRUE	3	2151.2	-2.2	23of 88	1.8155	FALSE	FALSE	::::::::::::::::::::
HDLVNIDLMEFSYNDE	14	3.43	0.026	2851	46.03	AE003683	TRUE	FALSE	3	1971.1	2.1	8of 60	1.1266	FALSE	FALSE	:::::::::Oxidation_M:::::::::
NEVMMILRRNPNFDLDVL	11	4.31	0.022	1608	61.36	AE003683	TRUE	FALSE	3	2206.6	2.4	20of 68	1.6849	FALSE	FALSE	:::::Oxidation_M::::::::::::
DDDRLSGRNNFNMMSNDYNNS	15	3.88	0.018	924	26.96	AE003683	TRUE	FALSE	3	2496.6	2.7	21of 80	2.2565	FALSE	FALSE	:::::::::::::Oxidation_M:::::::::
PDAEVEAKLRAMNAKIKAEMVTLM	14	7.16	0.011	1640	58.79	AE003683	TRUE	FALSE	3	2677.2	2.2	11of 92	1.3678	FALSE	FALSE	:::::::::::Oxidation_M::::::::::::
VHIRIHTGEKPYQCPHCPKTFSDNNNLAKHR	2	9.62	0.007	494	38.1	AE003683	TRUE	TRUE	3	3757.1	-1.5	19of120	1.6759	FALSE	FALSE	:::::::::::::Cys_CAM:::Cys_CAM:::::::::::::::
DAKIKLREKEESVR	4	9.76	0.007	2159	18.3	AE003683	TRUE	FALSE	2	1702	-0.9	4of 26	0.7113	FALSE	FALSE	::::::::::::::
WSIQEGGQKTDVGTFNLNVR	1	7.02	0.081	2010	40.2	AE003684	TRUE	FALSE	2	2250.5	-2.3	10of 38	1.4695	FALSE	FALSE	::::::::::::::::::
LLRATGRSNSTGQGSG	10	12.41	0.074	2488	16.2	AE003684	TRUE	FALSE	3	1562.7	2.2	17of 60	2.064	FALSE	FALSE	::::::::::::::::
LSSMKLQSPHGSMADK	3	9.89	0.073	1453	24.16	AE003684	TRUE	FALSE	2	1750	1.1	6of 30	1.0603	FALSE	FALSE	:::::Oxidation_M::::::::Oxidation_M::::
NFWSFGGQSLVAVRPPTKQA	2	11.49	0.053	881	47.8	AE003684	TRUE	FALSE	3	2262.6	2.2	19of 76	2.221	FALSE	FALSE	::::::::::::::::::
GLVFYKSRALQR	10	11.39	0.112	1125	32.1	AE003685	TRUE	TRUE	1	1438.7	2.1	9of 22	1.3801	FALSE	FALSE	::::::::::::
LNSYHHQVSGDVYAVNEY	8	5.05	0.091	2831	33.9	AE003685	TRUE	FALSE	2	2096.2	1.6	6of 34	1.1671	FALSE	FALSE	::::::::::::::::::
QRTEESSASQYFQFYGYLSQQQNMMQDYVR	15	4.45	0.031	1017	60.56	AE003685	TRUE	FALSE	3	3731	-1.1	9of116	1.0742	FALSE	FALSE	:::::::::::::::::::::::Oxidation_M:::::::
RSKLRKHMAIDEETISPVSGTIIRKLR	2	11.4	0.025	2361	52.33	AE003685	TRUE	TRUE	3	3136.7	-2.1	10of104	1.1435	FALSE	FALSE	::::::::::::::::::::::::::
VEEISGVAFIFNQ	11	3.13	0.015	1601	44.2	AE003685	TRUE	FALSE	2	1453.6	2	7of 24	0.9693	FALSE	FALSE	::::::::::::
MPKIQELHTLYPER	14	7.75	0.009	1104	35.63	AE003685	TRUE	FALSE	2	1772.1	0.7	12of 26	1.5318	FALSE	FALSE	:Oxidation_M:::::::::::
LAVATVFGLNWGRRGSVGPAAAGKQQVEQKDR	2	11.38	0.173	1822	59.2	AE003686	TRUE	TRUE	3	3368.8	-2.4	15of124	1.6291	FALSE	FALSE	::::::::::::::::::::::::::::
QRPTFLK	11	11.49	0.15	478	16.1	AE003686	TRUE	FALSE	1	890.1	0	6of 12	0.9625	FALSE	FALSE	::::::::
KRLVKQISQGDYYEPRKPSRASTLIR	9	10.91	0.104	2394	43.4	AE003686	TRUE	FALSE	3	3091.6	1.9	17of100	1.585	FALSE	FALSE	::::::::::::::::::::::::
DKTAIAVICERMKK	3	9.79	0.051	1553	26.93	AE003686	TRUE	FALSE	2	1664	0.3	7of 26	1.138	FALSE	FALSE	:::::::::Cys_CAM::::::
VNKKSNIKGQTHQLTFNIDDGD	8	7.77	0.029	2464	27	AE003686	TRUE	FALSE	2	2473.7	-0.1	11of 42	1.5879	FALSE	FALSE	::::::::::::::::::
LSAVRSQHEQTQESEKAEETSTIKKIK	1	7.76	0.022	172	27.3	AE003686	TRUE	FALSE	2	3087.4	2.3	10of 52	1.3327	FALSE	FALSE	::::::::::::::::::::::::
NEKTGTKRK	1	10.83	0.003	1094	-5.4	AE003686	TRUE	FALSE	1	1062.2	2.3	6of 16	1.2043	FALSE	FALSE	::::::::::
AFNASTASTTSRSFH	12	11.05	0.105	800	19.9	AE003687	TRUE	FALSE	3	1585.7	-2.2	13of 56	1.6508	FALSE	FALSE	::::::::::::::
NFVMEGGAMVLADGGVVCIDEFDKM	6	3.43	0.104	1596	74.19	AE003688	TRUE	FALSE	3	2754.1	2.1	16of 96	1.4474	FALSE	FALSE	:::::Oxidation_M::::::Oxidation_M::::::::Cys_CAM::::::::Oxidation_M:
AIPEKSKGLENDK	9	7.08	0.1	1249	14.6	AE003688	TRUE	FALSE	2	1429.6	1.6	10of 24	1.5751	FALSE	FALSE	::::::::::::::
MAYVYLANQCPCNGLLAIVIVEVIVIFVNCHR	14	6.91	0.066	1358	118.73	AE003688	TRUE	FALSE	3	3751.4	-0.3	24of124	3.0337	FALSE	FALSE	:::::::::Cys_CAM::Cys_CAM::::::::::::::::Cys_CAM:::
SHKSGVHRR	6	12.42	0.032	1810	-3.1	AE003688	TRUE	FALSE	2	1064.2	-0.6	9of 16	1.506	FALSE	FALSE	::::::::::
IEMLYESMTWRVS	8	4.27	0.031	2035	46.66	AE003688	TRUE	FALSE	2	1661.9	-1.6	8of 24	1.1429	FALSE	FALSE	:::Oxidation_M:::::::::::
FDMSCIRKVAVTEPLVDVVDPK	13	4.46	0.019	1072	60.03	AE003688	TRUE	FALSE	3	2535.9	1.7	8of 84	0.9253	FALSE	FALSE	:::Oxidation_M::Cys_CAM:::::::::::::::
NLYPLRSDITCSHPHT	11	7.32	0.012	1848	30.3	AE003688	TRUE	FALSE	2	1912.1	-2.7	8of 30	1.2954	FALSE	FALSE	:::::::::Cys_CAM:::::::
KGKKKKDKKERRRSRTKSETE	1	11.25	0.076	2320	-15.1	AE003689	TRUE	FALSE	3	2605	2.3	12of 80	1.4064	FALSE	FALSE	::::::::::::::::::
KGQPMGGVGVVQHVVQQ	6	10.1	0.042	2452	27.53	AE003689	TRUE	FALSE	2	1765	2.2	8of 32	0.88	FALSE	FALSE	:::::Oxidation_M:::::::::::
LEAYKFTNIVPINRGLKNHIWYRLESYVR	2	10.11	0.015	1914	83.4	AE003689	TRUE	FALSE	3	3595.2	-2.8	8of112	1.1831	FALSE	FALSE	::::::::::::::::::::::::::
IKKRPLQMDKLGMLR	9	11.57	0.002	1569	37.26	AE003689	TRUE	FALSE	3	1828.3	2.9	21of 56	2.947	FALSE	FALSE	::::::::::::::
LIEPPEVKHERLFVVSVLGLLVNLV	11	5.4	0.187	190	95.6	AE003690	TRUE	FALSE	2	2814.4	-2.8	5of 48	0.7897	FALSE	FALSE	::::::::::::::::::::::
STLELCEKYFGTRDVYK	9	6.47	0.091	2334	39.3	AE003690	TRUE	FALSE	2	2110.3	-1.9	6of 32	1.0517	FALSE	FALSE	::::::Cys_CAM:::::::::::
DERHLKDNIEMQLNNFK	1	5.39	0.076	222	31.13	AE003690	TRUE	FALSE	2	2145.4	1	7of 32	1.0782	FALSE	FALSE	::::::::::::::::

PEATQRVRDMSDR	13	7.1	0.048	2165	14.63	AE003690	TRUE	FALSE	3	1577.7	1	11of 48	1.1902	FALSE	FALSE	::::::::::Oxidation_M::::
EHVSRHKGAK	5	10.59	0.029	2979	-1.3	AE003690	TRUE	FALSE	2	1149.3	2.9	7of 18	1.1377	FALSE	FALSE	::::::::::
AIVETLRGLKYRVIWKYE	1	9.94	0.007	658	58	AE003690	TRUE	FALSE	3	2238.7	-2.9	17of 68	1.5683	FALSE	FALSE	::::::::::::::::::
PMAPRLANALTPLPLTPPPKKYICC	10	9.69	0.099	1888	70.83	AE003691	TRUE	FALSE	3	2821.4	3	13of 96	1.2422	FALSE	FALSE	::::::::::::::::::::::Cys_CAM:Cys_CAM:
HLQGELDMA	10	4.07	0.07	878	22.73	AE003691	TRUE	FALSE	2	1030.1	1.5	8of 16	0.775	FALSE	FALSE	:::::::Oxidation_M::
GKGLGGSANLNY	6	9.72	0.06	2810	18.4	AE003691	TRUE	FALSE	2	1151.3	-0.3	8of 22	1.1342	FALSE	FALSE	::::::::::::
TRPRRRPDWSEMMKEVESGKKLR	15	11.35	0.032	1028	31.16	AE003691	TRUE	TRUE	3	2890.4	-2.3	18of 88	2.0358	FALSE	FALSE	::::::::::Oxidation_M::::::::::::
PVATTSALKKKKEPTPPPESSSE	8	9.67	0.026	1735	23	AE003691	TRUE	FALSE	3	2410.7	2.4	9of 88	0.929	FALSE	FALSE	::::::::::::::::::::::
KFLVLNPAKRTSLSAVMSDK	1	10.83	0.011	2256	46.63	AE003691	TRUE	TRUE	3	2206.7	-3	12of 76	1.3103	FALSE	FALSE	::::::::::::::::::::
TFALDKSTPNRPAATSIR	10	11.33	0.009	1405	31.3	AE003691	TRUE	FALSE	3	1947.2	2.4	18of 68	2.3826	FALSE	FALSE	::::::::::::::::::
QIRRLEKNARQLKPVD	10	11.38	0.007	1730	27.3	AE003691	TRUE	FALSE	3	1965.3	1.8	22of 60	2.1937	FALSE	FALSE	::::::::::::::::
YREHAEHSPRAMYMRDWRSALR	9	10.19	0.003	2034	39.76	AE003691	TRUE	FALSE	3	2820.2	1.5	8of 84	0.9568	FALSE	FALSE	::::::::::::::::::::
PYITGHSPMHLAADVEALMSHQRLNKIVALGHGMGGR	3	9.72	0.135	2117	78.49	AE003692	TRUE	FALSE	3	4015.6	-0.1	9of144	1.0678	FALSE	FALSE	::::::::Oxidation_M::::::::::Oxidation_M::::::::::::::Oxidation_M::::
KSAASRFGAFEFLK	10	10.59	0.129	2100	34.1	AE003692	TRUE	FALSE	2	1559.8	0.7	9of 26	1.3064	FALSE	FALSE	::::::::::::::
KKRVLRPPGGGSSDIFGSEMPQTPRNVKNR	3	11.98	0.099	1916	37.73	AE003692	TRUE	FALSE	3	3326.8	0.3	18of116	1.7505	FALSE	FALSE	::::::::::::::::::Oxidation_M:::::::::
PYMGEVLLIAGSQSEFVTTTSIAVM	6	3.13	0.092	1836	78.66	AE003692	TRUE	FALSE	3	2662.1	1.3	7of 96	1.0121	FALSE	FALSE	:::Oxidation_M:::::::::::::::::::::
LGRVCLDVAITFMIYDSFMDLFNKV	10	4.18	0.086	2164	96.06	AE003692	TRUE	FALSE	3	2985.5	1.9	23of 96	2.7161	FALSE	FALSE	:::::Cys_CAM:::::::Oxidation_M:::::::::::
VVAMMREGYNAAGRKTRVR	4	11.96	0.068	1778	32.76	AE003692	TRUE	FALSE	3	2198.6	0.5	21of 72	2.4937	FALSE	FALSE	::::Oxidation_M:Oxidation_M::::::::::::::
ELRKATKDVHNLTDVLVNAKIALALSDDEVWYDGL	1	4.38	0.031	1758	91.1	AE003692	TRUE	FALSE	3	3927.4	-2.8	16of136	1.1436	FALSE	FALSE	::::::::::::::::::::::::::::::
TLMLRISIDVELTDKSTKLVSFMMK	4	9.76	0.028	1526	77.69	AE003692	TRUE	FALSE	3	2917.6	-1.8	9of 96	0.9295	FALSE	FALSE	:::Oxidation_M:::::::::::::::::::::
QMMDNFVKESLALK	3	6.99	0.005	1240	38.66	AE003692	TRUE	FALSE	3	1671	0.9	14of 52	0.8797	FALSE	FALSE	::Oxidation_M:::::::::::
SADTVKEESSTTTTSQLDQNPTNVTDK	1	3.85	0	2193	22.9	AE003692	TRUE	FALSE	3	2899	-1.8	17of104	1.5301	FALSE	FALSE	::::::::::::::::::::::::::
VMLGILR	2	11.05	0	1026	33.33	AE003692	TRUE	FALSE	1	802.1	2.5	7of 12	0.972	FALSE	FALSE	::::::::
ANYTVSCPMWLTLSEAECSLCTR	10	4.27	0	1996	64.13	AE003692	TRUE	FALSE	2	2751	0.5	15of 44	1.8104	FALSE	FALSE	::::::Cys_CAM::::::::::Cys_CAM:::Cys_CAM:::
YSETIKKESTG	15	7	0.096	527	10.5	AE003693	TRUE	FALSE	2	1243.4	2.9	10of 20	1.3732	FALSE	FALSE	::::::::::
ILGCIQVPPAGGPQVR	1	9.01	0.06	1942	42.3	AE003693	TRUE	FALSE	2	1662.9	2.8	9of 30	0.9897	FALSE	FALSE	::::Cys_CAM::::::::::::
LQEALGVSGDNA	13	3.01	0.029	544	25.3	AE003693	TRUE	FALSE	2	1174.3	0	7of 22	0.9625	FALSE	FALSE	::::::::::::
HTTSAPPPSLPLPPPPTTT	12	7.85	0.016	2058	34.7	AE003693	TRUE	FALSE	2	1910.2	2.7	7of 36	0.9911	FALSE	FALSE	::::::::::::::::::
RVKKFNVHDIK	12	10.83	0.01	1917	16.1	AE003693	TRUE	FALSE	3	1384.7	0.9	13of 40	1.2055	FALSE	FALSE	::::::::::::
INEDHMEFPDGGEEACP	9	3.44	0.074	2248	31.33	AE003694	TRUE	FALSE	2	1964	-2.1	8of 32	1.1455	FALSE	FALSE	:::::Oxidation_M::::::::Cys_CAM::
RMGKLCDVTLKVEDQTFSAHR	8	8.94	0.063	1701	39.23	AE003694	TRUE	TRUE	3	2508.8	-3	10of 80	1.0268	FALSE	FALSE	::Oxidation_M:::Cys_CAM::::::::::::::
IARMRKHLKDMRILKRFLSIRT	3	12.59	0.05	2237	56.86	AE003694	TRUE	FALSE	3	2816.5	0.8	19of 84	1.6174	FALSE	FALSE	:::Oxidation_M::::::Oxidation_M:::::::::::
RPVATTTLKPPPTI	15	11.49	0.042	2883	30.2	AE003694	TRUE	FALSE	2	1492.8	0	10of 26	1.2271	FALSE	FALSE	::::::::::::::
VNLRNEKPLQKMDRVVHTVTTTDDP	13	7.8	0.024	1683	41.13	AE003694	TRUE	FALSE	3	2908.3	2.3	8of 96	1.0527	FALSE	FALSE	::::::::::::::::::::::
VAREELIRSSH	15	7.86	0.009	304	21	AE003694	TRUE	FALSE	1	1297.5	-2.5	4of 20	0.4815	FALSE	FALSE	::::::::::
YLYGNGGPIIMVQVENEY	15	3.13	0.008	701	54.33	AE003694	TRUE	FALSE	3	2060.3	0.9	17of 68	1.5656	FALSE	FALSE	::::::::::::::::
RPRKVSI	15	12.42	0.004	444	10.9	AE003694	TRUE	FALSE	2	856.1	-1.4	7of 12	1.5112	FALSE	FALSE	::::::::
PEEDGPSSASET	9	2.89	0.118	1409	9.3	AE003695	TRUE	FALSE	2	1206.2	-2.6	11of 22	1.487	FALSE	FALSE	::::::::::::
KIRPTHQSLPVKRPPLPTTPANSNVRR	9	12.89	0.091	2338	39.1	AE003695	TRUE	FALSE	3	3062.6	-0.3	7of104	0.8532	FALSE	FALSE	::::::::::::::::::::::::
ELVTSDIAILK	8	4.08	0.074	2056	37.6	AE003695	TRUE	FALSE	1	1202.4	2.3	11of 20	1.3808	FALSE	FALSE	::::::::::::
RSLREQLLARI	9	12.11	0.045	962	32.8	AE003695	TRUE	FALSE	2	1355.6	2	9of 20	1.3003	FALSE	FALSE	::::::::::::
NVEYRIIMDEFFDIITR	2	4.07	0.036	594	62.23	AE003695	TRUE	TRUE	3	2191.5	2.6	18of 64	1.6252	FALSE	FALSE	:::::::Oxidation_M:::::::::
KPKPSPKPLPTLPSSLKAPEPMDNYSR	1	10.3	0.03	1448	43.83	AE003695	TRUE	FALSE	3	2993.5	0.3	22of104	1.8014	FALSE	FALSE	::::::::::::::::::::Oxidation_M:::::
PMMIKSYHKVHEGMRSLLPFSRK	10	10.89	0.023	1005	50.39	AE003695	TRUE	TRUE	2	2806.4	2.5	6of 44	1.075	FALSE	FALSE	::Oxidation_M:Oxidation_M:::::::::::::::::::
RSHTLTGNL	1	11.05	0.009	1753	13.7	AE003695	TRUE	FALSE	1	999.1	-2	4of 16	0.722	FALSE	FALSE	::::::::::
ERDEIVPSPLPKKR	8	9.88	0.008	1811	23.3	AE003695	TRUE	TRUE	2	1664.9	1.6	10of 26	1.5132	FALSE	FALSE	::::::::::::::::
KWDEDNLDSTALTPVKRAKLEAPDLPNVPQPEAAIDPE	1	3.94	0.006	1264	78.9	AE003695	TRUE	FALSE	3	4185.6	-1.7	17of148	1.5039	FALSE	FALSE	::::::::::::::::::::::::::::::::::::
PLPTLPSSLKAP	11	10.1	0.003	2626	32.4	AE003695	TRUE	FALSE	2	1221.5	-0.1	5of 22	0.9861	FALSE	FALSE	::::::::::::
GSLGGSSGSSGSKKSK	15	10.85	0	1003	-0.6	AE003695	TRUE	FALSE	1	1411.5	2.4	3of 30	0.1809	FALSE	FALSE	::::::::::::::::
VAIPRSGSFLNTGGLTRYK	5	11.39	0.147	2945	41.5	AE003696	TRUE	TRUE	3	2038.4	-1.3	15of 72	0.8341	FALSE	FALSE	::::::::::::::::::
YYNTSHTADIKTSVLFYCGK	3	8.74	0.064	2294	41.2	AE003696	TRUE	FALSE	2	2369.6	-1	10of 38	1.5491	FALSE	FALSE	::::::::::::::::::Cys_CAM:::
DQNPGQSPTGGASGPGEQGDENESYE	14	2.77	0.064	1702	14.9	AE003696	TRUE	FALSE	3	2608.5	1	11of100	1.2278	FALSE	FALSE	::::::::::::::::::::::::
LQGPVTITPQAHDNYGLESCALMIIP	2	4.07	0.041	1380	73.33	AE003696	TRUE	FALSE	3	2856.2	1.5	21of100	1.7561	FALSE	FALSE	::::::::::::::::::::Cys_CAM:::Oxidation_M::::
VAMVVGALTYTAFMITFMFPST	8	5.93	0.036	2235	85.89	AE003696	TRUE	FALSE	3	2431.9	2	13of 84	1.3787	FALSE	FALSE	::::::::::::Oxidation_M:::Oxidation_M:::::
AEIVETFTPPECEILNKVKNR	5	4.73	0.028	3040	49.2	AE003696	TRUE	FALSE	3	2488.8	-0.7	15of 80	1.5418	FALSE	FALSE	::::::::::::Cys_CAM:::::::::::
SSGLQAISW	14	6.02	0.026	2821	25.5	AE003696	TRUE	FALSE	2	949.1	-0.3	6of 16	1.0548	FALSE	FALSE	::::::::::
LPSTDEHLNQEVAAR	10	4.43	0.015	762	26.7	AE003696	TRUE	FALSE	2	1680.8	0.9	12of 28	1.6807	FALSE	FALSE	::::::::::::::
MYRMEEYLKATCISDFSSLPTR	10	6.47	0.158	1228	58.06	AE003697	TRUE	FALSE	3	2716.1	2.4	23of 84	2.6985	FALSE	FALSE	:::::Oxidation_M::::::::Cys_CAM:::::::::::
EESQQMSDTIGAMSKTDNSNM	5	3.59	0.091	2446	25.49	AE003697	TRUE	FALSE	2	2321.5	0	8of 40	1.1485	FALSE	FALSE	::::::::::::::::::::Oxidation_M:
MVMPRPEDALVVPAGL	15	4.08	0.123	2870	52.76	AE003698	TRUE	FALSE	3	1728.1	-2.2	11of 60	1.4616	FALSE	FALSE	:Oxidation_M::Oxidation_M:::::::::::::
IDALKSKRLLLDLIKTLTND	3	9.76	0.094	2597	59.5	AE003698	TRUE	FALSE	2	2284.7	2.5	11of 38	1.4157	FALSE	FALSE	::::::::::::::::::
QLDLGNNSLEVIPLSLADTNMS	8	2.88	0.087	1745	61.93	AE003698	TRUE	FALSE	3	2361.6	-0.5	25of 84	2.1838	FALSE	FALSE	::::::::::::::::::Oxidation_M:::
RADSDDPNASYIPYNNVPMGATHFR	4	5.2	0.037	2363	42.53	AE003698	TRUE	FALSE	3	2810	-1	15of 96	1.3619	FALSE	FALSE	::::::::::::::::::::::
PHGGYLLPPPSISK	4	9.72	0.031	2852	31.1	AE003698	TRUE	FALSE	2	1463.7	2.4	10of 26	1.0885	FALSE	FALSE	::::::::::::::
TPAASAAPSAATPSQKVAKK	11	10.85	0.157	1666	19.3	AE003699	TRUE	FALSE	3	1883.2	-1.1	17of 76	1.8188	FALSE	FALSE	::::::::::::::::::
MYQSSYLDKLKNRSRSIISTKFEPTYAR	1	10.31	0.123	240	54.93	AE003699	TRUE	FALSE	3	3400.9	-2	18of108	2.0585	FALSE	FALSE	:Oxidation_M:::::::::::::::::::::::
FEEWSGESRTRMKR	7	10.08	0.069	1579	21.83	AE003699	TRUE	FALSE	2	1800	-1.8	13	1.642	FALSE	FALSE	::::::::::::::
SKKYHPDANSQTRDSEVFMK	5	9.56	0.062	2920	19.03	AE003699	TRUE	FALSE	3	2369.6	-0.3	22of 76	2.0017	FALSE	FALSE	::::::::::::::::::
DLKMHILPGMLVKIVPSKDNKLKFSI	15	10.39	0.025	1015	74.36	AE003699	TRUE	FALSE	3	2998.7	2.8	20of100	1.7352	FALSE	FALSE	::::Oxidation_M::::::Oxidation_M:::::::::::::::
LVAIGLGLALTAFTVSTIVL	5	6.02	0.008	2360	85.6	AE003699	TRUE	FALSE	2	1973.4	-2.3	12of 38	1.2633	FALSE	FALSE	::::::::::::::::::
NDIVLSCEVSGGRPR	11	6.36	0.043	2428	28.8	AE003700	TRUE	FALSE	3	1659.8	1.4	10of 56	1.284	FALSE	FALSE	::::::Cys_CAM:::::::::
MPLQLVEALCGFQRIVKT	5	8.97	0.038	1281	60.73	AE003700	TRUE	FALSE	3	2120.5	-1.2	19of 68	1.8564	FALSE	FALSE	:Oxidation_M::::::::Cys_CAM:::::::::
QSPTHIRHLLPEVVPMQDLNYDY	10	5.12	0.221	1868	58.73	AE003701	TRUE	FALSE	3	2767.1	2.3	22of 88	2.2298	FALSE	FALSE	::::::::::::::::::::
LFTMCYAIVGIPLGL	7	5.33	0.173	2003	69.03	AE003701	TRUE	FALSE	2	1685	-0.5	54	1.0354	FALSE	FALSE	::::Oxidation_M:Cys_CAM:::::::::
EFCNYAQNLQPQGKDSFY	13	4.08	0.12	696	37.5	AE003701	TRUE	FALSE	3	2210.3	-1.7	17of 68	1.4994	FALSE	FALSE	:::Cys_CAM:::::::::::::
RKTLMLVGKGVTYDTGGADIKAGGVMAGMSRDK	8	10.29	0.048	2388	56.89	AE003701	TRUE	FALSE	3	3402	-0.8	24of128	2.7012	FALSE	FALSE	::::::::::::::::::::::::Oxidation_M:::::::
LFTIATLTGHAFISAGEGQSIAIDNSVAHR	2	6.03	0.031	1194	73.5	AE003701	TRUE	FALSE	3	3099.5	0.6	10of116	0.848	FALSE	FALSE	::::::::::::::::::::::::::::
HVGFLINERFINIPAQISVPLLQSLQQEIE	3	4.54	0.005	2105	100.4	AE003701	TRUE	FALSE	3	3448	-3	22of116	2.4704	FALSE	FALSE	::::::::::::::::::::::::::::
TKKRQGKDMPDILKPAK	3	10.71	0.001	1094	16.73	AE003701	TRUE	TRUE	3	1955.4	1.3	16of 64	1.3884	FALSE	FALSE	::::::::::::::::::
LDNSHDIIK	5	5.1	0.001	1972	18.3	AE003701	TRUE	FALSE	1	1055.2	0.5	6of 16	1.0977	FALSE	FALSE	::::::::::
YPWLLSRHGRIFPRFPGNFLFQPFRKPK	1	12.42	0.037	386	85.6	AE003702	TRUE	FALSE	3	3504.2	-1.6	14of108	1.4746	FALSE	FALSE	::::::::::::::::::::::::::
KNVMMDK	2	9.89	0.021	1365	11.46	AE003702	TRUE	FALSE	1	882.1	0.2	6of 12	1.4174	FALSE	FALSE	::::Oxidation_M::::
VPFKLRGLR	12	12.42	0.011	667	27.8	AE003702	TRUE	TRUE	2	1086.4	-0.8	8of 16	1.2955	FALSE	FALSE	::::::::::

LNMVDATTSTVDLLFSSGDSRSLTTQML	10	3.6	0.004	2151	72.86	AE003702	TRUE	FALSE	3	3005.4	1.8	14of108	1.2477	FALSE	FALSE	::::::::::::::::::::::::::::
RASSNASSCGRLSPIR	6	12.11	0.137	1176	20.5	AE003703	TRUE	FALSE	1	1719.9	-0.1	12of 30	1.932	FALSE	FALSE	::::::::Cys_CAM::::::::
NRSMHTATNYYLF	12	9.59	0.062	1949	29.83	AE003703	TRUE	FALSE	3	1618.8	2.3	14of 48	1.4387	FALSE	FALSE	::::::::::::::
LASPVLNICKK	9	9.91	0.01	1332	30.2	AE003703	TRUE	FALSE	2	1243.5	0.9	11of 20	1.3853	FALSE	FALSE	::::::::Cys_CAM:::
FKNLNLARGEVMLP	2	10.09	0.059	102	43.93	AE003704	TRUE	FALSE	2	1602.9	-1.6	9of 26	1.2557	FALSE	FALSE	::::::::::::::
EPPLGVFPAQGGPNGPPRRRK	7	12.12	0.035	1532	31	AE003704	TRUE	FALSE	3	2228.6	-1.2	74	1.4065	FALSE	FALSE	::::::::::::::::::::
KFKNLNLARGEVMLP	1	10.59	0.017	757	41.83	AE003704	TRUE	FALSE	2	1747.1	2.8	8of 28	1.1247	FALSE	FALSE	::::::::::::Oxidation_M:::
PPKETKNSSKNPS	11	10.32	0.008	310	-0.4	AE003704	TRUE	FALSE	3	1414.6	-0.9	13of 48	1.5189	FALSE	FALSE	::::::::::::::
SIGPLGKLLDCIPEDFDAMQLELTMWRDTY	1	3.69	0.001	1865	97.26	AE003704	TRUE	FALSE	3	3530	-2.6	15of116	1.7181	FALSE	FALSE	::::::::::Cys_CAM::::::::::::::::::::
DMMHNGNGNG	12	4.94	0	2313	6.76	AE003704	TRUE	FALSE	2	1063.1	1.6	6of 18	0.8391	FALSE	FALSE	:::Oxidation_M:::::::
VSAAVSNESVAGDSGVFEASRAHLPRK	1	7.83	0.074	906	43.2	AE003705	TRUE	FALSE	3	2743	0.2	12of104	1.269	FALSE	FALSE	::::::::::::::::::::::::::
KLVAGKGASTPDLSIMEAQATST	4	6.99	0.007	2165	42.03	AE003705	TRUE	FALSE	2	2293.6	-2.6	10of 44	1.4192	FALSE	FALSE	::::::::::::::::Oxidation_M:::::::
TTGGVASKTSASPGVVAKKSNTATKV	7	11.01	0.007	1915	22.6	AE003705	TRUE	FALSE	3	2448.8	-0.3	1	1.673	FALSE	FALSE	::::::::::::::::::::::::::
IYMIGCSVAGGGVRSPR	3	9.87	0.185	1528	39.03	AE003706	TRUE	FALSE	2	1797	0.3	11of 32	1.3728	FALSE	FALSE	:::Oxidation_M:::Cys_CAM::::::::::::
LNMARLSLAYLLK	9	10.4	0.111	1109	51.03	AE003706	TRUE	FALSE	2	1506.9	0.8	13of 24	1.5689	FALSE	FALSE	::::::::::::::
PEAFSSGNTLTVHSTPPAKFMPISPR	10	10.09	0.02	1969	52.73	AE003706	TRUE	FALSE	3	2771.2	-0.9	17of100	1.5126	FALSE	FALSE	::::::::::::::::::::::::::
FIMEDRDGCEFSLVLGGYYRLLTGNV	4	4.07	0.124	1950	83.53	AE003707	TRUE	FALSE	3	3026.4	0.6	16of100	1.6538	FALSE	FALSE	::::::::Cys_CAM:::::::::::::::::
PGLTNAGKFLTPLARGESMSSK	8	10.59	0.03	2483	41.63	AE003707	TRUE	FALSE	2	2263.6	-2.5	12of 42	1.9664	FALSE	FALSE	::::::::::::::::::::::::::
SNSDVYPLQNAANT	13	3.1	0.015	994	22.2	AE003707	TRUE	FALSE	2	1494.6	2.3	9of 26	1.1969	FALSE	FALSE	::::::::::::::
RVLLVSPRFGLSQISSAR	4	12.71	0.012	2934	51	AE003707	TRUE	FALSE	3	1987.4	-2.4	10of 68	0.9541	FALSE	FALSE	::::::::::::::::::
VKQDVPATPPSDAEPSPKQHRLGTQR	6	9.88	0.074	2907	26.7	AE003708	TRUE	FALSE	3	2841.2	1	24of100	1.8504	FALSE	FALSE	::::::::::::::::::::::::::
FEMDQYSFI	4	3.01	0.073	2635	34.73	AE003708	TRUE	FALSE	2	1196.3	2.7	5of 16	0.865	FALSE	FALSE	:::Oxidation_M:::::::
AQAPPPGPGAGLLGGLK	11	10.1	0.069	658	35.2	AE003708	TRUE	FALSE	3	1501.8	-2.3	14of 64	1.5437	FALSE	FALSE	::::::::::::::::
QAHLTIQS	15	7.85	0.067	1787	15.8	AE003708	TRUE	FALSE	2	898	0.3	7of 14	0.9858	FALSE	FALSE	::::::::
HQTEQTEMNYPLFSFSR	15	5.3	0.061	1806	36.03	AE003708	TRUE	FALSE	2	2132.3	2.3	11of 32	1.3562	FALSE	FALSE	::::::::Oxidation_M:::::::::
TSVTANNMAQVPVSKHSPEAKSAAVGGKGVFHEG	3	9.76	0.051	2462	42.73	AE003708	TRUE	FALSE	3	3410.8	2.1	25of132	1.9217	FALSE	FALSE	::::::::Oxidation_M:::::::::::::::::::::::
SLHSMYLKMDMCDFNTLGVPVHEK	14	6.03	0.03	1056	60.59	AE003708	TRUE	TRUE	3	2886.3	1	19of 92	1.8032	FALSE	FALSE	:::::Oxidation_M:::::Oxidation_M:Cys_CAM::::::::::::
HQIMVFVHARNATVR	2	12.41	0.262	1885	34.63	AE003709	TRUE	FALSE	2	1796.1	2.9	4of 28	0.9303	FALSE	FALSE	::::Oxidation_M:::::::::::
KDPTLEARRRALIMSAAMSLDKARMMR	1	11.85	0.14	1437	60.32	AE003709	TRUE	FALSE	3	3184.8	-0.5	7of104	1.0244	FALSE	FALSE	::::::::::::::Oxidation_M:::Oxidation_M::::::Oxidation_M:Oxidation_M::
MLTDYENIAFVCGFGSISPVPLFKLFTRK	9	8.85	0.118	2060	96.43	AE003709	TRUE	FALSE	3	3352.9	1.9	15of112	1.3924	FALSE	FALSE	::::::::::Cys_CAM:::::::::::::::::
CTGYRPILDAMKSFAVDSNVEV	7	4.31	0.017	1900	55.43	AE003709	TRUE	FALSE	2	2473.8	1.5	218	1.675	FALSE	FALSE	:Cys_CAM:::::::::::::::::::
PKYEKDACKLFCRMDMK	6	8.98	0.002	2235	33.46	AE003709	TRUE	FALSE	3	2253.6	-0.6	18of 64	1.7219	FALSE	FALSE	:::::::Cys_CAM:::Cys_CAM::Oxidation_M::Oxidation_M::
LLLLPGLLLMSSKSIINKR	1	11.64	0.08	640	72.83	AE003710	TRUE	FALSE	3	2126.7	-2.2	20of 72	1.9906	FALSE	FALSE	::::::::Oxidation_M:::::::::
DDIPIVGNSLSGKRAK	6	9.89	0.046	2296	26.1	AE003710	TRUE	FALSE	2	1670.9	-2.1	8of 30	0.9398	FALSE	FALSE	::::::::::::::::
RMQQIIRTDSHINMQTVRWPFMNR	2	12.41	0.044	2326	58.19	AE003710	TRUE	FALSE	3	3076.6	-1.3	8of 92	0.7722	FALSE	FALSE	::::::::::::::::::Oxidation_M:::
MDYTAAQGISK	4	6.68	0.017	2585	19.73	AE003710	TRUE	FALSE	2	1201.3	-2.5	7of 20	1.2476	FALSE	FALSE	:Oxidation_M:::::::::
YTVPTVLGTSSDVLLQTTVLTSL	1	3.1	0.005	1588	70	AE003710	TRUE	FALSE	2	2409.8	2.1	11of 44	1.4398	FALSE	FALSE	::::::::::::::::::::
RELMLVSDALRLGGAILAIYPNMLAPQLVGRL	6	9.84	0.143	2668	115.26	AE003711	TRUE	FALSE	3	3482.2	-0.3	22of124	1.9814	FALSE	FALSE	:::Oxidation_M:::::::::::::::::::::::::
VYSELQRSKMRDIR	15	10.39	0.116	2705	27.53	AE003711	TRUE	FALSE	3	1782.1	1.4	7of 52	0.8147	FALSE	FALSE	::::::::::::::
RVSEQVVFRDDQPGIQQITLMDYGYK	10	4.46	0.1	2125	60.93	AE003711	TRUE	FALSE	3	3087.5	2.8	21of100	1.8674	FALSE	FALSE	::::::::::::::::::::::::::
MQSNSIMVSSKLDYAVAGVRK	3	10.18	0.071	2534	43.86	AE003711	TRUE	FALSE	2	2285.7	0.6	12of 40	1.6009	FALSE	FALSE	::::::::::::::::::::
DPLHIDLSVEQSPITTVMESHLVNSQQIDLDLV	3	3.69	0.062	2255	90.83	AE003711	TRUE	FALSE	3	3688.1	2.5	21of128	2.0961	FALSE	FALSE	::::::::::::::::::::::::::::
SAIVVKCLLYFGGGVLLATT	12	8.88	0.229	1161	72.3	AE003712	TRUE	FALSE	3	2083.5	2	18of 76	1.9124	FALSE	FALSE	::::::Cys_CAM:::::::::::::
ERAARMNGTSASLPSNYRK	10	11.29	0.197	2112	21.93	AE003712	TRUE	FALSE	2	2110.4	1.3	10of 36	1.2671	FALSE	FALSE	::::::::::::::::::
EVHGIIGIVFSIIGLGMTALSIESPIYYLR	1	5.3	0.1	1360	111.43	AE003712	TRUE	FALSE	3	3279.9	1.5	9of116	1.1014	FALSE	FALSE	::::::::::::::::Oxidation_M:::::::::::::
LVAKVTAMVVLFCASAICGSIPFLLNR	15	9.15	0.09	1641	100.83	AE003712	TRUE	FALSE	3	2952.5	-3	18of104	1.8708	FALSE	FALSE	::::::::::::Cys_CAM::::Cys_CAM:::::::::
GNSNNSSATAASSNSSLHPYDHYPFR	8	7.85	0.073	1769	27.2	AE003712	TRUE	FALSE	3	2782.9	2.6	24of100	2.1643	FALSE	FALSE	::::::::::::::::::::::::::
GKPSADGGATGAAGNAT	12	6.76	0.037	1736	9.5	AE003712	TRUE	FALSE	2	1403.4	-2.7	9of 32	1.0856	FALSE	FALSE	::::::::::::::::::
PSVNLVTKLIDYHNNTLESMEKNIEKLKSQVTQVQK	4	9.46	0.027	2214	68.93	AE003712	TRUE	FALSE	3	4171.8	0.8	23of140	2.8381	FALSE	FALSE	::::::::::::::::::::::::::::::::::
NDDHEGAEEFR	11	3.92	0.017	684	10.3	AE003712	TRUE	FALSE	2	1319.3	-1.8	9of 20	1.3807	FALSE	FALSE	::::::::::::
TAGEKSGDSQLSRAERKAM	1	9.88	0.004	2372	16.23	AE003712	TRUE	FALSE	2	2023.2	2.4	13of 36	2.3086	FALSE	FALSE	::::::::::::::::::
KGDPGLNGISGEKGAAGKPGDKGQK	4	10.05	0.112	2737	12.1	AE003713	TRUE	FALSE	2	2367.6	1.8	12of 48	1.3539	FALSE	FALSE	::::::::::::::::::::::::::
GSVKVTDFGFCANIEGDEK	11	4.07	0.074	2696	35.8	AE003713	TRUE	FALSE	3	2074.2	2.9	15of 72	1.4928	FALSE	FALSE	::::::::::Cys_CAM:::::::::
GDPGEKGHKGDQGPMGLPGPMGMRGE	11	5.39	0.054	736	26.59	AE003713	TRUE	FALSE	3	2609.9	1.9	23of100	2.6128	FALSE	FALSE	::::::::::::::Oxidation_M:::::::::::
PEVEKRIESNAEQVIIIDK	8	4.36	0.047	3393	42.6	AE003713	TRUE	FALSE	3	2211.5	1.2	20of 72	2.0091	FALSE	FALSE	::::::::::::::::::
PEGVELLRLLTAVNRKVAYEYQSNTK	6	9.47	0.029	1907	59.9	AE003713	TRUE	FALSE	3	2993.4	-2.5	7of100	0.9099	FALSE	FALSE	::::::::::::::::::::::::::
EKAKRALDGSLRKGR	14	11.47	0.117	1214	12.8	AE003714	TRUE	FALSE	2	1686	2.2	4of 28	0.7705	FALSE	FALSE	::::::::::::::::
SAALGMTLLFFGSLVIISDPLQSILDTQLSLKPGT	11	3.89	0.088	145	120.23	AE003714	TRUE	FALSE	3	3649.3	-1	16of136	1.277	FALSE	FALSE	::::::::::::::::::::::::::::::::
LGAVIAQSCHATAAVIHLNSEDADTVAYLNDLDNMHK	5	4.51	0.077	2351	81.13	AE003714	TRUE	FALSE	3	3996.4	-0.9	26of144	3.3228	FALSE	FALSE	::::::::Cys_CAM::::::::::::::::::::::::Oxidation_M:::
RDEAQNQKSSKPGDQR	12	9.88	0.041	1196	-1.1	AE003714	TRUE	FALSE	3	1844.9	2.1	16of 60	1.3753	FALSE	FALSE	::::::::::::::::
PQSDLTQKQPYEMLYVACRSDASENYGK	11	4.56	0.019	1293	47.83	AE003714	TRUE	FALSE	3	3280.6	1.1	21of108	1.8324	FALSE	FALSE	::::::::::::::::Cys_CAM:::::::::::
DPLFEVLLK	6	4.08	0.012	1591	38.6	AE003714	TRUE	TRUE	1	1074.3	0.8	8of 16	1.6289	FALSE	FALSE	::::::::::
RYRNVTAPSMKELMNMKILSRMRQALAQRSPRS	12	12.41	0.004	2273	65.22	AE003714	TRUE	FALSE	3	3922.7	0.6	23of128	1.8407	FALSE	FALSE	::::::::::::::::::::::::::::::
VERSLTTSPASPRQPPR	12	12.11	0.084	1935	23	AE003715	TRUE	FALSE	2	1880.1	0.4	7of 32	0.9113	FALSE	FALSE	::::::::::::::::
SLSVSRFPYQESSCT	14	6.28	0.04	1828	30.4	AE003715	TRUE	FALSE	2	1748.9	2	6of 28	0.9019	FALSE	FALSE	::::::::::::Cys_CAM::
TDLIVLRDALK	8	6.9	0.006	2141	37	AE003715	TRUE	FALSE	1	1257.5	1.8	9of 20	1.9087	FALSE	FALSE	::::::::::
GMTFPTPNAAGKITHPTSSAKKAIRKEARPN	14	11.63	0.151	1980	36.23	AE003716	TRUE	FALSE	2	3295.8	1.8	9of 60	1.0819	FALSE	FALSE	::Oxidation_M:::::::::::::::::::::::::::
SLSGGSTVTRLQQSSGSNGRSNSPQNGNKK	1	12.43	0.145	2054	14	AE003716	TRUE	FALSE	3	3035.2	-0.5	24of116	2.0892	FALSE	FALSE	::::::::::::::::::::::::::::
SQNGSSTGKD	11	6.76	0.04	500	-2.9	AE003716	TRUE	FALSE	2	981	1.5	7of 18	0.9591	FALSE	FALSE	::::::::::
CLFCDFGQAALRDVNLLVEPPAVR	4	4.31	0.008	1938	78.3	AE003716	TRUE	FALSE	3	2762.1	-2.9	10of 92	1.2611	FALSE	FALSE	:Cys_CAM:::Cys_CAM:::::::::::::::::
LLKCGGDIDQPNR	11	6.24	0.003	542	24.9	AE003716	TRUE	FALSE	2	1486.6	1.4	11of 24	1.3136	FALSE	FALSE	:::::Cys_CAM:::::::::
LLGVLLLSMELVECALR	8	4.27	0.023	1955	78.03	AE003717	TRUE	FALSE	2	1930.4	-3	12of 32	1.6525	FALSE	FALSE	::::::::::::Cys_CAM::::
IVKIENLEKLANLRELYVSE	3	4.73	0.006	1188	61.9	AE003717	TRUE	FALSE	3	2374.8	-2.5	20of 76	1.859	FALSE	FALSE	::::::::::::::::::
NDQGSPAPERR	11	7.05	0.084	834	5.1	AE003718	TRUE	FALSE	2	1227.3	2.1	8of 20	1.304	FALSE	FALSE	::::::::::
MTIVAGSQAGHSK	8	10.1	0.075	3292	17.53	AE003718	TRUE	FALSE	2	1287.5	-1	11of 24	1.1009	FALSE	FALSE	::::::::::::
PSATPPKSSLCLESKESGGQHK	5	8.91	0.069	1510	19.8	AE003718	TRUE	FALSE	3	2326.5	2.5	24of 84	1.8765	FALSE	FALSE	::::::::Cys_CAM:::::::::::
FVQMLRLKQTLQSDKERHEK	6	10.32	0.055	1920	36.13	AE003718	TRUE	FALSE	3	2515.9	-1.1	16of 76	1.954	FALSE	FALSE	::::::::::::::::::::
KEKVVAVETEAPVVTKQILKQQ	8	9.67	0.03	1941	42.6	AE003718	TRUE	FALSE	3	2466.9	-2.1	13of 84	1.3123	FALSE	FALSE	::::::::::::::::::::
IDEEYMSLMAELGEGPPPPSASAKTDPPASNGPQL	7	3.44	0.023	1979	70.56	AE003718	TRUE	FALSE	3	3599	-0.6	134	2.2033	FALSE	FALSE	::::::::::::::::::::::::::::::::
ERMSNTLLEVIK	1	7.1	0.021	466	33.43	AE003718	TRUE	FALSE	2	1433.7	2.8	12of 22	1.5318	FALSE	FALSE	::::::::::::
AAPVASDSISFSLCDTITESP	11	2.88	0.016	793	50.3	AE003718	TRUE	FALSE	3	2169.3	-0.3	19of 80	1.8622	FALSE	FALSE	::::::::::::Cys_CAM:::::::
SILYTTSADGFFKKSSLLNLER	2	9.63	0.004	1153	58.6	AE003718	TRUE	FALSE	2	2491.8	2.8	8of 42	1.0586	FALSE	FALSE	::::::::::::::::::::
NGCYELTRPSSLKRASTASTTITTMTSG	1	9.75	0.175	1322	42.23	AE003719	TRUE	FALSE	3	2993.3	-1.6	15of108	1.4281	FALSE	FALSE	:::Cys_CAM:::::::::::::::::::::::

CDRLKKMTSITCSDSEDDSERR	4	4.72	0.149	2645	23.63	AE003719	TRUE	TRUE	2	2690.8	-2.5	11of 42	1.5931	FALSE	FALSE	:Cys_CAM::::::::::Cys_CAM:::::::::::
RYFGSKAHTHFCVTR	10	10.4	0.129	2139	23.6	AE003719	TRUE	FALSE	2	1868.1	-2.7	9of 28	1.3037	FALSE	FALSE	::::::::::Cys_CAM::::
GLSDSDLHSMDARMRPR	4	7.85	0.088	2373	27.16	AE003719	TRUE	FALSE	2	1961.2	-2.3	10of 32	1.2531	FALSE	FALSE	::::::::::Oxidation_M::::::::
ADSPPPPPR	10	6.79	0.04	2447	11.4	AE003719	TRUE	TRUE	2	934	-0.1	6of 16	0.9841	FALSE	FALSE	::::::::::
ASTASTTITTMTS	9	6.02	0.015	1521	19.93	AE003719	TRUE	FALSE	2	1273.4	-2.8	8of 24	1.0952	FALSE	FALSE	::::::::::::
SFRFVDWSPTGFK	9	10.09	0.094	1848	37.6	AE003720	TRUE	TRUE	3	1574.8	0.1	15of 48	1.6575	FALSE	FALSE	::::::::::::
WAQTMGDAAASGFDVI	14	2.93	0.215	2055	43.23	AE003721	TRUE	FALSE	2	1656.8	0.5	7of 30	1.2299	FALSE	FALSE	:::::Oxidation_M:::::::::::
WQQLVQHYESNRSGDPGPLAINSKLYVMNTRR	1	10.04	0.211	1081	64.13	AE003721	TRUE	FALSE	3	3760.2	-1.7	13of124	1.5539	FALSE	FALSE	::::::::::::::::::::::::::::::::
ALVAIITNPVNTCVPIAAEILKK	15	8.94	0.167	1619	72.3	AE003721	TRUE	TRUE	2	2449.9	-0.4	16of 44	2.219	FALSE	FALSE	::::::::::::Cys_CAM:::::::::::
ARIRFTHIHIGCDEVQRMGECTTCRQR	2	8.59	0.084	1898	47.23	AE003721	TRUE	FALSE	3	3389.7	2.4	9of104	0.8795	FALSE	FALSE	::::::::::Cys_CAM::::::::Cys_CAM:::Cys_CAM::::
PEFPMGGGPDGGGGGGGPGGMGP	11	3.01	0.073	2560	27.86	AE003721	TRUE	FALSE	3	1932	0.4	11of 88	1.1739	FALSE	FALSE	:::::Oxidation_M::::::::::::::Oxidation_M:::
HTHLIINKRQKGAKDNGNNN	2	10.83	0.072	2246	11.2	AE003721	TRUE	FALSE	2	2273.5	2.3	8of 38	1.0346	FALSE	FALSE	::::::::::::::::::::
QKAPLAQ	14	10.1	0.068	848	12	AE003721	TRUE	FALSE	1	755.9	0.5	9of 12	1.4507	FALSE	FALSE	::::::::
RAQERAQSGPRPSKQQERLNKMPKPPEGMSQADW	11	10.79	0.062	1384	37.16	AE003721	TRUE	FALSE	3	3921.4	2.6	23of132	2.9294	FALSE	FALSE	::::::::::::::::::::::::::::::::
QKAPLAQ	13	10.1	0.062	990	12	AE003721	TRUE	FALSE	1	755.9	1.3	8of 12	1.4439	FALSE	FALSE	::::::::
VDEVYAVESLIPSSLLER	5	3.69	0.055	2473	57.5	AE003721	TRUE	TRUE	2	2020.3	1	12of 34	1.6177	FALSE	FALSE	::::::::::::::::::
QQQLPTALCLYHFPGEVEGDLALQENELVTVLYR	12	4	0.048	2361	101.5	AE003721	TRUE	FALSE	3	3946.4	2.1	19of132	1.3532	FALSE	FALSE	::::::::Cys_CAM::::::::::::::::::::::
QANRVLRAERLKDNAVEK	5	10.57	0.041	1820	27.4	AE003721	TRUE	FALSE	2	2111.4	-1.4	6of 34	1.1132	FALSE	FALSE	::::::::::::::::::
KAMDKSKKVRMSKWHVIPLDENQLM	3	10.39	0.019	1716	50.29	AE003721	TRUE	FALSE	3	3046.6	0.5	19of 96	1.685	FALSE	FALSE	:::Oxidation_M:::::::::::::::::::Oxidation_M:
LPYDPHDAGGITPLDPRCDK	14	4.34	0	975	36.9	AE003721	TRUE	FALSE	3	2238.4	-2.2	20of 76	1.5361	FALSE	FALSE	:::::::::::::::::Cys_CAM:::
TACIWGVESARCLLQYQGHAGSVNSIKFHQQR	2	9.05	0.167	1896	66	AE003722	TRUE	FALSE	3	3704.1	2.8	10of124	1.2966	FALSE	FALSE	:::Cys_CAM::::::::Cys_CAM:::::::::::::::::::
NGGEIWNIFFGGRYII	15	6.89	0.101	1873	57.6	AE003722	TRUE	FALSE	2	1857.1	1.3	6of 30	1.0847	FALSE	FALSE	::::::::::::::::
QHSKLAINFVYMLLGMGLVAMCR	14	9.75	0.032	412	79.59	AE003722	TRUE	FALSE	3	2670.2	0.8	10of 88	1.1577	FALSE	FALSE	:::::::::::::::::::Oxidation_M:Cys_CAM::
LQVLAIMNGIDMEIE	11	2.95	0.028	361	58.06	AE003722	TRUE	FALSE	2	1722	3	7of 28	0.9383	FALSE	FALSE	::::::Oxidation_M::::Oxidation_M::::
KCMAVYQTYINAMNDR	6	8.81	0.101	2534	35.96	AE003723	TRUE	TRUE	2	1995.2	-0.6	9of 30	1.2644	FALSE	FALSE	::Cys_CAM::::::::::Oxidation_M::::
MGYGLGAALGLFSASVNPNMADPFANEK	8	4.08	0.009	2722	71.26	AE003723	TRUE	FALSE	3	2876.2	-3	15of108	1.4627	FALSE	FALSE	:Oxidation_M::::::::::::::::Oxidation_M:::::::::
RDVSGAMPTATVEEIDVP	9	3.59	0.182	278	38.73	AE003724	TRUE	FALSE	2	1888.1	-1	7of 34	1.2012	FALSE	FALSE	::::::::::::::::::
RKLYQHGEATKDYAAAASTTPAVGILTDMQK	10	9.43	0.128	1306	51.43	AE003724	TRUE	FALSE	3	3337.8	1	21of120	2.4995	FALSE	FALSE	::::::::::::::::::::::::::::::
TNPFYETIAAPVANLMMPS	13	3.3	0.104	318	57.06	AE003724	TRUE	FALSE	2	2100.4	1.4	5of 36	0.8352	FALSE	FALSE	::::::::::::::Oxidation_M:Oxidation_M:::
RKDQTASSLGEK	2	9.89	0.075	402	6.6	AE003724	TRUE	FALSE	2	1320.4	0.1	12of 22	1.316	FALSE	FALSE	::::::::::::
SQDPSAASGAISSTKSAK	9	9.89	0.065	1486	12.6	AE003724	TRUE	FALSE	2	1693.8	2.7	8of 34	1.2412	FALSE	FALSE	::::::::::::::::
QMADVKYSLDDN	12	3.6	0.058	745	22.83	AE003724	TRUE	FALSE	2	1399.5	-1.9	9of 22	1.2938	FALSE	FALSE	::::::::::::
SPTSTITTIPIVIDSK	15	6.76	0.024	2317	38.5	AE003724	TRUE	FALSE	3	1673.9	1.6	13of 60	1.9885	FALSE	FALSE	::::::::::::::::
DLYATPIRR	9	9.85	0.014	506	23.6	AE003724	TRUE	FALSE	2	1105.3	2.1	9of 16	1.2285	FALSE	FALSE	::::::::::
KRGVLTDTISICSSNG	7	8.97	0.17	1591	27.6	AE003725	TRUE	FALSE	2	1708.9	2.7	130	2.3269	FALSE	FALSE	::::::::::Cys_CAM::::::
YSYTQPPLSGYVIAGIRLIM	3	9.44	0.118	2367	67.63	AE003725	TRUE	FALSE	2	2259.7	0.7	12of 38	1.4767	FALSE	FALSE	:::::::::::::::::Oxidation_M:
HPTNPR	13	11.05	0.101	746	1.3	AE003725	TRUE	FALSE	1	721.8	-0.6	8of 10	1.2543	FALSE	FALSE	::::::
ATNRLRMRKGRSVVHK	8	12.89	0.008	3385	16.53	AE003725	TRUE	TRUE	3	1910.3	-2.6	7of 60	0.869	FALSE	FALSE	::::::::::::::::
SITLSDADVGSANVS	7	2.93	0.005	1181	28.9	AE003725	TRUE	FALSE	2	1436.5	2.9	304	1.1003	FALSE	FALSE	::::::::::::::
GEYTIAKYGRKMSDVMMAAPNANQEVDDK	10	4.65	0.07	2261	47.69	AE003726	TRUE	FALSE	2	3250.6	2.4	8of 56	1.1716	FALSE	FALSE	::::::::::Oxidation_M:::::::::::::::::
IVAVGTPHPKKGVALNPRVLGR	3	12.43	0.012	2635	45.5	AE003726	TRUE	FALSE	2	2280.8	1.5	10of 42	1.169	FALSE	FALSE	::::::::::::::::::::
YGRQLVAMVCKIR	2	10.4	0.006	369	36.63	AE003726	TRUE	FALSE	3	1594.9	2.9	16of 48	1.5514	FALSE	FALSE	::::::::::Cys_CAM::::
YSGFVVLPGGLSIILFQNKIGRK	4	10.71	0.187	1569	72.6	AE003727	TRUE	FALSE	3	2508	2.3	21of 88	2.042	FALSE	FALSE	::::::::::::::::::::::
SGDARVALIGFPSVGKSTMLST	7	10.09	0.157	1476	50.53	AE003727	TRUE	FALSE	2	2195.5	-1.5	382	1.3386	FALSE	FALSE	::::::::::::::::::::::
LALEKRLQCEVHMQAPKR	8	9.9	0.127	2151	38.13	AE003727	TRUE	FALSE	2	2224.6	0.6	10of 34	1.2526	FALSE	FALSE	::::::::Cys_CAM::::Oxidation_M::::::
KPNIYFKQKKGGGLSFNATC	1	10.3	0.112	1960	33	AE003727	TRUE	FALSE	2	2259.6	-1.9	7of 38	0.9462	FALSE	FALSE	::::::::::::::::::Cys_CAM:
ARIGQSLFFIGSVVGTLFYGLLSDKIGRV	6	10.39	0.112	1874	96.3	AE003727	TRUE	FALSE	3	3115.7	-0.3	20of112	2.1156	FALSE	FALSE	::::::::::::::::::::::::::::::
LVRSPNGKTNR	12	12.42	0.092	976	10.8	AE003727	TRUE	FALSE	2	1242.4	-0.6	8of 20	1.2142	FALSE	FALSE	::::::::::::
IFVAAFPLAPFFALLNNILEMR	7	6.98	0.051	1924	101.43	AE003727	TRUE	FALSE	3	2525.1	2.2	334	1.52	FALSE	FALSE	::::::::::::::::::Oxidation_M::
NINSSSSNTPISNLDR	14	6.79	0.039	783	21.7	AE003727	TRUE	FALSE	3	1719.8	-1	19of 60	1.678	FALSE	FALSE	::::::::::::::::
SFLHGSGILR	12	11.05	0.036	2311	28.2	AE003727	TRUE	FALSE	2	1087.3	0	7of 18	1.2187	FALSE	FALSE	::::::::::
EQLLRQVAAGSEI	13	4.27	0.003	1059	33.8	AE003727	TRUE	FALSE	2	1414.6	-2.8	10of 24	1.0163	FALSE	FALSE	::::::::::::
FLTPLINNASMSK	10	10.1	0.177	2344	38.13	AE003728	TRUE	FALSE	2	1452.7	-0.5	10of 24	1.3335	FALSE	FALSE	::::::::::Oxidation_M:::
THQLQFLEQADVIVIMDKGKISAMGTYESMAK	7	5.39	0.105	3431	78.19	AE003728	TRUE	FALSE	3	3585.2	-2.9	339	1.4495	FALSE	FALSE	::::::::::::::::::::::::::::::
FLVNLLPTRLHLLLDMPYERF	11	7.77	0.058	754	89.93	AE003728	TRUE	FALSE	3	2602.2	-0.6	21of 80	2.6031	FALSE	FALSE	::::::::::::::::::::
MQQEIYGVTLFYFWSTHFVGDFLIYAIYMGAL	4	4.07	0.026	2257	130.36	AE003728	TRUE	FALSE	3	3842.5	1.6	9of124	1.157	FALSE	FALSE	:Oxidation_M:::::::::::::::::::::::::::::
MEEANAVCSR	6	4.27	0.012	1440	17.93	AE003728	TRUE	FALSE	1	1183.2	0.9	8of 18	1.2129	FALSE	FALSE	:Oxidation_M::::::Cys_CAM:::
MGGQNPNQMGAGGPMVGNR	3	11.05	0.009	2206	23.99	AE003728	TRUE	FALSE	2	1890.1	2.7	6of 36	0.7712	FALSE	FALSE	:Oxidation_M:::::::::::::::::
VRRGNSDSAGSKMSIKSEKDI	4	10.32	0.008	1821	19.33	AE003728	TRUE	FALSE	3	2282.5	-1.1	20of 80	2.5557	FALSE	FALSE	::::::::::::Oxidation_M:::::::::
WAGNLMIIAGLSTYLIWLLP	1	5.93	0	2052	95.73	AE003728	TRUE	FALSE	2	2246.8	2.3	7of 38	0.771	FALSE	FALSE	::::::::::::::::::
LIFAGVYYQRDKTRLEVKTLQKQYQQR	3	10.31	0.068	888	59.5	AE003729	TRUE	FALSE	2	3374.9	-2.7	6of 52	1.0806	FALSE	FALSE	::::::::::::::::::::::::
TRLEVKTLQKQYQQRS	10	10.7	0.009	978	22.4	AE003729	TRUE	FALSE	2	2007.3	0.7	13of 30	2.2286	FALSE	FALSE	::::::::::::::
IVKEQGPLAMYNGISASMLRQ	10	9.72	0.208	1772	54.56	AE003730	TRUE	FALSE	3	2323.7	-2	22of 80	2.4638	FALSE	FALSE	::::::::::::::::Oxidation_M::::
PPPVTLHHHNDELDHD	15	5	0.02	1580	20.5	AE003730	TRUE	FALSE	2	1874	-2.5	7of 30	1.0991	FALSE	FALSE	::::::::::::::
VPPFMK	14	10.1	0	2775	20.53	AE003730	TRUE	FALSE	1	734.9	1.1	5of 10	0	FALSE	FALSE	:::::Oxidation_M::
RGKFNNALLELQEQGVLEK	3	7.16	0.177	1050	44.4	AE003731	TRUE	FALSE	3	2187.5	-0.6	18of 72	2.4062	FALSE	FALSE	::::::::::::::::::
INPMIYALFSNEFRIAFKR	5	10.39	0.165	1939	67.03	AE003731	TRUE	FALSE	2	2331.8	-1.1	5of 36	1.0316	FALSE	FALSE	::::::::::::::::::
ITDLPAPIGQTYGCP	10	3.1	0.111	2687	39	AE003731	TRUE	FALSE	2	1603.8	-0.7	4of 28	0.7698	FALSE	FALSE	::::::::::::Cys_CAM::
EKGSDFAILSSK	13	6.99	0.091	1477	21.9	AE003731	TRUE	FALSE	1	1282.4	0.2	11of 22	2.1913	FALSE	FALSE	::::::::::::
PKRELHISFDDEESMEFEDDSHH	9	4.18	0.087	330	35.93	AE003731	TRUE	FALSE	3	2831	-1.1	9of 88	0.8829	FALSE	FALSE	::::::::::::::::::
LKCMSDPTGPKLTLDRPISVNGIR	1	9.9	0.039	2316	53.03	AE003731	TRUE	FALSE	3	2670.1	-0.3	10of 92	1.1804	FALSE	FALSE	:::Cys_CAM:::::::::::::::::::
ISVSYPSSENISELAGHGDVGHERRQSGNALFAVHYN	11	5.77	0.015	1896	63.3	AE003731	TRUE	FALSE	3	4000.3	0.6	22of144	1.6651	FALSE	FALSE	::::::::::::::::::::::::::::::::
NYMRTLRLTDRLLTG	13	11.05	0.002	1469	41.83	AE003731	TRUE	FALSE	2	1840.2	-2.1	7of 28	1.1685	FALSE	FALSE	:::Oxidation_M:::::::::::::
GIKLDSLLGGSL	8	6.76	0.001	2884	36.9	AE003731	TRUE	FALSE	2	1173.4	-2.2	5of 22	0.7961	FALSE	FALSE	::::::::::::
PSNSIRRPPPTRSPVV	5	12.71	0.103	2885	25	AE003732	TRUE	FALSE	2	1761	0.1	7of 30	0.9615	FALSE	FALSE	::::::::::::::::
AKKALINLMNK	7	10.85	0.102	1080	25.63	AE003732	TRUE	FALSE	1	1244.6	1.1	319	0.5558	FALSE	FALSE	::::::::::::
SFLGDHSDTQFIEGDYTISRIIGMYCLLKAIA	1	4.44	0.096	1410	95.53	AE003732	TRUE	FALSE	3	3637.1	-2.2	17of124	1.8188	FALSE	FALSE	:::::::::::::::::::::::::Cys_CAM:::::::
APATVKGPDEDK	11	4.31	0.071	380	10.7	AE003732	TRUE	FALSE	2	1228.3	-1.9	13of 22	1.3596	FALSE	FALSE	::::::::::::
QPKTQWKRLEKQSVPQLANLTFQYFLK	3	10.63	0.068	1728	65.4	AE003732	TRUE	FALSE	3	3321.9	-2	20of104	2.1854	FALSE	FALSE	::::::::::::::::::::::::::::
ICDAKELPFLDTR	13	4.31	0.063	2441	37.7	AE003732	TRUE	FALSE	3	1578.8	-1.3	9of 48	1.0318	FALSE	FALSE	::Cys_CAM:::::::::::
SLGIGILFRK	15	11.49	0.017	1947	35.8	AE003732	TRUE	FALSE	1	1104.4	0.6	8of 18	1.2705	FALSE	FALSE	::::::::::
MNLVLFEDAMMHVCRINR	2	7.17	0.217	1453	59.69	AE003733	TRUE	FALSE	2	2250.7	0.9	7of 34	1.1017	FALSE	FALSE	::::::::::::Cys_CAM:::::
LDPEDPMGFNNMLIELMRDIMKMGSLIK	1	4.21	0.154	293	90.55	AE003733	TRUE	FALSE	3	3285.9	2.3	21of108	1.8482	FALSE	FALSE	::::::Oxidation_M::::::::::::::Oxidation_M::::::

QALQKSYQQRYKNDPNMSQLMLK	2	10.21	0.108	76	40.06	AE003733	TRUE	FALSE	2	2814.3	0.9	5of 44	0.9484	FALSE	FALSE	::::::::::::::::::::::
QIVLKVRLPRLVHEA	12	11.33	0.095	2063	46.4	AE003733	TRUE	FALSE	3	1772.2	-0.1	21of 56	2.1027	FALSE	FALSE	::::::::::::::
VVAVQVKSVQDAIRDKK	7	10.32	0.066	1559	29.7	AE003733	TRUE	FALSE	3	1884.2	2.1	252	2.3172	FALSE	FALSE	::::::::::::::::
PLMASMPHFYLGDPKLVADVDGLNPNEK	13	4.44	0.058	1403	71.66	AE003733	TRUE	FALSE	3	3070.5	1.4	8of108	0.7931	FALSE	FALSE	::::::::::::::::::::::::
SPNASMEQLEEHKLDTWRS	8	4.63	0.046	1971	32.63	AE003733	TRUE	FALSE	2	2275.5	-1.8	9of 36	1.5626	FALSE	FALSE	::::::Oxidation_M::::::::::::
HLRVFFVT	2	11.05	0.038	1474	32.2	AE003733	TRUE	FALSE	1	1019.2	0.1	3of 14	0.5863	FALSE	FALSE	::::::::
VEAQKLSKLNASSNAH	11	9.89	0.033	876	20.2	AE003733	TRUE	FALSE	3	1697.9	-2.5	18of 60	1.5081	FALSE	FALSE	::::::::::::::::
EVATDCGAGSGINDIAYQLARGEVGSK	15	4.07	0.02	1039	46.5	AE003733	TRUE	FALSE	3	2739.9	0.4	16of104	1.4514	FALSE	FALSE	::::::Cys_CAM::::::::::::::::::::
NFPFTGLSK	12	10.1	0	2054	23.8	AE003733	TRUE	FALSE	2	1011.2	-0.1	6of 16	0.3667	FALSE	FALSE	::::::::::
ALHTFLSPALLHSYEQR	15	7.92	0.148	385	47.5	AE003734	TRUE	FALSE	2	1984.3	0.4	6of 32	0.9314	FALSE	FALSE	::::::::::::::::
QPFIFEKTLKLSSGEEKR	1	9.76	0.085	2278	38.2	AE003734	TRUE	FALSE	3	2138.5	2.9	13of 68	1.6208	FALSE	FALSE	::::::::::::::::
NSINWVCSKNSNSVL	3	8.97	0.081	1039	31.6	AE003734	TRUE	FALSE	3	1722.9	2.3	15of 56	1.9207	FALSE	FALSE	::::::Cys_CAM::::::::
ADVLKLRCKAVVITRDGHFIDARR	7	10.56	0.04	1796	55	AE003734	TRUE	FALSE	3	2811.3	-0.3	7	1.7757	FALSE	FALSE	:::::::Cys_CAM::::::::::::::::
DVHPAAAAAMLLPSGQIVR	14	7.85	0.01	1645	50.23	AE003734	TRUE	FALSE	3	1918.3	-2.4	20of 72	1.4834	FALSE	FALSE	::::::::::::::::::
AGDTDATLSGADATMQTK	12	3.6	0.044	2729	21.93	AE003735	TRUE	FALSE	2	1754.9	-2.5	5of 34	0.8362	FALSE	FALSE	::::::::::::::::::
SYLQQYHLTNTVPYNLFYH	14	7.76	0.11	880	53	AE003736	TRUE	FALSE	3	2402.7	0.7	21of 72	2.7458	FALSE	FALSE	::::::::::::::::::
GPGQPNFR	1	11.05	0.077	701	10.5	AE003736	TRUE	FALSE	1	873	2.1	7of 14	1.3124	FALSE	FALSE	::::::::
QFRVKQLQCGHEHAVLLN	11	8.97	0.05	1714	40.4	AE003736	TRUE	FALSE	2	2178.5	-0.7	10of 34	1.2785	FALSE	FALSE	::::::::Cys_CAM:::::::::
QQVRKFAHQMFKGIA	5	11.64	0.038	3060	31.03	AE003736	TRUE	FALSE	2	1806.1	-1.1	4of 28	0.7713	FALSE	FALSE	::::::::Oxidation_M::::::
LLTLAVHEAVSSSRMMR	8	10.89	0.008	1752	47.16	AE003736	TRUE	FALSE	2	1918.3	-2.1	10of 32	1.2079	FALSE	FALSE	::::::::::::::Oxidation_M:::
TSLSLRQLFLAIALFGM	15	11.05	0.164	844	73.03	AE003737	TRUE	FALSE	3	1882.3	-2.3	16of 64	2.6589	FALSE	FALSE	::::::::::::::
TGTPKGVGMHR	9	11.49	0.091	888	8.33	AE003737	TRUE	FALSE	2	1141.3	2.5	11of 20	1.9504	FALSE	FALSE	::::::::::::
FPKTAHLLLSGSMDCRVK	5	9.91	0.083	3025	42.83	AE003737	TRUE	FALSE	3	2061.4	2	7of 68	0.9616	FALSE	FALSE	::::::::::::::Cys_CAM::::
ISMIVFFVEMSLKR	9	10.09	0.033	1481	58.16	AE003737	TRUE	FALSE	2	1701.1	2.8	12of 26	1.5973	FALSE	FALSE	::::::::::::::
LEEQIRILKNALDNSEAERK	3	4.8	0.032	2675	40.9	AE003737	TRUE	FALSE	2	2370.7	0.8	8of 38	1.1231	FALSE	FALSE	::::::::::::::::
EDKEVIEFALK	11	4.17	0.029	390	29.9	AE003737	TRUE	FALSE	2	1321.5	1	8of 20	1.2313	FALSE	FALSE	::::::::::::
RPPCPIVMLTGNESEAAQSLLFR	10	6.44	0.18	2558	63.33	AE003738	TRUE	FALSE	3	2588	0.5	11of 88	1.4781	FALSE	FALSE	::::Cys_CAM:::::::::::::::::
FEIRAISEMEAQQEHK	14	4.71	0.132	588	31.83	AE003738	TRUE	FALSE	3	1947.2	-0.9	10of 60	1.4512	FALSE	FALSE	::::::::::::::::
TATTTAISNSTNTTASPATTNTINTTTK	15	10.1	0.092	1984	27.5	AE003738	TRUE	FALSE	3	2787	1	22of108	1.8545	FALSE	FALSE	::::::::::::::::::::::::::
DKKEQANSRKASQV	3	10.32	0.046	2840	2.4	AE003738	TRUE	FALSE	2	1589.7	-2.8	9of 26	1.141	FALSE	FALSE	::::::::::::::
PTRAEASDVANAIFDGCDAVM	9	3.51	0.018	1337	46.33	AE003738	TRUE	FALSE	3	2211.4	-1.8	22of 80	1.8646	FALSE	FALSE	::::::::::::::Cys_CAM:::::
GLNCGPAATIQGGR	6	9.01	0.017	1662	22.7	AE003738	TRUE	FALSE	2	1372.5	2.7	9of 26	1.1023	FALSE	FALSE	:::Cys_CAM::::::::::
HIASFNIRCCELVSQMDY	7	5.22	0.014	1335	50.83	AE003738	TRUE	FALSE	2	2260.5	-1.8	377	1.5335	FALSE	FALSE	::::::::Cys_CAM:Cys_CAM:::::Oxidation_M:::
SVLAPMA	1	6.02	0.003	2325	24.43	AE003738	TRUE	FALSE	1	704.9	1.3	5of 12	0.9128	FALSE	FALSE	::::::Oxidation_M::
ELEPADLDYLGI	9	2.84	0.002	2699	42.6	AE003738	TRUE	FALSE	2	1348.5	-1.6	6of 22	0.7787	FALSE	FALSE	::::::::::::
RKKRANYNYNGIRTV	12	11.44	0.164	2206	16	AE003739	TRUE	FALSE	2	1854.1	0	5of 28	0.8005	FALSE	FALSE	::::::::::::::
AAKKAGKKQKTAAK	8	11.22	0.103	3316	-2.2	AE003739	TRUE	FALSE	2	1429.7	-1	8of 26	1.0855	FALSE	FALSE	::::::::::::::
GRYPALQHRVIIPEQETIR	5	9.84	0.099	1582	44.5	AE003739	TRUE	FALSE	2	2277.6	2.5	12of 36	1.7692	FALSE	FALSE	::::::::::::::::::
SHQADYEAGAGAAAAGGAVAAAH	4	5.05	0.063	2455	27.6	AE003739	TRUE	FALSE	2	2025.1	1.1	10of 44	1.1333	FALSE	FALSE	::::::::::::::::::::
FNMLYDRQGSARRM	12	11.05	0.061	2826	31.16	AE003739	TRUE	FALSE	2	1778	0.8	4of 26	0.9947	FALSE	FALSE	:::Oxidation_M::::::::::Oxidation_M:
FDAEPNSLYTILLVDPDAPSREDPK	8	3.69	0.053	2005	61.2	AE003739	TRUE	FALSE	3	2804.1	1.5	20of 96	2.2696	FALSE	FALSE	::::::::::::::::::::::
LRVRLARSLR	11	12.88	0.052	814	28.7	AE003739	TRUE	FALSE	2	1240.5	1.2	8of 18	1.3489	FALSE	FALSE	::::::::::
STSSSQQSEEA	14	3.13	0.052	1226	3.8	AE003739	TRUE	FALSE	1	1141.1	2.1	9of 20	1.5628	FALSE	FALSE	::::::::::
QMLAINRGEK	6	10.09	0.028	1582	20.63	AE003739	TRUE	FALSE	1	1160.4	2.7	9of 18	1.13	FALSE	FALSE	::::::::::
GNDVAMALLLTIMGRYTGEPVELDQK	3	4.07	0.021	1433	71.26	AE003739	TRUE	FALSE	3	2868.3	-2.2	9of100	1.0096	FALSE	FALSE	::::::Oxidation_M::::::Oxidation_M::::::::::::
VGCLRKVEFSADTLNLNLIDLAKSGSK	6	8.9	0.014	2549	65.6	AE003739	TRUE	FALSE	2	2950.4	-1.8	10of 52	1.2176	FALSE	FALSE	:::Cys_CAM::::::::::::::::::::
REELMCAK	10	6.44	0.003	2265	17.73	AE003739	TRUE	FALSE	2	1053.2	2.5	4of 14	0.7054	FALSE	FALSE	:::::Oxidation_M:Cys_CAM:::
GGQNHPEFFRPPLVTKDDYK	2	7.73	0.089	2146	34	AE003740	TRUE	FALSE	2	2346.6	-2.1	7of 38	0.7147	FALSE	FALSE	::::::::::::::::::
LSLSVRSTQSIAGIRSD	3	10.89	0.078	1897	36.4	AE003740	TRUE	FALSE	2	1791	-2.8	6of 32	1.318	FALSE	FALSE	::::::::::::::::
KLPMILALHLKRFKYMEQF	11	10.45	0.066	1317	67.66	AE003740	TRUE	FALSE	3	2424	-2.7	13of 72	1.6028	FALSE	FALSE	::::Oxidation_M:::::::::::::::
RSDISDRLRLDQWTFDKVR	5	10.08	0.035	2981	42	AE003740	TRUE	FALSE	3	2407.7	2.5	11of 72	1.2568	FALSE	FALSE	::::::::::::::::::
AAMALRSIQTK	1	11.49	0.027	678	24.73	AE003740	TRUE	FALSE	1	1190.4	2.5	9of 20	1.1767	FALSE	FALSE	::::::::::::
YRSLPRGIERGPSGCGRFGLR	1	11.82	0.019	1353	39.5	AE003740	TRUE	FALSE	3	2392.7	2.1	22of 80	2.1759	FALSE	FALSE	::::::::::::::Cys_CAM:::::::
LLALLACAICSQASLE	3	3.3	0.012	2049	61.8	AE003740	TRUE	FALSE	2	1734	2.1	11of 30	1.4385	FALSE	FALSE	::::::Cys_CAM:::Cys_CAM::::::
GAQDMKSVGCQYMAAVRALKASGYQ	11	9.51	0.118	270	45.16	AE003741	TRUE	FALSE	3	2708	1.7	12of 96	1.1601	FALSE	FALSE	:::::Oxidation_M:::::Cys_CAM:::::::::::::::
SYIMTTKEFLPK	3	9.63	0.063	896	33.53	AE003741	TRUE	FALSE	2	1474.8	2.8	9of 22	1.4485	FALSE	FALSE	::::Oxidation_M:::::::::
NHALRNANGQLRRKSAGGASVPPSGPKKAAK	8	12.72	0.063	2217	23.7	AE003741	TRUE	TRUE	3	3140.6	-2.5	21of120	1.7343	FALSE	FALSE	::::::::::::::::::::::::::::
FKFSGTSGHGSLLHKSTA	7	10.6	0.059	1828	25.8	AE003741	TRUE	FALSE	2	1863.1	-2.1	3	1.1752	FALSE	FALSE	::::::::::::::::
HYGPRWMANRAPFELK	5	10.39	0.043	2681	37.93	AE003741	TRUE	FALSE	2	1974.3	-0.6	11of 30	1.5118	FALSE	FALSE	::::::::::::::::
YVPDEEVGGHLGMR	14	4.43	0.018	2789	29.23	AE003741	TRUE	FALSE	3	1559.7	1.7	7of 52	0.8313	FALSE	FALSE	::::::::::::::
VGENAWAK	9	6.95	0.041	1018	16	AE003742	TRUE	FALSE	2	875	-2.4	10of 14	1.5864	FALSE	FALSE	::::::::
EMYLLKMATAALDIDAIQG	14	3.71	0.006	1687	62.46	AE003742	TRUE	FALSE	2	2084.5	-0.4	6of 36	0.8881	FALSE	FALSE	::::::Oxidation_M::::::::::::
DNIAAFGGDPNQVTIFGES	13	2.88	0.055	1334	42.1	AE003743	TRUE	FALSE	2	1953.1	2.8	7of 36	0.957	FALSE	FALSE	::::::::::::::::::
HAILNNNGVQMLMRDK	9	10.09	0.05	1941	35.06	AE003743	TRUE	FALSE	2	1871.2	0.1	12of 30	1.6575	FALSE	FALSE	::::::::::Oxidation_M:::::::
FSLIQQSNCIYCYRSR	2	9.01	0.043	1785	42.8	AE003743	TRUE	FALSE	2	2096.3	-0.9	4of 30	0.7715	FALSE	FALSE	::::::::Cys_CAM:::Cys_CAM:::::
VKSGSPLSLAICHRGVEFK	14	9.91	0.014	2771	41.5	AE003743	TRUE	FALSE	3	2086.4	2.9	8of 72	0.9625	FALSE	FALSE	::::::::::Cys_CAM::::::::
IFHSRKNNKALAELKGHQGPVWQV	5	10.83	0.001	2595	44.7	AE003743	TRUE	FALSE	3	2759.2	0.3	22of 92	1.5335	FALSE	FALSE	::::::::::::::::::::::
SLFERLWNESLIRR	15	10.8	0.287	2741	48	AE003744	TRUE	FALSE	3	1820.1	2	13of 52	2.0138	FALSE	FALSE	::::::::::::::
EELYRRQIPLSSVMGRNPDR	10	9.84	0.083	814	41.43	AE003744	TRUE	FALSE	3	2433.7	-1.8	9of 76	1.0319	FALSE	FALSE	::::::::::::Oxidation_M::::::
SNASGSKEASTQAGASQSGGATSGQDAAAG	9	4.08	0.033	2258	13.2	AE003744	TRUE	FALSE	3	2612.6	-0.7	18of116	1.4945	FALSE	FALSE	::::::::::::::::::::::::::
EASTQAGASQSGGATSGQDAAA	10	3.01	0.016	1824	14.9	AE003744	TRUE	FALSE	2	1923.9	-0.4	15of 42	1.6423	FALSE	FALSE	::::::::::::::::::::
IVPLLAIAIVMYLKLMPIVADGPR	2	9.72	0.005	1405	101.86	AE003744	TRUE	TRUE	3	2640.3	3	10of 92	1.4015	FALSE	FALSE	::::::::::Oxidation_M::::Oxidation_M::::::::
SPVHKATGSGPGSPKTK	2	10.85	0.09	573	4.6	AE003745	TRUE	FALSE	2	1636.8	-2.8	6of 32	0.8657	FALSE	FALSE	::::::::::::::::
IHITSQTSAENGISLMQGQ	5	5.13	0.006	2943	36.43	AE003745	TRUE	FALSE	3	2032.2	-1.2	8of 72	0.6424	FALSE	FALSE	::::::::::::::Oxidation_M::::
DETVACEDNGSVISEYSR	14	3.51	0.139	1531	28.8	AE003746	TRUE	FALSE	2	2032	2.9	9of 34	1.1553	FALSE	FALSE	::::::Cys_CAM::::::::::::
PYVYGWYSNTFDVNLSEAMYP	8	3.01	0.134	1707	64.63	AE003746	TRUE	FALSE	3	2517.8	-1.5	12of 80	1.3989	FALSE	FALSE	::::::::::::::::::
SCSSGDTKGAR	12	8.97	0.123	1160	1.7	AE003746	TRUE	FALSE	2	1126.1	1.4	9of 20	1.2355	FALSE	FALSE	::Cys_CAM:::::::::
KEGEGFIDSLRK	2	7.11	0.106	529	20.6	AE003746	TRUE	FALSE	2	1379.6	-2.1	12of 22	1.4238	FALSE	FALSE	::::::::::::
AQYKHSDIVILSPYNGQI	3	7.68	0.101	2272	43.1	AE003746	TRUE	FALSE	2	2047.3	-1.6	9of 34	1.2418	FALSE	FALSE	::::::::::::::::::
LFSGSGTSFGAPLNSSVAYFD	2	3.1	0.083	2089	54.6	AE003746	TRUE	FALSE	2	2125.3	2	7of 40	1.0778	FALSE	FALSE	::::::::::::::::::::
TPAAQKSSDAIEV	9	4.08	0.073	609	19.8	AE003746	TRUE	FALSE	2	1317.4	-0.8	11of 24	1.2962	FALSE	FALSE	::::::::::::
IFRYLYGASTKVIYRPHR	3	10.66	0.068	1776	47.7	AE003746	TRUE	FALSE	2	2241.6	2.5	10of 34	1.1602	FALSE	FALSE	::::::::::::::::
EDQTNEVEALDSIYCGDMEILATEPH	5	3.28	0.067	2783	58.83	AE003746	TRUE	FALSE	3	2981.1	0.2	9of100	1.044	FALSE	FALSE	::::::::::::::Cys_CAM:::::::::::

YWMQCPVTLELQTVGDKKDVVFK	6	6.41	0.065	1155	63.93	AE003746	TRUE	FALSE	3	2802.2	-0.8	22of 88	2.4264	FALSE	FALSE	:::Oxidation_M::Cys_CAM::::::::::::::::::
KTRAAVAALKRQVA	9	12.43	0.064	846	23.3	AE003746	TRUE	FALSE	3	1483.8	-0.9	20of 52	2.0094	FALSE	FALSE	::::::::::::::
MPAEDAISKMRCGG	6	6.36	0.063	2852	25.06	AE003746	TRUE	FALSE	2	1539.7	2.4	8of 26	1.0993	FALSE	FALSE	:::::::::Oxidation_M::Cys_CAM:::
SIWPMATPTPAPSSGVSSTK	13	10.1	0.045	2600	37.23	AE003746	TRUE	FALSE	2	2003.3	-1.9	6of 38	0.6933	FALSE	FALSE	::::::::::::::::::
KLPVVKKSQVEEKK	4	10.39	0.043	2818	16.6	AE003746	TRUE	TRUE	2	1641	0.6	6of 26	0.8178	FALSE	FALSE	::::::::::::::
VNAVTTSSTQITIAPT	1	6.02	0.029	972	32.8	AE003746	TRUE	FALSE	1	1604.8	-2.8	13of 30	1.2818	FALSE	FALSE	::::::::::::::::
FLLQAGADQE	15	3.01	0.008	1470	29.4	AE003746	TRUE	FALSE	1	1092.2	0.2	11of 18	1.6634	FALSE	FALSE	::::::::::
MQAQVVRAKRDLRAELNAK	14	11.38	0.141	1902	34.43	AE003747	TRUE	FALSE	3	2214.6	2.4	21of 72	1.6355	FALSE	FALSE	:Oxidation_M:::::::::::::::::
DTNRNQRQRRSPSPEAP	1	11.93	0.116	202	5.9	AE003747	TRUE	FALSE	2	2010.1	0.8	7of 32	1.0717	FALSE	FALSE	::::::::::::::::
AKSPIIFNRREKT	5	11.47	0.091	1346	22.4	AE003747	TRUE	FALSE	2	1560.8	1.8	10of 24	1.3654	FALSE	FALSE	::::::::::::::
HGIRGEINVIVK	9	10.09	0.066	536	27.5	AE003747	TRUE	FALSE	2	1335.6	1.6	14of 22	1.8383	FALSE	FALSE	::::::::::::::
SPSNGRPRRKAKTSSSSATTQERPLR	4	12.59	0.049	2822	11.8	AE003747	TRUE	FALSE	3	2857.2	0.5	23of100	1.9338	FALSE	FALSE	::::::::::::::::::::::::
TQFVVTLNGDKALGGKNVKGGASRKR	15	11.63	0.034	1658	32.7	AE003747	TRUE	TRUE	3	2703.1	-1.1	24of100	2.0873	FALSE	FALSE	::::::::::::::::::::::
LVKPYIKGFSVETTTEGTDSQAVSAAP	14	4.45	0.016	1924	52.7	AE003747	TRUE	FALSE	2	2798.1	3	9of 52	1.1463	FALSE	FALSE	::::::::::::::::::::::
IEEQKKDNAVFFRLFKR	11	10.32	0.01	180	41.1	AE003747	TRUE	FALSE	2	2169.5	-0.4	8of 32	1.0973	FALSE	FALSE	::::::::::::::::
RGAPGGPGPKRGRYEGGPYGQR	3	11.27	0.007	1793	14	AE003747	TRUE	TRUE	2	2271.5	0.8	9of 42	1.3598	FALSE	FALSE	::::::::::::::::::::
MKPKPMSTPKRRYDWSYSKRP	5	11.04	0.002	1760	26.86	AE003747	TRUE	FALSE	3	2657.1	-2.1	11of 80	1.0475	FALSE	FALSE	::::::Oxidation_M:::::::::::::::
NCWPTILTLLIVANLVDALK	9	6.1	0.002	2056	80.8	AE003747	TRUE	FALSE	3	2268.7	3	25of 76	2.8062	FALSE	FALSE	::Cys_CAM:::::::::::::::::
VHHPRTEFAPSSAFYIPYSASKFKAFK	12	10.21	0.195	829	57.6	AE003748	TRUE	FALSE	3	3115.6	0.2	7of104	0.8479	FALSE	FALSE	::::::::::::::::::::::::
LREICVDGSFLRVTVEGGGCS	7	4.45	0.113	3315	52.5	AE003748	TRUE	FALSE	3	2312.5	2.4	210	1.3054	FALSE	FALSE	:::::Cys_CAM::::::::::::Cys_CAM:::
KINRDDGLPQEICRQCMA	5	6.27	0.083	2111	35.03	AE003748	TRUE	FALSE	2	2221.4	2.4	12of 34	2.0184	FALSE	FALSE	:::::::::::Cys_CAM:::Cys_CAM:Oxidation_M:::
RKCTVSHSGLFCK	10	9.93	0.081	305	19.5	AE003748	TRUE	FALSE	3	1580.8	-2.4	16of 48	1.8683	FALSE	FALSE	:::Cys_CAM::::::::Cys_CAM:::
WQMFAFMSPFDTYSKLIN	1	6.68	0.039	2196	65.86	AE003748	TRUE	FALSE	2	2243.6	0	7of 34	1.0082	FALSE	FALSE	:::Oxidation_M:::::::::::::::
SIRYSAQRQKLDVTIHKIQK	7	10.89	0.012	2213	32.6	AE003748	TRUE	FALSE	2	2413.8	-0.6	75	1.5381	FALSE	FALSE	::::::::::::::::::::
PRRRKDSDQSPPRR	4	12.24	0.009	1959	0.9	AE003748	TRUE	FALSE	2	1751.9	-1.5	5of 26	0.7754	FALSE	FALSE	::::::::::::::
FPRPSQLTLH	15	11.05	0.002	1830	26	AE003748	TRUE	FALSE	2	1196.4	-1.8	6of 18	0.9321	FALSE	FALSE	::::::::::
QILTQVLATKGAAMAEG	15	6.95	0.087	1623	41.93	AE003749	TRUE	FALSE	2	1703	-2.8	6of 32	1.2285	FALSE	FALSE	::::::::::::::::
EQCDRGYYVQV	14	4.08	0.048	203	22.1	AE003749	TRUE	FALSE	2	1417.5	1.6	8of 20	1.5912	FALSE	FALSE	:::Cys_CAM:::::::::
FFEAEFLPKINH	8	5.3	0.044	2363	41.2	AE003749	TRUE	FALSE	1	1492.7	-0.6	10of 22	1.4642	FALSE	FALSE	::::::::::::
QVVQEIRKKMCNLSSMVPTNVQ	9	9.91	0.035	2554	46.46	AE003749	TRUE	FALSE	3	2623	2.9	9of 84	1.1659	FALSE	FALSE	:::::::::Oxidation_M:Cys_CAM:::::Oxidation_M:::::::
PNVENMQTRAKRKADHSPIKNDK	10	10.55	0.032	1016	14.33	AE003749	TRUE	FALSE	3	2679	2	21of 88	2.7874	FALSE	FALSE	::::::::::::::::::::
RELDSERKELDKLR	5	7.21	0.02	2046	21.8	AE003749	TRUE	FALSE	3	1788	-1.5	14of 52	2.5595	FALSE	FALSE	::::::::::::::
APTDGR	8	6.79	0.004	3331	4	AE003749	TRUE	TRUE	1	616.7	-0.7	4of 10	0.8833	FALSE	FALSE	::::::
LCMVDDLYEQLT	5	2.88	0.001	2997	44.03	AE003749	TRUE	FALSE	2	1500.7	-1.7	8of 22	0.9893	FALSE	FALSE	::Cys_CAM:::::::::
VAVHMEIEGTAQCPSQVMLAAALGCEE	7	3.79	0.292	1685	69.16	AE003750	TRUE	FALSE	3	2903.2	1.7	303	1.9531	FALSE	FALSE	:::::::::::Cys_CAM::::::::::Cys_CAM:::
KAPVLVIHGTDDEVIDFSHGIGIYER	1	4.61	0.093	1141	65	AE003750	TRUE	FALSE	3	2882.2	1.9	22of100	2.3753	FALSE	FALSE	::::::::::::::::::::::
PLEVDLKRLEDLSDSIVRD	9	4	0.092	1505	51.1	AE003750	TRUE	FALSE	3	2213.5	2.1	19of 72	1.8998	FALSE	FALSE	::::::::::::::::::
ETSTEADISTEPSAEVEK	14	3.51	0.049	1400	23.2	AE003750	TRUE	FALSE	3	1924	-1.9	21of 68	2.1276	FALSE	FALSE	::::::::::::::::::
IWSLDQPSNDLKANI	14	3.89	0.044	1747	40.5	AE003750	TRUE	FALSE	2	1714.9	-2.5	6of 28	1.0587	FALSE	FALSE	::::::::::::::
ITNWVPNEVSSTLIR	2	6.98	0.037	2452	43.8	AE003750	TRUE	FALSE	2	1730	-2.3	7of 28	0.9454	FALSE	FALSE	::::::::::::::
GNLITCIYVRC	15	8.29	0.032	1161	36.8	AE003750	TRUE	FALSE	1	1369.5	-0.5	6of 20	1.2853	FALSE	FALSE	:::::Cys_CAM::::Cys_CAM:
LPVGSVGPSSIAPLIAK	3	10.1	0.025	1131	47.9	AE003750	TRUE	FALSE	3	1606.9	2.4	15of 64	1.1298	FALSE	FALSE	::::::::::::::::
TSMAAISGCAAGILGLSGTLGF	8	5.33	0.02	2603	62.93	AE003750	TRUE	FALSE	2	2072.3	3	10of 42	1.2962	FALSE	FALSE	:::Oxidation_M::::::Cys_CAM:::::::::::::
NSTGNNVLT	10	6.02	0.016	394	12.1	AE003750	TRUE	FALSE	2	920	-0.4	8of 16	0.6718	FALSE	FALSE	::::::::::
DVPNGTL	6	3.1	0	2812	15.1	AE003750	TRUE	FALSE	1	715.8	1	8of 12	1.0824	FALSE	FALSE	::::::::
ATKSMRANA	15	11.49	0.16	727	8.63	AE003751	TRUE	FALSE	1	966.1	2.1	8of 16	1.3891	FALSE	FALSE	:::::Oxidation_M:::::
GWPMTQVHELL	14	5.13	0.15	1649	36.93	AE003751	TRUE	FALSE	2	1311.5	0.6	8of 20	1.3271	FALSE	FALSE	::::::::::::
DLHYFFSTALQADIRLK	14	7.74	0.141	1283	52.4	AE003751	TRUE	FALSE	2	2039.3	2.7	8of 32	1.4513	FALSE	FALSE	::::::::::::::::
LWLIFQLFSVGMFVSSTALLPSSFSMYFGC	2	5.33	0.139	1704	128.36	AE003751	TRUE	FALSE	3	3438	2.8	7of116	0.8751	FALSE	FALSE	:::::::::::::::::::::::::::::Cys_CAM:
DLVIKPATAKGDNYASVMTRVRILFLKSGAK	1	10.62	0.067	1940	72.83	AE003751	TRUE	FALSE	3	3381	-1.3	13of120	1.3778	FALSE	FALSE	:::::::::::::::::Oxidation_M:::::::::::::
EGNEFAQNAMKPYDIFNR	5	4.45	0.064	2687	37.33	AE003751	TRUE	FALSE	2	2161.4	-1.1	12of 34	1.371	FALSE	FALSE	:::::::::Oxidation_M:::::::::
GHGDYV	2	4.94	0.061	2277	7.2	AE003751	TRUE	FALSE	1	647.7	0.9	4of 10	0.6642	FALSE	FALSE	::::::
PPPAQPAAPPAPLNILESK	9	6.95	0.039	2737	43.8	AE003751	TRUE	FALSE	3	1909.2	-2.3	12of 72	1.1237	FALSE	FALSE	::::::::::::::::::
PGQKYKLRGLPDLKSHLEEDMAE	14	5.47	0.038	2824	42.53	AE003751	TRUE	FALSE	3	2656	2.4	9of 88	1.0742	FALSE	FALSE	::::::::::::::::::::::
PTNKPGKHLK	4	10.85	0.035	35	3.5	AE003751	TRUE	FALSE	2	1120.3	-0.7	7of 18	1.062	FALSE	FALSE	::::::::::
EDASIEQVLSSSESGMRFKNSVYESE	14	3.89	0.027	815	46.43	AE003751	TRUE	FALSE	3	2910.1	1.6	19of100	1.687	FALSE	FALSE	::::::::::::::::::::::::
FSIFDPLRNGAARAIR	3	12.11	0.021	1919	44.5	AE003751	TRUE	TRUE	2	1805.1	-1.1	13of 30	1.3327	FALSE	FALSE	::::::::::::::::
TLLGCLDRSQMEIKNDR	2	6.42	0.015	2093	37.63	AE003751	TRUE	TRUE	2	2066.3	3	6of 32	0.8475	FALSE	FALSE	:::::Cys_CAM::::::Oxidation_M:::::::
MFQREHQVYHNVLPKLE	13	7.9	0.011	1433	41.03	AE003751	TRUE	FALSE	2	2169.5	-0.1	4of 32	0.7137	FALSE	FALSE	::::::::::::::::
YWYPDPEFMNK	6	4.08	0.002	1684	34.03	AE003751	TRUE	FALSE	2	1490.7	-1.1	7of 20	1.2243	FALSE	FALSE	::::::::::
QSVTIMYLLR	5	9.85	0.129	2323	38.43	AE003752	TRUE	FALSE	2	1240.5	-0.9	10of 18	1.4292	FALSE	FALSE	:::::Oxidation_M:::::
EHRDNGQAGGYFTRY	13	7.7	0.069	1785	16.5	AE003752	TRUE	FALSE	2	1771.8	-2.5	4of 28	0.873	FALSE	FALSE	::::::::::::::
RAELDRVRR	12	11.93	0.066	2400	14	AE003752	TRUE	FALSE	2	1171.3	-1	5of 16	1.0209	FALSE	FALSE	::::::::::
VYAYWCEMQR	14	6.28	0.059	516	33.43	AE003752	TRUE	FALSE	2	1406.6	-0.4	8of 18	1.2756	FALSE	FALSE	:::::Cys_CAM:::::
ALLQHGANHTIR	15	11.05	0.059	1942	22.6	AE003752	TRUE	FALSE	2	1331.5	0.4	7of 22	1.1948	FALSE	FALSE	::::::::::::
QPKEAVTPAAQLLQKR	9	10.59	0.054	1042	28.1	AE003752	TRUE	FALSE	3	1779.1	-1.7	19of 60	1.4828	FALSE	FALSE	::::::::::::::
DKALVDGAWVDSSNAKATFEVR	10	4.46	0.054	1521	44.3	AE003752	TRUE	FALSE	2	2380.6	0.6	11of 42	1.1693	FALSE	FALSE	::::::::::::::::::
ALKIIDERFGKMF	10	9.89	0.053	1049	42.93	AE003752	TRUE	FALSE	2	1568.9	1.2	11of 24	2.447	FALSE	FALSE	::::::::::::
IGGGIGCPSHK	12	8.97	0.049	947	14.2	AE003752	TRUE	FALSE	1	1083.2	-0.2	11of 20	1.2719	FALSE	FALSE	::::::Cys_CAM:::::
ELILEPDLIKPLEHVV	12	4.16	0.047	936	60.5	AE003752	TRUE	FALSE	3	1858.2	-2.1	18of 60	1.4921	FALSE	FALSE	::::::::::::::
AMGGSNKSGSSGR	6	11.49	0.034	2936	2.63	AE003752	TRUE	FALSE	2	1196.3	2.2	14of 24	1.5412	FALSE	FALSE	::::::::::::::
AGMRFEDLQLVGFSMGAHVAGLAGK	14	7.82	0.028	734	64.86	AE003752	TRUE	FALSE	3	2564	2.8	10of 96	1.2318	FALSE	FALSE	::::::::::::::::::::::
LTGAKMLQVLAHLATQR	4	11.49	0.022	2223	45.13	AE003752	TRUE	TRUE	2	1868.2	2.4	9of 32	1.2382	FALSE	FALSE	::::::Oxidation_M:::::::::::
KMAIANQQLREIFVATEAN	1	7.1	0.124	214	48.43	AE003753	TRUE	FALSE	3	2164.5	-0.4	15of 72	1.6227	FALSE	FALSE	::Oxidation_M:::::::::::::::
RKTKPRPKSPRRR	12	13.01	0.111	679	-2.9	AE003753	TRUE	FALSE	3	1664	0.9	18of 48	2.1415	FALSE	FALSE	::::::::::::::
RAEAGNGNVATTTTGTATGSSQH	2	7.85	0.03	2216	12.6	AE003753	TRUE	FALSE	3	2190.2	-2.3	10of 88	0.9557	FALSE	FALSE	::::::::::::::::::::
QKSLAKNNEENIKLR	11	10.32	0.024	362	18.9	AE003753	TRUE	FALSE	3	1786	-0.8	17of 56	1.9204	FALSE	FALSE	::::::::::::::::
GHRSIGNRVMWL	13	12.41	0.01	2529	30.33	AE003753	TRUE	FALSE	2	1426.7	1.3	6of 22	1.0979	FALSE	FALSE	::::::::::::
QTCKKNYMEFIQTAK	4	9.6	0.131	1701	25.53	AE003754	TRUE	TRUE	2	1891.2	-2.6	9of 28	1.5559	FALSE	FALSE	:::Cys_CAM:::::::::::::
AEEFVEPEDGWTTVRR	11	4.01	0.106	1092	35.3	AE003754	TRUE	FALSE	2	1922.1	2.1	11of 30	1.6763	FALSE	FALSE	::::::::::::::::
KSQNTMAQAMKGVTKAMQNMNRQLNLPQIQK	15	11.8	0.064	1765	48.12	AE003754	TRUE	FALSE	3	3533.2	2.1	20of120	1.6122	FALSE	FALSE	::::::::::::::::::::::::::::
KFMLMKANIQAVSLKIQTLKSQNTMA	4	11.01	0.052	1471	65.99	AE003754	TRUE	FALSE	3	2971.6	-2.9	24of100	1.8664	FALSE	FALSE	:::Oxidation_M::::::::::::::::::::Oxidation_M:::
VVGDTWCAVTDPLR	10	3.89	0.095	950	39.3	AE003755	TRUE	FALSE	3	1589.8	0.8	17of 52	1.7877	FALSE	FALSE	::::::Cys_CAM:::::::

GCALDSGTLTTDTEIIRMSHCGKFYYDDK	15	4.55	0.018	1675	57.23	AE003755	TRUE	TRUE	3	3372.6	-1.5	26of112	2.7328	FALSE	FALSE	::Cys_CAM::::::::::::::Oxidation_M::::Cys_CAM:::::::::
AKFASLNRCMDTPDDSPVRRR	7	10.1	0.055	1517	33.03	AE003756	TRUE	TRUE	3	2493.8	-0.5	99	1.9264	FALSE	FALSE	::::::::Cys_CAM::::::::::::
SADPGIGDVCGIRLDHREICK	14	5.33	0.03	1805	40	AE003756	TRUE	FALSE	2	2369.6	1.4	10of 40	1.2908	FALSE	FALSE	::::::::::Cys_CAM::::::::::Cys_CAM::
SSSGDDNDDSDQEEGIAR	13	3.23	0.001	1486	10.2	AE003756	TRUE	FALSE	2	1897.8	2.4	6of 34	0.9018	FALSE	FALSE	::::::::::::::::
CAGEVAAARDNGIC	13	4.08	0.088	2525	25.3	AE003757	TRUE	FALSE	2	1464.5	2	8of 26	0.9836	FALSE	FALSE	:Cys_CAM::::::::::::Cys_CAM:
AATPASTSSNAGAGSVAGAGAVASTK	3	10.1	0.06	2009	27.3	AE003757	TRUE	FALSE	2	2163.3	-3	9of 50	1.0809	FALSE	FALSE	::::::::::::::::::::::::
IGGSGVSPVPALAGPVSYSAAPQASVHK	11	9.72	0.042	1792	52	AE003757	TRUE	FALSE	2	2606	-0.6	11of 54	1.4873	FALSE	FALSE	::::::::::::::::::::::::
PPKRVSDVNAMGPSAPMMGGGAT	3	10.09	0.011	2182	36.89	AE003757	TRUE	FALSE	2	2245.6	-1	12of 44	1.7084	FALSE	FALSE	::::::::::::::::::::Oxidation_M:::::::
FSAFNSLTQR	10	11.05	0.003	837	25.3	AE003757	TRUE	FALSE	1	1171.3	-0.3	5of 18	0.7426	FALSE	FALSE	::::::::::::
DPVFIRIGTCGGIGVDGGTVIITEDALD	11	3.37	0.127	1086	76.7	AE003758	TRUE	FALSE	3	2862.2	0.1	13of108	1.3262	FALSE	FALSE	::::::::::Cys_CAM:::::::::::::::::
VQKAKEAFMDNIGESLKTLFPKGVPPPIGDFMKYV	13	9.46	0.071	310	89.16	AE003758	TRUE	FALSE	3	3897.6	-1.3	15of136	1.4147	FALSE	FALSE	::::::::::::::::::::::::::::::::::
QAGSGHLQETAAAFKATQR	6	10.09	0.045	1834	23.1	AE003758	TRUE	FALSE	2	1973.2	1.5	10of 36	1.3901	FALSE	FALSE	::::::::::::::::::::
SRLLASTKTDLRE	2	10.09	0.062	798	25.1	AE003759	TRUE	FALSE	2	1490.7	2.1	10of 24	1.6025	FALSE	FALSE	::::::::::::::
THLENLMDFVHWQMMDK	10	5.12	0.028	860	49.89	AE003759	TRUE	FALSE	3	2176.5	1.6	24of 64	2.5096	FALSE	FALSE	::::::::::::::::
IHGWTQRYSDDMNTR	6	7.76	0.009	1434	23.53	AE003759	TRUE	FALSE	3	1897	-1.9	18of 56	2.6874	FALSE	FALSE	::::::::::::Oxidation_M::::
NCGFRYRSPEE	14	6.43	0.115	131	17.2	AE003760	TRUE	FALSE	3	1415.5	-0.4	13of 40	1.3264	FALSE	FALSE	::Cys_CAM:::::::::
QLTSLGVPVTALEVH	12	5.13	0.105	2690	43.1	AE003760	TRUE	FALSE	3	1564.8	-1.8	11of 56	1.3576	FALSE	FALSE	::::::::::::::::
VKQRLLKIRGDPPVQRPRLG	2	12.42	0.077	1340	40.9	AE003760	TRUE	FALSE	2	2327.8	0.4	7of 38	0.959	FALSE	FALSE	::::::::::::::::::::
VKSPKAKQPTLKVRNVRVEGEGLEAS	5	10.55	0.07	1354	37.1	AE003760	TRUE	FALSE	3	2822.3	2.5	21of100	2.0162	FALSE	FALSE	::::::::::::::::::::::::::
IIEEDVSIKTKMCEE	9	4.01	0.062	484	36.13	AE003760	TRUE	FALSE	3	1841	-0.1	16of 56	1.5634	FALSE	FALSE	::::::::::::Oxidation_M:Cys_CAM:::
AAVDVPETDPDPAQLTVSQSQSSSTVARR	12	3.97	0.03	2130	43.4	AE003760	TRUE	FALSE	2	3014.2	2.2	5of 56	0.8311	FALSE	FALSE	::::::::::::::::::::::::::
YMPKGGEKKIVTTKLQWNAKSKIGS	3	10.6	0.171	1415	38.83	AE003761	TRUE	FALSE	3	2810.3	-1.2	20of 96	2.0545	FALSE	FALSE	::Oxidation_M:::::::::::::::::::::
LLTTARPYLQVLSLFGLT	14	9.85	0.109	623	71	AE003761	TRUE	FALSE	3	2007.4	-1.8	17of 68	1.8635	FALSE	FALSE	::::::::::::::::::
DIYRQQGRIGISRTCAPTM	1	9.87	0.044	2272	37.83	AE003761	TRUE	FALSE	3	2240.5	-1.9	16of 72	1.3615	FALSE	FALSE	::::::::::::::Cys_CAM:::Oxidation_M:
RAGSPDMLILVGVNCSTF	2	6.1	0.021	502	52.63	AE003761	TRUE	FALSE	3	1938.2	-1.7	12of 68	1.3323	FALSE	FALSE	::::::::::::::Cys_CAM:::::
LCPYFDGQDAASCK	8	3.89	0.086	1845	29.8	AE003762	TRUE	FALSE	2	1632.7	0.4	7of 26	1.1904	FALSE	FALSE	::Cys_CAM::::::::::Cys_CAM::
LVNACLGIQATVQCTDA	10	3.1	0.066	2411	45.4	AE003762	TRUE	FALSE	2	1835	0.4	8of 32	1.1645	FALSE	FALSE	:::::Cys_CAM::::::::Cys_CAM::::
SPDGSLGGLTLGR	15	6.79	0.054	2226	25.3	AE003762	TRUE	FALSE	2	1230.4	0.3	7of 24	1.1099	FALSE	FALSE	::::::::::::::
RSALTPPVRSARSIAPVANIVAIARAKKK	11	12.89	0.051	1453	56	AE003762	TRUE	FALSE	3	3043.7	0.8	16of112	1.353	FALSE	FALSE	::::::::::::::::::::::::::::
NSIAEQQDKSGHKGNAPS	7	7.8	0.05	1596	6.2	AE003762	TRUE	FALSE	2	1869	-1.1	125	1.3153	FALSE	FALSE	::::::::::::::::
SSYWKKCDHSAMKFYFILDQESKQNMELSSKLR	6	9.39	0.044	1996	68.96	AE003762	TRUE	TRUE	3	4103.6	0.5	10of128	1.4205	FALSE	FALSE	::::::Cys_CAM::::::::::::::::::Oxidation_M::::::::
QVDDASNPPSVRSTPSPVPSNSSSSK	1	6.9	0.033	146	22.3	AE003762	TRUE	FALSE	2	2628.8	-2.7	10of 50	1.5974	FALSE	FALSE	::::::::::::::::::::::
PELRDTMERYYSCIQPFGTK	15	6.47	0.015	2918	44.63	AE003762	TRUE	FALSE	3	2492.8	-1.2	8of 76	1.0957	FALSE	FALSE	::::::::::::Cys_CAM::::::::
PQAYANQSLQNDDNRSQRRLLLK	1	10.39	0.007	62	37.2	AE003762	TRUE	FALSE	2	2730	2.4	7of 44	0.9305	FALSE	FALSE	::::::::::::::::::::
AVANYLAMR	3	9.85	0.047	1157	27.93	AE003763	TRUE	FALSE	2	1009.2	-2.9	6of 16	0.7085	FALSE	FALSE	::::::::::
SRLYNEP	15	6.89	0.007	376	14.3	AE003763	TRUE	FALSE	2	879	2.5	9of 12	1.1754	FALSE	FALSE	::::::::
SSSNNAPSNA	10	6.02	0.089	2696	3.4	AE003764	TRUE	FALSE	2	948.9	2.2	7of 18	1.2653	FALSE	FALSE	::::::::::
PIDTHIGIAHTR	9	8	0.277	1581	22.6	AE003765	TRUE	FALSE	2	1331.5	0.1	16of 22	2.412	FALSE	FALSE	::::::::::::
AMNLQSMGASQFIGPFLETVNK	10	6.95	0.091	640	59.46	AE003765	TRUE	FALSE	3	2400.8	2.4	21of 84	2.267	FALSE	FALSE	::Oxidation_M:::::::::::::::::
IENMNSVMDDNK	14	3.71	0.09	627	20.86	AE003765	TRUE	FALSE	2	1410.6	2.9	6of 22	0.6851	FALSE	FALSE	::::::::::::
LKVRSNLSRNDRLK	9	12.14	0.053	950	21.9	AE003765	TRUE	FALSE	3	1700	0.7	15of 52	1.6099	FALSE	FALSE	::::::::::::
SRSGRIVKGRGVFRFR	6	13.01	0.038	3088	27.5	AE003765	TRUE	FALSE	2	1879.2	-2.6	9of 30	1.038	FALSE	FALSE	::::::::::::::::
PDWLMNYQGMVGLAASQVWWTAE	13	3.01	0.014	1912	76.86	AE003765	TRUE	FALSE	2	2655	-2.8	10of 44	1.1281	FALSE	FALSE	::::::::::::::::::::
VNKRDAGATRPR	11	12.12	0.006	1017	7.1	AE003765	TRUE	FALSE	2	1341.5	-1.7	11of 22	1.3473	FALSE	FALSE	::::::::::::
GKALIHILANDGNHQLLERALNACKSPIDLEIE	5	5.29	0.092	2415	83.1	AE003766	TRUE	FALSE	3	3668.2	0.7	10of128	1.1545	FALSE	FALSE	:::::::::::::::::::::Cys_CAM:::::::::
YICMGTVISEMLVITTSTC	9	3.3	0.056	277	63.96	AE003766	TRUE	FALSE	3	2196.5	0.4	21of 72	1.3785	FALSE	FALSE	:::Cys_CAM:Oxidation_M::::::::::::::Cys_CAM:
DGQEAAGGLK	1	4.08	0.036	1317	10.7	AE003766	TRUE	FALSE	1	946	1.8	9of 18	1.3412	FALSE	FALSE	::::::::::
DEDDDSTNMDIYLPIR	10	3.27	0.023	1057	36.23	AE003766	TRUE	FALSE	3	1913	2.6	22of 60	2.2074	FALSE	FALSE	::::::::::::::::
ATSQDDKLIDVDADVGGLPK	6	3.7	0.011	1266	36.4	AE003766	TRUE	FALSE	2	2058.2	0.4	14of 38	2.3225	FALSE	FALSE	::::::::::::::::::::
KPQGGSTQVELILNTERR	7	10.09	0.153	1881	29.5	AE003767	TRUE	FALSE	2	2027.3	-1.3	384	1.3067	FALSE	FALSE	::::::::::::::::
GKEAPETATAIASTEPT	8	3.97	0.128	2244	22.6	AE003767	TRUE	FALSE	2	1674.8	2.2	9of 32	1.1345	FALSE	FALSE	::::::::::::::::
WPLEGGTLIATPSILGQSIH	8	5.13	0.045	2303	60.5	AE003767	TRUE	FALSE	2	2091.4	2.3	13of 38	2.2595	FALSE	FALSE	::::::::::::::::::
VFHASGLMRCRISPTGDKLVLCTSGGYI	2	9.05	0.034	1550	71.03	AE003767	TRUE	FALSE	3	3097.5	3	10of108	1.1261	FALSE	FALSE	::::::::::Cys_CAM::::::::::Cys_CAM::::::
QMQFQFTQQTTISTAALLR	4	11.05	0.021	2170	50.93	AE003767	TRUE	FALSE	2	2230.5	2.9	11of 36	1.7019	FALSE	FALSE	::Oxidation_M:::::::::::::::
FKLLIQSRK	14	11.64	0.01	1052	26.7	AE003767	TRUE	FALSE	1	1133.4	-0.1	12of 16	1.8404	FALSE	FALSE	::::::::::
DESPMQMFYKD	14	3.71	0.009	606	24.86	AE003767	TRUE	FALSE	2	1407.6	1.8	8of 20	1.4596	FALSE	FALSE	::::::Oxidation_M:::::
KSSSSSCVPSPRCAAAFFRR	5	11.23	0.004	3027	31.3	AE003767	TRUE	FALSE	3	2259.5	0.4	12of 76	1.329	FALSE	FALSE	::::::Cys_CAM::::::Cys_CAM::::::::
GVMLLVVRSFSPSDVGTY	2	6.7	0.002	1229	55.53	AE003767	TRUE	FALSE	2	1944.3	1.8	5of 34	0.7147	FALSE	FALSE	:::Oxidation_M:::::::::::::::
MSMTHVPGGGQPMGAPLLRTSSR	15	12.41	0	1981	42.29	AE003767	TRUE	FALSE	3	2401.8	3	13of 88	1.173	FALSE	FALSE	:Oxidation_M::::::::::Oxidation_M:::::::::
TGCDTPQVCVETCPRETFVWDTMK	11	4.07	0.198	1771	51.93	AE003768	TRUE	FALSE	3	2919.1	1.5	14of 92	1.8113	FALSE	FALSE	:::Cys_CAM::::::Cys_CAM:::Cys_CAM:::::::::::
VERTIDSLNEVEKL	9	4.17	0.153	1508	34.2	AE003768	TRUE	FALSE	2	1645.9	2.9	7of 26	1.0061	FALSE	FALSE	::::::::::::::
ERELLPWKSAFDNLQ	12	4.45	0.129	454	44.1	AE003768	TRUE	FALSE	2	1847.1	1.5	8of 28	0.9153	FALSE	FALSE	::::::::::::::
YFMDNVDFIYKFYHPLTKDMS	9	5.2	0.107	2659	65.46	AE003768	TRUE	FALSE	3	2692.1	0	23of 80	1.6993	FALSE	FALSE	:::Oxidation_M:::::::::::::::::
GKLSISTTCQGVNCCAMR	10	8.58	0.084	1246	32.93	AE003768	TRUE	FALSE	2	2044.2	1	5of 34	0.8166	FALSE	FALSE	::::::::Cys_CAM::::Cys_CAM:Cys_CAM::::
GDLNKLLVPTDSFNRK	8	9.89	0.066	24	34	AE003768	TRUE	FALSE	2	1818.1	-0.9	7of 30	1.0852	FALSE	FALSE	::::::::::::::::
AAKTFYMSAGAVNVPIVFR	11	10.4	0.058	2716	55.53	AE003768	TRUE	FALSE	2	2043.4	-2.6	5of 36	0.8032	FALSE	FALSE	::::::::::::::::::
FDNLQFVSGILR	9	6.79	0.056	365	43.4	AE003768	TRUE	FALSE	3	1409.6	-2.9	16of 44	1.997	FALSE	FALSE	::::::::::::
HEQLQIQGNQVRFVHTLLTE	11	6.03	0.036	181	47.6	AE003768	TRUE	FALSE	2	2391.7	2.9	7of 38	0.9616	FALSE	FALSE	::::::::::::::::::
IQIMPILPPGATVMGGTPGTGGH	15	7.85	0.027	1730	54.86	AE003768	TRUE	FALSE	3	2203.6	2.1	23of 88	2.4031	FALSE	FALSE	::::::::::::::::::::
RDALESS	14	4.08	0.018	1270	10.4	AE003768	TRUE	FALSE	1	777.8	-0.1	8of 12	1.06	FALSE	FALSE	::::::::
TIAALADAKNTSYIR	6	9.72	0.011	1446	33.3	AE003768	TRUE	FALSE	1	1608.8	0.1	4of 28	0.883	FALSE	FALSE	::::::::::::::
VPIGKAKVMR	5	11.64	0.006	3101	21.93	AE003768	TRUE	FALSE	2	1099.4	-0.1	10of 18	1.7104	FALSE	FALSE	::::::::::
AATLALLFASSLLLLSAA	3	6.02	0.018	2859	76.8	AE003769	TRUE	FALSE	2	1747.1	1.9	4of 34	0.62	FALSE	FALSE	::::::::::::::::::
MISFGVAHVFYISAFGWKPIK	8	10.18	0.08	2778	74.23	AE003770	TRUE	FALSE	3	2399.9	-1.8	15of 80	1.5318	FALSE	FALSE	::::::::::::::::::::
KTTRSQAMAKK	9	11.73	0.078	1090	3.63	AE003770	TRUE	TRUE	2	1250.5	2.4	7of 20	1.0488	FALSE	FALSE	::::::::::
RKAMNCCDLFRPTKTFNG	9	9.92	0.036	2526	33.63	AE003770	TRUE	FALSE	3	2217.5	-1.1	18of 68	1.4075	FALSE	FALSE	:::::Cys_CAM:Cys_CAM::::::::::
PLPSQFR	9	11.05	0.019	1036	19.4	AE003770	TRUE	FALSE	2	845	-2.4	6of 12	0.929	FALSE	FALSE	::::::::
SGKDPPTMGVASP	12	6.76	0.001	1041	16.43	AE003770	TRUE	FALSE	2	1244.4	1.4	9of 24	1.1113	FALSE	FALSE	::::::::::::
FIVAQTSASENSNVSCT	5	3.3	0.166	3043	32.4	AE003771	TRUE	FALSE	2	1815.9	-2.3	5of 32	0.7028	FALSE	FALSE	::::::::::::::Cys_CAM::
QRVLVSAFIRAMRDP	6	12.11	0.125	1262	43.33	AE003771	TRUE	FALSE	2	1760.1	2.6	6of 28	1.0613	FALSE	FALSE	::::::::::::::::
SKLYLSLKSERR	5	10.7	0.098	1680	23.9	AE003771	TRUE	FALSE	2	1480.8	-1.7	12of 22	1.589	FALSE	FALSE	::::::::::::
VDQSDVSAQKSDSTSATTTATSSL	1	3.6	0.093	2108	24.2	AE003771	TRUE	FALSE	2	2388.5	-0.5	6of 46	1.021	FALSE	FALSE	::::::::::::::::::::::
FGEDSWFVSSTPLAEVMGV	4	2.95	0.078	1650	59.63	AE003771	TRUE	FALSE	2	2059.3	-0.7	11of 36	1.2065	FALSE	FALSE	::::::::::::::::::

TECPKALAFPALHHDVQAARPQLDLK	1	7.32	0.075	2102	57.2	AE003771	TRUE	FALSE	3	2928.3	-0.2	12of100	1.3	FALSE		FALSE	:::Cys_CAM::::::::::::::::::::::
ENTNGGGQSSPSHSDATTATIA	13	4.07	0.061	1856	14.4	AE003771	TRUE	FALSE	3	2104.1	0.3	13of 84	1.3508	FALSE		FALSE	::::::::::::::::::::
VASTAVDVDLKVMVVNYFGSVALTK	15	6.81	0.044	1403	71.53	AE003771	TRUE	FALSE	3	2628.1	1.1	15of 96	1.4831	FALSE		FALSE	::::::::::::::::::::
VKDKNGIVLFRTAGGVHIMVR	6	11.47	0.041	2847	50.63	AE003771	TRUE	FALSE	3	2327.8	2.4	22of 80	1.7376	FALSE		FALSE	::::::::::::::::::Oxidation_M:::
RTCASLVLTIGFF	10	9.01	0.029	756	49.6	AE003771	TRUE	FALSE	2	1485.7	0.8	13of 24	1.6991	FALSE		FALSE	:::Cys_CAM:::::::::
KRAVKEEKEMSRRARARAKKIRNTEARAAK	10	12.06	0.025	2271	19.33	AE003771	TRUE	FALSE	3	3557.2	-2.2	16of116	1.3173	FALSE		FALSE	:::::::::Oxidation_M:::::::::::::::::::
KGENSQMIVDLNQ	11	4.08	0.022	941	23.63	AE003771	TRUE	FALSE	2	1492.6	2.4	12of 24	1.9285	FALSE		FALSE	::::::Oxidation_M::::::
RNLLGKTVTDRMLCAGYLKGGTDACQMDSGGPLSVR	10	9.03	0.018	2400	71.46	AE003771	TRUE	FALSE	3	3900.4	-0.7	25of140	1.9468	FALSE		FALSE	:::::::::::::Cys_CAM::::::::::Cys_CAM:::::::::::
PNIMKAKKKPLK	10	11.13	0.011	846	15.93	AE003771	TRUE	FALSE	2	1412.8	-0.1	11of 22	1.1041	FALSE		FALSE	::::Oxidation_M:::::::::
NPEFEASTLPYVFQVEEGKAQASVGV	9	3.8	0.001	2156	60.3	AE003771	TRUE	FALSE	2	2798.1	-2.9	11of 50	1.4787	FALSE		FALSE	::::::::::::::::::::::::
EMGVIMNPGTPDEQLVVMGMYSSYDEK	1	3.51	0	1614	66.22	AE003771	TRUE	FALSE	3	3054.4	1.8	8of104	0.8036	FALSE		FALSE	::::::Oxidation_M::::::::::::Oxidation_M:::::::::::
AEGINISVVYLRKEIAR	3	9.72	0.205	2871	46.7	AE003772	TRUE	FALSE	2	1932.3	1.9	7of 32	1.2601	FALSE		FALSE	::::::::::::::::::
ITVLVPQFLNALEDRRASL	3	7.05	0.148	2229	63.8	AE003772	TRUE	FALSE	2	2156.5	2.9	10of 36	1.4836	FALSE		FALSE	::::::::::::::::::
PTAQEGSAQPQDLAKVFTELR	4	4.45	0.019	2901	39.8	AE003772	TRUE	FALSE	3	2287.5	-2.4	9of 80	1.0173	FALSE		FALSE	::::::::::::::::::::
KESRRSSHPHGDGEYR	3	9.72	0.016	2085	-0.2	AE003772	TRUE	FALSE	2	1899	-1	7of 30	1.2508	FALSE		FALSE	::::::::::::::::::
EQPSTSKKA	10	9.89	0.002	680	1.1	AE003772	TRUE	FALSE	2	976.1	2.8	9of 16	1.3087	FALSE		FALSE	::::::::::
CYVHPK	13	8.88	0	899	9.9	AE003772	TRUE	FALSE	1	803.9	1.2	2of 10	0.4768	FALSE		FALSE	:Cys_CAM::::::
SSNSEQSEKVFFFK	14	7.07	0.073	1705	25.9	AE003773	TRUE	FALSE	2	1664.8	2.3	12of 26	2.8375	FALSE		FALSE	::::::::::::::
PKLRIETLATTTGLKYLMLTPD	9	9.63	0.132	2212	63.23	AE003774	TRUE	FALSE	2	2493	-2.9	6of 42	1.0348	FALSE		FALSE	::::::::::::::::::Oxidation_M:::::
HAFSSDFGSKTFLIVDKNSNQRYQMVPT	11	9.63	0.067	1345	56.33	AE003774	TRUE	FALSE	3	3219.6	2.9	24of108	2.8606	FALSE		FALSE	::::::::::::::::::::::::::
NVETNFISPPVIVKLVQALLKCHTIEEFR	6	7.17	0.011	1598	87.5	AE003774	TRUE	FALSE	3	3397	2.5	21of112	2.4727	FALSE		FALSE	:::::::::::::::::::::::Cys_CAM::::::::
HYYVDVKDISRQEYD	15	4.44	0.104	2927	27.6	AE003775	TRUE	FALSE	2	1931.1	-2.4	7of 28	0.9768	FALSE		FALSE	::::::::::::::::
AFARRDKLVIHMNKFKH	10	11.57	0.07	2173	34.13	AE003775	TRUE	FALSE	2	2128.5	2	7of 32	0.9513	FALSE		FALSE	::::::::::::Oxidation_M:::::::
RPSLPTEYDEIFQ	15	3.83	0.039	841	34.3	AE003775	TRUE	FALSE	2	1595.7	1.6	11of 24	1.9388	FALSE		FALSE	::::::::::::::
DAAVALPSFQ	13	3.1	0.037	1442	29.2	AE003775	TRUE	FALSE	1	1019.1	1.6	8of 18	1.5509	FALSE		FALSE	::::::::::
SENVELPLLTLD	10	2.95	0.035	1954	41.6	AE003775	TRUE	FALSE	2	1343.5	1.4	8of 22	1.1259	FALSE		FALSE	::::::::::::
DGRVRKGYK	10	10.7	0.183	2230	3.9	AE003777	TRUE	TRUE	2	1079.2	2.8	7of 16	1.1146	FALSE		FALSE	::::::::::
YLGEELALAP	15	3.13	0.045	1488	36.8	AE003777	TRUE	FALSE	2	1076.2	1.2	9of 18	1.2326	FALSE		FALSE	::::::::::
QRPLINNYRSIQDTNSR	1	11.05	0.041	2282	26.2	AE003777	TRUE	TRUE	3	2076.3	-0.7	9of 64	0.9582	FALSE		FALSE	::::::::::::::::
LTVGQLLGNIVTGEFFTYNG	9	3.3	0.015	1981	63.3	AE003777	TRUE	FALSE	2	2144.4	-0.3	11of 38	2.0884	FALSE		FALSE	::::::::::::::::::
VEFPAISVCSL	11	3.3	0.007	1278	40.9	AE003777	TRUE	FALSE	2	1222.4	-2.6	7of 20	0.9066	FALSE		FALSE	::::::::Cys_CAM:::
DLCLNSPYRCHS	6	7	0.175	1986	24.4	AE003778	TRUE	FALSE	3	1522.6	1.5	16of 44	1.6221	FALSE		FALSE	:::Cys_CAM::::::Cys_CAM:::
VVVVQAICALCTKYPRKHT	3	9.69	0.137	1620	45.5	AE003778	TRUE	FALSE	2	2244.6	1.8	11of 36	1.4873	FALSE		FALSE	:::::::Cys_CAM:::Cys_CAM:::::::::
LQETRTFNETPVNPRK	14	10.09	0.02	1824	24.7	AE003778	TRUE	FALSE	2	1931.2	-1.4	5of 30	0.8319	FALSE		FALSE	::::::::::::::::
TMAEVKQGMMK	5	9.89	0	2867	20.89	AE003778	TRUE	FALSE	2	1286.6	0.7	9of 20	1.2047	FALSE		FALSE	::Oxidation_M::::::Oxidation_M:::
LRDHVGTVWYERTFFVPRSWKTMQR	6	11.22	0.083	2990	65.03	AE003779	TRUE	FALSE	3	3197.7	0.2	8of 96	0.8947	FALSE		FALSE	::::::::::::::::::::::
FGGRLANGEYSGGVGR	7	9.85	0.065	3381	25.6	AE003779	TRUE	FALSE	3	1597.7	3	57	1.7346	FALSE		FALSE	::::::::::::::
MLWYVHGRR	6	11.14	0.059	1700	28.43	AE003779	TRUE	FALSE	1	1218.5	-1.6	5of 16	1.0184	FALSE		FALSE	::::::::::
IDFTSVSPQGTQDIRLSGH	10	5.1	0.056	870	35.9	AE003779	TRUE	FALSE	2	2059.2	-1	12of 36	1.8517	FALSE		FALSE	::::::::::::::::::
IVSLPSYSHAKKSLIVSGLGFLIISFFNTI	3	10.18	0.03	2230	104.3	AE003779	TRUE	FALSE	3	3253.9	-0.2	21of116	2.2428	FALSE		FALSE	::::::::::::::::::::::::::::
KRQKVRKSSAMDSVFNSPPR	4	12.15	0.023	1686	20.33	AE003779	TRUE	FALSE	3	2319.7	-2.3	20of 76	1.8679	FALSE		FALSE	::::::::::::::::::
FELFVASNEK	6	4.27	0.022	1347	30.6	AE003779	TRUE	FALSE	1	1184.3	-0.4	13of 18	1.7449	FALSE		FALSE	::::::::::
MKTIPIAISLVASQLSAISIMTIP	6	10.1	0.019	1483	84.96	AE003779	TRUE	FALSE	3	2516.1	-1.2	10of 92	0.9649	FALSE		FALSE	:Oxidation_M:::::::::::::::::::::
TCPVDLLSLE	12	3.01	0.011	989	35.6	AE003779	TRUE	FALSE	2	1147.3	2	9of 18	1.1222	FALSE		FALSE	::Cys_CAM:::::::::
TNSLDQMEITAKKVTR	11	9.89	0.004	2411	25.53	AE003779	TRUE	FALSE	2	1836.1	1.7	8of 30	1.0291	FALSE		FALSE	::::::::::::::::
LEHEVGLKFASRRLAR	9	11.23	0.014	822	37.2	AE003780	TRUE	FALSE	3	1883.2	-1.8	19of 60	2.2096	FALSE		FALSE	::::::::::::::::
NAAQNIALNSSVAAPR	14	11.05	0.361	532	29.7	AE003781	TRUE	TRUE	2	1597.8	0.2	20of 30	3.8917	FALSE		FALSE	::::::::::::::::
NAAQNIALNSSVAAPR	13	11.05	0.005	708	29.7	AE003781	TRUE	TRUE	2	1597.8	0.1	13of 30	1.7785	FALSE		FALSE	::::::::::::::::
FRHRGTEFRIDPSDAKYVESMHTSANFGF	13	7.9	0.165	312	54.93	AE003782	TRUE	FALSE	3	3404.7	2.8	14of112	1.4021	FALSE		FALSE	::::::::::::::::::::::::::::
SPVDFDLTPVIVEMNNHTRYSIDLKEMI	11	4.2	0.078	1168	78.66	AE003782	TRUE	FALSE	3	3278.8	-0.8	20of108	2.2454	FALSE		FALSE	::::::::::::::::::::::::::
TFDQDPTNLRTSYTQSLEQC	5	3.71	0.065	1744	35.7	AE003782	TRUE	FALSE	3	2405.5	0.9	15of 76	1.6233	FALSE		FALSE	:::::::::::::::::::Cys_CAM:
IIHCPALAAQKVKLISRGAMEIHTTK	3	10.32	0.018	1643	59.73	AE003782	TRUE	FALSE	3	2904.5	-2.8	21of100	2.4687	FALSE		FALSE	::::Cys_CAM::::::::::::::Oxidation_M:::::::
RFLHTSSVMTKSSS	3	11.49	0.016	1389	22.13	AE003782	TRUE	FALSE	2	1568.8	-0.4	10of 26	1.1582	FALSE		FALSE	::::::::::::::
MLREMNSRNGLYS	1	9.85	0.014	2297	29.86	AE003782	TRUE	FALSE	2	1587.8	1.3	8of 24	1.157	FALSE		FALSE	:::::Oxidation_M:::::::::
LRETPSILDGISFETERRYR	4	7.15	0.013	2689	47.3	AE003782	TRUE	FALSE	2	2439.7	0.9	10of 38	1.1726	FALSE		FALSE	::::::::::::::::::
RMAKARMAYRIVRR	10	12.59	0.198	420	28.86	AE003783	TRUE	FALSE	2	1795.2	1.8	8of 26	1.23	FALSE		FALSE	::::::Oxidation_M:::::::::
QPKIEGQKTEQQ	10	7.07	0.104	1301	7.8	AE003783	TRUE	FALSE	2	1414.6	1.7	9of 22	1.0161	FALSE		FALSE	::::::::::
AKRRQNCTADRK	7	11.38	0.114	3316	0.8	AE003784	TRUE	TRUE	2	1504.7	-2.3	86	1.0767	FALSE		FALSE	::::::Cys_CAM:::::::
RTKAKMPVAERMGLM	1	11.47	0.099	1530	31.79	AE003784	TRUE	FALSE	2	1752.2	-2.6	5of 28	0.852	FALSE		FALSE	::::::::::::Oxidation_M:::Oxidation_M:
STSLTETALAKTAATVLPLYAVVSKNRELESITK	3	9.56	0.064	2021	78	AE003784	TRUE	TRUE	3	3608.2	0.1	15of132	1.442	FALSE		FALSE	::::::::::::::::::::::::::::::::
ISSLAASMQASHQR	11	11.05	0.051	418	23.53	AE003784	TRUE	TRUE	3	1503.7	-0.5	16of 52	1.5751	FALSE		FALSE	:::::::Oxidation_M:::::::
GKASSVRVNGSAPPPPNSAAALKREAQRKLLLEMKR	11	12	0.233	234	56.93	AE003785	TRUE	FALSE	3	3846.5	1.9	17of140	1.5018	FALSE		FALSE	::::::::::::::::::::::::::::::::Oxidation_M:::
LSMVFLGARGSTSGEMNEILKLDDMVTFNPHLIFK	8	5.39	0.094	2333	104.69	AE003785	TRUE	FALSE	3	3929.6	1.9	20of136	1.9094	FALSE		FALSE	::::::::::::::::Oxidation_M:::::::::::::::::::
MFFQVHPTVR	4	11.05	0.091	1461	31.63	AE003785	TRUE	FALSE	2	1262.5	1.3	10of 18	1.7784	FALSE		FALSE	::::::::::
QPEYQYPPSGEREEDK	13	4.01	0.014	1479	16.5	AE003785	TRUE	FALSE	2	1953	1.5	8of 30	1.011	FALSE		FALSE	::::::::::::::::
AAYHIPPMLASSTTVTTSSTK	8	9.72	0.008	2580	38.53	AE003785	TRUE	FALSE	2	2181.5	-0.9	12of 40	1.5046	FALSE		FALSE	::::::::Oxidation_M:::::::::::::
PLTSHYGGSTLATMLSEEDEDITEFTESS	10	3.38	0.003	1554	59.23	AE003785	TRUE	FALSE	3	3149.3	-2.8	8of112	0.9277	FALSE		FALSE	::::::::::::::::::::::::::
TDSRADGNEVLQAATALVSSPRYNIK	8	7	0.002	2567	45.5	AE003785	TRUE	FALSE	3	2778.1	2.1	23of100	2.5557	FALSE		FALSE	::::::::::::::::::::::::
RAIKHVFNVE	11	10.09	0	2624	23.2	AE003785	TRUE	FALSE	2	1213.4	2.2	4of 18	0.6876	FALSE		FALSE	::::::::::
TTYFTGSLNITHLPKSNEIFK	1	9.63	0.085	1062	49.1	AE003786	TRUE	FALSE	3	2412.7	1.6	10of 80	1.1932	FALSE		FALSE	::::::::::::::::::
LGPVNANLELETSHK	10	5.3	0.131	2676	30.3	AE003787	TRUE	FALSE	2	1622.8	0.1	6of 28	1.2416	FALSE		FALSE	::::::::::::::
PCSINWLGSAWKWIAG	10	8.97	0.075	2191	54.4	AE003787	TRUE	FALSE	2	1847.1	-3	7of 30	0.9287	FALSE		FALSE	::Cys_CAM:::::::::::::
GMLSRWKMWSPQYKILRNHLINFKSVSTYK	12	11.05	0.016	1982	78.56	AE003787	TRUE	FALSE	3	3730.4	0.5	20of116	1.7798	FALSE		FALSE	:::::::Oxidation_M:::::::::::::::::::::
CRSHNGS	8	9.02	0	2849	-1.3	AE003787	TRUE	FALSE	1	817.8	-2	3of 12	0.2934	FALSE		FALSE	:Cys_CAM:::::::
NIIGQFGVGFYSSFIVANKVEVFTR	15	9.72	0.237	1714	77.9	AE003789	TRUE	FALSE	3	2794.2	-0.7	11of 96	1.6391	FALSE		FALSE	::::::::::::::::::::::
HCININHPTMA	12	7.32	0.059	1415	22.13	AE003789	TRUE	FALSE	2	1324.5	2.2	10of 20	1.1243	FALSE		FALSE	::Cys_CAM::::::::Oxidation_M::
IELITRQMLETMVEETQYLAVYF	11	3.8	0.131	1188	84.86	AE003790	TRUE	FALSE	3	2822.3	-2.7	20of 88	1.8536	FALSE		FALSE	::::::::::::::::::::
RVIQFMQKWVMAVRHAAFEEPSV	10	10.09	0.121	1910	68.06	AE003790	TRUE	FALSE	3	2777.3	-0.2	12of 88	1.3707	FALSE		FALSE	::::::::::Oxidation_M:::::::::::::
SELAIYGTSAIMLAVAYAK	15	6.81	0.112	2862	59.53	AE003790	TRUE	FALSE	3	1973.3	0.5	7of 72	0.9954	FALSE		FALSE	::::::::::::::::::::
ASRIKHSLDALMQRIK	3	11.47	0.105	2145	32.83	AE003790	TRUE	FALSE	2	1884.3	-2.1	11of 30	1.3374	FALSE		FALSE	::::::::::Oxidation_M:::::
CDGHQDAGWGCGYR	9	5.1	0.087	1350	17.4	AE003790	TRUE	FALSE	2	1639.6	1.2	8of 26	1.1609	FALSE		FALSE	:Cys_CAM::::::::Cys_CAM::::
NAVIQAGLVQTILPMLEIHQPPVVFK	9	7.82	0.068	2440	86.83	AE003790	TRUE	TRUE	3	2857.5	2.6	22of100	2.3924	FALSE		FALSE	::::::::::::::::::::::::
RVGLVLWHPSALNV	10	11.05	0.057	886	48.4	AE003790	TRUE	FALSE	3	1561.9	-2.3	15of 52	1.5063	FALSE		FALSE	::::::::::::::

EGRVIAVLFYDNN	9	4.08	0.021	1106	39.4	AE003790	TRUE	FALSE	2	1510.7	1.1	11of 24	1.5028	FALSE	FALSE	::::::::::::::
DNPFINPWANGGGGDV	7	2.93	0.191	1955	33.1	AE003791	TRUE	FALSE	2	1630.7	0.9	205	1.4663	FALSE	FALSE	::::::::::::::::
VILIASFTVGLEAR	15	6.98	0.091	399	53.8	AE003791	TRUE	FALSE	3	1489.8	1.5	16of 52	1.547	FALSE	FALSE	::::::::::::::
FNAGGARGNAGGRGGADRFGGAAGGAVAGAGMGQR	10	12.41	0.015	2122	38.53	AE003791	TRUE	FALSE	3	3078.3	-2.7	24of136	1.695	FALSE	FALSE	::::::::::::::::::::::::::::::::
LRTPVCAVGDEAALQLAR	2	6.36	0.01	2416	47.4	AE003791	TRUE	FALSE	2	1941.2	2.1	7of 34	1.1446	FALSE	FALSE	::::::Cys_CAM::::::::::::
AYMHDEDYVINAPPPSYEEVMR	14	3.92	0.009	1547	52.16	AE003791	TRUE	FALSE	3	2643.9	1.7	19of 84	1.8387	FALSE	FALSE	:::::::::::::::::::Oxidation_M:::
IRSEPDNDPEAVGEDK	12	3.76	0.008	2131	18.6	AE003791	TRUE	FALSE	2	1771.8	-2.3	5of 30	0.7553	FALSE	FALSE	::::::::::::::::
FSPMEQTGQRYI	4	6.89	0	2825	28.23	AE003791	TRUE	FALSE	2	1473.6	-2.2	4of 22	0.2747	FALSE	FALSE	::::Oxidation_M:::::::::
DKRRQGSQRRPAIA	7	12.41	0	1507	8.7	AE003791	TRUE	FALSE	2	1639.9	1.3	10	0.8054	FALSE	FALSE	::::::::::::::::
VQHQQFSSGMSRS	9	11.05	0.21	591	14.93	AE003792	TRUE	FALSE	2	1479.6	0.9	11of 24	1.7225	FALSE	FALSE	::::::::::::::
VRAISVDEETRSGRY	15	7.08	0.131	2926	24.5	AE003792	TRUE	FALSE	2	1738.9	2.1	6of 28	0.8022	FALSE	FALSE	::::::::::::::::
SVFFVHHNQQNAMQLR	6	11.05	0.07	2280	35.63	AE003792	TRUE	FALSE	2	1973.2	1.7	8of 30	1.1912	FALSE	FALSE	::::::::::::Oxidation_M::::
YKCNIKCQLERDSTKWLNAQGRMDLDLMN	2	8.27	0.057	1625	63.96	AE003792	TRUE	FALSE	3	3619	0.7	9of112	1.0221	FALSE	FALSE	:::Cys_CAM::::Cys_CAM::::::::::::::::Oxidation_M::::::::
SPPPRRRSPPMAMHSGMDRRGGPR	9	12.71	0.05	2048	23.89	AE003792	TRUE	FALSE	3	2688.1	2.5	16of 92	1.3373	FALSE	FALSE	::::::::::::::::::::::::
VLQNASRARSGIYTCVGSNR	9	11.05	0.02	937	33.2	AE003792	TRUE	FALSE	3	2210.4	-1.9	19of 76	1.8556	FALSE	FALSE	::::::::::::::::Cys_CAM::::::
VEHGIDPRIILFANDP	15	4.3	0.011	260	47.4	AE003792	TRUE	FALSE	3	1807.1	1.4	16of 60	1.4218	FALSE	FALSE	::::::::::::::::
MRVLNLVNVTTMHCPIMHV	3	9.02	0.028	1313	59.99	AE003793	TRUE	FALSE	3	2298.8	2	21of 72	2.4386	FALSE	FALSE	:Oxidation_M::::::::::::Cys_CAM:::Oxidation_M:::
APRYDKDVKFIQVD	5	6.89	0.006	1776	29.8	AE003793	TRUE	FALSE	1	1694.9	1	8of 26	1.0926	FALSE	FALSE	::::::::::::::
LSKMEPAQNLTLLR	11	10.09	0.083	1658	40.13	AE003794	TRUE	FALSE	3	1614.9	-1.3	11of 52	1.1922	FALSE	FALSE	::::::::::::::
HGSKSMSFSSQGLTTPALRWIGLHPSEIPALGTGAVAL	2	10.09	0.137	1902	90.53	AE003795	TRUE	FALSE	3	3893.5	-0.2	11of148	1.2627	FALSE	FALSE	::::::Oxidation_M:::::::::::::::::::::::::::::::
SWLRHFESTGSSQGGCGGYARSSLPQI	15	8.9	0.093	2959	47.8	AE003795	TRUE	FALSE	3	2927.1	2.4	9of104	1.1063	FALSE	FALSE	::::::::::::::::Cys_CAM::::::::::::
DTKNNDTVLAMRATFK	5	9.89	0.057	1643	26.93	AE003795	TRUE	FALSE	2	1826.1	2.6	10of 30	1.2587	FALSE	FALSE	::::::::::::::::
PAGTGPTPAARSSSSTTSTSGSAS	9	11.05	0.051	1654	14.2	AE003795	TRUE	FALSE	3	2124.2	-1.8	20of 92	1.7219	FALSE	FALSE	::::::::::::::::::::::::
QEGLMYFIAFGVKNKQRELGKNAVKMK	13	10.47	0.045	1206	58.66	AE003795	TRUE	FALSE	3	3145.8	-0.2	11of104	0.9467	FALSE	FALSE	::::::Oxidation_M:::::::::::::::::::::
SISTAQRLFKKQFSIYQTPPTNVIK	1	10.9	0.013	138	55.7	AE003795	TRUE	FALSE	3	2897.4	-0.1	11of 96	1.2484	FALSE	FALSE	::::::::::::::::::::::::
GSDGRNSIGAYSK	9	9.72	0.003	1121	9.6	AE003795	TRUE	TRUE	3	1312.4	-0.2	12of 48	1.3393	FALSE	FALSE	::::::::::::::
MTLDNGADAPKAVVLR	13	6.9	0.125	2409	37.23	AE003796	TRUE	FALSE	3	1672	-2.9	15of 60	1.5094	FALSE	FALSE	::::::::::::::
INNILRSPTKAPNGVRQRSVF	15	12.71	0.088	1240	41.3	AE003796	TRUE	FALSE	3	2368.7	1.8	20of 80	1.9122	FALSE	FALSE	::::::::::::::::::
TNVQRLPYLHVRR	10	12.11	0.079	1726	28.8	AE003796	TRUE	TRUE	2	1652.9	1.3	12of 24	2.4352	FALSE	FALSE	::::::::::::
FPSPMPPPPFAMDR	15	6.79	0.071	460	40.66	AE003796	TRUE	FALSE	3	1619.9	-1.7	16of 52	1.8784	FALSE	FALSE	:::::Oxidation_M::::::Oxidation_M:::
QTHPQASLKNVAQFKDVVSIK	8	10.32	0.065	2400	36	AE003796	TRUE	FALSE	2	2339.7	2.3	10of 40	1.273	FALSE	FALSE	::::::::::::::::::
KFEKGEVTWKMG	15	9.76	0.05	2875	23.53	AE003796	TRUE	FALSE	2	1440.7	-1.7	6of 22	0.874	FALSE	FALSE	::::::::::::
NKMEAGQRNSPNPSSSKRQK	2	11.57	0.028	2252	2.33	AE003796	TRUE	FALSE	3	2261.5	2.1	12of 76	1.1943	FALSE	FALSE	::::Oxidation_M:::::::::::::::
AAAQKQFKLQRYRILMTILTVVNILCLLCR	5	10.69	0.026	2709	104.73	AE003796	TRUE	FALSE	3	3636.4	-0.2	17of116	1.7256	FALSE	FALSE	:::::::::::::::::::::::Cys_CAM:::Cys_CAM::
HEGFGGMGGGR	5	7.85	0.023	3061	10.83	AE003796	TRUE	FALSE	2	1062.1	-2.7	8of 20	0.814	FALSE	FALSE	::::::::::
AATGHKPNQPMHVSTDQMQR	14	10.09	0.015	2797	17.56	AE003796	TRUE	FALSE	3	2267.5	0.7	12of 76	1.3547	FALSE	FALSE	:::::::::Oxidation_M::::::Oxidation_M:::
ASDRVMMYIDPLDNVKVTDWSFDHTPL	1	4.04	0.014	1884	73.46	AE003796	TRUE	FALSE	3	3199.6	-0.9	16of104	1.403	FALSE	FALSE	::::::Oxidation_M:Oxidation_M:::::::::::::::::
LSKLNTTGLVSIAA	1	10.1	0.014	2280	38.6	AE003796	TRUE	FALSE	2	1388.6	3	5of 26	0.5982	FALSE	FALSE	::::::::::::::
GGDMAGREALHAMALAAAAHAAANRLSSS	6	8	0.003	2107	51.46	AE003796	TRUE	FALSE	3	2812.1	0	23of112	1.3385	FALSE	FALSE	::::Oxidation_M::::::::Oxidation_M:::::::::::::::
IVLYIWMMSSSTGMFR	11	9.85	0.003	2652	65.09	AE003796	TRUE	FALSE	3	1923.4	2.5	11of 60	1.1259	FALSE	FALSE	::::::::::::::::
VTKTAP	8	10.1	0	2731	8.1	AE003796	TRUE	FALSE	1	616.7	-1.6	5of 10	0.8856	FALSE	FALSE	::::::
KKGIKDKALTKKAKKEAQKMEPK	1	10.7	0.074	2028	10.83	AE003797	TRUE	TRUE	2	2628.2	2.2	4of 44	0.8087	FALSE	FALSE	::::::::::::::::::::
ATHSFSVTMASDGSELPGISIR	11	5.22	0.034	1298	45.93	AE003797	TRUE	FALSE	3	2280.5	2.1	20of 84	1.961	FALSE	FALSE	::::::::Oxidation_M:::::::::::::
RYLAMKERR	13	11.29	0.033	572	17.33	AE003797	TRUE	FALSE	2	1239.5	-2.1	6of 16	1.0671	FALSE	FALSE	:::::Oxidation_M:::::
APVHQQATTSGNNNYSSLESN	5	5.13	0.032	2524	20.4	AE003797	TRUE	FALSE	2	2220.3	-2.1	10of 40	1.2932	FALSE	FALSE	::::::::::::::::::
EKKDSKFNSRNGGRLPVVMLPSA	9	10.82	0.029	1877	37.43	AE003797	TRUE	FALSE	3	2547.9	-2	17of 88	1.7566	FALSE	FALSE	::::::::::::::::Oxidation_M::::::
KRPRMGIGH	12	12.42	0.01	1096	9.13	AE003797	TRUE	FALSE	1	1068.3	-2.1	9of 16	1.1992	FALSE	FALSE	:::::Oxidation_M:::::
DQGLFMGPSTSGAAANRGKNWKLVMAQTRRL	8	12.14	0.002	3241	60.26	AE003797	TRUE	FALSE	2	3363.9	0.2	8of 60	1.1434	FALSE	FALSE	::::::::::::::::::::::::::::::
VFTELTKPLPK	11	9.89	0.182	664	31.4	AE003798	TRUE	FALSE	1	1273.6	0.5	8of 20	1.1259	FALSE	FALSE	::::::::::::
YTNLVHSTYHKKGGHF	2	9.94	0.147	454	19.7	AE003798	TRUE	FALSE	2	1890.1	-2	8of 30	1.4311	FALSE	FALSE	::::::::::::::::
DYWRDNYLTKWDER	6	4.46	0.095	2554	33.1	AE003798	TRUE	FALSE	2	1961.1	0.1	11of 26	1.4976	FALSE	FALSE	::::::::::::::
DLMEHVVYATSTSTKVTSETEI	7	4.16	0.078	1431	44.23	AE003798	TRUE	FALSE	3	2458.7	1.4	219	1.8292	FALSE	FALSE	:::Oxidation_M:::::::::::::::::
TTTTETPITSTTPAEDR	14	3.83	0.058	647	19.8	AE003798	TRUE	FALSE	2	1822.9	0	12of 32	1.9754	FALSE	FALSE	::::::::::::::::
LHFESGVVFANGIR	5	7.85	0.326	1610	40.9	AE003799	TRUE	TRUE	1	1546.8	0.2	11of 26	1.6659	FALSE	FALSE	::::::::::::::
SGHRIIASNSHLYSLGGYNPRSAMSASRHGRCLL	8	11.1	0.173	3259	60.23	AE003799	TRUE	FALSE	3	3728.2	-0.2	23of132	2.2822	FALSE	FALSE	:::::::::::::::::::::::::::::::::Cys_CAM:::
YRVVMLGDAGVGKTALVN	9	9.72	0.119	2128	47.13	AE003799	TRUE	FALSE	2	1864.2	-1.2	6of 34	0.9727	FALSE	FALSE	::::::::::::::::
EIVAMEITERHPAGLEQVRQVQDYMEKIVRPYLAK	4	5.55	0.069	2633	86.46	AE003799	TRUE	FALSE	3	4174.8	0.7	8of136	0.939	FALSE	FALSE	:::::Oxidation_M::::::::::::::::::Oxidation_M:::::::::::
GANVRQFMSKHDVHVELPPSELKSD	13	6.04	0.047	311	43.03	AE003799	TRUE	FALSE	3	2822.2	2.6	15of 96	1.1645	FALSE	FALSE	::::::::::::::::::::::::
TNPADVARVEGKTFISTDSKEQTVPVT	8	4.56	0.026	2149	43.1	AE003799	TRUE	FALSE	3	2892.2	1	8of104	0.8501	FALSE	FALSE	::::::::::::::::::::::::
VDTMNNEPLSLAK	6	4.08	0.018	1502	29.13	AE003799	TRUE	FALSE	1	1432.6	0.6	10of 24	1.5444	FALSE	FALSE	::::::::::::
IVLTAR	5	11.05	0	2673	22.5	AE003799	TRUE	FALSE	1	672.8	1.1	4of 10	0.912	FALSE	FALSE	::::::
NNPFLMATPKKASQGRSISVGTGVGVNGIINS	10	11.64	0.09	1789	59.13	AE003800	TRUE	FALSE	3	3216.7	0.3	25of124	2.3068	FALSE	FALSE	::::::::::::::::::::::::::::
GMHSST	12	7.85	0.064	1987	3.43	AE003800	TRUE	FALSE	1	619.7	-1.6	5of 10	1.1255	FALSE	FALSE	::::::
KASQGRSISVGTGVGVNGIINSIFKLKGTSKEQ	12	10.99	0.06	1572	52.7	AE003800	TRUE	FALSE	3	3362.9	-0.2	12of128	1.2112	FALSE	FALSE	::::::::::::::::::::::::::::
PPKSQMDKSGGYRY	8	9.94	0.046	1936	13.13	AE003800	TRUE	FALSE	2	1630.8	1	6of 26	0.8413	FALSE	FALSE	::::::Oxidation_M:::::::::
EVDDGFRYLRLKNAEYDLRSTARDYMQR	3	7.05	0.04	2517	57.93	AE003800	TRUE	FALSE	3	3482.9	-0.8	12of108	1.3156	FALSE	FALSE	::::::::::::::::::::::::
KFALAIVLVDLLDFPCSIWPGMQNILGAKR	6	8.93	0.03	2198	110.23	AE003800	TRUE	FALSE	3	3404.1	-2.3	22of116	2.3868	FALSE	FALSE	::::::::::::::Cys_CAM::::::Oxidation_M:::::::::
RVRLADNTPITILGESLLDLLTRELNDTSVVLGTR	8	4.65	0.029	2037	100	AE003800	TRUE	FALSE	3	3866.5	-1.4	25of136	2.4473	FALSE	FALSE	::::::::::::::::::::::::::::
RPVFLVGNKVDLLPRDSNIY	6	9.72	0.026	1388	58.8	AE003800	TRUE	FALSE	2	2316.7	2.7	11of 38	1.6711	FALSE	FALSE	::::::::::::::::
TMTAEGTTMSEHRLSVR	9	7.86	0.017	2149	26.86	AE003800	TRUE	FALSE	2	1924.2	-2	10of 32	1.2506	FALSE	FALSE	::Oxidation_M:::::::::::::
QLDNAMLSMKMVEKERNKDEQQIR	13	7.18	0.009	343	41.99	AE003800	TRUE	FALSE	2	2968.4	2.4	4of 46	0.8412	FALSE	FALSE	::::::Oxidation_M:::Oxidation_M:::::::::::::::
TDGPTQTGKPERRKRLNPPKDKLIDMDDADNPITK	2	9.6	0.008	1924	39.33	AE003800	TRUE	FALSE	3	3979.5	-2.3	22of136	2.3487	FALSE	FALSE	:::::::::::::::::::::::::Oxidation_M:::::::::
GIKNLRSSSRFSMDSQDVSNPK	8	10.58	0.048	2204	28.53	AE003801	TRUE	FALSE	3	2454.7	2.4	17of 84	1.6283	FALSE	FALSE	::::::::::::::::::::::
ISSAVSEAK	15	6.95	0	461	14.8	AE003801	TRUE	FALSE	2	892	2.5	10of 16	1.5331	FALSE	FALSE	::::::::::
VKWDVNHVIHQHSNYSD	5	6.31	0.218	2127	26.1	AE003802	TRUE	FALSE	2	2079.2	1.4	9of 32	1.8885	FALSE	FALSE	::::::::::::::::::
TSFPESDKIMENFR	11	4.45	0.114	2681	30.43	AE003802	TRUE	FALSE	3	1701.9	1.1	8of 52	1.0978	FALSE	FALSE	::::::::::::::
ELVLQYFERSGTNNER	10	4.56	0.06	1826	34.9	AE003802	TRUE	FALSE	2	1956.1	2.8	9of 30	1.2331	FALSE	FALSE	::::::::::::::::::
VTMVRRASSVPHLNSSGGSSADSAGTSGSRR	13	12.41	0.055	1892	30.33	AE003802	TRUE	FALSE	3	3076.3	0.3	23of120	1.6383	FALSE	FALSE	::::::::::::::::::::::::::::
CMRTYRGHLNEFYCSNSNFSTT	7	8.28	0.037	1664	41.03	AE003802	TRUE	FALSE	3	2746.9	1.1	20	2.8737	FALSE	FALSE	:Cys_CAM::::::::::Cys_CAM:::::::::
DYYYIGA	9	3.1	0.035	1312	22.9	AE003802	TRUE	FALSE	1	864.9	0	6of 12	0.9635	FALSE	FALSE	::::::::
GDGPKRDLLEEIR	9	4.56	0.035	2789	24.5	AE003802	TRUE	FALSE	2	1498.7	0.3	5of 24	0.8053	FALSE	FALSE	::::::::::::::
PKEGDIGLDLSGSDSMDSEVESMRRCPRR	14	4.45	0.034	1548	44.26	AE003802	TRUE	FALSE	3	3281.6	2	18of112	1.7295	FALSE	FALSE	:::::::::::::::::::::::::::Cys_CAM::::
LIFLMLGIVGLNVSSIFGAGLDTLMAH	3	4.94	0.033	2140	108.96	AE003802	TRUE	FALSE	2	2804.4	-1.8	12of 52	1.8477	FALSE	FALSE	::::::::::::::::::::::::::

KSHSLDASHVLSPSSNMI	2	7.97	0.029	2168	30.23	AE003802	TRUE	FALSE	3	1911.1	2	11of 68	1.2557	FALSE	FALSE	::::::::::::::::::
PELDGSELAELVKLYMVENESLR	6	3.89	0.028	2035	66.33	AE003802	TRUE	FALSE	3	2636	-2.1	13of 88	1.3437	FALSE	FALSE	::::::::::::::::::::::
ELGENNASLANLPTGEAAKER	4	4.26	0.027	2555	34.2	AE003802	TRUE	FALSE	2	2185.4	-2.6	13of 40	1.4206	FALSE	FALSE	::::::::::::::::::::
DLLEEIREKTNMQE	7	4.01	0.017	1289	31.03	AE003802	TRUE	FALSE	2	1764.9	2.2	324	0.9765	FALSE	FALSE	::::::::::Oxidation_M:::
RPTMLALIPPYMVGWVLMLFAKNVTMLYFGRF	2	10.56	0.016	2205	134.02	AE003802	TRUE	FALSE	3	3826.7	2.5	22of124	2.2476	FALSE	FALSE	::::::::::Oxidation_M::::::Oxidation_M::::::::Oxidation_M::::::
ATHLLVEGFSNVK	14	7.82	0.009	1431	32.8	AE003802	TRUE	FALSE	2	1415.6	1.4	12of 24	1.5526	FALSE	FALSE	::::::::::::
HYYDESLLYRPSNTLH	12	6.03	0.125	2850	35.9	AE003803	TRUE	FALSE	2	2009.2	1.6	4of 30	0.7957	FALSE	FALSE	::::::::::::::::
KTPTPPTLPPGVTKTCHIVK	8	10.33	0.12	1669	32.5	AE003803	TRUE	FALSE	2	2173.6	2.3	8of 38	1.1471	FALSE	FALSE	::::::::::::::Cys_CAM:::::
IAESLFDNAMLGAGQLASTSVGMC	10	3.01	0.049	2664	66.56	AE003803	TRUE	FALSE	3	2444.7	-2.9	19of 92	1.7078	FALSE	FALSE	::::::::::::::::::::::Cys_CAM:
GNSVYIYLMVCVGGAVLLEVSSAKQRPESCIEAIMR	1	6.37	0.013	1853	102.76	AE003803	TRUE	TRUE	3	4034.6	2.6	8of140	0.803	FALSE	FALSE	::::::::Oxidation_M::Cys_CAM::::::::::::::::::Cys_CAM::::Oxidation_M::
MEKALKFAQSKAAGFSKVD	12	10.16	0.012	2088	35.13	AE003803	TRUE	FALSE	3	2057.4	2	11of 72	1.1796	FALSE	FALSE	::::::::::::::::::
SAKKSGMEMGMKSKKPKK	1	10.92	0.003	854	5.99	AE003803	TRUE	TRUE	2	1982.5	2.9	8of 34	1.0602	FALSE	FALSE	::::::::::::::::::
TRGDNGYKLIVADGPNGYVPGKTYNLL	3	9.36	0.239	2232	55.2	AE003804	TRUE	FALSE	3	2897.3	-1.5	14of104	1.7153	FALSE	FALSE	::::::::::::::::::::::::::
AHEDAQSAGHNSSSGDSSSLMNS	13	4.29	0.067	1753	13.73	AE003804	TRUE	FALSE	3	2277.3	1.6	20of 88	1.8023	FALSE	FALSE	::::::::::::::::::::::
HQQSGSHEELPTYPR	10	6.03	0.06	2389	14	AE003804	TRUE	FALSE	2	1766.9	-0.6	6of 28	0.7261	FALSE	FALSE	::::::::::::::::
TTAVGKPAQVTQKTTPTSNFR	3	11.64	0.052	2121	23.9	AE003804	TRUE	FALSE	2	2234.5	-1.9	12of 40	1.5651	FALSE	FALSE	::::::::::::::::::::
TPTATSTPTATPSIAMTTSLTTAVGK	11	10.1	0.036	1709	43.13	AE003804	TRUE	FALSE	2	2524.8	0.9	10of 50	1.1205	FALSE	FALSE	::::::::::::::Oxidation_M:::::::::
PSEALTVPPELIAVPIPGQPNCFQIAK	14	4.27	0.101	322	76.8	AE003805	TRUE	FALSE	3	2888.3	0	9of104	1.1603	FALSE	FALSE	::::::::::::::::::::Cys_CAM:::::::
VVAASNGDRYKK	5	10.18	0.013	2931	12.9	AE003805	TRUE	FALSE	2	1308.5	-0.2	6of 22	0.9352	FALSE	FALSE	::::::::::::
SAQRTDVFSLKAMAPRPNAGPGGWLC	3	10.11	0.099	1900	56.13	AE003806	TRUE	FALSE	3	2789.2	-2.4	24of100	1.9965	FALSE	FALSE	:::::::::::::::::::::::::Cys_CAM:
GDNTLALLSGILAVGVGDTAASVVGSK	12	3.89	0.086	1076	65.1	AE003806	TRUE	FALSE	3	2486.8	2.1	16of104	1.6418	FALSE	FALSE	::::::::::::::::::::::::::
LSDTPANMMTPSIFAQAAVDALC	3	2.93	0.069	2109	64.96	AE003806	TRUE	FALSE	2	2441.7	-2.1	10of 44	1.2341	FALSE	FALSE	::::::::Oxidation_M::::::::::::Cys_CAM:
LVFYMLLVVLTCLTVAWQIGSSAKANTR	7	9.75	0.06	1807	101.33	AE003806	TRUE	FALSE	3	3156.8	2.8	3	2.3727	FALSE	FALSE	::::::::::Cys_CAM::::::::::::::::
RRWQNRPESRRETN	9	12.23	0.059	2664	9.2	AE003806	TRUE	FALSE	2	1886	-1.4	8of 26	1.2449	FALSE	FALSE	::::::::::::::
GNIHKIR	9	11.49	0.046	800	9.2	AE003806	TRUE	TRUE	2	838	-2.8	7of 12	1.0095	FALSE	FALSE	::::::::
LLNGTLARTNGLTHAASVATSSSGSYGSSSAAGSNAGSGG	11	9.85	0.044	1728	50.2	AE003806	TRUE	FALSE	3	3598.8	-2.3	27of156	2.6705	FALSE	FALSE	::::::::::::::::::::::::::::::::::::
HGVPPYLLKDCMTGRPTRSIIQFLYQ	15	9.56	0.003	1452	70.73	AE003806	TRUE	FALSE	3	3092.6	-2.5	9of100	1.086	FALSE	FALSE	::::::::::Cys_CAM::::::::::::::
VGNVCSFAQMDVR	11	6.1	0.146	388	31.83	AE003807	TRUE	FALSE	2	1483.6	2.5	9of 24	1.3679	FALSE	FALSE	:::::Cys_CAM::::::::
ITVKCHTHRLASKNR	12	11.48	0.104	1037	15.9	AE003807	TRUE	FALSE	2	1822.1	2.2	10of 28	1.2758	FALSE	FALSE	:::::Cys_CAM:::::::::
VWGTIGFGATAMLAGIVVNWWT	4	6.02	0.075	1646	84.33	AE003807	TRUE	FALSE	3	2351.8	1.2	25of 84	2.8279	FALSE	FALSE	::::::::::::::::::::
WLLISECSALFDEGEGKH	11	4.16	0.07	1448	51.7	AE003807	TRUE	FALSE	2	2092.3	1.8	7of 34	1.0195	FALSE	FALSE	::::::Cys_CAM::::::::::
TVFYCGPPQLAK	3	8.88	0.057	931	32.6	AE003807	TRUE	FALSE	2	1381.6	0.8	12of 22	1.6296	FALSE	FALSE	:::::Cys_CAM::::::::
ARSEDKNWSR	6	10.09	0.039	1198	7.8	AE003807	TRUE	FALSE	2	1249.3	1.7	8of 18	1.3493	FALSE	FALSE	::::::::::
GRSESESAFDEK	6	4.17	0.039	2783	10.1	AE003807	TRUE	FALSE	2	1342.4	2.2	10of 22	1.2842	FALSE	FALSE	::::::::::::
DNQKSCCDSWKR	3	8.29	0.011	1014	8.6	AE003807	TRUE	FALSE	3	1584.6	0.7	15of 44	1.5398	FALSE	FALSE	::::::Cys_CAM:Cys_CAM::::::
IDNGKISLVIQTASK	14	9.89	0.008	2076	32.7	AE003807	TRUE	FALSE	3	1587.9	-0.7	11of 56	1.1315	FALSE	FALSE	::::::::::::::
HGIGGYFDTHLYK	13	7.84	0.005	1669	26.5	AE003807	TRUE	FALSE	2	1508.7	1.4	12of 24	2.4343	FALSE	FALSE	::::::::::::
FLAFLSGMHHQISGMSVMY	8	7.91	0.001	3392	62.69	AE003807	TRUE	FALSE	3	2189.6	-0.6	7of 72	0.9312	FALSE	FALSE	::::::::::::::Oxidation_M:::Oxidation_M::
PVLRPSHK	6	11.49	0	3042	12.1	AE003807	TRUE	TRUE	2	934.1	-1.2	4of 14	0.5354	FALSE	FALSE	::::::::
GNGGKHNKHKSSKGGKGQQQQ	9	11.13	0.182	1532	-17.5	AE003808	TRUE	FALSE	3	2191.4	-1	21of 80	2.4292	FALSE	FALSE	::::::::::::::::::::
MKISKFVQASDYVRERIADKK	8	10.29	0.175	2452	38.43	AE003808	TRUE	FALSE	2	2530	1.4	4of 40	0.8193	FALSE	FALSE	:Oxidation_M:::::::::::::::::::
SGASLKLTILNRNRGRIWTMVAGGGASVIYSDTIC	13	9.75	0.108	347	87.03	AE003808	TRUE	FALSE	3	3600.1	2.2	9of132	0.9761	FALSE	FALSE	::::::::::::::::::Oxidation_M::::::::::::::Cys_CAM:
PNLILNVDGV	10	3.1	0.091	768	34.4	AE003808	TRUE	FALSE	1	1054.2	-1.3	9of 18	2.0765	FALSE	FALSE	::::::::::
SENKTMNVIT	3	6.95	0.076	2765	16.73	AE003808	TRUE	FALSE	2	1153.3	0.5	4of 18	0.765	FALSE	FALSE	::::::Oxidation_M:::::
VTKDARH	9	10.09	0.056	586	3	AE003808	TRUE	FALSE	2	826.9	-1.7	8of 12	1.0577	FALSE	FALSE	::::::::
SSSVPGSWQSPAGLPTIPSDELIKQMR	1	7.02	0.053	134	57.93	AE003808	TRUE	FALSE	3	2870.2	2	13of104	1.4639	FALSE	FALSE	::::::::::::::::::::::::::
KAEESQKVELKDSEAK	10	4.8	0.046	464	12.9	AE003808	TRUE	FALSE	2	1820	0.6	8of 30	0.8278	FALSE	FALSE	::::::::::::::::
PGQEKVEVVENSGQENLQHGDG	7	4	0.037	1439	23.3	AE003808	TRUE	FALSE	3	2351.4	1	121	2.1501	FALSE	FALSE	::::::::::::::::::::
RNAVESTNGFR	15	10.89	0.034	1101	14	AE003808	TRUE	FALSE	2	1251.3	-2.3	10of 20	1.1693	FALSE	FALSE	::::::::::::
GGGESADAKAKGKKKKKEDEPEGGDGGYERR	3	9.38	0.028	1883	0.9	AE003808	TRUE	FALSE	3	3236.5	2.1	24of120	2.4403	FALSE	FALSE	::::::::::::::::::::::::::::
QSFDKMEEELSLSAPIRKRKK	10	10.16	0.021	2576	34.53	AE003808	TRUE	FALSE	2	2537.9	2.7	6of 40	0.8009	FALSE	FALSE	::::::Oxidation_M:::::::::::::
MDEDIRRLHMGLQVIEK	15	5.39	0.019	1906	44.06	AE003808	TRUE	FALSE	3	2116.5	2.3	15of 64	1.5518	FALSE	FALSE	:Oxidation_M::::::::Oxidation_M::::::::
YNKGFGIELMALLVDR	3	6.94	0.003	2662	54.43	AE003808	TRUE	FALSE	3	1840.2	2.6	13of 60	1.325	FALSE	FALSE	::::::::::::::::
QIAHQMKDGTIGA	9	7.82	0	1924	20.53	AE003808	TRUE	FALSE	1	1386.6	1.2	5of 24	0.886	FALSE	FALSE	::::::Oxidation_M:::::::
TSPSIHPHPYAANPRR	11	11.14	0.141	1502	18.1	AE003809	TRUE	FALSE	2	1802	2.5	9of 30	1.2431	FALSE	FALSE	::::::::::::::::
FMLGVGMGLASAPPGVYAAE	15	3.3	0.124	83	61.96	AE003809	TRUE	FALSE	2	1971.3	-0.1	7of 38	0.9398	FALSE	FALSE	::Oxidation_M::::Oxidation_M:::::::::::::
KYTPPPSYTTATGARLAKLLR	12	10.79	0.097	1831	41.9	AE003809	TRUE	FALSE	2	2306.7	0.3	10of 40	1.2811	FALSE	FALSE	::::::::::::::::::::
WFASVNALSAPIGGLLSGFLLDRIGRKK	9	11.47	0.053	2656	86.1	AE003809	TRUE	FALSE	3	2988.5	0.2	16of108	1.399	FALSE	FALSE	::::::::::::::::::::::::
ILQAEDNSGGRVVRALFNTIAADNLVME	15	4.07	0.041	1760	75.33	AE003809	TRUE	FALSE	3	3018.4	2.5	22of108	1.6359	FALSE	FALSE	::::::::::::::::::::::::
MDKVAQTTEMRQALRRR	9	11.95	0.03	1038	26.16	AE003809	TRUE	FALSE	3	2107.5	-1.6	13of 64	1.5294	FALSE	FALSE	::::::::Oxidation_M:::::::
EEIQTYIKR	10	7.02	0.006	2353	19.4	AE003809	TRUE	TRUE	2	1180.3	0.5	5of 16	0.8494	FALSE	FALSE	::::::::
CSKFNVTNLIQILK	5	9.91	0.134	2371	41.7	AE003810	TRUE	FALSE	2	1679	2.3	11of 26	1.6238	FALSE	FALSE	:Cys_CAM:::::::::::
GAAPPPPPPHTPLLATPR	3	11.05	0.059	1495	36.5	AE003810	TRUE	FALSE	2	1788.1	-1.6	10of 34	1.1638	FALSE	FALSE	::::::::::::::::::
VIQYPVTPLPPVKSTTLRTIIHPDSEK	10	9.63	0.056	2567	64.3	AE003810	TRUE	FALSE	3	3031.6	1.5	11of104	1.3061	FALSE	FALSE	::::::::::::::::::::::::
AIRIVPDLLPPRV	12	10.89	0.05	1053	48	AE003810	TRUE	FALSE	2	1459.8	2.2	10of 24	1.3196	FALSE	FALSE	::::::::::::
LMIKKSLLEGMPSPPQLDSSES	11	4.45	0.005	852	53.86	AE003810	TRUE	FALSE	3	2404.8	2.9	21of 84	1.5294	FALSE	FALSE	::::::::::Oxidation_M:::::::::::
TEMSRAEAAALLEKKHLKECEE	5	4.92	0.022	2984	38.43	AE003811	TRUE	FALSE	3	2590.9	2.2	12of 84	1.1932	FALSE	FALSE	:::Oxidation_M::::::::::::::::Cys_CAM:::
EKYVAFNGEGETIFGTDF	14	3.69	0.18	1498	44.6	AE003812	TRUE	FALSE	2	2025.2	1.6	6of 34	0.8357	FALSE	FALSE	::::::::::::::::
VRYCEALALEKPSEEEQR	14	4.43	0.105	296	36.3	AE003812	TRUE	FALSE	3	2208.4	-0.5	16of 68	1.8083	FALSE	FALSE	::::Cys_CAM:::::::::::::
MADVNIRAKKHCQTALMLAVSHGNGDMVNM	6	8.94	0.094	2500	60.92	AE003812	TRUE	FALSE	3	3314.8	-1.3	24of116	2.2813	FALSE	FALSE	::::::::::Cys_CAM:::::::::::::::
MKTIRLGDVLYDDQKR	12	9.63	0.094	2396	34.23	AE003812	TRUE	FALSE	2	1968.3	2.4	7of 30	1.0285	FALSE	FALSE	:Oxidation_M:::::::::::::::
RRRLLSE	13	12.11	0.072	1917	15.3	AE003812	TRUE	FALSE	1	930.1	-0.1	5of 12	0.9716	FALSE	FALSE	::::::::
SPTLDMSNAGGSTAEPASSP	6	3.01	0.047	1344	26.13	AE003812	TRUE	FALSE	3	1878	-1.5	23of 76	1.5971	FALSE	FALSE	::::::::::::::::::
HFLRMHRELQYDINKTRRHVSAGSGSSGS	6	11.22	0.046	2260	37.63	AE003812	TRUE	FALSE	3	3328.7	1.7	21of112	1.9061	FALSE	FALSE	::::::::::::::::::::::::::
NGWHMLALESKPQNIEY	11	5.3	0.039	1566	42.83	AE003812	TRUE	FALSE	2	2031.3	-1.8	6of 32	0.8122	FALSE	FALSE	::::::::::::::::
VKVIPDMELELNSLR	10	4.45	0.035	952	48.13	AE003812	TRUE	FALSE	2	1757.1	-0.9	11of 28	1.5553	FALSE	FALSE	::::::::::::::
MQQQIDAEMGGSIKNLETQLSAKR	3	7.11	0.112	1427	42.86	AE003813	TRUE	FALSE	3	2710.1	1	15of 92	1.2531	FALSE	FALSE	:Oxidation_M::::::::Oxidation_M:::::::::::::::
DGIGAAMQLASMA	6	3.1	0.071	2794	34.16	AE003813	TRUE	FALSE	2	1268.4	-1.1	5of 24	0.7482	FALSE	FALSE	::::::Oxidation_M::::Oxidation_M::
FELSHFTGCDLAKSSMYINVNSVDGANFR	8	5.28	0.028	2726	68.83	AE003813	TRUE	FALSE	3	3281.6	0.6	17of112	1.468	FALSE	FALSE	::::::::Cys_CAM::::::::::::::::::
LLEEAIVLNEDEQIFGLSKAVLQMQT	2	3.59	0.004	1668	85.03	AE003813	TRUE	FALSE	3	2949.4	-0.4	19of100	1.522	FALSE	FALSE	::::::::::::::::::::::Oxidation_M:::
TCPGRIKVYPIQKPIGGCLVMTVNAVIY	8	9.54	0.108	2325	80.63	AE003814	TRUE	FALSE	3	3149.7	-1.9	19of108	2.1633	FALSE	FALSE	::Cys_CAM::::::::::::::Cys_CAM:::::::::::
LRRSKSESLPKRGRPRGQKQRKNR	11	12.81	0.1	2836	7.1	AE003814	TRUE	FALSE	3	2920.4	1.9	10of 92	1.539	FALSE	FALSE	::::::::::::::::::::::
HIILGPPGKKLLHSD	1	9.89	0.095	2088	34.3	AE003814	TRUE	FALSE	2	1626	-2.2	5of 28	0.7263	FALSE	FALSE	::::::::::::::::

QPEPLGTQLR	15	6.98	0.083	237	21.1	AE003814	TRUE	FALSE	1	1139.3	0.5	10of 18	1.5781	FALSE	FALSE	::::::::::
VLDDEAADEAEDALDPDSSISIPVRGGGR	11	3.45	0.069	1533	55.1	AE003814	TRUE	FALSE	3	2971.1	-2.8	21of112	2.1094	FALSE	FALSE	::::::::::::::::::::::::::::
TLSKSTVSSVARAKSTGSLSAVLGETPADE	14	7.11	0.015	1300	47.5	AE003814	TRUE	FALSE	3	2951.3	-2	21of116	1.4561	FALSE	FALSE	::::::::::::::::::::::::::::
CIVTALADPNTFLLDPLLSLKPVR	5	6.24	0.476	2425	84.8	AE003815	TRUE	TRUE	2	2668.2	0.8	18of 46	4.5161	FALSE	FALSE	:Cys_CAM:::::::::::::::::::
PSKTRPTFERYVSK	6	10.7	0.12	1739	18.1	AE003815	TRUE	FALSE	2	1696.9	2.5	7of 26	1.1697	FALSE	FALSE	::::::::::::::
ERMQSESSLVVVGSADDALRVPKS	10	4.56	0.111	2545	45.83	AE003815	TRUE	FALSE	2	2577.9	-3	11of 46	1.2712	FALSE	FALSE	:::Oxidation_M:::::::::::::::
YRIFIVEQTNGKPFNRAAMMNIGYLEALK	2	9.94	0.087	2158	82.86	AE003815	TRUE	FALSE	3	3406	0.9	14of112	1.3546	FALSE	FALSE	:::::::::::::::::Oxidation_M:::::::::
MRKTMETVAAERLNKIGK	1	10.82	0.082	1997	30.66	AE003815	TRUE	FALSE	2	2093.5	1.8	14of 34	1.3853	FALSE	FALSE	:::::Oxidation_M:::::::::::::
TPAAQFANDGGKPDKRSR	6	10.58	0.077	2366	12.5	AE003815	TRUE	FALSE	2	1917.1	1.8	12of 34	1.7194	FALSE	FALSE	::::::::::::::::::
MLACQFEIDK	6	4.08	0.07	1863	32.93	AE003815	TRUE	FALSE	1	1271.4	-0.4	9of 18	1.4761	FALSE	FALSE	:Oxidation_M:::Cys_CAM::::::
VIRLPRIQQHWMH	9	12.41	0.05	532	38.83	AE003815	TRUE	FALSE	2	1731.1	1.8	8of 24	1.2612	FALSE	FALSE	::::::::::::Oxidation_M:::
LVRDEAMTLSTSHPLCDSD	4	3.97	0.049	2684	41.03	AE003815	TRUE	FALSE	2	2148.3	-1	8of 36	0.9404	FALSE	FALSE	:::::::::::::::Cys_CAM::::
PSGMVTSGSITAVSKPG	6	10.1	0.049	1231	26.63	AE003815	TRUE	FALSE	2	1592.8	1.5	11of 32	1.6993	FALSE	FALSE	::::Oxidation_M:::::::::::::
KKLNEPLTTIEFK	5	9.76	0.048	2114	30.2	AE003815	TRUE	FALSE	2	1561.9	1.8	11of 24	1.9469	FALSE	FALSE	::::::::::::::
PIRSANKSPLIISQK	7	11.64	0.047	1261	30.3	AE003815	TRUE	FALSE	3	1653	1.5	289	1.9903	FALSE	FALSE	::::::::::::::::
GSQNSFNTMVDIKLR	9	10.09	0.033	1056	30.43	AE003815	TRUE	FALSE	3	1726.9	-1.6	17of 56	1.7352	FALSE	FALSE	::::::::Oxidation_M:::::::
PKPGSVIKPQ	10	10.6	0.016	1300	13.8	AE003815	TRUE	FALSE	2	1051.3	-1.6	11of 18	1.2684	FALSE	FALSE	::::::::::
DVPLRLAK	1	10.09	0.006	764	22.7	AE003815	TRUE	FALSE	1	912.1	0.6	7of 14	1.5507	FALSE	FALSE	::::::::
GNITINVNATEIFAPYD	7	3.01	0.004	1768	46.3	AE003815	TRUE	FALSE	2	1853	0.9	97	1.7971	FALSE	FALSE	::::::::::::::::::
VLPQERK	8	10.09	0	3201	13.5	AE003815	TRUE	FALSE	1	870	3	3of 12	0.5206	FALSE	FALSE	:::::::
IANQLIDASVREVVDAK	5	4.31	0.131	2865	41.9	AE003816	TRUE	FALSE	3	1842.1	-2.6	11of 64	1.3703	FALSE	FALSE	::::::::::::::::::
RFQLKSPALTTVMKDGK	9	10.83	0.128	958	32.93	AE003816	TRUE	FALSE	3	1921.3	-0.1	18of 64	2.1307	FALSE	FALSE	::::::::::::::::::
HSVQIRDFK	9	10.09	0.091	1129	15.7	AE003816	TRUE	FALSE	1	1130.3	2.3	8of 16	1.4549	FALSE	FALSE	::::::::::
LKAKAAAAGGASNTAVLVAK	9	10.85	0.075	2530	35.3	AE003816	TRUE	FALSE	3	1813.2	-2	15of 76	1.1064	FALSE	FALSE	::::::::::::::::::::
TNVTPKILSYVGANK	5	10.18	0.052	1987	29.4	AE003816	TRUE	FALSE	2	1605.9	0.2	9of 28	1.174	FALSE	FALSE	::::::::::::::
TTETGNLEPVVVEDVSTTVKEDKVVVK	11	4.13	0.021	1380	50.6	AE003816	TRUE	FALSE	3	2917.3	0.7	27of104	2.6858	FALSE	FALSE	::::::::::::::::::::::::::
GTDVPINEIK	14	4.08	0.099	971	20.8	AE003817	TRUE	FALSE	1	1086.2	1.6	7of 18	1.1929	FALSE	FALSE	::::::::::
SIVSWALCALMAYK	5	8.88	0.056	2636	53.53	AE003817	TRUE	FALSE	3	1613.9	2.1	8of 52	0.8918	FALSE	FALSE	::::::::Cys_CAM:::::::
KASRPNPLQ	13	11.49	0.056	651	10.6	AE003817	TRUE	FALSE	2	1011.2	-0.2	11of 16	1.16	FALSE	FALSE	::::::::::
MGCDGGFQEYGFEYIR	8	3.83	0.052	3435	41.73	AE003817	TRUE	FALSE	2	1930.1	-0.6	7of 30	1.2756	FALSE	FALSE	:::Cys_CAM::::::::::::
SNMNGNAARLAR	13	12.41	0.042	2517	16.23	AE003817	TRUE	FALSE	2	1275.4	0.3	5of 22	0.9105	FALSE	FALSE	::::::::::::
IKRLLKEIKGKCKKQR	12	11.17	0.027	2327	20.7	AE003817	TRUE	FALSE	2	2027.5	-0.1	9of 30	1.0409	FALSE	FALSE	::::::::::Cys_CAM:::::
RGCMAGAAVCVAAVR	5	9.2	0.023	2881	34.13	AE003817	TRUE	FALSE	2	1549.8	1.4	8of 28	1.0575	FALSE	FALSE	:::Cys_CAM::::::Cys_CAM::::::
YQPSVGSIISTVAIAQ	11	5.93	0.007	984	42.5	AE003817	TRUE	FALSE	3	1634.9	-1.3	18of 60	1.4996	FALSE	FALSE	::::::::::::::::
LFLKPRTNLHHV	2	11.49	0.001	1189	32.5	AE003817	TRUE	FALSE	2	1475.8	2.2	10of 22	1.3131	FALSE	FALSE	::::::::::::
RENANAIDSSSSGGGR	3	7.05	0.167	1823	8.9	AE003818	TRUE	FALSE	2	1578.6	1.4	12of 30	1.5193	FALSE	FALSE	::::::::::::::::
AADFLRNATQSSEPFFAMVA	3	4.08	0.105	1081	55.23	AE003818	TRUE	FALSE	3	2190.4	2.7	23of 76	2.0203	FALSE	FALSE	::::::::::::::::Oxidation_M:::
FVWQSGTIVAQEPLPLERQSAAATSNVSVSAV	8	4.27	0.1	2385	80.5	AE003818	TRUE	FALSE	3	3344.7	0.5	24of124	2.2116	FALSE	FALSE	::::::::::::::::::::::::::::::
IMKNSAMVMQI	10	10.1	0.095	252	35.49	AE003818	TRUE	FALSE	2	1282.6	-2	9of 20	1.2803	FALSE	FALSE	::Oxidation_M:::::::::
IDFIVCLGGDGTLLYASQLFQQSV	2	2.93	0.081	2298	82.5	AE003818	TRUE	FALSE	3	2646	-0.4	14of 92	1.4982	FALSE	FALSE	::::::Cys_CAM:::::::::::::
IAGIRLNDVVKNLACGDDPENWAK	12	4.46	0.07	446	55.1	AE003818	TRUE	FALSE	2	2670	-0.4	8of 46	1.0997	FALSE	FALSE	::::::::::::::Cys_CAM:::::::::
MFTQGGSGKNGSSVAGTSVLSPSIPLTLVVLP	5	10.1	0.067	2366	78.33	AE003818	TRUE	FALSE	3	3119.6	-2	19of124	1.6568	FALSE	FALSE	:Oxidation_M:::::::::::::::::::::::::::::
IHRRRGRGQLNAQTGDAGNTR	6	12.58	0.061	2850	13.8	AE003818	TRUE	FALSE	3	2335.6	1.2	19of 80	1.9449	FALSE	FALSE	::::::::::::::::::::
LISANTCANGSQEMM	3	3.3	0.048	857	33.06	AE003818	TRUE	FALSE	2	1627.8	-0.5	10of 28	0.9154	FALSE	FALSE	::::::Cys_CAM:::::::::
LMSDNDLRQSMPTESKT	12	4.31	0.039	1830	28.06	AE003818	TRUE	FALSE	2	1970.2	1.5	10of 32	1.2718	FALSE	FALSE	::Oxidation_M:::::::::::::::
SSCSSVSGMGMLADRFTDDK	8	4.18	0.035	1641	33.96	AE003818	TRUE	FALSE	3	2168.3	0.9	16of 76	1.4887	FALSE	FALSE	:::Cys_CAM::::::Oxidation_M:::::::::::
ADPEHYHTLMMVDLDV	13	3.96	0.023	995	43.86	AE003818	TRUE	FALSE	2	1903.1	0.8	4of 30	0.7136	FALSE	FALSE	:::::::::Oxidation_M:::::::
VGMRRKLRHLRRQLKKVRNPKNLVDKCF	5	12.42	0.018	2450	48.23	AE003818	TRUE	FALSE	3	3548.3	-0.6	19of108	1.6153	FALSE	FALSE	::::::::::::::::::::::::::Cys_CAM::
QMYGSNSSIKSAPHYN	3	9.53	0.166	2757	19.53	AE003819	TRUE	FALSE	3	1800.9	2.7	7of 60	0.9406	FALSE	FALSE	::Oxidation_M:::::::::::::::
LCLNDMKALMTGLGSAEYWALK	3	6.36	0.104	1908	69.96	AE003819	TRUE	FALSE	3	2486.9	-2.7	10of 84	1.2808	FALSE	FALSE	::Cys_CAM:::::::::::::::::::
SAESRMATSGIVE	14	4.27	0.062	1322	23.33	AE003819	TRUE	FALSE	2	1354.5	1.1	12of 24	1.6285	FALSE	FALSE	::::::Oxidation_M:::::::
YLSLDMQLYIISPILLISLYK	2	6.58	0.047	2333	96.73	AE003819	TRUE	FALSE	2	2517.1	2	12of 40	1.6708	FALSE	FALSE	::::::Oxidation_M:::::::::::::::
FKEVYLHPMVRDAHGRKMSK	5	10.44	0.018	1827	34.96	AE003819	TRUE	FALSE	3	2462.9	1	13of 76	1.2603	FALSE	FALSE	::::::::Oxidation_M::::::::Oxidation_M:::
QLKSLGSSYDWTR	8	9.72	0.017	2173	26.8	AE003819	TRUE	FALSE	2	1541.7	0.7	10of 24	1.2387	FALSE	FALSE	::::::::::::::
KTVSPMATPKKTATEKTPVKKR	4	11.19	0.015	2402	16.23	AE003819	TRUE	FALSE	2	2444.9	-1.1	9of 42	1.0846	FALSE	FALSE	::::::Oxidation_M:::::::::::::::
FALYPPSK	5	9.72	0.009	1631	24.4	AE003819	TRUE	FALSE	1	923.1	-2.2	3of 14	0.6544	FALSE	FALSE	::::::::
FLEPPLILQFADGVAMLR	2	4.08	0.245	1848	75.03	AE003820	TRUE	TRUE	2	2031.5	2.1	16of 34	1.7036	FALSE	FALSE	::::::::::::::::::
EAGVETGDEEDLSTPNEK	2	3.38	0.162	396	20.9	AE003820	TRUE	TRUE	2	1920.9	0.3	18of 34	2.2903	FALSE	FALSE	::::::::::::::::::
RILPEAGTPVFHRVD	13	7.85	0.097	1481	38	AE003820	TRUE	FALSE	2	1708	2.4	6of 28	1.1054	FALSE	FALSE	::::::::::::::::
SPKGGPAGVANSTGGAQNGDPAA	3	6.76	0.033	1525	16.9	AE003820	TRUE	FALSE	2	1982.1	-2.5	7of 44	0.9635	FALSE	FALSE	::::::::::::::::::::::
PMHKEVLNPIHSPTDR	5	7.97	0	1531	26.23	AE003820	TRUE	FALSE	2	1888.2	1.7	10of 30	1.8528	FALSE	FALSE	::Oxidation_M:::::::::::::
SMYHRPEHGPLLLAWMLLR	12	9.85	0.068	731	66.16	AE003821	TRUE	FALSE	2	2321.8	2.3	6of 36	1.062	FALSE	FALSE	::::::::::::::::::
GPPVPTRCQVLGRGAYGTVFKAIYRDR	10	10.55	0.035	1685	56.3	AE003821	TRUE	FALSE	3	3036.5	2.7	9of104	1.1663	FALSE	FALSE	::::::::Cys_CAM:::::::::::::::::
DCVPNIGESIVTYMRDFL	7	3.71	0.009	1521	56.13	AE003821	TRUE	FALSE	2	2146.4	2	135	1.5216	FALSE	FALSE	::Cys_CAM::::::::::Oxidation_M:::::
CLNVCTALLPLVDEEIFSR	12	3.83	0.002	1740	68.7	AE003821	TRUE	FALSE	2	2250.5	3	8of 36	1.0356	FALSE	FALSE	:Cys_CAM:::Cys_CAM:::::::::::::
IVDDLKSM	6	3.89	0.001	1427	24.13	AE003821	TRUE	FALSE	1	937.1	-2.5	4of 14	0.7956	FALSE	FALSE	:::::::Oxidation_M:
EELQSLLGD	12	2.95	0.24	1925	26.3	AE003822	TRUE	FALSE	1	1004.1	2.5	6of 16	1.1066	FALSE	FALSE	::::::::
LYYPLENTSVNLTGLAST	11	3.3	0.186	762	51.5	AE003822	TRUE	FALSE	2	1957.2	1.1	6of 34	1.3648	FALSE	FALSE	::::::::::::::::
VLLLAVYFTESINEFAANNWSSFSR	8	4.27	0.144	2211	84.9	AE003822	TRUE	FALSE	3	2880.2	-0.3	11of 96	1.3205	FALSE	FALSE	::::::::::::::::::::::::
LKRKTVAQAQTAPRKSSAVEEPPQTPQ	6	10.82	0.124	2099	30.2	AE003822	TRUE	FALSE	3	2948.4	1.7	9of104	1.1039	FALSE	FALSE	::::::::::::::::::::::::
PLLLWAPACHMSGLSPLKE	1	7.16	0.065	318	63.73	AE003822	TRUE	FALSE	2	2121.5	-0.6	7of 36	1.1905	FALSE	FALSE	::::::::Cys_CAM:::::::::::
EGLELQQNVEATHFGR	7	4.54	0.062	1703	31.5	AE003822	TRUE	FALSE	2	1829	0.6	362	1.3215	FALSE	FALSE	::::::::::::::::
YYRQHAKHPFATTMAEEIFQSGVLPSDSDFR	10	6.04	0.061	2145	64.83	AE003822	TRUE	TRUE	3	3631	2.7	21of120	2.0445	FALSE	FALSE	::::::::::::::::::::::::::::
TPYLCMMSLLFYGGALLINLLSTLH	8	7.15	0.036	2441	104.66	AE003822	TRUE	FALSE	3	2875.4	-1.3	20of 96	2.1115	FALSE	FALSE	:::::Cys_CAM:Oxidation_M:Oxidation_M:::::::::::::::::
KAGSTSFSQNVGLMSKGMMS	3	10.6	0.028	2266	33.99	AE003822	TRUE	FALSE	2	2065.4	-3	11of 38	1.3352	FALSE	FALSE	::::::::::::::::Oxidation_M:::
DAEAKDFVAAFPDFVHVMEWPSIFKRY	8	4.63	0.019	1968	81.33	AE003822	TRUE	FALSE	3	3233.7	1.2	22of104	2.1918	FALSE	FALSE	::::::::::::::::Oxidation_M:::::::::
ILQCPSSFDSVLCWPRTNAGSLAVLPCFEEF	4	3.83	0.014	2523	101.5	AE003822	TRUE	FALSE	3	3603	2.9	24of120	2.0248	FALSE	FALSE	::::Cys_CAM::::::::Cys_CAM::::::::::::Cys_CAM:::::
PNLPFDQIENPQRPAYNPSDNMGGYDK	6	3.97	0.014	1126	46.13	AE003822	TRUE	FALSE	3	3095.3	0.2	19of104	1.6356	FALSE	FALSE	::::::::::::::::::::Oxidation_M:::::::
LLGKRAGKPSFTEIEQEL	6	7.16	0.01	2971	42.3	AE003822	TRUE	FALSE	2	2017.3	-2.5	6of 34	0.8765	FALSE	FALSE	::::::::::::::::::
YQKIQELKKHKEKANQQLTEARK	12	10.35	0.005	2836	20.1	AE003822	TRUE	TRUE	3	2841.3	1.2	8of 88	0.9077	FALSE	FALSE	::::::::::::::::::::::
AFSVALESIPLALAENSGLHPIETLSELK	3	4.25	0.275	2257	87.7	AE003823	TRUE	TRUE	2	3051.5	2.1	13of 56	2.3611	FALSE	FALSE	::::::::::::::::::::::::::::
IASQLMLR	13	11.05	0.125	1434	30.33	AE003823	TRUE	FALSE	1	932.2	1.1	8of 14	1.6761	FALSE	FALSE	::::::::
QAISVWLLAVVKHCSQRPAVLA	13	10.11	0.109	402	67.9	AE003823	TRUE	FALSE	2	2447.9	-0.2	7of 42	1.1245	FALSE	FALSE	::::::::::::Cys_CAM:::::::::

SKKQQILLSTQLVK	12	10.85	0.098	968	30.6	AE003823	TRUE	FALSE	2	1615	1.9	7of 26	1.1712	FALSE	FALSE	::::::::::::::
NVKLAILTCPFEPPKPKTKHKL	7	10.39	0.091	3324	46.5	AE003823	TRUE	FALSE	3	2561.1	-0.8	92	0.7268	FALSE	FALSE	::::::::Cys_CAM::::::::::::
AGAGMGVGMSATMPRPHTQSRRVSR	12	12.88	0.074	996	31.89	AE003823	TRUE	FALSE	3	2648	-2.3	8of 96	0.833	FALSE	FALSE	:::::Oxidation_M:::Oxidation_M:::Oxidation_M::::::::::::
AFSVALESIPLALAENSGLHPIETLSELK	2	4.25	0.053	1698	87.7	AE003823	TRUE	TRUE	2	3051.5	0.5	12of 56	1.8466	FALSE	FALSE	::::::::::::::::::::::::::::
IASQLMLR	12	11.05	0.032	1652	30.33	AE003823	TRUE	FALSE	1	932.2	1.5	7of 14	1.2855	FALSE	FALSE	::::::::
DNPNLLFNMSGF	15	3.1	0.03	203	37.93	AE003823	TRUE	FALSE	2	1369.5	2.1	12of 22	2.1915	FALSE	FALSE	::::::::::::
FRKQHAVVVVRR	6	12.71	0.024	1792	24.1	AE003823	TRUE	FALSE	2	1495.8	-1.4	9of 22	1.0811	FALSE	FALSE	::::::::::::
QHNGSTSGLPRLPGLP	6	11.05	0.004	2146	26.6	AE003823	TRUE	FALSE	1	1631.8	-1.7	11of 30	1.4499	FALSE	FALSE	::::::::::::::
IGYNPAAVAFVPISGWHGDNMLEPSTNMPWFK	6	5.22	0.409	2252	91.16	AE003824	TRUE	TRUE	3	3549.1	1.6	31of124	4.9272	FALSE	FALSE	::::::::::::::::::::::::::::::
SYLELKELYIHMSYLM	9	5.3	0.117	1922	61.96	AE003824	TRUE	FALSE	3	2050.4	-2.9	16of 60	1.8758	FALSE	FALSE	::::::::::::::Oxidation_M:
DHLDNSDMLLAGENEVK	9	3.84	0.112	2242	33.83	AE003824	TRUE	FALSE	2	1917.1	-0.4	11of 32	1.3965	FALSE	FALSE	:::::::Oxidation_M:::::::::
QTHNIRPNSVYGSSEELRERFLLVEESQHLEK	1	5.4	0.06	1506	61.3	AE003824	TRUE	FALSE	3	3827.2	-2.8	23of124	1.6593	FALSE	FALSE	::::::::::::::::::::::::::::
QHQVRHHHNDPSLLLRRQQHEKKQK	1	11.47	0.018	976	13.2	AE003824	TRUE	FALSE	3	3179.6	2.5	21of 96	2.8832	FALSE	FALSE	::::::::::::::::::::::::
MFQSIGAISVPPLA	4	6.02	0.008	3009	48.93	AE003824	TRUE	FALSE	2	1431.7	-0.1	8of 26	1.0878	FALSE	FALSE	::::::::::::::
HFLYMLYESSAIGDLELRH	4	5.18	0.002	1395	61.43	AE003824	TRUE	FALSE	2	2311.6	2	5of 36	1.0708	FALSE	FALSE	:::::Oxidation_M::::::::::::::
EMMYGRQHCNVPPATNKLNKWYMPS	2	9.51	0	777	50.69	AE003824	TRUE	FALSE	3	3070.5	-0.1	13of 96	1.35	FALSE	FALSE	:::Oxidation_M::::::Cys_CAM::::::::::::::::
FFVIIFVPETRGKSLEEIER	14	4.73	0.073	1352	67.9	AE003825	TRUE	FALSE	3	2410.8	-0.9	15of 76	1.8861	FALSE	FALSE	::::::::::::::::::::
VERHQESAGAAADGAGIVQPL	15	4.43	0.058	2895	36.4	AE003825	TRUE	FALSE	3	2077.3	0.1	11of 80	1.1199	FALSE	FALSE	::::::::::::::::::::
RNVSHGNSTEVSELSHLT	10	6.03	0.031	1285	22.6	AE003825	TRUE	FALSE	2	1968.1	1.4	6of 34	1.1	FALSE	FALSE	::::::::::::::::::
AAQCIELSVARLQMAVELMFTK	4	6.44	0.024	1769	71.36	AE003825	TRUE	FALSE	2	2527	1.9	13of 42	2.4442	FALSE	FALSE	::::Cys_CAM::::::::::::::Oxidation_M::::
TPSGAVGSASNPITIDDFDAPLNLSMKPSDK	15	3.88	0.021	1213	58.83	AE003825	TRUE	FALSE	3	3147.5	1.1	16of120	1.3945	FALSE	FALSE	::::::::::::::::::::::::::::::
GGPALAPP	1	6.02	0	2214	17.7	AE003825	TRUE	FALSE	1	679.8	0.2	7of 14	0	FALSE	FALSE	::::::::
WNLGQQR	12	11.05	0.128	2295	15.5	AE003826	TRUE	FALSE	2	902	-2	4of 12	0.5404	FALSE	FALSE	::::::::
GGAPGAPGSPGGGGFGGQGGGGGGYGGGAGRGGAPGAPGSPG	10	9.85	0.103	1360	28.8	AE003826	TRUE	FALSE	3	3095.2	1.6	29of160	2.25	FALSE	FALSE	::::::::::::::::::::::::::::::::::::::
RGGFGGGGYGGGGY	12	9.59	0.072	1188	14.5	AE003826	TRUE	FALSE	2	1219.3	-1.5	11of 26	1.3357	FALSE	FALSE	::::::::::::::
PSPSGGAPPTSGPPI	13	6.02	0.053	824	20.8	AE003826	TRUE	FALSE	2	1319.5	1.9	8of 28	1.0045	FALSE	FALSE	::::::::::::::
KERQLKMAGSADPDVKMVANVTPATGSQPM	5	9.76	0.048	2625	48.09	AE003826	TRUE	FALSE	3	3207.7	-1.9	18of116	1.9609	FALSE	FALSE	::::::Oxidation_M::::::::Oxidation_M::::::::::::Oxidation_M:
GGFGGGFGGGFQRTRVVTRTRYR	8	12.58	0.045	2140	36	AE003826	TRUE	FALSE	3	2490.8	-2.2	21of 88	1.7552	FALSE	FALSE	::::::::::::::::::::::
QFVTAAATMIKTESPDAVKFTEDGVRGTIMLDGYHRI	1	5.42	0.024	1420	84.56	AE003826	TRUE	FALSE	3	4087.7	-1.8	22of144	1.7874	FALSE	FALSE	::::::::Oxidation_M:::::::::::::::::::::::::::
PLTHPRARNHYPSEDLAEEPL	7	5.26	0.012	1731	38.7	AE003826	TRUE	FALSE	3	2443.7	-0.6	88	0.8311	FALSE	FALSE	::::::::::::::::::::
PRQRMEVSMMR	13	12.11	0.203	1228	22.69	AE003827	TRUE	FALSE	2	1437.7	0.7	10of 20	1.7038	FALSE	FALSE	:::::::::Oxidation_M::
QKFIVAISSLRKSVWLSPL	7	11.64	0	3382	64.4	AE003827	TRUE	FALSE	2	2173.6	-2.4	451	0.346	FALSE	FALSE	::::::::::::::::::
TPHRPVPTNLQPAPMLMNQSSVQR	11	12.41	0.085	1064	45.56	AE003828	TRUE	FALSE	3	2717.1	-0.4	24of 92	2.2515	FALSE	FALSE	::::::::::::::::Oxidation_M:::::::::
SEDEDETPQNGISEKEVQTIQK	6	3.74	0.07	2939	23.5	AE003828	TRUE	FALSE	2	2505.6	2.9	9of 42	1.4051	FALSE	FALSE	::::::::::::::::::::
QLANGHGRGSLSISGSSSSLNVVQ	11	11.05	0.058	1912	37.6	AE003828	TRUE	FALSE	2	2356.6	2.1	12of 46	1.284	FALSE	FALSE	::::::::::::::::::::
KHKFGRFFSILILVMG	4	11.64	0.039	1934	58.33	AE003828	TRUE	FALSE	2	1894.4	-2.5	8of 30	0.9513	FALSE	FALSE	::::::::::::::::
AEETEVRQNGNESMSKVEIRNSEIK	12	4.56	0.035	2050	31.53	AE003828	TRUE	FALSE	3	2879.1	-2.2	8of 96	0.9109	FALSE	FALSE	::::::::::::::::::::::
IQRALEMTLNDDGCSQSPK	9	4.31	0.026	2220	33.93	AE003828	TRUE	FALSE	2	2164.4	-2.8	7of 36	0.8415	FALSE	FALSE	::::::::::::Cys_CAM::::::
GLRGLTSKSNALLENR	2	11.33	0.004	910	30.8	AE003828	TRUE	FALSE	2	1730	1.9	10of 30	1.7425	FALSE	FALSE	::::::::::::::::
QGVAWDPCNQYIATMSTDR	6	3.89	0.031	2610	39.83	AE003829	TRUE	FALSE	2	2214.4	-1	9of 36	1.3018	FALSE	FALSE	:::::::Cys_CAM::::::::::
SVKGQLTMVMS	10	10.1	0.015	1964	27.06	AE003829	TRUE	FALSE	2	1213.5	-1.6	3of 20	0.6734	FALSE	FALSE	:::::::Oxidation_M::Oxidation_M::
FVFFMIGAGIGLFWD	5	3.1	0.094	2837	76.23	AE003830	TRUE	FALSE	3	1737.1	-2.6	9of 56	1.4265	FALSE	FALSE	:::::Oxidation_M:::::::::
NTYYFDTKTNAFR	12	9.53	0.054	1555	25.3	AE003830	TRUE	FALSE	2	1641.8	-0.4	9of 24	1.0853	FALSE	FALSE	::::::::::::
RALVMRPFAPLQTVQLSELSSS	2	10.89	0.019	1950	63.73	AE003830	TRUE	FALSE	2	2447.9	1.6	15of 42	2.0821	FALSE	FALSE	:::::Oxidation_M:::::::::::::::
CIYGDDQSYLQN	15	2.93	0.015	755	26.5	AE003830	TRUE	FALSE	3	1476.5	-1.3	14of 44	1.4242	FALSE	FALSE	:Cys_CAM:::::::::
LNPMQMQSVQTLAGYGSSSQR	6	9.85	0.004	2131	38.96	AE003830	TRUE	FALSE	2	2300.6	2.4	11of 40	1.417	FALSE	FALSE	:::::Oxidation_M:::::::::::::::
RHANRSRLWDSQSAFYIAGG	14	11.05	0.194	314	37.6	AE003831	TRUE	FALSE	3	2293.5	1.4	21of 76	1.8195	FALSE	FALSE	::::::::::::::::::::
NVFIIGATNRPDIIDPAILRPGR	14	10.8	0.148	1366	65.8	AE003831	TRUE	TRUE	3	2520	1.1	27of 88	3.6304	FALSE	FALSE	::::::::::::::::::::::
IVQVCRWYMSAYHAGR	15	9.62	0.125	2844	43.63	AE003831	TRUE	TRUE	3	2014.3	-1.3	10of 60	0.9278	FALSE	FALSE	:::::Cys_CAM:::Oxidation_M:::::::
IQEASDLKHAQEAF	10	4.43	0.121	1234	27.6	AE003831	TRUE	FALSE	2	1587.7	0.7	11of 26	1.4619	FALSE	FALSE	::::::::::::::
FGMQPSRGVLFYGPPG	7	9.85	0.11	2248	43.73	AE003831	TRUE	FALSE	2	1727	1	65	1.4903	FALSE	FALSE	:::Oxidation_M:::::::::::::
LILPDSQNIR	1	6.79	0.075	716	31.8	AE003831	TRUE	FALSE	1	1169.4	0.6	9of 18	1.7461	FALSE	FALSE	::::::::::
NVFIIGATNRPDIIDPAILRPGR	13	10.8	0.063	1449	65.8	AE003831	TRUE	TRUE	3	2520	2.3	26of 88	2.8423	FALSE	FALSE	::::::::::::::::::::::
LRTSNGNGNVRLSGSGNTKDAVTTSVESTAALTAGNDLNE	8	4.56	0.062	2520	52.7	AE003831	TRUE	FALSE	3	3994.2	1.6	25of156	2.1487	FALSE	FALSE	::::::::::::::::::::::::::::::::::::
AISTTEGLSSSHNTLETFENQANLR	8	4.54	0.051	1996	44	AE003831	TRUE	FALSE	3	2721.9	-0.6	15of 96	1.4867	FALSE	FALSE	::::::::::::::::::::::
TLNEIQAKMG	15	6.95	0.034	1273	21.83	AE003831	TRUE	FALSE	2	1105.3	0.5	9of 18	1.2429	FALSE	FALSE	::::::::::
ERAENQNSAMDMDEDDPVPE	9	3.24	0.033	1792	27.26	AE003831	TRUE	FALSE	3	2325.4	1.8	20of 76	1.9544	FALSE	FALSE	:::::::::Oxidation_M::Oxidation_M:::::::::
PEVARQELMQLTHTTK	12	7.83	0.029	2120	29.93	AE003831	TRUE	FALSE	2	1883.2	1.7	6of 30	0.9759	FALSE	FALSE	::::::::::::::::
KNEEMSRKFSTLLQELNK	3	9.76	0.017	2270	33.33	AE003831	TRUE	TRUE	2	2196.5	-2.3	8of 34	1.1615	FALSE	FALSE	::::::::::::::::::
VNRVWGQTTFDNRNQYQEKYRGPIRESTILALEP	8	9.52	0.016	2827	71.3	AE003831	TRUE	FALSE	3	4081.5	0	9of132	0.8147	FALSE	FALSE	::::::::::::::::::::::::::::::
YMDPRNGR	7	9.85	0.012	3369	10.23	AE003831	TRUE	FALSE	2	1009.1	-1	2	0.9573	FALSE	FALSE	::::::::
PALDDWDEDGSAPSAFRER	4	3.69	0.006	2644	36.2	AE003831	TRUE	FALSE	2	2135.2	0.8	13of 36	1.5552	FALSE	FALSE	::::::::::::::::
LYPKTLENRARVDEFLEWQHLNIRLA	5	7.75	0.067	1835	77.2	AE003832	TRUE	FALSE	3	3226.7	1.7	22of100	3.5991	FALSE	FALSE	::::::::::::::::::::::::
GTSTPSASSAANSREK	11	10.09	0.067	2739	5.8	AE003832	TRUE	FALSE	2	1551.6	1.1	9of 30	1.3594	FALSE	FALSE	::::::::::::::::
RVSKRRLEPHERSLVF	4	11.95	0.052	1911	31.5	AE003832	TRUE	FALSE	2	2010.4	-1.8	5of 30	0.9334	FALSE	FALSE	::::::::::::::::
HHDAGQKDK	8	7.94	0.031	2842	-6.2	AE003832	TRUE	FALSE	2	1036.1	1.6	5of 16	0.9095	FALSE	FALSE	::::::::
RGRALIFPFGSGKVR	3	12.71	0.024	2004	36	AE003832	TRUE	FALSE	2	1662	2.7	7of 28	1.2174	FALSE	FALSE	::::::::::::::
GIPFGASPMIPPPPVPNHSVSCQFYMDREEQLYRR	15	7.16	0.016	2476	84.66	AE003832	TRUE	FALSE	3	4075.6	-2.8	10of136	1.139	FALSE	FALSE	::::::::::::::::::::Cys_CAM:::::::::::::
HRLLHEHRVLQDPGPADGL	14	6.32	0.015	1778	37	AE003832	TRUE	FALSE	2	2161.4	2.7	8of 36	1.0975	FALSE	FALSE	::::::::::::::::::
SSGERVNLADEIRKL	2	7.14	0.014	1117	28.5	AE003832	TRUE	FALSE	2	1687.9	2.1	7of 28	1.3898	FALSE	FALSE	::::::::::::::
NFGDKTANLFSK	5	9.89	0.008	1954	21.3	AE003832	TRUE	TRUE	1	1342.5	-0.6	12of 22	1.7728	FALSE	FALSE	::::::::::::
IFLPKKLF	6	10.6	0.137	1398	37.6	AE003833	TRUE	FALSE	1	1006.3	1.6	7of 14	1.2676	FALSE	FALSE	::::::::
ARLEVEAERSGLAA	9	4.56	0.06	798	30.9	AE003833	TRUE	FALSE	3	1472.6	-2.1	17of 52	1.8052	FALSE	FALSE	::::::::::::::
FFMMLFMELCTADVILESLMHSIVSAFAY	4	3.83	0.024	1893	125.12	AE003833	TRUE	FALSE	3	3483.1	-2	24of112	1.879	FALSE	FALSE	:::Oxidation_M:Oxidation_M:::Oxidation_M:::Cys_CAM::::::::::Oxidation_M:::::::::
NSFGAPNTERAVTKCFFDIREEVR	5	6.55	0.015	3051	49.5	AE003833	TRUE	FALSE	3	2845.1	-2.7	15of 92	1.2193	FALSE	FALSE	::::::::::::::Cys_CAM:::::::::::
AVKQLLPVA	10	10.1	0.005	973	30.1	AE003833	TRUE	FALSE	2	939.2	0.6	9of 16	1.3649	FALSE	FALSE	::::::::::
SLSMAIDNYAPSSGDLDMDLDMEMGMDMDLDM	11	2.55	0.005	1723	89.91	AE003833	TRUE	FALSE	3	3564	1.1	25of124	2.9824	FALSE	FALSE	::::Oxidation_M::::::::::::::::::::::::Oxidation_M:
KAEELYKRVHLGVWLR	9	10.18	0.172	2257	44.1	AE003834	TRUE	FALSE	2	1998.4	-2	9of 30	1.4418	FALSE	FALSE	::::::::::::::::
DSIGGGGAGQGGSAGAAALGAAAGAVGAAGGGGGGGGGQA	8	3.1	0.112	2605	40.3	AE003834	TRUE	FALSE	3	2884	-0.9	21of156	1.6348	FALSE	FALSE	::::::::::::::::::::::::::::::::::::
KATLPTSSSSQMITFTFKNGLVV	6	10.6	0.108	1326	55.93	AE003834	TRUE	FALSE	3	2458.9	1	18of 88	1.9097	FALSE	FALSE	::::::::::::::::::::::
GFVPGMLGVSHGAI	14	7.85	0.105	1432	40.03	AE003834	TRUE	FALSE	1	1342.6	2.8	5of 26	1.0071	FALSE	FALSE	::::::::::::::
EKVRPSVIMDIIYSGEQLRFK	5	9.63	0.1	2052	56.83	AE003834	TRUE	FALSE	2	2526	-2.4	8of 40	1.0979	FALSE	FALSE	::::::::Oxidation_M:::::::::::
LGVLYIK	11	9.72	0.085	760	30.8	AE003834	TRUE	FALSE	1	806	-0.4	8of 12	1.3473	FALSE	FALSE	::::::::

VLKMSIVTMAMLSLACCVLE	10	6.14	0.05	1810	79.79	AE003834	TRUE	FALSE	2	2302.8	2.3	10of 38	1.4377	FALSE	FALSE	::::Oxidation_M:::::Oxidation_M:::::::Cys_CAM:Cys_CAM::::
GVAFVIGNIVVVMMESKMATM	15	6.95	0.05	1627	72.42	AE003834	TRUE	FALSE	3	2228.8	2.2	23of 80	2.274	FALSE	FALSE	::::::::::::::::::
GFNSDPLHSEGRLMLPK	14	7.82	0.041	1435	37.03	AE003834	TRUE	FALSE	2	1915.2	0.4	11of 32	1.4651	FALSE	FALSE	::::::::::::::Oxidation_M::::
DNNEEEEEEAAVGAEPATGSQLTGDEDDIR	5	3.14	0.033	1734	37.6	AE003834	TRUE	FALSE	3	3063	-2.9	22of112	1.9222	FALSE	FALSE	::::::::::::::::::::::::::::
ALGAFYLRLTGAALDCYKYLEP	3	6.35	0.026	2278	73.5	AE003834	TRUE	FALSE	2	2506.9	-0.8	11of 42	1.5498	FALSE	FALSE	::::::::::::::::Cys_CAM::::::
SLCAVKVLRLEEFIDDVRHGMALQL	15	5.39	0.017	1666	79.93	AE003834	TRUE	FALSE	3	2914.4	2.7	20of 96	1.8572	FALSE	FALSE	:::Cys_CAM:::::::::::::::::::
IVIQIVGSIVGMLVLRRVLKMSIVTMAMLSLA	11	12.42	0.013	1053	129.92	AE003834	TRUE	FALSE	3	3473.5	-2	25of124	2.2936	FALSE	FALSE	:::::::::::::::::::::Oxidation_M:::::::::::
AIDFRIVKSLHKKLKKRCVLNVMKIIFMFLTT	1	11.17	0.001	2162	101.66	AE003834	TRUE	FALSE	3	3925.9	-2.1	8of124	0.9924	FALSE	FALSE	::::::::::::::::::Cys_CAM:::::Oxidation_M:::::Oxidation_M:::::
NELSHVISALVSR	9	7.85	0.446	2008	32.8	AE003835	TRUE	TRUE	2	1425.6	1.3	20of 24	4.0511	FALSE	FALSE	::::::::::::::
DHSDSLIAEAILTGNVDAAVELCLEAQR	15	3.76	0.16	1793	70.4	AE003835	TRUE	FALSE	3	3012.3	2.1	19of108	1.985	FALSE	FALSE	:::::::::::::::::::::::Cys_CAM::::::
PVPGCGEVYTRSNRIVGGH	11	8.9	0.104	818	30.3	AE003835	TRUE	FALSE	3	2056.3	-2.5	20of 72	1.9953	FALSE	FALSE	:::::Cys_CAM::::::::::::::
SLQAQDAAGDQLHIALGTYKGS	1	5.1	0.072	1786	40	AE003835	TRUE	FALSE	2	2245.5	-0.2	6of 42	0.7556	FALSE	FALSE	::::::::::::::::::::
QLNRCSEKTTVDAAASLSTSKP	2	8.93	0.062	2242	28.7	AE003835	TRUE	FALSE	3	2365.6	-2.3	20of 84	1.4433	FALSE	FALSE	:::::Cys_CAM::::::::::::::::
NDYSLQDLDSASEATSSPQSAS	3	2.79	0.023	2168	29	AE003835	TRUE	FALSE	2	2274.3	1.3	11of 42	1.5167	FALSE	FALSE	::::::::::::::::::::
PPRPLSNASSSGGPPPAGGASSSGGSGLSGR	6	12.41	0.023	2228	29	AE003835	TRUE	FALSE	3	2707.9	1.9	28of120	1.9121	FALSE	FALSE	::::::::::::::::::::::::::::
LTSLAGK	9	10.1	0.003	456	16.3	AE003835	TRUE	TRUE	1	689.8	0.6	7of 12	1.1737	FALSE	FALSE	::::::::
SDPAVEIIPAPSVELPQGELITVPKQLVP	6	3.69	0.001	1888	83.9	AE003835	TRUE	FALSE	3	3038.6	-1.9	21of112	1.9052	FALSE	FALSE	::::::::::::::::::::::::::::
EVWSPDMGLVTAAFK	1	4.08	0.093	536	45.93	AE003836	TRUE	TRUE	2	1651.9	2.9	12of 28	1.6706	FALSE	FALSE	::::::::::::::::
RSVGIFSIVFYCIYL	5	8.83	0.053	2575	66.9	AE003836	TRUE	FALSE	2	1838.2	-2.6	7of 28	1.064	FALSE	FALSE	::::::::::Cys_CAM::::
EKPDIYLK	13	6.92	0.047	998	19.1	AE003836	TRUE	FALSE	1	1006.2	1.1	8of 14	1.2326	FALSE	FALSE	::::::::
NGEFFIGLEKLHR	1	7.83	0.021	410	36.2	AE003836	TRUE	FALSE	2	1560.8	0.7	10of 24	1.7608	FALSE	FALSE	::::::::::::
IELPRAALIDNSE	12	3.83	0.021	1914	38	AE003836	TRUE	FALSE	2	1441.6	1.3	11of 24	1.3605	FALSE	FALSE	::::::::::::
LFCGPTHARNLYWNMTRVGDVNVQPCPGGAAG	4	8.29	0.015	2350	70.63	AE003836	TRUE	FALSE	3	3517.9	-1.3	11of124	1.2123	FALSE	FALSE	:::Cys_CAM:::::::::::::::::::::::Cys_CAM::::::::
TNENTPKTDDT	9	3.71	0.087	2720	2.6	AE003837	TRUE	FALSE	2	1236.2	0.9	5of 20	0.9786	FALSE	FALSE	::::::::::::
LARCNPRCSRGRKPTLCTKLR	11	11.85	0.041	2849	31.1	AE003837	TRUE	TRUE	2	2602	-2	9of 40	0.94	FALSE	FALSE	::::Cys_CAM:::Cys_CAM::::::::Cys_CAM:::::
VSYFSTSPELSNK	6	6.87	0.019	2820	25.9	AE003837	TRUE	FALSE	2	1459.6	2.5	9of 24	1.1204	FALSE	FALSE	::::::::::::::
MAIGIGAGAGSSPLR	7	11.05	0.012	1219	34.63	AE003837	TRUE	FALSE	2	1358.6	3	181	1.2125	FALSE	FALSE	::::::::::::::
SELSNSSNAHAYEGTVLK	9	5.3	0.003	2086	26.1	AE003837	TRUE	FALSE	2	1908	2.7	4of 34	0.7405	FALSE	FALSE	::::::::::::::::
DHNPSPKCSDSSGK	9	7.16	0.001	2781	-0.9	AE003837	TRUE	TRUE	2	1516.5	-0.9	4of 26	0.8089	FALSE	FALSE	::::::::Cys_CAM::::::::
SVFSGFSGFGKPAASPAAGSPFSFLANVTAPATTSSSEPK	14	9.89	0.359	1689	78.1	AE003838	TRUE	TRUE	3	3864.3	0.2	32of156	3.7718	FALSE	FALSE	::::::::::::::::::::::::::::::::::::
SNTLQKATLLTMDNAVCRSRF	11	10.11	0.135	2575	46.63	AE003838	TRUE	FALSE	2	2427.7	-1.5	10of 40	1.2739	FALSE	FALSE	:::::::::::::::::Cys_CAM::::::
DLSSNLPIFCGGSIVSERYIMTAAH	3	5.22	0.112	1540	67.53	AE003838	TRUE	FALSE	3	2756.1	-0.2	20of 96	1.7755	FALSE	FALSE	::::::::::Cys_CAM::::::::::Oxidation_M::::::
INILRTLSGRGLQLTRR	14	12.88	0.102	866	44.8	AE003838	TRUE	FALSE	2	1968.4	2.7	10of 32	1.2293	FALSE	FALSE	::::::::::::::::
ASSVKLTNKAGKNKFNKG	7	11.13	0.094	1271	12.7	AE003838	TRUE	FALSE	2	1893.2	2.4	51	1.5503	FALSE	FALSE	::::::::::::::::
YEVARMLK	6	9.72	0.058	1860	23.53	AE003838	TRUE	FALSE	1	1010.2	0.5	8of 14	1.2989	FALSE	FALSE	::::::::
TTFTFGKPSAPIGASVSPLAKK	3	10.85	0.055	1824	43.2	AE003838	TRUE	FALSE	2	2206.6	1.1	13of 42	1.5484	FALSE	FALSE	::::::::::::::::::::
SALMGPWLMRSFNR	5	12.41	0.052	1830	45.76	AE003838	TRUE	FALSE	2	1699	0.2	9of 26	1.0628	FALSE	FALSE	:::Oxidation_M:::::Oxidation_M:::::
KCMCPTNFILADDGR	15	6.1	0.047	2680	35.83	AE003838	TRUE	FALSE	3	1799	-2.6	11of 56	1.521	FALSE	FALSE	::Cys_CAM::Cys_CAM:::::::::::
TLAVHDPRKLSSGSITMKKIIRKQVTGKTRKQFEA	3	11.63	0.041	2114	54.23	AE003838	TRUE	FALSE	3	3971.7	-0.5	22of136	2.0729	FALSE	FALSE	::::::::::::::Oxidation_M:::::::::::::::::
IKTPAQSTRPPRILVKSFLAL	9	12.43	0.025	1017	57.6	AE003838	TRUE	FALSE	3	2337.9	1.1	20of 80	2.2532	FALSE	FALSE	::::::::::::::::::::
KLQWQPTLGNCMLRA	3	10.11	0.018	1561	42.33	AE003838	TRUE	FALSE	2	1817.1	1.4	10of 28	1.4428	FALSE	FALSE	:::::::::Cys_CAM:::::
LDNQSKASNEAETEKAIPAVIEDTEKEK	1	4.16	0.017	2033	36.1	AE003838	TRUE	FALSE	3	3089.3	-2	10of108	1.2068	FALSE	FALSE	::::::::::::::::::::::::::
KDKSRKCPFGR	14	10.82	0.011	2725	5	AE003838	TRUE	FALSE	2	1379.6	-2.1	8of 20	0.914	FALSE	FALSE	::::::Cys_CAM:::::
ELQRLRGKDAEELIA	10	4.65	0.004	2686	35.7	AE003838	TRUE	FALSE	2	1742	-2.7	4of 28	0.6863	FALSE	FALSE	::::::::::::::::
IGGTPIIGGQYVVSCDLIPQLPVIK	6	6.09	0.335	2158	79	AE003839	TRUE	TRUE	2	2639.1	-0.4	18of 48	3.9218	FALSE	FALSE	::::::::::::::Cys_CAM:::::::::::
IGGTPIIGGQYVVSCDLIPQLPVIK	7	6.09	0.313	1936	79	AE003839	TRUE	TRUE	2	2639.1	0.3	1	3.9566	FALSE	FALSE	::::::::::::::Cys_CAM:::::::::::
DPASPEGGEIIFGGSDPNHYTGEFTYLPVTR	1	3.92	0.246	1288	63.9	AE003839	TRUE	TRUE	3	3325.6	2.6	32of120	2.6682	FALSE	FALSE	::::::::::::::::::::::::::::
ESAAYAPRGGYSPYPPR	10	9.44	0.142	1842	26.6	AE003839	TRUE	FALSE	2	1840	-1.9	10of 32	1.272	FALSE	FALSE	::::::::::::::::
LLSIWKNLPEHPLQEQ	13	5.3	0.06	1090	49.8	AE003839	TRUE	FALSE	3	1946.3	0.6	17of 60	1.723	FALSE	FALSE	::::::::::::::::
QLDTRVNIIPVIAKA	5	10.09	0.056	2903	43.8	AE003839	TRUE	FALSE	2	1652	2.4	6of 28	0.988	FALSE	FALSE	::::::::::::::::
RVDQLDRNNSDLPECVDR	14	4.13	0.05	2624	29.5	AE003839	TRUE	FALSE	3	2202.3	-1.2	17of 68	1.5303	FALSE	FALSE	::::::::::::::Cys_CAM::::
EGILPRMLTEILD	7	3.83	0.042	1308	48.83	AE003839	TRUE	FALSE	2	1500.8	0.4	72	1.604	FALSE	FALSE	::::::::::::::
KLLMTPAVGTANELAGARGAKSTISQYFSTTSC	4	9.66	0.036	2243	66.73	AE003839	TRUE	FALSE	3	3433.9	0.2	23of128	2.477	FALSE	FALSE	:::::::::::::::::::::::::::::::Cys_CAM:
RWVRRTTLVDSRTSVTDVEFAPKYLGL	6	10.38	0.035	1663	68.5	AE003839	TRUE	FALSE	3	3167.6	1.8	20of104	1.7712	FALSE	FALSE	::::::::::::::::::::::::::::
IVIGNQTCVFEKENDPSLL	9	3.83	0.035	2689	53	AE003839	TRUE	FALSE	3	2177.4	-0.4	17of 72	1.6428	FALSE	FALSE	::::::::Cys_CAM:::::::::::
MFMPESKASDLHQILTQMD	9	4.3	0.035	2423	49.79	AE003839	TRUE	FALSE	3	2255.6	1.9	19of 72	1.5008	FALSE	FALSE	:Oxidation_M::Oxidation_M:::::::::::::::
PVFALGVAR	9	11.05	0.03	998	31.4	AE003839	TRUE	FALSE	2	930.1	2.1	9of 16	1.0305	FALSE	FALSE	::::::::::
HPLQEQEPLGDR	11	4.43	0.026	912	19.7	AE003839	TRUE	FALSE	2	1419.5	-2.6	10of 22	1.2594	FALSE	FALSE	::::::::::::
YERKLPIDDTQ	6	4.31	0.009	2790	21.4	AE003839	TRUE	FALSE	2	1378.5	-0.1	8of 20	1.1109	FALSE	FALSE	::::::::::::
RMMEKMNRTILKKFS	11	11.57	0	840	33.59	AE003839	TRUE	FALSE	2	1930.4	0.9	10of 28	1.6934	FALSE	FALSE	:::Oxidation_M:::::::::::
YACSCGILNPINTLFFCR	14	8.01	0.247	1694	61.9	AE003840	TRUE	TRUE	2	2207.4	1.6	18of 34	2.7764	FALSE	FALSE	:::Cys_CAM::Cys_CAM::::::::::Cys_CAM::
WEPLEATELV	9	3.03	0.207	904	37.9	AE003840	TRUE	FALSE	2	1187.3	-2.2	7of 18	1.047	FALSE	FALSE	::::::::::
LAPRSRSPGGQSAASGGGKVVTLGK	7	12.43	0.182	1847	29.4	AE003840	TRUE	FALSE	2	2339.7	1.5	5	1.5123	FALSE	FALSE	::::::::::::::::::::::
SATGMQYMIDKKAVLDVDILLM	2	4.18	0.153	1800	70.79	AE003840	TRUE	FALSE	2	2457	2.2	11of 42	2.3418	FALSE	FALSE	::::::::::::::::::::::
SSPMQETTGDMNDVLPDELMESPEER	13	3.28	0.149	984	49.09	AE003840	TRUE	FALSE	3	2955.2	-1.7	20of100	2.1155	FALSE	FALSE	::::::::::Oxidation_M:::::::::::::
VQVLDESLDSQSNPSLYSLQTTTTTNTSDESDTVR	13	3.32	0.125	1413	57.3	AE003840	TRUE	FALSE	3	3732.9	2.6	25of132	2.6776	FALSE	FALSE	::::::::::::::::::::::::::::
VVQGRSINLALSQR	10	12.41	0.097	1029	33.2	AE003840	TRUE	FALSE	3	1541.8	1.9	18of 52	2.6232	FALSE	FALSE	::::::::::::::
EAPKDRPKRKLKPQPKKDSK	13	10.9	0.07	2534	3.5	AE003840	TRUE	FALSE	3	2375.8	-2.3	12of 76	1.317	FALSE	FALSE	::::::::::::::::::
EETSMPSSNLLKATAR	7	7.1	0.068	1739	27.23	AE003840	TRUE	FALSE	2	1736	-1.2	459	1.0945	FALSE	FALSE	::::::::::::::::
AIVTGGAIYAQR	9	9.85	0.061	2519	29.9	AE003840	TRUE	FALSE	2	1220.4	-2	8of 22	1.0628	FALSE	FALSE	::::::::::::
PTPLGANQKR	10	11.49	0.038	961	11.2	AE003840	TRUE	TRUE	2	1082.2	-1.2	9of 18	1.1147	FALSE	FALSE	::::::::::
FTSNAVAILVGGAQEALDSHPGK	8	5.22	0.035	2617	47.8	AE003840	TRUE	FALSE	2	2283.5	-0.4	11of 44	1.2952	FALSE	FALSE	::::::::::::::::::::
KESVTAESCKLD	9	4.45	0.012	1066	16.1	AE003840	TRUE	FALSE	2	1367.5	-0.3	10of 22	1.4119	FALSE	FALSE	::::::::Cys_CAM::::
RRKKTRRTHV	11	12.89	0.005	2580	-2.5	AE003840	TRUE	FALSE	2	1338.6	-1.8	6of 18	1.0915	FALSE	FALSE	::::::::::
SRSGSQSMPRANR	14	12.71	0.136	684	6.13	AE003841	TRUE	FALSE	2	1434.6	0	11of 24	1.8821	FALSE	FALSE	::::::::::::
EDKVADIADMIR	10	3.97	0.105	2654	28.33	AE003841	TRUE	FALSE	2	1392.6	-0.4	7of 22	1.1057	FALSE	FALSE	:::::::::Oxidation_M:::
TLLKYMTDGMLLREAMSDPMLDQY	1	3.97	0.101	228	75.42	AE003841	TRUE	FALSE	3	2853.4	0.6	14of 92	1.8198	FALSE	FALSE	::::::::::::::Oxidation_M:::::::::
APTTPDLKQIFPNIDPSQLKR	6	9.89	0.082	2218	45.1	AE003841	TRUE	FALSE	2	2380.7	-2.8	6of 40	0.9524	FALSE	FALSE	::::::::::::::::::::
QHESVSQISPKSSSHRSPDRQR	1	11.23	0.075	122	8.2	AE003841	TRUE	FALSE	2	2534.7	-0.6	11of 42	1.1955	FALSE	FALSE	::::::::::::::::::::
MSSLSIKRTER	11	11.33	0.072	718	18.83	AE003841	TRUE	FALSE	2	1308.5	2.4	10of 20	1.2126	FALSE	FALSE	::::::::::::
ALDSAMSMTPYSDEFME	8	2.84	0.051	1748	45.89	AE003841	TRUE	FALSE	2	1974.1	2.8	8of 32	1.2742	FALSE	FALSE	::::::Oxidation_M::Oxidation_M::::::::Oxidation_M::
QQRIFEPAPPPNANGAIGR	3	10.89	0.032	2253	35.2	AE003841	TRUE	FALSE	2	2034.3	1.8	9of 36	1.3234	FALSE	FALSE	::::::::::::::::::::
IVTCPVAGYPIDSIVWERDNRALPINRKQK	4	9.66	0.021	2389	73.1	AE003841	TRUE	FALSE	3	3511	-1.4	22of116	1.6329	FALSE	FALSE	::::Cys_CAM:::::::::::::::::::::::::

VMTPGQAFTIRENGATVATGMVTQRLPSLDLPK	5	10.09	0.006	1715	77.46	AE003841	TRUE	FALSE	3	3502.1	-1.8	22of128	2.5641	FALSE	FALSE	::::::::::::::::::::::::::::::::
AIKLPTRTHELF	10	10.09	0.003	1314	33.2	AE003841	TRUE	FALSE	2	1426.7	1.5	11of 22	1.3277	FALSE	FALSE	::::::::::::
SGASSSSPMSGEPAKKKGVR	11	10.83	0.104	2717	10.93	AE003842	TRUE	FALSE	2	1949.2	1.8	6of 38	0.8293	FALSE	FALSE	::::::::::::::::::
ALCGGAVFGVAFLGMYVALK	7	8.88	0.091	1929	73.23	AE003842	TRUE	FALSE	2	2045.5	-2.6	7	1.4649	FALSE	FALSE	:::Cys_CAM:::::::::::::::
GRPLFPHSSSPRR	6	12.71	0.05	1178	17.5	AE003842	TRUE	FALSE	2	1494.7	2.6	8of 24	1.3919	FALSE	FALSE	::::::::::::
METQYEELLKGPK	14	4.56	0.043	2029	27.73	AE003842	TRUE	TRUE	2	1566.8	0.5	9of 24	1.3197	FALSE	FALSE	::::::::::::
WRVCFLYGDQQKYYR	11	9.44	0.002	442	42.8	AE003842	TRUE	FALSE	3	2083.3	0	16of 56	1.6663	FALSE	FALSE	::::Cys_CAM:::::::::::
RREKNAPRSCPACN	11	10.12	0.142	2558	9	AE003843	TRUE	FALSE	3	1716.8	-0.2	12of 52	1.4695	FALSE	FALSE	:::::::::Cys_CAM:::Cys_CAM::
CNNNNLGVNLSNELSNISAK	15	6.29	0.093	1531	35.3	AE003843	TRUE	FALSE	2	2176.3	2	13of 38	1.9528	FALSE	FALSE	:Cys_CAM:::::::::::::::::
LVASNEKGEAVSQIVNLVDIPEEE	10	3.51	0.091	812	58.8	AE003843	TRUE	FALSE	3	2583.9	2.9	21of 92	2.5409	FALSE	FALSE	::::::::::::::::::::::
RHLLIPTGVPLGNGR	15	12.41	0.073	2951	36.8	AE003843	TRUE	FALSE	3	1600.9	-2.5	20of 56	1.8692	FALSE	FALSE	::::::::::::::::
QTSSCSDTSMNSPHILETL	5	4.07	0.026	2900	33.13	AE003843	TRUE	FALSE	3	2125.2	0.8	20of 72	2.2044	FALSE	FALSE	:::::Cys_CAM::::Oxidation_M:::::::::
EKNGSSSISADDK	3	4.31	0.025	1569	5.1	AE003843	TRUE	FALSE	2	1338.4	-0.8	7of 24	0.9803	FALSE	FALSE	::::::::::::::
VTNDKTSEVNRSTEEQKSTFGRLR	1	9.88	0.009	782	24.1	AE003843	TRUE	FALSE	3	2784	1.5	8of 92	1.1812	FALSE	FALSE	::::::::::::::::::::::
TSNAAVAGAASVNIAANTNNQPSGQQIR	6	11.05	0.009	1394	37.4	AE003843	TRUE	FALSE	3	2726.9	-2	28of108	2.6818	FALSE	FALSE	::::::::::::::::::::::::::
EKVDKNCNATSLAQPAKGSGEPMVQHGNAANNQN	2	7.17	0.006	2398	30.23	AE003843	TRUE	FALSE	3	3581.8	-0.1	17of132	1.5758	FALSE	FALSE	::::::Cys_CAM:::::::::::::::::::::::
VPIGTK	10	10.1	0	453	12.7	AE003843	TRUE	FALSE	1	614.8	0.5	6of 10	1.2118	FALSE	FALSE	::::::
DRQKITNGR	9	11.33	0.063	468	4.1	AE003844	TRUE	FALSE	2	1088.2	-0.3	11of 16	1.5132	FALSE	FALSE	::::::::
CGPLPLANDKCKLDTEKTNK	5	8.28	0.042	2308	28.4	AE003844	TRUE	FALSE	3	2303.6	-0.5	19of 76	1.8165	FALSE	FALSE	:Cys_CAM::::::::Cys_CAM:::::::::
TDVNETAIVSGDTIESLK	7	3.59	0.035	1524	36	AE003844	TRUE	FALSE	3	1893.1	3	2	2.2997	FALSE	FALSE	::::::::::::::::::
SYAESGLPTSDSLASVKTIDTWTHNDAELGIK	14	4.2	0.077	1906	62.3	AE003845	TRUE	FALSE	3	3408.7	2.9	24of124	2.6391	FALSE	FALSE	::::::::::::::::::::::::::::::::
GGLNSMPHSNSALPFTAHK	4	10.1	0.132	1575	29.93	AE003846	TRUE	TRUE	2	1967.2	-2.5	7of 36	0.978	FALSE	FALSE	::::::::::::::::::
AFYMVGPIEEVVEKADRLAK	12	4.65	0.129	1209	55.13	AE003846	TRUE	FALSE	3	2282.7	-0.5	21of 76	1.9133	FALSE	FALSE	::::Oxidation_M:::::::::::::::
GGSTMTFFRHNK	11	11.49	0.049	320	16.93	AE003846	TRUE	FALSE	3	1399.6	0.3	14of 44	1.5064	FALSE	FALSE	:::::Oxidation_M:::::::
TSIQNSTDLGHPNKNK	5	9.89	0.035	2130	10.2	AE003846	TRUE	FALSE	2	1754.9	2.7	11of 30	1.3011	FALSE	FALSE	::::::::::::::::
EYLTINGR	13	6.89	0.021	1848	20.3	AE003846	TRUE	FALSE	2	966.1	0.4	8of 14	1.4005	FALSE	FALSE	::::::::
DTNEVDGKSGSSLPQRSQID	2	3.97	0.02	2350	20.3	AE003846	TRUE	FALSE	2	2134.2	-1.9	7of 38	0.9811	FALSE	FALSE	::::::::::::::::::
EEIHQGISQMASDMAQKLGISYDDAYR	6	4.2	0.099	2264	53.36	AE014155	TRUE	FALSE	3	3058.4	2.9	17of104	1.5787	FALSE	FALSE	::::::::::::::::::::::::::::
TQIKAIMEKHNGDMSQLSSAEK	15	7.77	0.019	953	31.16	AE014155	TRUE	FALSE	3	2463.8	-2.4	8of 84	0.9399	FALSE	FALSE	:::::::::::::Oxidation_M:::::::::
KCIMEILLYYNNINMDT	10	4.08	0.011	1124	59.06	AE014844	TRUE	FALSE	3	2165.5	0.2	21of 64	2.513	FALSE	FALSE	::Cys_CAM::::::::::::Oxidation_M:::
IVKNRKRNLEMKRIWVQSIFR	8	12.42	0.021	2680	53.73	AE014851	TRUE	TRUE	3	2732.3	-0.7	17of 80	1.6779	FALSE	FALSE	:::::::::::Oxidation_M:::::::::::
ILGNSITAVKPDNESSK	14	6.99	0.151	1032	27.6	AE014896	TRUE	FALSE	2	1774	-0.5	6of 32	1.0105	FALSE	FALSE	::::::::::::::::
NRKQISELVFRFCLER	10	10.1	0.171	1764	44.9	AE017256	TRUE	FALSE	2	2096.4	-1.7	6of 30	1.1697	FALSE	FALSE	:::::::::::::Cys_CAM::::
SKLKYDMAMKKAQKVK	2	10.6	0.152	434	20.06	AE017256	TRUE	FALSE	3	1930.4	0.3	10of 60	1.8398	FALSE	FALSE	::::::Oxidation_M::Oxidation_M:::::::
MFTKLSVPVIGIVENMSYFIQSGSK	14	9.63	0.128	1200	74.76	AE017256	TRUE	FALSE	3	2793.3	-3	8of 96	1.0281	FALSE	FALSE	:::::::::::::::Oxidation_M:::::::::
KVQRLDRPYIKK	11	10.89	0.11	2748	19.7	AE017256	TRUE	FALSE	2	1544.9	-1.9	5of 22	1.078	FALSE	FALSE	::::::::::::
DGLLPISQWALHFY	15	4.94	0.108	2022	54.8	AE017256	TRUE	FALSE	2	1660.9	1.8	6of 26	0.9742	FALSE	FALSE	::::::::::::
FTLDVPIFKRGVNAFGVSKAKMDAK	1	10.55	0.101	1850	59.13	AE017256	TRUE	FALSE	3	2741.3	0.9	12of 96	1.1447	FALSE	FALSE	::::::::::::::::::::::::
FLTNLVADKIMEEK	8	4.45	0.094	2027	42.43	AE017256	TRUE	FALSE	2	1652	-0.3	5of 26	1.0683	FALSE	FALSE	::::::::::::
TVVVTGANSPVGLRSMPVR	3	12.41	0.092	2065	43.23	AE017256	TRUE	FALSE	2	1941.3	-0.1	6of 36	0.8194	FALSE	FALSE	::::::::::::::::::
ILVPDNRIAGVAFTGSTQTAQIINKMLANRD	4	10.09	0.091	1503	75.93	AE017256	TRUE	FALSE	3	3329.8	-1.8	12of120	1.2732	FALSE	FALSE	::::::::::::::::::::::::::::
AIVAPDVGAIGRARAFAK	8	11.33	0.08	3266	43.4	AE017256	TRUE	FALSE	3	1784.1	-1.7	7of 68	0.9666	FALSE	FALSE	::::::::::::::::::
DGWKVPFVPDKFKGVRL	11	10.32	0.077	1529	45.2	AE017256	TRUE	FALSE	2	1989.4	-0.1	10of 32	1.3737	FALSE	FALSE	::::::::::::::::
RLLENGANSSF	14	6.98	0.063	948	25	AE017256	TRUE	FALSE	2	1208.3	1.9	13of 20	2.3324	FALSE	FALSE	::::::::::::
EVADTNNNDSDKVT	5	3.51	0.062	1804	10.8	AE017256	TRUE	FALSE	2	1522.5	-1.8	9of 26	1.1043	FALSE	FALSE	::::::::::::::
SSIYEALKANSDLRK	13	9.63	0.06	1728	27.4	AE017256	TRUE	FALSE	2	1695.9	-2.1	7of 28	1.0103	FALSE	FALSE	::::::::::::::::
FLGPTGVGKTELAK	2	9.89	0.059	185	30.8	AE017256	TRUE	FALSE	2	1418.7	2.2	13of 26	2.1158	FALSE	FALSE	::::::::::::::
YVHQKVDLPEIRPYVVIGTWSLLEMQKKKK	5	10.04	0.054	2390	75.83	AE017256	TRUE	FALSE	3	3628.4	-1.9	12of116	1.1949	FALSE	FALSE	::::::::::::::::::::::::::::
KSLSDIDKYMHALSALIR	5	9.63	0.049	2427	46.03	AE017256	TRUE	FALSE	2	2062.4	2.8	6of 34	0.9103	FALSE	FALSE	::::::::::::::::::
THVTKIASMKGDA	9	9.89	0.029	1033	16.63	AE017256	TRUE	FALSE	2	1375.6	2.5	10of 24	1.3	FALSE	FALSE	::::::::Oxidation_M:::::
FYPYITISKHDYPRIAKYRG	2	9.96	0.024	1796	47.2	AE017256	TRUE	FALSE	3	2489.9	1	9of 76	1.0838	FALSE	FALSE	::::::::::::::::::
TKKFPIKIVAAGRVYRNDFDATHTPMFHQI	9	10.44	0.024	2318	66.23	AE017256	TRUE	FALSE	3	3520.1	3	25of116	2.3506	FALSE	FALSE	:::::::::::::::::::::::::Oxidation_M:::::
NDYLLGYFPKKMSTEFK	9	9.43	0.021	1105	43.53	AE017256	TRUE	FALSE	3	2082.4	-1.8	18of 64	2.0068	FALSE	FALSE	::::::::::::::::::
LGNSYPIFRKTEIGGDSLVNASVRFGNLGKPTVHFK	12	10.44	0.021	1679	78.4	AE017256	TRUE	FALSE	3	3921.5	2.8	21of140	2.4777	FALSE	FALSE	::::::::::::::::::::::::::::::::::
DIKGRFLSPEEGKEFFQK	3	7.16	0.02	2062	37.8	AE017256	TRUE	TRUE	2	2156.4	-0.8	4of 34	0.6966	FALSE	FALSE	::::::::::::::::::
SIEDFSKDMRD	14	3.97	0.018	2709	19.63	AE017256	TRUE	FALSE	2	1359.5	-0.2	4of 20	0.6287	FALSE	FALSE	::::::::Oxidation_M:::
LEFVKDVLESK	12	4.45	0.014	1819	32.3	AE017256	TRUE	FALSE	2	1307.5	1.7	8of 20	1.2085	FALSE	FALSE	::::::::::::
VETLAEAVADQQKIMAICIIVSAVAA	12	3.83	0.009	2080	80.53	AE017256	TRUE	FALSE	3	2716.2	-1.2	10of100	1.2015	FALSE	FALSE	:::::::::::::::::Cys_CAM:::::::::
KYREISSCSCNCGAFQARRMNTKYSSETDKKMK	3	10.05	0.008	2363	33.66	AE017256	TRUE	FALSE	3	3896.3	-0.9	19of124	2.1089	FALSE	FALSE	::::::::Cys_CAM:::Cys_CAM:::::::Oxidation_M::::::::::::Oxidation_M::
DPIGNGVLLR	8	6.79	0.005	2073	29.2	AE017256	TRUE	FALSE	1	1054.2	1	6of 18	0.9269	FALSE	FALSE	::::::::::
RRTKNNPVLIGEPGVGK	1	11.47	0	1109	24	AE017256	TRUE	FALSE	2	1836.1	2.5	8of 32	1.3923	FALSE	FALSE	::::::::::::::::::
LFPAEAKELIARGAKVQVGK	3	10.32	0	1959	46.6	AE017256	TRUE	FALSE	2	2126.6	-0.1	9of 38	0.9557	FALSE	FALSE	::::::::::::::::::
GVLKAVQAVNGIIAD	8	6.76	0.175	2488	41	AE017257	TRUE	FALSE	2	1468.7	-2.1	8of 28	1.3192	FALSE	FALSE	::::::::::::::
DTLWPDFSCQDLSK	15	3.6	0.171	1280	36.4	AE017257	TRUE	FALSE	2	1712.8	0.5	5of 26	0.9098	FALSE	FALSE	::::::::Cys_CAM:::::
LGLECFEVLDEFMNLVLQFE	2	2.85	0.148	834	86.73	AE017257	TRUE	FALSE	3	2446.8	2.7	8of 76	0.9652	FALSE	FALSE	:::::Cys_CAM:::::::::::::::
GDEFIQEKEDGIVQTKRR	13	4.73	0.138	947	26.4	AE017257	TRUE	TRUE	3	2149.4	-1.5	20of 68	1.7322	FALSE	FALSE	::::::::::::::::
AITFNSGEPLIEESVLNIDKETISKRIVIPT	8	4.36	0.126	2785	84.3	AE017257	TRUE	FALSE	2	3428.9	0.9	5of 60	0.7432	FALSE	FALSE	::::::::::::::::::::::::::::
VWNNIVLLKELNALRKERTEARLSGNLDLEER	3	7.28	0.111	2383	83.8	AE017257	TRUE	FALSE	3	3794.3	-2.3	21of124	1.8247	FALSE	FALSE	::::::::::::::::::::::::::::
PAGVIVQGGVKVKISMS	5	10.6	0.091	1944	39.13	AE017257	TRUE	FALSE	2	1671.1	1.6	10of 32	1.1051	FALSE	FALSE	::::::::::::::::
SSVLDKLKGASDEEQIGINIIKKVLSAPIR	5	9.67	0.08	2387	69.1	AE017257	TRUE	FALSE	3	3223.8	2.8	16of116	1.3777	FALSE	FALSE	::::::::::::::::::::::::::::
IQEFAKTMEELIK	9	4.56	0.08	1397	38.23	AE017257	TRUE	FALSE	2	1580.9	-2.1	10of 24	1.2846	FALSE	FALSE	::::::::::::
KSNDKEELVKE	2	4.65	0.078	213	9.5	AE017257	TRUE	FALSE	2	1319.5	-0.4	14of 20	2.2158	FALSE	FALSE	::::::::::
KETEKSDLDEKSSKKTS	13	7.14	0.065	1539	1.7	AE017257	TRUE	FALSE	2	1941.1	2.5	7of 32	1.0135	FALSE	FALSE	::::::::::::::::
SVEELLSYPEESAGRLIHKDMVI	12	4.36	0.054	2866	62.13	AE017257	TRUE	FALSE	2	2633	1.4	7of 44	1.0878	FALSE	FALSE	::::::::::::::::::Oxidation_M:::
DEILPWIIEEYGLGEILRWVKDKGKAIR	9	4.85	0.05	1469	89.1	AE017257	TRUE	TRUE	3	3341.9	1.7	21of108	2.3014	FALSE	FALSE	::::::::::::::::::::::::::
CNKKYIKDALCSK	7	9.57	0.041	1164	18.2	AE017257	TRUE	TRUE	3	1628.8	2.5	30	2.4514	FALSE	FALSE	:Cys_CAM::::::::Cys_CAM:::
EISKRDKYDYVIINDDIDKSVE	13	4.11	0.028	2376	43.9	AE017257	TRUE	FALSE	2	2658.9	2.4	5of 42	1.0468	FALSE	FALSE	::::::::::::::::::::::
EKLVNILDQHLL	12	5.22	0.022	2067	41.3	AE017257	TRUE	FALSE	3	1435.7	-0.3	12of 44	1.3401	FALSE	FALSE	::::::::::::
LEVIQERLEREFDLDLTATAPSVIYR	13	4.13	0.022	1441	79.8	AE017257	TRUE	FALSE	3	3078.5	2.9	13of100	1.2136	FALSE	FALSE	::::::::::::::::::::::::
QVELWKVSLVTFPANLAAQVINVKNQ	6	9.89	0.02	2589	77.1	AE017257	TRUE	FALSE	2	2911.4	2.5	6of 50	1.0897	FALSE	FALSE	::::::::::::::::::::::::
QKKLNVNVSFDSKLAQYLTEMAETQNK	7	9.51	0.018	1397	49.43	AE017257	TRUE	FALSE	3	3145.6	-0.2	140	1.8246	FALSE	FALSE	::::::::::::::::::Oxidation_M::::::
EVGTHDFLMSKDGLYAK	10	5.28	0.016	1050	36.53	AE017257	TRUE	FALSE	3	1928.2	-1.2	19of 64	1.5699	FALSE	FALSE	::::::::Oxidation_M:::::::::
MLIIHMLLAKYR	11	10.4	0.016	1221	51.86	AE017257	TRUE	FALSE	1	1519	-0.9	8of 22	1.7283	FALSE	FALSE	:Oxidation_M:::::::::::

HSILQYMPKIEKERRKNWVRK	5	11	0.014	2156	37.83	AE017257	TRUE	FALSE	3	2757.3	2.9	19of 80	1.6557	FALSE	FALSE	::::::Oxidation_M::::::::::::::
LHVAGMSSIVGAINFIVTIFNMR	9	11.05	0.013	1533	79.86	AE017257	TRUE	FALSE	3	2508	0.9	20of 88	2.2593	FALSE	FALSE	::::::Oxidation_M::::::::::::::::
KTGEILGSHM	13	7.82	0.012	1800	17.93	AE017257	TRUE	FALSE	1	1089.3	2.4	6of 18	1.0582	FALSE	FALSE	::::::::::Oxidation_M:
MFRYAGAEVPSDAILEE	13	3.69	0.012	1742	49.13	AE017257	TRUE	FALSE	2	1915.1	2.8	7of 32	1.115	FALSE	FALSE	:Oxidation_M::::::::::::::
DNHQFYNAKYIEDSRAAIIVKQNSEAKKNL	4	9.39	0.009	2278	49.1	AE017257	TRUE	FALSE	3	3509.9	1.2	13of116	1.2565	FALSE	FALSE	::::::::::::::::::::::::::::
LGWSHGNDEIISDEQAIEWFNLESIGRSP	5	3.82	0.008	2666	75	AE017257	TRUE	FALSE	3	3301.6	2.8	21of112	2.0763	FALSE	FALSE	::::::::::::::::::::::::::::
YVSGQEKVVVDENS	14	3.83	0.007	1472	23.6	AE017257	TRUE	FALSE	2	1553.7	1.3	12of 26	1.897	FALSE	FALSE	::::::::::::::
PVMEGKAVLFKRF	4	10.59	0.005	2816	39.93	AE017257	TRUE	FALSE	2	1522.9	-1.7	8of 24	1.023	FALSE	FALSE	::::::::::::::
LSKAGLSITEW	8	6.95	0.003	2593	33.4	AE017257	TRUE	FALSE	2	1205.4	-2.7	7of 20	1.5251	FALSE	FALSE	::::::::::::
GMRIVNSKKEI	2	10.59	0.001	858	20.63	AE017257	TRUE	FALSE	1	1275.6	0.7	8of 20	1.1161	FALSE	FALSE	::::::::::::
DLHISPQSPTPSSSGYSSPSTPSSRR	2	9.85	0.167	2281	25.9	AE017258	TRUE	TRUE	3	2716.9	2.3	8of100	1.1884	FALSE	FALSE	::::::::::::::::::::::::
NRFIRVDKFHEPGLAPVYDE	8	5.39	0.162	2647	48.6	AE017258	TRUE	FALSE	2	2403.7	-0.2	11of 38	1.2881	FALSE	FALSE	::::::::::::::::::::
DFYFTFIELPKFPKTKEDQLES	8	4.29	0.146	1840	62.9	AE017258	TRUE	FALSE	3	2724.1	-2.7	9of 84	0.9421	FALSE	FALSE	::::::::::::::::::::
SLTKFGFEKNNPI	4	9.89	0.145	2758	29.6	AE017258	TRUE	FALSE	2	1495.7	-1.6	8of 24	1.2456	FALSE	FALSE	::::::::::::::
MGGWLMLLTALQFPEK	2	6.95	0.115	408	63.56	AE017258	TRUE	FALSE	2	1836.3	-0.7	8of 30	1.1267	FALSE	FALSE	::::::::::::::::
ARIMLGMATIMVALAAPFQLFMGDR	10	10.89	0.106	509	93.62	AE017258	TRUE	FALSE	3	2758.4	1.9	22of 96	1.6392	FALSE	FALSE	::::Oxidation_M:::Oxidation_M::::::::::::::::::
GNTHEINLADGMLKV	8	5.22	0.071	3320	32.23	AE017258	TRUE	FALSE	2	1612.8	-2.2	6of 28	0.8867	FALSE	FALSE	::::::::::::::::
KGDCASMAVIELVDRD	7	3.97	0.069	2028	36.23	AE017258	TRUE	FALSE	2	1780	-2.6	125	0.9348	FALSE	FALSE	::::Cys_CAM::::::::::::
PYCGLSCNLDLSYRNLSNIK	2	8.27	0.057	698	50.9	AE017258	TRUE	FALSE	3	2388.6	0.4	15of 76	1.4236	FALSE	FALSE	:::Cys_CAM::::Cys_CAM::::::::::::
NVFHKGFAIAEDKHGWFHIDINGNPVYR	2	7.96	0.054	1440	63.8	AE017258	TRUE	FALSE	3	3283.7	-2.3	10of108	1.4168	FALSE	FALSE	::::::::::::::::::::::::::::
KSREQFEMRTSRRLIVLHDLTPTMMQML	1	11.16	0.053	1969	74.22	AE017258	TRUE	FALSE	3	3514.1	1.3	18of108	1.5133	FALSE	FALSE	::::::::Oxidation_M::::::::::::::Oxidation_M:Oxidation_M::Oxidation_M::
AQSRKQIIYASASLILSGVFAVGTSLTMSHLGISIS	5	10.4	0.052	2091	99.73	AE017258	TRUE	FALSE	3	3725.3	3	27of140	2.2401	FALSE	FALSE	::::::::::::::::::::::::::::Oxidation_M::::::::
KVLKTKNIVIATGSDVISLPGINIDEK	13	9.67	0.049	1391	64.5	AE017258	TRUE	FALSE	3	2867.4	0.1	18of104	1.3462	FALSE	FALSE	::::::::::::::::::::::::::
NNPLFMFGLCNIATGLLTIGITLSYNNLTLL	5	5.33	0.046	1794	118.43	AE017258	TRUE	FALSE	3	3430	-1.2	29of120	3.2805	FALSE	FALSE	:::::Oxidation_M:::Cys_CAM::::::::::::::::::::
YPTLTKAIMGTVAALISLKVVAVGLGYGFTL	3	9.94	0.044	1260	105.13	AE017258	TRUE	FALSE	3	3185.9	-1.4	20of120	1.5671	FALSE	FALSE	::::::::Oxidation_M:::::::::::::::::::::
VLPADDIQSLSERILAEEHK	12	4.28	0.043	1377	48.6	AE017258	TRUE	FALSE	3	2264.5	-0.6	19of 76	1.7845	FALSE	FALSE	::::::::::::::::::::
LFNFDNQGQLALNGNTMLYSQ	15	3.1	0.043	291	58.43	AE017258	TRUE	FALSE	3	2389.6	0.3	12of 80	1.4577	FALSE	FALSE	::::::::::::::::::::
LICHQAERENIPIVINVTR	1	7.17	0.041	877	52.6	AE017258	TRUE	FALSE	3	2276.6	-2.4	20of 72	2.3137	FALSE	FALSE	:::Cys_CAM::::::::::::::::
RKISPPSRAEMKKSMEALIHHFK	5	10.97	0.036	2042	37.86	AE017258	TRUE	FALSE	2	2739.3	1.4	7of 44	1.0059	FALSE	FALSE	::::::::::Oxidation_M::::::::::::
HIETARRVISRTLKRSGKV	9	12.42	0.035	2452	27.9	AE017258	TRUE	FALSE	2	2208.6	-1.6	8of 36	1.2796	FALSE	FALSE	::::::::::::::::::
YNIKLIIQE	14	6.87	0.031	1051	33.2	AE017258	TRUE	FALSE	1	1134.4	1.3	12of 16	2.1666	FALSE	FALSE	::::::::::
HVAISSSNYDER	9	5.22	0.024	1218	16.3	AE017258	TRUE	FALSE	2	1378.4	-0.7	9of 22	1.288	FALSE	FALSE	::::::::::::
FSTRKGDCASMAVIELVDRDIAA	10	4.46	0.024	2438	55.53	AE017258	TRUE	FALSE	2	2526.8	-1.9	10of 44	1.1058	FALSE	FALSE	:::::::Cys_CAM::::::::::::::
MELNTILK	1	6.95	0.021	857	28.13	AE017258	TRUE	FALSE	1	978.2	0.7	9of 14	1.8853	FALSE	FALSE	:Oxidation_M:::::::
AKIIDDEIK	10	4.31	0.018	2436	21.5	AE017258	TRUE	FALSE	2	1045.2	2.9	7of 16	1.2189	FALSE	FALSE	::::::::::
NFVEAKEI	9	4.27	0.015	1197	22	AE017258	TRUE	FALSE	2	950.1	1.6	8of 14	1.373	FALSE	FALSE	::::::::::
RVLFHVSGSR	7	12.41	0.013	3402	22.3	AE017258	TRUE	FALSE	2	1158.3	0.3	184	0.9809	FALSE	FALSE	::::::::::
VRQNALFYGAIVKANGLADRTLRTYLR	3	11.27	0.004	1891	70.2	AE017258	TRUE	FALSE	3	3081.6	-2.1	16of104	1.5313	FALSE	FALSE	::::::::::::::::::::::::
CIACHSFEKGGMN	10	7.01	0	1980	23.93	AE017258	TRUE	FALSE	3	1511.6	-2.3	9of 48	0.3331	FALSE	FALSE	:Cys_CAM:::Cys_CAM:::::::::
QLNSLLIESRSVKEYL	15	7.02	0.195	1856	47.6	AE017259	TRUE	FALSE	3	1893.2	-2.6	17of 60	2.1503	FALSE	FALSE	::::::::::::::::
NNENDKEKIKKILQERLKV	8	10.05	0.157	2771	26.6	AE017259	TRUE	FALSE	2	2340.7	1.1	12of 36	1.6226	FALSE	FALSE	::::::::::::::::::
LIPCLAGKKSDYR	9	9.66	0.152	1713	29.7	AE017259	TRUE	TRUE	2	1521.8	-2.4	8of 24	1.2871	FALSE	FALSE	::::Cys_CAM:::::::::
HSRVARSNIR	14	12.71	0.113	595	9.5	AE017259	TRUE	FALSE	2	1196.4	2.1	7of 18	1.1151	FALSE	FALSE	::::::::::
YQTKNVVGGFLVQENND	13	4.08	0.09	1048	33.3	AE017259	TRUE	FALSE	2	1926.1	3	5of 32	0.7672	FALSE	FALSE	::::::::::::::::
NDQTAKVFLGGKGLKGETGATGPKGA	5	10.16	0.08	1568	30	AE017259	TRUE	FALSE	3	2503.8	-2.2	10of100	1.3179	FALSE	FALSE	::::::::::::::::::::::::
VSKANCILIFINQIR	3	10.11	0.066	1608	51.3	AE017259	TRUE	FALSE	2	1790.1	2.3	9of 28	1.4262	FALSE	FALSE	::::::Cys_CAM:::::::::
VDTGIKVNPGDKLSFSLVPR	14	9.89	0.061	2741	45.5	AE017259	TRUE	FALSE	3	2143.5	3	11of 76	0.963	FALSE	FALSE	::::::::::::::::::
MPIVVIGAGLTAIDTATE	9	3.01	0.056	897	56.53	AE017259	TRUE	FALSE	3	1789.1	-2.2	15of 68	1.2926	FALSE	FALSE	:Oxidation_M::::::::::::::::
FEMNTPEAVEKR	15	4.56	0.051	1904	23.23	AE017259	TRUE	FALSE	3	1451.6	-2.9	12of 44	1.7345	FALSE	FALSE	::::::::::::
VKWREMVLYMSSRGINKFVEIGPNKVLSNLVKR	13	11	0.037	414	87.76	AE017259	TRUE	TRUE	3	3925.7	0.2	14of128	1.1638	FALSE	FALSE	::::::Oxidation_M:::Oxidation_M:::::::::::::::::::::
AADWTVELSKVAKKIYVIHR	6	10.05	0.035	2645	49.9	AE017259	TRUE	FALSE	2	2328.8	-2.9	11of 38	1.4992	FALSE	FALSE	::::::::::::::::::::
MLSPFGRLRLDFGFPLVK	10	11.33	0.035	682	67.53	AE017259	TRUE	FALSE	3	2094.6	0.8	17of 68	1.3146	FALSE	FALSE	::::::::::::::::::
NKNRINGFITAKEVRLVDHSGEMVGIVPIER	13	9.88	0.035	1701	68.73	AE017259	TRUE	FALSE	3	3494.1	-2.8	22of120	1.9732	FALSE	FALSE	::::::::::::::::::::::::::::::
NFDRAATQVL	3	6.79	0.033	1074	24.8	AE017259	TRUE	FALSE	2	1135.3	-1.8	12of 18	1.188	FALSE	FALSE	::::::::::
INFNKIKNIGFRERDANTSVNGRGT	5	11.38	0.033	1802	38.1	AE017259	TRUE	FALSE	3	2823.1	-1.4	23of 96	2.1384	FALSE	FALSE	::::::::::::::::::::::::
KVLTLEWIEATPIYEV	14	3.97	0.033	1611	60.7	AE017259	TRUE	FALSE	3	1905.2	2.3	20of 60	3.0548	FALSE	FALSE	::::::::::::::::::
EQTRIRNILAEHKEKALISR	10	10.57	0.025	810	37.4	AE017259	TRUE	FALSE	3	2406.8	-0.2	19of 76	1.7181	FALSE	FALSE	::::::::::::::::::::
IFFPVLLSTIPMLIFGPTTLGVVLTAIGTIFAIKGGVE	1	6.95	0.023	2128	153.63	AE017259	TRUE	FALSE	3	3948.9	3	26of148	2.6046	FALSE	FALSE	::::::::::::::::::::::::::::::::
FQGLISILENQMDY	15	3.01	0.022	379	49.43	AE017259	TRUE	FALSE	2	1671.9	0.1	10of 26	1.4733	FALSE	FALSE	::::::::::::
TINIVTRTISDIDLK	3	6.9	0.021	1147	41.4	AE017259	TRUE	TRUE	3	1703	-0.4	14of 56	1.3724	FALSE	FALSE	::::::::::::
VIVFTLMTAYDAQRIK	9	9.72	0.016	810	53.73	AE017259	TRUE	FALSE	2	1870.3	-2.2	7of 30	1.0435	FALSE	FALSE	::::::::::::::
KFFSAAALATLLSLSNSAFSDPVGPISDEET	9	3.59	0.013	1278	82.8	AE017259	TRUE	FALSE	3	3187.5	1.8	12of120	1.1783	FALSE	FALSE	::::::::::::::::::::::::::
TPILVSKELWERSGHWDKFRENMFIVDE	2	4.82	0.012	1953	79.03	AE017259	TRUE	FALSE	3	3463.9	-0.1	12of108	1.2052	FALSE	FALSE	::::::::::::::::::::::::
LKTNSDLPIIEIVPHDDKLTR	13	5.33	0.011	1174	50.7	AE017259	TRUE	FALSE	3	2418.8	-0.8	21of 80	2.2347	FALSE	FALSE	::::::::::::::::::
QLEEKLGSLTIT	15	4.27	0.011	441	32.6	AE017259	TRUE	FALSE	2	1332.5	-1	5of 22	0.686	FALSE	FALSE	::::::::::
SVKELILYLMERFKIKRDMIFSH	1	10.05	0.01	1593	75.66	AE017259	TRUE	FALSE	3	2930.5	2.7	20of 88	2.3085	FALSE	FALSE	::::::::Oxidation_M::::::::Oxidation_M::::
AEMIENNNKTTLE	11	3.97	0.005	1065	23.63	AE017259	TRUE	FALSE	2	1507.7	-1.7	8of 24	1.2137	FALSE	FALSE	::::::::::::
NCGIGMVLIVSSENMQNVK	15	6.29	0.003	1355	47.96	AE017259	TRUE	FALSE	2	2110.4	-2.5	10of 36	2.0447	FALSE	FALSE	::Cys_CAM:::Oxidation_M:::::::::::
KTNNEAGNLSLSKRKIANINVITLSIDR	2	10.82	0	2329	54.1	AE017259	TRUE	FALSE	3	3084.5	-2	16of108	0.3571	FALSE	FALSE	::::::::::::::::::::::::::
KDFNLLGVDNK	15	6.88	0.17	981	24.1	AE017260	TRUE	FALSE	1	1263.4	0.6	11of 20	1.5844	FALSE	FALSE	::::::::::
LARAIAGEANVPFFSISGSDFVEMFVGVGASR	6	4.45	0.147	2530	91.83	AE017260	TRUE	FALSE	3	3303.8	-0.3	24of124	1.9786	FALSE	FALSE	::::::::::::::::::::::::::::
HSVEHAVLPFKDLFLGLFFMTVGM	8	6.03	0.139	2203	89.86	AE017260	TRUE	FALSE	3	2737.3	-0.6	21of 92	2.6502	FALSE	FALSE	::::::::::::::::::::::
KKKPKPYIHK	13	10.76	0.136	584	3.3	AE017260	TRUE	FALSE	2	1267.6	-1.8	7of 18	1.3841	FALSE	FALSE	::::::::::
NVLAGEEENAILNNTGVSTQE	3	2.96	0.131	1203	40.2	AE017260	TRUE	FALSE	3	2203.3	1	23of 80	2.2938	FALSE	FALSE	::::::::::::::::::
LVGSAGSNLFASLSAGVATLWGPA	1	6.02	0.108	1176	69.7	AE017260	TRUE	FALSE	2	2247.6	3	16of 46	2.4728	FALSE	FALSE	::::::::::::::::::::
MEFKRLLKALIIIFLPVFLVLK	4	10.83	0.1	1407	108.83	AE017260	TRUE	FALSE	3	2646.5	-0.4	16of 84	1.5018	FALSE	FALSE	::::::::::::::::::::
LLLPLVDGQGNFGSIDGDPPASMRYTEAR	14	3.97	0.099	527	72.23	AE017260	TRUE	FALSE	3	3091.5	-1.2	19of112	1.4872	FALSE	FALSE	::::::::::::::::::::::::
YEKRPSPFKNQLIKEFASPNEKAK	5	10.19	0.094	2244	36.8	AE017260	TRUE	FALSE	3	2851.3	0.2	15of 92	1.7209	FALSE	FALSE	::::::::::::::::::::::
IVPLHDNNIIKLGTLFIFIGLSIKMALFPLSRWL	12	10.59	0.079	2685	142.63	AE017260	TRUE	FALSE	3	3895.8	1.2	10of132	1.1157	FALSE	FALSE	::::::::::::::::::::::::::::
IYSGLYHVLGGR	9	9.59	0.076	2279	34.1	AE017260	TRUE	FALSE	1	1335.5	2.4	4of 22	0.6687	FALSE	FALSE	::::::::::::
IRGRKSKFTKGKNISREVIIPDKITIR	14	12.01	0.064	306	47.7	AE017260	TRUE	FALSE	3	3155.8	-0.4	9of104	1.0499	FALSE	FALSE	::::::::::::::::::::::::
KYKSSSISRKISAMKNFYKCL	15	10.53	0.064	2854	37.43	AE017260	TRUE	FALSE	3	2541	2.8	7of 80	0.9791	FALSE	FALSE	::::::::::::::::::Cys_CAM:::
PLEANLGGPGILCKR	1	8.97	0.059	508	37.5	AE017260	TRUE	FALSE	2	1595.8	-0.4	9of 28	1.0966	FALSE	FALSE	:::::::::::::Cys_CAM:::

EGKLKALRR	2	11.47	0.058	458	13.7	AE017260	TRUE	FALSE	2	1071.3	-1.5	9of 16	1.4718	FALSE	FALSE	::::::::::
LVNAVEVDVDAVCDGEK	12	3.43	0.057	844	39.6	AE017260	TRUE	FALSE	3	1833	2.4	20of 64	1.91	FALSE	FALSE	:::::::::::Cys_CAM:::::
NKMTNENLGQPVQNKFR	15	10.59	0.052	1948	23.03	AE017260	TRUE	FALSE	3	2035.3	1.5	20of 64	2.3056	FALSE	FALSE	:::Oxidation_M::::::::::::::
VVLAFRNAESNLHK	11	10.09	0.045	846	33.2	AE017260	TRUE	FALSE	2	1598.8	1.7	12of 26	1.6145	FALSE	FALSE	::::::::::::::
NAVLPIMAASLLSS	12	6.02	0.045	751	49.03	AE017260	TRUE	FALSE	3	1387.7	2.2	15of 52	1.8263	FALSE	FALSE	::::::::::::::
FQSKIMAIGEGKIEEVEKWLMIKL	2	7.17	0.033	2390	76.16	AE017260	TRUE	FALSE	3	2838.4	2.8	10of 92	1.1565	FALSE	FALSE	:::::::::::::::::::Oxidation_M::::
GYTNRTSVMFGMPG	9	9.85	0.033	1421	29.86	AE017260	TRUE	FALSE	2	1518.7	1.8	9of 26	1.3483	FALSE	FALSE	::::::::::::::
IDEIHTIIGAGSTSGSFLDAGNLLKPALAR	11	5.28	0.027	1146	76	AE017260	TRUE	FALSE	3	3039.5	-1.3	19of116	1.8342	FALSE	FALSE	::::::::::::::::::::::::::::::
LRFPLGGFYK	7	10.4	0.024	3211	35.8	AE017260	TRUE	FALSE	2	1198.5	-1.7	299	1.1958	FALSE	FALSE	::::::::::
TIQKEGRGLKMKKQ	6	10.99	0.023	1779	13.33	AE017260	TRUE	FALSE	2	1646	0.5	4of 26	0.7312	FALSE	FALSE	::::::::::::::
GFIFTTAMSPVLAAAAKASVEHLK	8	9.89	0.018	1856	64.73	AE017260	TRUE	FALSE	3	2477.9	2.4	26of 92	2.2449	FALSE	FALSE	:::::::Oxidation_M:::::::::::::::
KSFLNGIDIFR	9	10.09	0.017	1561	35.6	AE017260	TRUE	FALSE	3	1310.5	2.9	16of 40	1.7459	FALSE	FALSE	::::::::::
DITSGTGLGLSTVYGI	4	3.1	0.014	1514	41.3	AE017260	TRUE	FALSE	2	1554.7	-0.9	10of 30	1.3391	FALSE	FALSE	::::::::::::::::
KWDRPGGGGGESTIIF	2	7.02	0.013	107	31.7	AE017260	TRUE	FALSE	2	1677.9	2.4	9of 30	0.9906	FALSE	FALSE	::::::::::::::::
TFIDTPGHEAFTAMR	1	5.22	0.011	2293	35.33	AE017260	TRUE	FALSE	2	1694.9	0.6	6of 28	0.9263	FALSE	FALSE	::::::::::::::::
KQRFGIRGRKSK	8	12.72	0.01	3291	6.8	AE017260	TRUE	FALSE	2	1461.8	0.9	7of 22	1.1998	FALSE	FALSE	::::::::::::
SVAHVGGEPWM	11	5.13	0.01	1069	26.73	AE017260	TRUE	FALSE	1	1186.3	0.4	3of 20	0.5983	FALSE	FALSE	:::::::::::Oxidation_M:
YIILALSFNSK	2	9.72	0.008	1016	42.5	AE017260	TRUE	FALSE	1	1269.5	0.5	9of 20	1.7873	FALSE	FALSE	::::::::::::
IAKAAKMKNVPMMIHFSAMG	2	10.85	0.005	2104	50.62	AE017260	TRUE	FALSE	2	2209.8	-1.6	4of 38	0.5914	FALSE	FALSE	:::::::::::::Oxidation_M::::::Oxidation_M::
LQHSYDCMYDAGMTSGQA	11	3.88	0.004	425	32.86	AE017260	TRUE	FALSE	3	2036.2	1.6	13of 68	1.2782	FALSE	FALSE	:::::::Cys_CAM::::::::::::
VLDHGFIRVVD	9	5.1	0.003	1242	36.1	AE017260	TRUE	FALSE	2	1270.5	-1.7	9of 20	1.0813	FALSE	FALSE	::::::::::::
SDPIHKATIIPRGMALGLVMR	4	11.33	0.002	2310	57.26	AE017260	TRUE	FALSE	2	2277.8	-2.4	11of 40	1.4022	FALSE	FALSE	::::::::::::::::::::
VLGIAQQAANVAGTAR	12	11.05	0.055	1417	34.5	AF018999	TRUE	FALSE	3	1540.8	2.2	19of 60	1.8641	FALSE	FALSE	::::::::::::::::
MSTQMLLQMESASA	5	3.3	0.004	2363	37.89	AF032870	TRUE	FALSE	2	1528.8	-1	11of 26	1.6015	FALSE	FALSE	::::::::::::::
WVEMDAMAILVPPLWPFLSHST	13	4.07	0.019	630	87.86	AF033104	TRUE	FALSE	3	2558	-2.6	19of 84	1.6785	FALSE	FALSE	:::::Oxidation_M:::::::::::::::::::
GEAEQSAGHP	10	4.25	0	624	5.5	AF041038	TRUE	FALSE	2	983	0.6	7of 18	1.2067	FALSE	FALSE	::::::::::::
QDVMVLLETTNDMLRMPD	6	3.51	0.056	1211	54.59	AF045771	TRUE	FALSE	2	2138.5	-1.7	7of 34	1.0986	FALSE	FALSE	:::::::::::::::Oxidation_M:::
KSQMPEEAAMQMIHAMEMMKNGSMWIVNMGQLK	15	7.78	0.011	49	81.84	AF045793	TRUE	FALSE	3	3845.6	0.3	11of128	1.2083	FALSE	FALSE	:::::::::::Oxidation_M:::::::::::Oxidation_M:::::::::
RTLSAVPPSALKLAAAANCQVSK	9	10.59	0.103	1684	47.5	AF079765	TRUE	FALSE	3	2354.7	-0.9	22of 88	1.8681	FALSE	FALSE	:::::::::::::::::::Cys_CAM::::::
KQEKRDGSSTNDPYVAFRRR	3	10.68	0.01	2007	15.9	AF079765	TRUE	FALSE	2	2411.6	-1.4	13of 38	1.338	FALSE	FALSE	::::::::::::::::::::
AKGTAKAKAVALLNAKKVQKKIIKAFGTRARKIR	15	12.74	0.005	1902	52	AF080130	TRUE	FALSE	3	3679.6	-0.5	21of132	1.6052	FALSE	FALSE	::::::::::::::::::::::::::::::
FSALVVAWYSSACHVSNTLR	9	8.9	0.01	494	57.7	AF095136	TRUE	FALSE	3	2269.5	2.6	21of 76	2.1011	FALSE	FALSE	:::::::::::Cys_CAM:::::::::
NETDQGSGNAPAASAGAG	12	3.01	0.022	1347	11.5	AF096896	TRUE	FALSE	3	1575.5	-2.1	19of 68	1.7695	FALSE	FALSE	::::::::::::::::::
STDLGYANGNLVHGSNQK	5	7.74	0.005	2151	21.5	AF097535	TRUE	FALSE	2	1876	-2.8	10of 34	0.9859	FALSE	FALSE	::::::::::::::::::
GTARAIQFLHQDSPSLIHGDIKSSNVLLDERLMPK	7	7.95	0.004	1629	80.23	AF103876	TRUE	FALSE	3	3905.5	0.9	5	2.2856	FALSE	FALSE	:::::::::::::::::::::::::::::::Oxidation_M:::
AAKKAEQKAENASTAAANNSGGDSAEDHAA	3	4.7	0.123	1329	15.1	AF113612	TRUE	FALSE	3	2887	2.4	19of116	1.9366	FALSE	FALSE	::::::::::::::::::::::::::::
DIDKTYSGFVN	9	3.89	0.117	1049	22.9	AF114160	TRUE	FALSE	2	1259.4	2.2	12of 20	1.5324	FALSE	FALSE	::::::::::::
VHDEEGIQKLVTEVF	9	4.16	0.007	2451	38.3	AF114160	TRUE	FALSE	2	1744	-1.7	6of 28	0.9436	FALSE	FALSE	::::::::::::::::
TAPFPGCCPIFTCEEGAKLEYPELPTPPPEGEK	7	3.96	0.052	1749	75.7	AF117598	TRUE	TRUE	3	3721.1	2.2	146	2.5171	FALSE	FALSE	:::::::Cys_CAM:Cys_CAM::::Cys_CAM::::::::::::::::::::
DCGPLPLANPK	4	6.1	0.013	1653	24.1	AF117598	TRUE	FALSE	1	1182.3	1.4	11of 20	1.344	FALSE	FALSE	::Cys_CAM:::::::::
VETGVLKPGTVVVFAPANITTEVKSVEMHHEALAE	7	4.8	0.003	1499	82.53	AF124488	TRUE	FALSE	3	3705.3	0.2	73	2.5682	FALSE	FALSE	::::::::::::::::::::::::::::::::
EDKTIELLIKILVNL	7	4.45	0.002	1639	57.8	AF132032	TRUE	FALSE	2	1755.1	-1.7	122	1.1481	FALSE	FALSE	::::::::::::::::
RKVQTESSTGSVGSNR	11	11.33	0.123	1612	7.2	AF139828	TRUE	FALSE	2	1693.8	1.5	7of 30	1.3342	FALSE	FALSE	::::::::::::::::
DSPASLAVVPFSAVGITYNNYGV	5	3.1	0.11	1858	61.2	AF141673	TRUE	FALSE	3	2342.6	2.6	23of 88	2.7359	FALSE	FALSE	::::::::::::::::::::
LKDIIMAFRWIK	1	10.59	0.012	1124	50.13	AF159419	TRUE	FALSE	2	1534.9	2	11of 22	1.6467	FALSE	FALSE	::::::::::::
PAASVQNNQDESEQDTSASASDSSFDESTAR	12	3.28	0.215	2332	27	AF162792	TRUE	FALSE	3	3233.2	2.4	16of120	1.7465	FALSE	FALSE	::::::::::::::::::::::::::::
FLMISSFFVMMSCQREEFEMAYIEER	14	4.09	0.007	300	95.22	AF180467	TRUE	FALSE	3	3344.8	-2.1	8of100	0.9409	FALSE	FALSE	:::::::::Oxidation_M::Cys_CAM::::::Oxidation_M:::::::
EDKKANYIK	1	9.56	0.072	632	8.3	AF181637	TRUE	TRUE	1	1109.3	1.8	11of 16	1.992	FALSE	FALSE	::::::::::
LFYNVLSSDIGYMMPLVYTPTVGLACQR	6	6.08	0.493	2479	95.46	AF187998	TRUE	TRUE	2	3210.7	1.8	18of 54	3.6977	FALSE	FALSE	:::::::::::::::::::::::::Cys_CAM:::
LFMMLVFVVMSIACFRWRMNR	6	12.11	0.015	2455	95.82	AF190455	TRUE	FALSE	2	2757.4	1.6	6of 40	0.9637	FALSE	FALSE	:::Oxidation_M:Oxidation_M::::::::::Cys_CAM::::Oxidation_M:::
LYITETDEKKINR	15	7.04	0.05	296	25.6	AF195418	TRUE	FALSE	2	1623.8	0.6	5of 24	0.8521	FALSE	FALSE	::::::::::::::
QALYKYNHHVVIANSLDTRR	3	10.04	0.206	1152	38.5	AF198100	TRUE	TRUE	3	2399.7	-2.7	22of 76	2.1487	FALSE	FALSE	::::::::::::::::::::
IELQKDDFEGLVKILSV	12	4.07	0.032	1826	55.2	AF210453	TRUE	FALSE	2	1947.3	0.2	11of 32	1.5836	FALSE	FALSE	::::::::::::::::::
MVGPVAAHPTPGRRIY	9	11.14	0.039	1145	34.33	AF216752	TRUE	FALSE	3	1723	-1.2	19of 60	1.7405	FALSE	FALSE	::::::::::::::::
EKPFLCWARKLVGDPNLEFVAMPALLPPEVK	3	6.55	0.008	1875	100.43	AF220950	TRUE	FALSE	3	3567.2	1.7	19of120	2.618	FALSE	FALSE	:::::Cys_CAM::::::::::::::::::::::
LVRNKQTLNAKQDNIN	10	10.59	0.001	1851	24.2	AF222049	TRUE	FALSE	2	1870.1	-0.1	13of 30	1.1591	FALSE	FALSE	::::::::::::::::
TQGLSGKLVSVLESTLSK	10	9.89	0.096	790	39.3	AF223578	TRUE	FALSE	2	1848.1	2.6	9of 34	1.1692	FALSE	FALSE	::::::::::::::::::
ASTSPVAIEDDEPGSVVAEFCAEVQR	10	3.44	0.021	1114	54.1	AF250878	TRUE	FALSE	3	2764.9	0.9	20of100	1.3831	FALSE	FALSE	:::::::::::::::::::Cys_CAM::::::
GGGAGVAGGGGTGAGLAVTSDGR	1	6.79	0.004	2073	24.5	AF251243	TRUE	FALSE	3	1802.9	0.6	27of 88	2.1446	FALSE	FALSE	::::::::::::::::::::
VTMTSVAGGVGGGPGGAAAAGVMSSVGSSMPGPS	11	6.02	0.009	900	55.59	AF251251	TRUE	FALSE	3	2850.2	-0.1	27of132	3.0463	FALSE	FALSE	::::::::::::::::::::::::::::::
LWKFETPKYSVTIIDAPGHRDFIK	10	9.56	0.005	1236	64.1	AF251762	TRUE	FALSE	3	2863.3	0.8	25of 92	2.4953	FALSE	FALSE	::::::::::::::::::::::
DGSMGISTGSVAMDIPRNYR	14	6.85	0.085	1227	37.36	AF254372	TRUE	FALSE	2	2160.4	1.9	7of 38	0.9914	FALSE	FALSE	:::Oxidation_M::::::::Oxidation_M:::::::
HSLGAVNMASARTPATRKTTR	10	12.71	0.097	2212	23.83	AF254373	TRUE	FALSE	2	2243.5	0.3	8of 40	1.0844	FALSE	FALSE	:::::::Oxidation_M::::::::::::
VMLRSTPGTATSASSSAAVSGVSGG	9	11.05	0.086	2792	37.63	AF254373	TRUE	FALSE	3	2255.5	2.5	16of 96	1.5042	FALSE	FALSE	::Oxidation_M:::::::::::::::::::::
AGANAGTGAASGGAASGGGPAG	12	6.02	0.081	1099	15.8	AF255326	TRUE	FALSE	3	1587.6	2	18of 84	1.6952	FALSE	FALSE	::::::::::::::::::::
PKIVVEGSDGSVRPGKKSGK	14	10.55	0.16	1691	17.3	AF262038	TRUE	FALSE	2	2026.3	-1.7	11of 38	1.6339	FALSE	FALSE	::::::::::::::::::
VWSVSGCRLMSTVR	14	10.9	0.02	578	38.63	AF262038	TRUE	FALSE	2	1638.9	2.7	7of 26	1.0665	FALSE	FALSE	:::::::Cys_CAM::::::::
VDQLSGEQEVLKGELEAAKQAKVKLENRIK	3	7.22	0.044	2061	54.2	AF262046	TRUE	TRUE	3	3352.9	0.4	23of116	2.3784	FALSE	FALSE	::::::::::::::::::::::::::::
IVEEGPVPSK	8	4.27	0.027	3250	21.1	AF262375	TRUE	FALSE	2	1055.2	1.5	9of 18	1.0661	FALSE	FALSE	::::::::::
LRVWVKGQRWADAYY	12	10.04	0.141	2788	45.4	AF264924	TRUE	FALSE	3	1912.2	-0.5	7of 56	1.0415	FALSE	FALSE	::::::::::::::
LSRSSAGSSTPLPSIIGK	5	11.49	0.018	1270	33.3	AF274591	TRUE	TRUE	2	1759	-0.9	6of 34	1.0182	FALSE	FALSE	::::::::::::::::
MGKRVLHCGPQGAGLAAKLAN	9	10.59	0.002	1162	39.13	AF309689	TRUE	FALSE	3	2150.5	1.2	21of 80	1.8343	FALSE	FALSE	:::::::Cys_CAM:::::::::::::
NYNHILSALSEQER	12	5.3	0.131	1171	28	AF313479	TRUE	FALSE	2	1674.8	0.8	9of 26	1.5447	FALSE	FALSE	::::::::::::::
KNFFLR	6	11.49	0.039	1618	21	AF313479	TRUE	TRUE	1	825	1.1	8of 10	1.5461	FALSE	FALSE	::::::
EYMLVVMKEMLK	14	7	0.013	1186	45.29	AF313479	TRUE	FALSE	2	1530.9	-0.8	6of 22	1.4759	FALSE	FALSE	:::::::::Oxidation_M:::
YNTGNLTEDLK	5	4.08	0.056	1968	19.7	AF313480	TRUE	FALSE	1	1268.4	1.4	10of 20	1.812	FALSE	FALSE	::::::::::::
WHKMRGAQMIVAMK	7	11.64	0.097	2070	34.69	AF317058	TRUE	FALSE	2	1720.1	-2.5	47	1.2968	FALSE	FALSE	:::::::::Oxidation_M:::Oxidation_M::
IIAFHDEHLSVLLRSITSIINR	2	8	0.026	634	71.7	AF324751	TRUE	FALSE	3	2549	0.7	12of 84	1.1214	FALSE	FALSE	::::::::::::::::::::
TASQPPETPPQPSDSK	7	4.08	0.003	1269	11.8	AF344878	TRUE	FALSE	3	1667.8	2.3	114	1.5595	FALSE	FALSE	::::::::::::::::
STPLILLSLGGLPPLTGFMPK	10	10.1	0.004	649	75.73	AF353202	TRUE	FALSE	2	2169.7	0.1	12of 40	2.4696	FALSE	FALSE	:::::::::::::::::::Oxidation_M:::
EWTFTLYDFDNNGK	4	3.71	0.161	2804	36.8	AF358134	TRUE	FALSE	3	1750.9	-1.1	9of 52	1.187	FALSE	FALSE	::::::::::::::::
VDDDSILEYDSDTIN	12	2.67	0.159	1199	34.1	AF364549	TRUE	FALSE	3	1714.7	-0.3	16of 56	1.8124	FALSE	FALSE	::::::::::::::::
HERYTFATSFARSQEDR	8	7.77	0.034	3356	24	AF364549	TRUE	FALSE	3	2102.2	0.8	15of 64	1.3852	FALSE	FALSE	::::::::::::::::

MRADPDDPHTDVQEKIK	5	4.55	0.028	2553	19.53	AF364549	TRUE	FALSE	2	1996.2	-0.6	6of 32	0.9219	FALSE	FALSE	::::::::::::::::
KQHRAQVHSAPRSDR	10	12.12	0.017	1534	2.7	AF364549	TRUE	FALSE	3	1774	-1.3	9of 56	1.4686	FALSE	FALSE	::::::::::::::
IYDLSQHSIQINE	11	4.07	0.07	784	33	AF364550	TRUE	FALSE	3	1560.7	2	11of 48	1.3487	FALSE	FALSE	::::::::::::
QMNNNTLDFTDVSD	11	2.82	0.011	878	26.53	AF365402	TRUE	FALSE	2	1630.7	-1.3	5of 26	0.7723	FALSE	FALSE	::Oxidation_M::::::::::::
VALGPLSVFSNTADLRNSVLSYSQQPHQ	3	7.76	0.009	1392	63.7	AF395904	TRUE	FALSE	3	3030.4	2.5	13of108	1.3134	FALSE	FALSE	::::::::::::::::::::::::::
DQPQEYFMELTFNQAAKGVNKEFTVNIMDTCER	7	4.13	0.009	1936	73.76	AF411044	TRUE	FALSE	3	3956.4	2.2	428	2.874	FALSE	FALSE	::::::::::::::::::::::::::::::::::Cys_CAM:::
ASLTSSLYGGSMNSSLDLKYSFLGGGDSVSGGISGTSTLR	9	6.77	0.018	1825	80.73	AF411457	TRUE	FALSE	3	3932.3	2.1	25of156	2.3184	FALSE	FALSE	::::::::::::::::::::::::::::::::::::::
DRGEYKRMMDLADSPRRGDRDGR	2	9.71	0.081	838	23.26	AF416331	TRUE	FALSE	3	2770	1.8	13of 88	1.5903	FALSE	FALSE	:::::::::Oxidation_M:::::::::::::::
IPFHPYHSHKDMLLLTL	6	7.98	0.014	1940	54.13	AF420147	TRUE	FALSE	2	2063.5	1.4	14of 32	2.0476	FALSE	FALSE	::::::::::::::::::
DIGTAWPSSPALMLL	9	3.1	0.142	2041	54.23	AF420149	TRUE	FALSE	2	1572.9	2.8	11of 28	1.4549	FALSE	FALSE	::::::::::::::
LVCAKNDIFK	6	8.94	0.131	1232	28.6	AF421370	TRUE	FALSE	2	1208.4	2.2	7of 18	1.3735	FALSE	FALSE	:::Cys_CAM::::::::
GPATPNGQ	14	6.02	0.096	750	5.6	AF421370	TRUE	FALSE	1	741.8	2.7	7of 14	0.7888	FALSE	FALSE	::::::::
EDARTPTGVHR	9	7.85	0.076	625	8	AF427496	TRUE	FALSE	3	1239.3	-2.3	17of 40	2.0338	FALSE	FALSE	::::::::::::
TLAAERSLDMVELKSRQCIINSFAGKISEIGE	6	4.8	0.059	2064	79.13	AF427496	TRUE	FALSE	3	3568	0.8	25of124	2.0005	FALSE	FALSE	::::::::::::::::Cys_CAM::::::::::::::
QLSPAEQNVAAILGVSESFIGKKASGQAIGK	1	9.76	0.15	1033	62.2	AF436845	TRUE	FALSE	3	3100.5	0.4	22of120	1.8878	FALSE	FALSE	::::::::::::::::::::::::::::
ISALVKQTMNGFY	1	9.72	0.008	1346	38.13	AF480611	TRUE	FALSE	1	1488.7	-0.7	4of 24	0.702	FALSE	FALSE	::::::::Oxidation_M::::::
ISRTLNEHEVNYSAIEK	9	5.4	0.091	581	31.9	AF492764	TRUE	FALSE	3	2004.2	-0.4	22of 64	2.0431	FALSE	FALSE	::::::::::::::::::
KQIIHISYKEMTLE	13	7.73	0.071	1215	36.63	AF492764	TRUE	FALSE	2	1734.1	2.6	10of 26	1.0326	FALSE	FALSE	::::::::::::::
ANKRNKRRPSSQIRISDAM	9	12.42	0.124	1097	18.13	AF500094	TRUE	FALSE	3	2245.6	0.2	20of 72	2.432	FALSE	FALSE	::::::::::::::::::Oxidation_M:
YLDKEVDAVEAGWNEGR	13	3.93	0.041	592	35.4	AF518015	TRUE	FALSE	3	1952.1	-0.7	21of 64	2.0621	FALSE	FALSE	::::::::::::::::::
TSHNDPVYRK	2	9.72	0.003	462	6.7	AF541948	TRUE	TRUE	2	1217.3	2	6of 18	0.8822	FALSE	FALSE	::::::::::
NIAGEVIRTLGVTNLTTWTELRT	5	7.13	0	1368	62.9	AF541948	TRUE	FALSE	2	2559.9	0.1	6of 44	0.9118	FALSE	FALSE	::::::::::::::::::::::::
FGFAKMVPSNQPVGCSPSYR	5	9.75	0.061	2660	42.53	AF542390	TRUE	FALSE	2	2230.5	1.6	9of 38	1.0142	FALSE	FALSE	::::::::::::::Cys_CAM:::::::
AKIVKPMTLK	9	10.85	0.036	731	24.33	AJ009736	TRUE	FALSE	2	1129.5	1.5	9of 18	1.597	FALSE	FALSE	::::::::::
TKPKMQKVKT	14	11.01	0.006	276	5.33	AJ009736	TRUE	FALSE	1	1189.5	1.1	8of 18	1.5904	FALSE	FALSE	::::::::::
ISCPAHGCNILVDDNTVMRLITDSK	7	5.19	0.038	2013	58.33	AJ130976	TRUE	FALSE	2	2831.1	1.3	1	1.9257	FALSE	FALSE	:::Cys_CAM:::::Cys_CAM:::::::::::::::
LRELMLRAQVGDSCGISAYMVPSD	9	4.31	0.013	1446	65.16	AJ131920	TRUE	FALSE	3	2702	-1.3	10of 92	1.0688	FALSE	FALSE	:::::Oxidation_M::::::::Cys_CAM::::::Oxidation_M:::::
HCAGKSLSLP	12	8.97	0.057	2310	18	AJ237969	TRUE	FALSE	2	1070.2	2.5	7of 18	0.8553	FALSE	FALSE	::Cys_CAM::::::::
GDKAVVKKSTPPADGENQEPVKVKGRK	7	10.27	0.057	1655	18.6	AJ271449	TRUE	FALSE	3	2864.3	2.5	453	2.0285	FALSE	FALSE	::::::::::::::::::::::::::
ELMQNKSTSNGGTVSVPEPR	10	7.1	0.099	1847	26.13	AJ272505	TRUE	TRUE	2	2132.4	-2.7	7of 38	1.0622	FALSE	FALSE	::::::::::::::::::
RPANIVLDR	1	10.89	0.162	1345	22.9	AJ298995	TRUE	FALSE	1	1054.2	0.3	11of 16	1.6153	FALSE	FALSE	::::::::
WLGRVDWKQFQYRL	3	10.39	0.052	2867	48.1	AJ606680	TRUE	FALSE	2	1896.2	1.1	5of 26	0.6827	FALSE	FALSE	::::::::::::::
QLKAPREFGGWLGAFLLLLLL	3	10.09	0.029	1655	93.6	AJ606680	TRUE	FALSE	3	2356.9	1.5	26of 80	2.7889	FALSE	FALSE	::::::::::::::::::::
RETEDTKTADSDRDVF	6	4	0.025	2940	16.4	AK028532	TRUE	FALSE	2	1885.9	2.1	5of 30	0.9417	FALSE	FALSE	::::::::::::::::
HLFRTLNPQMLQK	10	11.49	0.097	1453	35.13	AK029881	TRUE	FALSE	2	1643	-2.3	6of 24	1.0618	FALSE	FALSE	::::::::Oxidation_M::::
VVVAGALYLLFSGM	2	5.93	0.001	844	60.83	AK044591	TRUE	FALSE	2	1456.8	1.5	9of 26	1.299	FALSE	FALSE	:::::::::::Oxidation_M:
VLMALCLMALPFIPASNLFFPVGFVVAER	8	6.29	0.019	2015	127.46	AK044857	TRUE	FALSE	3	3256.9	2.4	25of112	2.1641	FALSE	FALSE	::Oxidation_M::Cys_CAM::Oxidation_M::::::::::::::::::::
ICDVALNIVECLLQLGVVPCVEKNR	8	4.45	0.12	2684	82.3	AK081235	TRUE	TRUE	3	2913.3	-0.5	25of 96	2.0711	FALSE	FALSE	::Cys_CAM::::::::Cys_CAM::::::::Cys_CAM:::::::
RMGVPFLLHED	12	5.22	0.005	1959	35.23	AK081235	TRUE	FALSE	3	1330.5	-0.4	13of 40	1.3417	FALSE	FALSE	::Oxidation_M:::::::::::
INEMVHFDLPGQEERE	2	4	0.023	2430	37.23	AK091144	TRUE	FALSE	2	1960.1	-1.6	6of 30	0.8164	FALSE	FALSE	::::Oxidation_M::::::::::::
KNSETSILQAMSRGLSTS	3	10.09	0.039	1269	28.93	AK092764	TRUE	FALSE	2	1927.1	2.3	8of 34	0.9373	FALSE	FALSE	:::::::::Oxidation_M:::::::
WDKNKSAFPFSDKLGELSDK	6	7.04	0.1	2943	37.1	AK092765	TRUE	FALSE	3	2313.6	0	11of 76	1.3314	FALSE	FALSE	::::::::::::::::::
LNRKGCCPICTEK	7	8.58	0.041	1333	21.4	AK096150	TRUE	FALSE	2	1636.8	2.9	28	1.0079	FALSE	FALSE	::::::Cys_CAM:Cys_CAM:::Cys_CAM::::
RSPSEIDDEAKLGRGQLVKEPP	8	4.73	0.042	1925	34.1	AL033125	TRUE	FALSE	3	2422.7	-2	11of 84	0.9512	FALSE	FALSE	::::::::::::::::::::::
NNKGNGLINTNIGSSNVKPNIR	9	11.64	0.041	1113	27.9	AL034557	TRUE	FALSE	3	2325.6	-2.2	20of 84	2.0454	FALSE	FALSE	::::::::::::::::::::::
FMEVIKGQEAYSRRKVLAGIVMTENMNFCEAKVSPQ	10	8.83	0.08	2127	86.29	AL035207	TRUE	FALSE	3	4163.8	1.8	9of140	1.1846	FALSE	FALSE	::::::::::::::::::::::::::Cys_CAM:::::::
QIYLHEGIGN	7	5.13	0.039	1379	25.4	AL035476	TRUE	FALSE	2	1144.3	-0.4	9	1.2529	FALSE	FALSE	::::::::::
LATSLPRLMNSQDDQGKFSTLSLLLGYLK	8	9.63	0.08	2111	81.93	AL109823	TRUE	FALSE	3	3227.7	2.8	24of112	3.1055	FALSE	FALSE	::::::::Oxidation_M::::::::::::::::::
TAAHHPVQGHGAAAL	12	8.09	0.027	1965	19	AL121804	TRUE	FALSE	2	1438.6	-2.4	11of 28	1.4539	FALSE	FALSE	::::::::::::::::
CRPAASPAPPPSRPSSPVHVAFERLELK	6	10.1	0.036	2354	54.3	AL133380	TRUE	FALSE	3	3055.5	1.5	21of108	1.4014	FALSE	FALSE	:Cys_CAM:::::::::::::::::::::::
TGRLVSLSACGRTARRQQ	12	12.41	0.081	955	25.8	AL136870	TRUE	FALSE	3	2018.3	2.9	19of 68	1.6843	FALSE	FALSE	:::::::::Cys_CAM:::::::::
EQYFYQNKPGSNK	1	9.47	0.091	1248	14.4	AL353822	TRUE	FALSE	1	1603.7	0.2	9of 24	1.6134	FALSE	FALSE	::::::::::::::
PPGLARRKKSP	9	12.43	0.011	1474	10.3	AL353822	TRUE	FALSE	2	1207.5	2.8	11of 20	1.3231	FALSE	FALSE	::::::::::::
MMGVGSGGGGTKKHKR	15	11.73	0.104	499	6.26	AL354513	TRUE	FALSE	3	1588.9	-0.8	16of 60	1.6473	FALSE	FALSE	::::::::::::::::
RPSASDSRPTTSLNQAV	9	10.89	0.194	2398	19.9	AL355930	TRUE	FALSE	2	1787.9	1	10of 32	1.4479	FALSE	FALSE	::::::::::::::::
RCTQPSSAQLQGMRGARR	11	12.41	0.116	460	19.63	AL355930	TRUE	FALSE	3	2061.3	1	25of 68	2.4182	FALSE	FALSE	::Cys_CAM:::::::::::::::
LLNAGTQDDCHL	9	3.88	0.051	1178	27	AL355930	TRUE	FALSE	2	1357.4	1.5	9of 22	1.1829	FALSE	FALSE	:::::::::Cys_CAM:::
KPKAKEHQTLKQRFR	12	11.63	0.149	2079	10.2	AL356173	TRUE	FALSE	2	1896.2	1.1	6of 28	1.0237	FALSE	FALSE	::::::::::::::
SVHKYADQAFFPAEINEA	5	4.43	0.096	2334	40.5	AL356246	TRUE	FALSE	2	2038.2	0.8	5of 34	0.637	FALSE	FALSE	::::::::::::::::
VATSAAGGGDATRV	11	6.79	0.035	1665	18	AL356713	TRUE	FALSE	1	1233.3	-1.3	6of 26	1.1063	FALSE	FALSE	::::::::::::
VATSAAGGGDATRV	14	6.79	0.002	1719	18	AL356713	TRUE	FALSE	1	1233.3	-1.4	6of 26	1.1035	FALSE	FALSE	::::::::::::
LPATALR	9	11.05	0.024	1104	22.2	AL358652	TRUE	FALSE	1	741.9	0.3	7of 12	1.0152	FALSE	FALSE	:::::::
KEDEERQMGHMK	14	5.44	0.081	479	7.46	AL389891	TRUE	FALSE	3	1534.7	0.9	12of 44	1.6377	FALSE	FALSE	::::::::::Oxidation_M::
SRHCLCRLSPCAFPHLCVHRVTHTHT	10	8.76	0.001	1020	47.9	AL446005	TRUE	FALSE	3	3241.6	-0.3	19of100	2.4354	FALSE	FALSE	::::Cys_CAM::Cys_CAM::::Cys_CAM::::::Cys_CAM:::::::::
LQTMKAVAAESETRAADIQAVR	1	7.14	0.098	2254	43.13	AL449144	TRUE	FALSE	3	2360.7	-0.1	21of 84	1.9978	FALSE	FALSE	::::::::::::::::::::::
KGSGVGAAGPSSEAEEAAATAAANGREGKR	1	7.22	0.086	234	22.2	AL449144	TRUE	FALSE	2	2758.9	1.7	10of 58	1.1357	FALSE	FALSE	::::::::::::::::::::::::::
IAGCVHNALMSPR	3	9.02	0.001	1197	30.93	AL449144	TRUE	FALSE	2	1442.6	-0.5	12of 24	1.3748	FALSE	FALSE	:::Cys_CAM::::::Oxidation_M::::
FAQFSEALFMADRHARE	10	5.35	0.004	2070	44.83	AL451018	TRUE	FALSE	2	2027.3	-1.8	6of 32	0.9124	FALSE	FALSE	::::::::::::::::
AEMLEGGIKEAR	12	4.56	0.009	901	25.23	AL451020	TRUE	FALSE	2	1304.5	-1.9	9of 22	1.1758	FALSE	FALSE	::::::::::::
ARGSSGSRAVSHTNTISMSSS	2	12.41	0.071	414	17.23	AL512294	TRUE	FALSE	3	2097.2	-2.2	14of 80	1.4457	FALSE	FALSE	::::::::::::::::Oxidation_M::::
RRATDSVRR	12	12.41	0.006	701	5.2	AL512294	TRUE	FALSE	2	1117.3	-0.9	11of 16	1.5632	FALSE	FALSE	::::::::
YEILTISNRGERQRYLSVKQR	11	10.54	0.129	108	42.1	AL513463	TRUE	TRUE	3	2611	-1.5	11of 80	1.2404	FALSE	FALSE	::::::::::::::::::
WFTHAEATPAVGGGTDEAR	2	4.43	0.087	2429	32.8	AL590734	TRUE	FALSE	2	1974.1	-2.7	6of 36	0.7461	FALSE	FALSE	::::::::::::::::::
RFVTSRADVAAALRDR	6	11.93	0.035	1203	32.6	AL590734	TRUE	FALSE	2	1805	0.8	12of 30	1.7247	FALSE	FALSE	::::::::::::::::
TVSGSNVVMGGVHSTGGGTNNVR	5	11.05	0.077	1992	26.03	AL669989	TRUE	FALSE	3	2204.4	2.9	26of 88	1.878	FALSE	FALSE	::::::::Oxidation_M:::::::::::::
KGAPPPLHGLGRSMTEGF	11	10.09	0.145	1526	33.73	AL669990	TRUE	FALSE	2	1853.1	2.7	10of 34	1.3208	FALSE	FALSE	::::::::::::::::::
LVIDHPSNALPAILALS	14	4.94	0.027	1494	59.3	AL670004	TRUE	FALSE	2	1745.1	1.4	12of 32	2.0284	FALSE	FALSE	::::::::::::::::::
EEDLSPIDGALKASTTAGNKR	13	4.56	0.104	748	29.2	AL670542	TRUE	FALSE	3	2174.4	0.8	21of 80	1.6713	FALSE	FALSE	::::::::::::::::::::
SSNDDANADSDA	4	2.75	0.013	3000	5	AL670542	TRUE	FALSE	2	1182.1	0	11of 22	1.5089	FALSE	FALSE	::::::::::::
RSWGIAHRCGQLHSLSRLAQQNLETLKK	11	11.38	0.004	1237	53.2	AL832473	TRUE	FALSE	3	3289.7	0	22of108	2.1862	FALSE	FALSE	::::::::Cys_CAM:::::::::::::::::
RRLTRRAPPEPGPESGQARGE	2	11.81	0.014	1040	20.2	AL834341	TRUE	FALSE	2	2318.6	-0.9	4of 40	0.8651	FALSE	FALSE	::::::::::::::::::::
KWKYEEPIINIDNGFGSGYPGD	13	4.07	0.002	1007	48.3	AL844505	TRUE	FALSE	3	2500.7	-0.6	17of 84	1.2972	FALSE	FALSE	::::::::::::::::::::
HEQGSENLNMKSKNMIEE	3	4.71	0.043	1583	22.26	AL844506	TRUE	FALSE	3	2151.3	-3	22of 68	2.7227	FALSE	FALSE	::::::::::Oxidation_M::::Oxidation_M::::

EDYIKREDTQNGEHMT	13	4.28	0.013	1651	16.73	AL844506	TRUE	FALSE	2	1983.1	-2.9	9of 30	1.1252	FALSE	FALSE	::::::::::::::Oxidation_M::
HIVSNFQRYKNIPM	8	10.4	0.132	3345	33.73	AL844507	TRUE	FALSE	3	1764.1	2.4	7of 52	1.1186	FALSE	FALSE	::::::::::::Oxidation_M:
AAQTIGICYDKRRKNR	2	10.69	0.111	1174	19.9	AL844507	TRUE	TRUE	2	1951.2	2.4	7of 30	1.0109	FALSE	FALSE	:::::::Cys_CAM::::::::
HHTDDFNKSYKHKDSK	6	9.51	0.107	2955	-1.9	AL844507	TRUE	FALSE	2	1988.1	-0.9	6of 30	1.1123	FALSE	FALSE	::::::::::::::
MPYYSKHSRISHKQDDYKYADNYRSKFNNKSYE	7	9.67	0.031	3250	35.03	AL844507	TRUE	FALSE	3	4165.5	1.6	75	1.6349	FALSE	FALSE	::::::::::::::::::::::::::::::
YIELKMKKM	7	10.05	0.01	1144	25.86	AL844507	TRUE	FALSE	2	1184.5	0.3	13	1.2439	FALSE	FALSE	::::::::::
IKNETIKNFIYVFPK	9	10.05	0.02	925	44.1	AL929351	TRUE	FALSE	3	1855.2	0.7	13of 56	1.506	FALSE	FALSE	::::::::::::::
DTYIMK	1	6.68	0.002	930	16.13	AL929351	TRUE	FALSE	1	770.9	1.1	6of 10	1.4096	FALSE	FALSE	::::::
TYNNTNKNISNISNSLIFSR	10	10.4	0.102	1493	37	AL929353	TRUE	FALSE	3	2301.5	-2.7	19of 76	2.237	FALSE	FALSE	::::::::::::::::::
EIYSNKKDNDLRER	9	7.07	0.019	1234	15.8	AL929354	TRUE	FALSE	3	1780.9	-0.1	14of 52	1.5245	FALSE	FALSE	::::::::::::::
TEIVGVDVSVRALTIASRRLKLDRMGERQAAR	10	11.74	0.059	2085	69.93	AL939125	TRUE	FALSE	3	3585.2	-1.7	19of124	2.158	FALSE	FALSE	:::::::::::::::::::::Oxidation_M:::::::
PYAASSLLAVALSSVFSSAMRGVCKSRPERAAE	11	9.74	0.044	1536	74.73	AL939125	TRUE	FALSE	3	3486.9	-1.7	24of128	1.7776	FALSE	FALSE	:::::::::::::::::Oxidation_M::::Cys_CAM:::::::::
FRYPHLSAAPMIPSGYFNQFQR	15	10.2	0.003	1275	59.83	AL-DROME	TRUE	FALSE	2	2645	0.8	11of 42	2.0439	FALSE	FALSE	::::::::::Oxidation_M:::::::::::
GVVPLFGSEDEVTTQGLDDLAAR	2	3.43	0.478	1290	56	ALF-DROME	TRUE	TRUE	2	2390.6	1.3	24of 44	5.1412	FALSE	FALSE	::::::::::::::::::::
NTPSYQSILENANVLAR	1	6.89	0.38	1246	38	ALF-DROME	TRUE	TRUE	2	1891.1	2.3	15of 32	2.5722	FALSE	FALSE	::::::::::::::::
ALSDHHVYLEGTLLKPNMVTAGQSAK	11	7.88	0.336	986	53.13	ALF-DROME	TRUE	TRUE	2	2782.2	0.7	22of 50	4.7205	FALSE	FALSE	::::::::::::::::::::::
YVAGSAGAGSGSLFVANHAY	5	7.7	0.206	1484	41.1	ALF-DROME	TRUE	FALSE	2	1900.1	0.5	16of 38	2.0403	FALSE	FALSE	::::::::::::::::::
DRAQKVTETVLAAVYK	7	9.63	0.191	1107	31.3	ALF-DROME	TRUE	FALSE	3	1793.1	1.6	48	2.4153	FALSE	FALSE	::::::::::::::
KNTPEEIALATVQALR	8	7.1	0.051	2176	36.7	ALF-DROME	TRUE	TRUE	2	1755	-0.5	10of 30	1.7422	FALSE	FALSE	::::::::::::::
VYLEGTLLKPNMVTAGQSAK	9	9.63	0.036	1756	47.23	ALF-DROME	TRUE	FALSE	3	2121.5	-0.1	22of 76	2.4179	FALSE	FALSE	::::::::::::::::::
GLLFGILLLSIGSLIRQR	14	12.41	0.016	1447	76.7	ALG8-DROME	TRUE	FALSE	2	1970.5	1.3	7of 34	1.2497	FALSE	FALSE	::::::::::::::::
WGFLASGQALTFVDNHDNQR	10	5.1	0.029	1058	46.7	AMYR-DROAN	TRUE	FALSE	3	2277.5	-2.9	11of 76	1.0158	FALSE	FALSE	::::::::::::::::
SPKPYKMATAFHLAYPY	9	9.79	0.113	2414	41.33	AMYR-DROER	TRUE	FALSE	3	1986.3	-2.6	14of 64	1.7833	FALSE	FALSE	::::::::::::::::
QLHAAMAGIGTEEATLVEIL	2	3.96	0.017	1070	59.63	ANXX-DROME	TRUE	FALSE	2	2068.4	1.5	7of 38	1.1441	FALSE	FALSE	::::::::::::::::
YLVTILTGVLAFRVAGGTSRSFR	5	12.11	0.03	1991	70.4	APH1-DROME	TRUE	FALSE	3	2485.9	1.5	12of 88	1.172	FALSE	FALSE	::::::::::::::::::
NDPMFYETISYANGPGYWDH	9	3.7	0.074	1813	47.53	APH4-DROME	TRUE	FALSE	3	2378.5	-1	21of 76	2.0784	FALSE	FALSE	::::::::::::::::
ERGDESNGFVLLVEGGR	9	4.17	0.061	830	35	APH4-DROME	TRUE	FALSE	3	1835	0	18of 64	1.9204	FALSE	FALSE	::::::::::::::
VFANLFKGLFGKKEMRILMVGLDAAGKTTILYK	4	10.47	0.016	1875	101.16	ARF1-DROME	TRUE	FALSE	3	3707.5	-2	22of128	1.7299	FALSE	FALSE	::::::::::::::Oxidation_M:::Oxidation_M:::::::::::::::
LTISSLLTRLFGKKQMRILMVGLDAAGK	11	11.57	0.104	1308	84.46	ARF2-DROME	TRUE	FALSE	3	3078.8	-2.3	9of108	1.1316	FALSE	FALSE	::::::::::::::::::Oxidation_M:::::::::
WIAANTKECPR	12	8.97	0.042	1967	23.2	ARI1-DROME	TRUE	FALSE	2	1346.5	1.4	9of 20	1.2283	FALSE	FALSE	:::::::Cys_CAM:::
GMDAGMVAWKGAAIMSVLES	1	4.08	0.118	313	57.09	ARP8-DROME	TRUE	FALSE	2	2025.4	-0.6	10of 38	1.2484	FALSE	FALSE	::::::::::::::::::
VRPANGITAHK	12	11.49	0.16	833	13.4	ARS2-DROME	TRUE	TRUE	2	1164.4	-1.1	8of 20	1.1341	FALSE	FALSE	::::::::::
RGGASAGGGGARHR	12	12.71	0.095	1918	0.7	ARS2-DROME	TRUE	FALSE	2	1267.4	1.6	11of 26	1.5007	FALSE	FALSE	::::::::::::::
NARERNRVKQVNNGF	15	12.12	0.075	1177	14.7	AST3-DROME	TRUE	FALSE	2	1803	-0.3	4of 28	0.7439	FALSE	FALSE	::::::::::::::
RYQHIMPAPSPLIPGGNQNQPAGTMPIKTRKYTPR	13	11.44	0.024	1279	60.06	AST4-DROME	TRUE	FALSE	3	3950.6	-1.7	22of136	2.4072	FALSE	FALSE	::::::Oxidation_M::::::::::::::::Oxidation_M:::::::::::
NLDDDLDELPSTSKDSKQPK	1	3.94	0.11	1973	23.5	ASX-DROME	TRUE	FALSE	2	2246.4	2.8	9of 38	1.4445	FALSE	FALSE	::::::::::::::::::
VAEVFTGHAGKLVPLEQTIK	4	7.8	0.071	2098	49.4	ATPB-DROME	TRUE	FALSE	2	2138.5	-2.1	10of 38	1.3655	FALSE	FALSE	::::::::::::::::::
AMDLGPGVNLSER	14	4.08	0.033	540	30.23	AY007228	TRUE	FALSE	2	1359.5	-2	9of 24	1.1771	FALSE	FALSE	::::::::::::
LRSKKASSAKFQMANKVAVSQK	1	11.86	0.164	1628	27.23	AY010627	TRUE	FALSE	2	2408.9	2	12of 42	1.6694	FALSE	FALSE	::::::::::::::::::
AVLVDGAPPQGGA	9	3.1	0.068	826	27.7	AY035993	TRUE	FALSE	2	1152.3	-3	9of 24	1.1156	FALSE	FALSE	::::::::::::::
KKMKPDYGKASTELK	14	10.19	0.005	2659	13.13	AY052131	TRUE	FALSE	3	1725.1	-2.2	12of 56	1.0973	FALSE	FALSE	::::::::::::::
LQLKSLGVAQQQR	15	11.49	0.055	2771	28.2	AY052143	TRUE	FALSE	2	1469.7	-1.8	7of 24	0.9281	FALSE	FALSE	::::::::::::::
EDEESYIEMEEHR	10	3.8	0.109	1422	21.33	AY057989	TRUE	TRUE	2	1696.7	1	5of 24	1.1049	FALSE	FALSE	::::::::::::::
SPPERKLQRYAWRKRWFVLRRGRMSGN	10	12.54	0.042	2391	54.23	AY057989	TRUE	FALSE	3	3433	1.6	16of104	1.5806	FALSE	FALSE	::::::::::::::::::::::::::
LNITLK	11	10.1	0	668	21.5	AY060257	TRUE	FALSE	1	701.9	-0.2	8of 10	1.3658	FALSE	FALSE	::::::
QTQLSCIIRRMFESNLCFNK	6	9.15	0.243	1732	54.73	AY060474	TRUE	FALSE	2	2546.9	-2.1	5of 38	1.073	FALSE	FALSE	:::::Cys_CAM::::::::::Cys_CAM::::
LASNRCECLAAADHKEISCAAG	1	5.35	0.1	484	39.8	AY060692	TRUE	FALSE	2	2405.5	0.8	4of 42	0.6437	FALSE	FALSE	:::::Cys_CAM::Cys_CAM::::::::::Cys_CAM::::
GIVRRMTKQKDGGR	11	12.14	0.102	2789	12.13	AY060761	TRUE	FALSE	3	1602.9	-2.2	19of 52	2.1419	FALSE	FALSE	::::::::::::::
GIVRRMTKQKDGGR	4	12.14	0.045	2970	12.13	AY060761	TRUE	FALSE	3	1602.9	-2.7	19of 52	2.1748	FALSE	FALSE	::::::::::::::
QLEEGIQESVNQAKSIESGM	9	3.8	0.083	1289	36.13	AY060925	TRUE	FALSE	3	2178.4	1.8	23of 76	2.4147	FALSE	FALSE	::::::::::::::::::
KSKSPDEITEKSSAGGGSGTSGT	2	7.08	0.101	558	7.1	AY060926	TRUE	FALSE	3	2169.3	2.8	24of 88	1.8804	FALSE	FALSE	::::::::::::::::::::
EKLKRTLLNEK	11	10.32	0.14	1560	19.6	AY061291	TRUE	FALSE	3	1372.7	-2.4	10of 40	1.4587	FALSE	FALSE	::::::::::::
PMAGAPKEHGNMGAMSSGGDSMQFKR	1	9.89	0.006	2273	32.42	AY061377	TRUE	FALSE	3	2713	2.9	13of100	1.2306	FALSE	FALSE	::::::::::Oxidation_M::::::::::Oxidation_M:::::
KINNTNLHYK	9	10.18	0	2515	12.5	AY061377	TRUE	FALSE	2	1245.4	2.9	4of 18	0.938	FALSE	FALSE	::::::::::
IASSFREFQEFSK	10	7.1	0.073	2667	32.6	AY069148	TRUE	FALSE	2	1576.7	0.8	6of 24	0.9801	FALSE	FALSE	::::::::::::
QMDPTSNFNSYR	6	6.7	0.059	2059	18.73	AY069263	TRUE	FALSE	2	1460.6	-2.8	9of 22	1.0541	FALSE	FALSE	::::::::::::
GIALPINTAGGSVIAGALAGGGGAG	15	6.02	0.019	1036	55.4	AY069281	TRUE	FALSE	3	2023.3	2.1	26of 96	1.8557	FALSE	FALSE	::::::::::::::::::::::
HVATGNAETKLSNFRDSN	8	7.82	0.002	2776	20.5	AY069771	TRUE	FALSE	2	1962.1	-2.8	8of 34	0.9617	FALSE	FALSE	::::::::::::::::::
RIKKKGMTFPTPNAAGKITHPTSSAKKAIR	2	12.46	0.071	2357	34.93	AY069785	TRUE	FALSE	3	3237.9	-2.3	14of116	1.3085	FALSE	FALSE	::::::::::::::::::::::::::::
VFASHMNMLYNLPNLSK	4	9.72	0.001	2049	50.56	AY069828	TRUE	FALSE	2	1996.4	-1.8	4of 32	0.7161	FALSE	FALSE	:::::::Oxidation_M:::::::::
SETGFYEMPCSIVNGTTGDMFPPKMNVNDEIT	11	3.51	0.035	1217	71.89	AY070904	TRUE	FALSE	3	3615.9	1.8	23of124	1.9251	FALSE	FALSE	:::::::Oxidation_M::Cys_CAM::::::::Oxidation_M:::::::::::
SNNCYSSCKISINSRSNP	9	9.05	0.066	2315	20.2	AY071461	TRUE	FALSE	2	2089.2	1.2	5of 34	0.7952	FALSE	FALSE	::::Cys_CAM::::Cys_CAM:::::::::
GSAADASHSSELEPRLQQRTNTQRSAQHCIRLLS	2	9.02	0.004	1626	47.4	AY071461	TRUE	FALSE	3	3807.1	-0.4	8of132	1.002	FALSE	FALSE	::::::::::::::::::::::::::Cys_CAM:::::
HVKCGVSVIRVSGPQTK	3	10.59	0.062	2848	24.9	AY071544	TRUE	FALSE	3	1853.1	-0.9	13of 64	1.4977	FALSE	FALSE	::::Cys_CAM:::::::::::
MTDVDVLSSR	14	3.89	0.078	2832	23.63	AY071605	TRUE	FALSE	2	1123.3	-1	10of 18	1.2447	FALSE	FALSE	::::::::::
LPPTNLHGCRLIKISYDVFFVIEPKSMEK	15	8.83	0.05	1955	84.13	AY071606	TRUE	FALSE	3	3450	0.4	24of112	2.0421	FALSE	FALSE	::::::::Cys_CAM::::::::::::::Oxidation_M:::
YVRANLIQ	2	9.85	0.071	837	25.8	AY071642	TRUE	FALSE	1	977.2	1.4	8of 14	1.8117	FALSE	FALSE	::::::::
HSSMDQQIGLLENMGKS	3	5.22	0.087	2088	30.16	AY071688	TRUE	FALSE	2	1892.1	0.6	8of 32	0.9792	FALSE	FALSE	::::Oxidation_M::::::::::::
EQNDKLHGDVANIRKQER	3	7.8	0.059	1785	16.2	AY075270	TRUE	TRUE	2	2151.3	-1.9	9of 34	1.1078	FALSE	FALSE	::::::::::::::::
AYGDHEVTTK	14	5.22	0.009	2057	9.6	AY075276	TRUE	TRUE	2	1121.2	-0.7	9of 18	1.5956	FALSE	FALSE	::::::::::
LDKILTEAGNENFKQLK	3	7.08	0.026	1061	37.1	AY075291	TRUE	FALSE	3	1962.3	2.6	22of 64	2.3914	FALSE	FALSE	::::::::::::::::
EVLPVHGKQSAGHGGRTEGSAK	7	9.89	0.077	2009	16.5	AY084098	TRUE	FALSE	2	2203.4	0	301	1.6236	FALSE	FALSE	::::::::::::::::::
SCILAGFVIYPTNVQIQFGERQFSKAVWSKAKR	1	10.45	0.013	2100	86.1	AY089324	TRUE	FALSE	3	3831.4	2.6	11of128	1.2537	FALSE	FALSE	::Cys_CAM:::::::::::::::::::::::::::
LFQHPYARFGSSMNFSMIGLRFKDKDATKALTS	1	10.44	0.018	2161	77.86	AY089334	TRUE	FALSE	3	3767.4	1.7	11of128	1.1212	FALSE	FALSE	::::::::::::::::::::::::::::
SFYNMKFGKYPKILKKVGAKIKVEMGGGKVHEK	8	10.52	0.119	1759	57.56	AY089357	TRUE	FALSE	3	3774.6	-0.5	15of128	1.5041	FALSE	FALSE	:::::Oxidation_M::::::::::::::::Oxidation_M:::::::::
PLQANVMAPQLLGAGVVETHNLS	8	5.13	0.012	1688	60.73	AY089420	TRUE	FALSE	2	2376.7	-2.6	14of 44	2.5452	FALSE	FALSE	::::::Oxidation_M:::::::::::::
LMEQNSTAAGNANPATVPAKRGTQQGR	7	11.33	0.057	2276	29.63	AY089597	TRUE	TRUE	3	2786.1	1.4	441	1.5462	FALSE	FALSE	::Oxidation_M:::::::::::::::::::::::
MEQNSTAAGNANPATVPAKRGTQQGRKK	8	11.57	0.051	1749	17.33	AY089597	TRUE	FALSE	3	2929.2	-2.9	16of108	1.4806	FALSE	FALSE	:Oxidation_M:::::::::::::::::::::::
GGVGGIQNMMRQLQQGAAGGLGGLESMK	10	10.09	0	1832	53.09	AY094660	TRUE	FALSE	3	2763.2	2.4	24of108	1.901	FALSE	FALSE	:::::::::Oxidation_M:::::::::::::::::
WDNSLMVPGKDSTSRK	3	9.89	0.138	1176	24.23	AY094807	TRUE	FALSE	2	1838	0.8	13of 30	1.6203	FALSE	FALSE	:::::Oxidation_M:::::::::
MSMSCFPPGTMAR	14	9.01	0.054	2795	32.69	AY094828	TRUE	FALSE	2	1505.7	2.4	7of 24	1.0144	FALSE	FALSE	:::Oxidation_M::Cys_CAM:::::Oxidation_M:::
NLLSKQRRGSAFTVPIPK	6	12.43	0.07	2542	36.7	AY095064	TRUE	FALSE	2	2013.4	-2.1	9of 34	1.4968	FALSE	FALSE	::::::::::::::::::
LKNLNTDHGFASGARAYIAQEVIDMGGEAISKS	15	5.39	0.147	1671	65.23	AY098450	TRUE	FALSE	3	3481.9	-1.1	23of128	1.8709	FALSE	FALSE	::::::::::::::::::::::::Oxidation_M:::::::::

CADASIVSSMVVAEKRTMRSGQGNVIDAVMNIMGIR	11	8.97	0.006	129	82.92	AY102675	TRUE	FALSE	3	3901.5	1	16of140	1.4461	FALSE	FALSE	:Cys_CAM::::::::::::::Oxidation_M::::::::::::Oxidation_M::::
AAKERVYNTYQ	10	9.53	0.084	733	16.4	AY102699	TRUE	FALSE	2	1343.5	-1.1	9of 20	1.1493	FALSE	FALSE	::::::::::
GKRYGPQSHADFESYRHNMAKLSEMK	3	9.86	0.01	2262	31.36	AY113218	TRUE	FALSE	3	3085.4	-1.7	22of100	2.3247	FALSE	FALSE	:::::::::::::::::::::Oxidation_M:::
SLSLMRADSHELEIVVVENR	12	4.63	0.03	1381	53.23	AY113256	TRUE	FALSE	3	2314.6	1.2	25of 76	1.6978	FALSE	FALSE	:::::Oxidation_M:::::::::::::
GVMVGMEKIWHHTFYNELR	11	7.9	0.092	753	52.86	AY113405	TRUE	FALSE	3	2380.7	2.4	17of 72	1.7983	FALSE	FALSE	:::Oxidation_M:::Oxidation_M::::::::::::
PDMMSTATSTELGMGIGMGIGGGINGGMGGTGM	8	3.01	0.051	2634	67.78	AY113420	TRUE	FALSE	3	3064.5	-2.4	23of128	2.0762	FALSE	FALSE	:::::::::::::::::::::::::::::::Oxidation_M:
MAPWENIFDNISID	6	2.88	0.12	1950	48.73	AY113457	TRUE	FALSE	2	1681.9	2.8	6of 26	1.0969	FALSE	FALSE	:Oxidation_M:::::::::::::
RINYQPPTVVPGGDLAK	6	9.72	0	1444	35.1	AY113631	TRUE	FALSE	2	1826.1	1.1	15of 32	2.1202	FALSE	FALSE	::::::::::::::::::
RINYQPPTVVPGGDLAK	7	9.72	0	1252	35.1	AY113631	TRUE	FALSE	2	1826.1	0.5	1	2.6238	FALSE	FALSE	::::::::::::::::::
LGFSDDEDSDDEVEEFEEESDAEPVEEIPETFVD	8	2.46	0.009	2877	74.1	AY113649	TRUE	FALSE	3	3894.9	-0.9	25of132	2.1171	FALSE	FALSE	::::::::::::::::::::::::::::::::::
SLDMWSVGVIIYVSLSGTFPFNEEEDIN	15	2.8	0.011	1355	92.33	AY118312	TRUE	FALSE	3	3163.5	-2.2	25of108	2.3323	FALSE	FALSE	::::::::::::::::::::::::::
TPVLSSSSSMPPGLGNLSSYSSK	4	9.72	0.135	2295	41.03	AY118524	TRUE	FALSE	2	2284.5	0.6	11of 44	1.3069	FALSE	FALSE	::::::::::::::::::::::
LQRNSLAESNAGTKEKISPQFSI	7	9.89	0.12	1737	40.9	AY118541	TRUE	FALSE	3	2519.8	0	174	0.9543	FALSE	FALSE	::::::::::::::::::::::
VMGIQGGGGIGSWLGHLLLLGGH	2	8	0.038	2258	68.43	AY118717	TRUE	FALSE	3	2246.6	-0.2	14of 88	1.5959	FALSE	FALSE	::Oxidation_M::::::::::::::::::::
GFYGRRSHAKSR	1	12.13	0.052	2333	7.8	AY118864	TRUE	FALSE	3	1422.6	-2.4	10of 44	1.2421	FALSE	FALSE	::::::::::::
PNLAPEFSKEETTTKKKKK	4	10.27	0.094	1910	13.9	AY119069	TRUE	TRUE	2	2205.6	-0.1	4of 36	0.7183	FALSE	FALSE	::::::::::::::::::
LRNYGCPTPSEIIWNLLH	11	7.16	0.057	413	56.4	AY119114	TRUE	FALSE	3	2184.5	1.9	22of 68	2.0761	FALSE	FALSE	::::::Cys_CAM::::::::::::
RSQRPAVGMPGSWPLDFRR	11	12.41	0.059	1581	40.53	AY119524	TRUE	TRUE	3	2214.6	0.6	17of 72	1.6543	FALSE	FALSE	::::::::::::::::::
KVIGLTAALGSGMPLGRGGPFVHIASIVAQLLSK	11	11.64	0.079	202	95.23	AY119539	TRUE	FALSE	3	3361.1	1.2	18of132	1.523	FALSE	FALSE	::::::::::::::::::::::::::::::::::
LEPLELTYLAHILR	2	5.3	0.024	2001	56.5	AY121624	TRUE	FALSE	2	1682	2.2	8of 26	1.1361	FALSE	FALSE	::::::::::::::
ELTYLAHILR	14	7.77	0.002	644	37.2	AY121624	TRUE	FALSE	3	1229.5	2.5	11of 36	1.5301	FALSE	FALSE	::::::::::
KVDELLHTGENYDLVG	12	4.06	0.062	1541	36.8	AY121671	TRUE	FALSE	2	1803	-2.5	6of 30	0.9995	FALSE	FALSE	::::::::::::::::
QMGGTGGGGRKSF	9	11.49	0.03	1266	10.13	AY121677	TRUE	FALSE	2	1240.4	-1.1	11of 24	1.2957	FALSE	FALSE	::::::::::::::
ASGTVVATSGAARAGTTNTMK	12	11.49	0.081	1253	24.23	AY122136	TRUE	FALSE	3	1953.2	-2	20of 80	1.7433	FALSE	FALSE	::::::::::::::::::::
MLPRLAR	15	12.41	0	992	24.53	AY122136	TRUE	FALSE	1	873.1	0.8	8of 12	1.3946	FALSE	FALSE	:Oxidation_M::::::
NSIASHWHGHGPK	10	10.1	0.078	482	10.4	AY122176	TRUE	FALSE	3	1428.6	2.1	15of 48	1.7371	FALSE	FALSE	::::::::::::::
HRLWLSKISEQNSWLPAPANSLQMTR	10	11.33	0.045	1324	65.23	AY122251	TRUE	FALSE	3	3065.5	-2.4	21of100	2.4445	FALSE	FALSE	::::::::::::::::::::::::
IQFIKTEGLTFALLAGPMGQAASM	3	6.95	0.036	1552	75.76	AY122262	TRUE	FALSE	3	2529	0	16of 92	1.4567	FALSE	FALSE	:::::::::::::::::Oxidation_M:::::Oxidation_M:
MDRVKMSKLQWRINISLSLNTVQID	1	10.58	0.065	1632	70.16	AY122267	TRUE	FALSE	3	3006.6	2	22of 96	2.6361	FALSE	FALSE	:Oxidation_M:::::::::::::::::::::
GGSLGSAISALGHATMNGYLSQHAPLGQNSS	5	7.91	0.028	2533	52.63	AY128459	TRUE	FALSE	3	3001.3	2	24of120	2.0699	FALSE	FALSE	:::::::::::::::Oxidation_M::::::::::::::
IQNVPRDFEIKMPTLVRESPPSQAPKGR	2	10.57	0.009	1402	54.33	AY135563	TRUE	FALSE	3	3208.7	1.1	7of108	0.8646	FALSE	FALSE	:::::::::::Oxidation_M::::::::::::::
EDKILTISPRAMFVSSKG	13	9.89	0.034	415	41.83	AY136549	TRUE	FALSE	2	1996.3	-2.7	7of 34	1.0647	FALSE	FALSE	:::::::::::Oxidation_M::::::::
MQNEAAGGGSDQVPSMSLKL	10	4.08	0.007	1594	35.66	AY142213	TRUE	FALSE	2	2037.3	1.5	12of 38	1.5234	FALSE	FALSE	:Oxidation_M:::::::::::::::::
SKTHAASAYSVDAR	13	9.72	0.127	1320	12.9	AY150698	TRUE	FALSE	2	1464.6	-1.9	9of 26	1.6109	FALSE	FALSE	::::::::::::::
EGKVIFSLSRMGSAIAMAALTTF	14	10.09	0.118	1098	69.86	AY150698	TRUE	FALSE	3	2418.9	2.5	16of 88	1.9221	FALSE	FALSE	:::::::::Oxidation_M::::::::::
ANCIYKTVVDSKSYWVELEK	13	6.47	0.162	1152	48.6	AY180917	TRUE	FALSE	3	2433.7	1.9	8of 76	1.0771	FALSE	FALSE	:::Cys_CAM:::::::::::::
TDFGWIVSGCKKSKGKETIVATT	2	9.7	0.058	517	40.6	AY180917	TRUE	FALSE	3	2514.8	1.3	17of 88	1.7705	FALSE	FALSE	:::::::::Cys_CAM::::::::::::
EMVSDLTSDAFLAALRR	13	4.31	0.016	1392	49.43	AY180917	TRUE	FALSE	2	1896.2	1.2	10of 32	1.221	FALSE	FALSE	::::::::::::::::::
LKGSIDNIMEIYAWSDSTITLAWINSGQSKIK	2	6.96	0.003	1290	86.03	AY180917	TRUE	TRUE	3	3585.1	2.2	25of124	2.7023	FALSE	FALSE	::::::::::::::::::::::::::::
CTGYRPILEGYKTFTKEFACGMGDKCCXVSG	2	7.84	0.044	2161	61.73	AY219192	TRUE	FALSE	3	3624	-2	13of120	1.1207	FALSE	FALSE	:Cys_CAM::::::::::::::::Cys_CAM::Oxidation_M:::Cys_CAM:Cys_CAM:::::
VASNQATHDPIGKPKVHVXALKQATGEA	11	9.76	0.011	696	35.3	AY219199	TRUE	FALSE	3	2882.3	1.1	20of108	1.6813	FALSE	FALSE	::::::::::::::::::::::::
PMDASAPGGMIAYRR	9	9.85	0.013	554	31.36	AY219217	TRUE	FALSE	3	1609.9	1.6	12of 56	1.4356	FALSE	FALSE	:::::::::Oxidation_M::::::
YAGGPMRGGPPGGYQR	2	10.2	0.046	2354	20.13	AY223154	TRUE	FALSE	3	1621.8	-0.1	31of 60	2.6075	FALSE	FALSE	::::::::::::::::
QSLNSRVSGYSFG	7	9.85	0.004	1236	23.3	AY223170	TRUE	FALSE	2	1402.5	-1.1	23	0.8227	FALSE	FALSE	::::::::::::::
ETDKEEYNDIPTGVDISR	13	3.76	0.09	1316	27.7	AY223295	TRUE	FALSE	3	2082.2	-2.3	17of 68	2.0942	FALSE	FALSE	::::::::::::::::::
HLVNESIIPDQDT	15	3.7	0.025	148	29.1	AY223318	TRUE	FALSE	3	1481.6	-1.4	16of 48	1.6212	FALSE	FALSE	::::::::::::::
NTDAIIYVVDSMDRDR	14	3.88	0.026	2864	36.23	AY223381	TRUE	FALSE	3	1884.1	0.8	13of 60	1.4496	FALSE	FALSE	::::::::::::::::
NCGVSIMRSGEAMERGLR	5	9.01	0.108	1294	34.96	AY223453	TRUE	FALSE	3	2040.3	2.6	22of 68	2.6219	FALSE	FALSE	::Cys_CAM::::Oxidation_M:::::::::::
YLNIRVIWLLILLTTSIGAIVVYVDLNELYQTVR	5	6.85	0.125	2719	143.3	AY226549	TRUE	FALSE	3	3979.8	-2.8	23of132	2.5993	FALSE	FALSE	::::::::::::::::::::::::::::::::
ATKAAANRAKLLAARKKKVAAKK	4	12.47	0.079	1847	23.3	AY231643	TRUE	FALSE	3	2409	-2.1	14of 88	1.5776	FALSE	FALSE	::::::::::::::::::::::
DMSESEEFK	12	3.69	0.059	2557	14.63	AY231678	TRUE	TRUE	2	1102.2	-0.1	5of 16	0.8718	FALSE	FALSE	::::::::::
VVAKTSTAIQTSQEVPGISGSPGKPTVTEPTNQTETAK	2	7.13	0.088	646	48.6	AY231682	TRUE	FALSE	3	3842.2	-0.8	20of148	1.4997	FALSE	FALSE	::::::::::::::::::::::::::::::::::
EYMDTLTHK	11	5.22	0.005	1002	16.43	AY231705	TRUE	FALSE	1	1138.3	0.8	7of 16	1.9517	FALSE	FALSE	::::::::::
KHPELESIPNLHVIKALQSLHSR	5	9.89	0.069	2467	48.1	AY231709	TRUE	FALSE	2	2648.1	0.9	10of 44	1.3074	FALSE	FALSE	::::::::::::::::::::::
TLEAYVQDQA	10	3.01	0.077	1032	23.5	AY231716	TRUE	FALSE	2	1138.2	1.4	7of 18	1.1393	FALSE	FALSE	::::::::::
LQCSGNSTSSR	13	9.01	0.209	2586	9.1	AY231731	TRUE	FALSE	2	1197.2	2.1	5of 20	1.0564	FALSE	FALSE	:::Cys_CAM:::::::::
RLGVVRPKGLVCNPTFRGA	9	12.12	0.051	1960	43.4	AY231760	TRUE	FALSE	3	2098.5	-2.4	21of 72	2.0866	FALSE	FALSE	:::::::::::Cys_CAM::::::::
SRNRTEMNKNRGGNASQNQRGGRPGGGNRNNVGNRPG	3	12.8	0.039	882	4.33	AY231761	TRUE	FALSE	3	3953.2	0.7	25of144	2.0194	FALSE	FALSE	::::::Oxidation_M:::::::::::::::::::::::::::
VLASGLLLVTGPFALNSCPLR	15	9.01	0.356	1818	75.9	AY231788	TRUE	TRUE	2	2199.6	0.3	18of 40	4.3575	FALSE	FALSE	:::::::::::::::::Cys_CAM::::
NLTPGTVLILLAGR	13	11.05	0.207	1693	48.4	AY231788	TRUE	TRUE	2	1438.8	1.6	19of 26	3.9847	FALSE	FALSE	::::::::::::::
HIDFSLK	9	7.82	0.131	1376	19.4	AY231798	TRUE	TRUE	2	860	0.3	12of 12	2.4986	FALSE	FALSE	::::::::
AVKIKKNPTNTKFK	9	11.13	0.049	421	14	AY231803	TRUE	TRUE	3	1618	2.5	8of 52	0.9403	FALSE	FALSE	::::::::::::::
IFNVTQHAVGVIVNKRVRGKIL	15	12.43	0.175	1033	56.9	AY231806	TRUE	FALSE	3	2463	0.9	20of 84	3.524	FALSE	FALSE	::::::::::::::::::::::
WKANPFGGASHAKGI	8	10.6	0.068	2640	24.6	AY231818	TRUE	FALSE	2	1541.8	-1.1	10of 28	1.1635	FALSE	FALSE	::::::::::::::
VIHNASIMNAVGCCGLQLYK	15	8.29	0.501	1196	54.23	AY231829	TRUE	TRUE	2	2249.6	1	26of 38	4.7723	FALSE	FALSE	:::::::::::Cys_CAM:Cys_CAM::::::
QLTDRRRNISSINTQLQDVQRIMVQNI	3	11.93	0.134	2365	58.33	AY231832	TRUE	FALSE	3	3257.7	2.9	12of104	1.5841	FALSE	FALSE	:::::::::::::::::::::Oxidation_M:::::
QMHEDNEQVR	3	4.43	0.003	2794	9.63	AY231837	TRUE	FALSE	2	1286.4	-2.1	5of 18	1.0037	FALSE	FALSE	::::::::::
GRKKVQIVHKPMDAKT	12	10.99	0.042	929	16.43	AY231857	TRUE	FALSE	3	1837.2	-1.2	14of 60	1.5759	FALSE	FALSE	::::::::::::::
EFFLSFAKDPQMFI	7	4.08	0.036	1221	56.43	AY231861	TRUE	FALSE	2	1721	1.7	151	0.9668	FALSE	FALSE	::::::::::::::
QLIHGKFPATFTSIK	11	10.6	0.018	1122	37.6	AY231865	TRUE	FALSE	2	1689	-0.8	7of 28	1.1807	FALSE	FALSE	::::::::::::::
YCRNKGIKTSIR	10	10.7	0.159	490	16.1	AY231870	TRUE	FALSE	3	1496.7	-1.9	16of 44	1.6647	FALSE	FALSE	::Cys_CAM:::::::::::
DIDSAAKFIGA	11	3.89	0.013	326	26.8	AY231917	TRUE	FALSE	2	1108.2	2.3	8of 20	1.3753	FALSE	FALSE	::::::::::
MACATLKRALDWESMNQRPPKRRR	14	11.85	0.035	2857	42.56	AY231927	TRUE	FALSE	3	2973.5	1.1	7of 92	0.975	FALSE	FALSE	:::Cys_CAM:::::::::::::::::::
KPATAPTKTGPTGPK	9	10.85	0.092	1193	7.7	AY231928	TRUE	FALSE	2	1452.7	-1	11of 28	1.6624	FALSE	FALSE	::::::::::::::
LTRPVAATDVKRRVGGAASAPFKR	2	12.42	0.097	793	39.4	AY231931	TRUE	FALSE	3	2526	-2.8	15of 92	1.4289	FALSE	FALSE	::::::::::::::::::::::
VDNHLFNKENMPS	2	5.22	0.01	163	23.83	AY231943	TRUE	FALSE	3	1561.7	0	11of 48	1.2393	FALSE	FALSE	:::::::::Oxidation_M:::
KVAVSGMPGTSSTVQAGNVVSSVQMHGQAR	11	11.49	0.082	209	43.06	AY231954	TRUE	FALSE	2	2988.4	2.8	5of 58	0.7635	FALSE	FALSE	:::::::::::::::::::::::Oxidation_M:::::
TGLWQRNEAKATGGSVAVVPAYHGELPKE	2	7.73	0.058	2425	52.5	AY231965	TRUE	FALSE	3	3067.4	1.8	20of112	1.6467	FALSE	FALSE	::::::::::::::::::::::::::
DGDVILIATDGVFDNVPEDLM	1	2.67	0.154	110	65.33	AY231981	TRUE	FALSE	2	2265.5	-1.4	6of 40	0.9454	FALSE	FALSE	:::::::::::::::::::Oxidation_M:
RSPCQNILDLCCHISNKR	8	8.58	0.046	1812	34	AY231998	TRUE	FALSE	2	2272.5	1.8	10of 34	1.3017	FALSE	FALSE	::::Cys_CAM::::::Cys_CAM:Cys_CAM::::::
IEGRITNGYPAEEGKAPY	15	4.56	0.128	1769	31.8	AY232010	TRUE	FALSE	2	1966.2	2.7	10of 34	1.3309	FALSE	FALSE	::::::::::::::::
MTSQLSQASSTLSR	9	11.05	0.023	565	23.33	AY232012	TRUE	FALSE	3	1513.7	1.7	15of 52	1.6033	FALSE	FALSE	:Oxidation_M:::::::::::::
VIDTPITEMGFAGIAVGAAMA	11	3.01	0.01	1324	65.26	AY232099	TRUE	FALSE	2	2036.4	2.5	12of 40	1.2407	FALSE	FALSE	::::::::::::::::::::

AKAILNINKTKEQTHTACLHGLRVFSVLWTM	1	10.32	0.019	1482	79.03	AY232101	TRUE	FALSE	3	3583.2	3	14of120	1.5327	FALSE	FALSE	::::::::::::::::Cys_CAM::::::::::::
QQVLQTNVMGVVYCTRRAFESMRQR	8	10.98	0.054	2775	55.26	AY232112	TRUE	FALSE	3	3075.5	2.2	18of 96	1.5363	FALSE	FALSE	::::::::::::Cys_CAM::::::::Oxidation_M::::
DYKKTIGVDFLKRQIEIDGEDVRIMLWDT	13	4.39	0.041	1908	79.23	AY232118	TRUE	FALSE	3	3499	-0.2	21of112	1.4143	FALSE	FALSE	::::::::::::::::::::::::::::
PLMVSSTVEKIVEVDKHIGCATSGLMADAR	6	5.39	0.112	1294	68.56	AY232148	TRUE	FALSE	3	3216.7	1.4	21of116	3.3007	FALSE	FALSE	::::::::::::::::::Cys_CAM:::::::::::
VCCETAQLESYDRAQSERTINAPSAIR	7	4.65	0.076	1965	49.3	AY232183	TRUE	TRUE	3	3127.3	1.6	214	1.5907	FALSE	FALSE	::Cys_CAM:Cys_CAM:::::::::::::::::::::
PFGVDWKKVAEYAMR	11	9.63	0.008	1694	39.23	AY232216	TRUE	FALSE	2	1814.1	-1.6	9of 28	1.2596	FALSE	FALSE	::::::::::::Oxidation_M::
PERPAVGRLAT	6	10.89	0.069	1242	21.4	AY232226	TRUE	FALSE	2	1167.4	-1.5	6of 20	1.1329	FALSE	FALSE	::::::::::::
PPQVLQVSTVLENPTR	8	6.98	0.04	2671	38.1	AY271259	TRUE	FALSE	2	1779	-0.1	8of 30	1.2434	FALSE	FALSE	::::::::::::::::
SYCQKHSMSKGKKENAGSHGGG	7	9.97	0.065	3468	0.73	AY321364	TRUE	FALSE	3	2352.5	-2.6	168	1.5088	FALSE	FALSE	:::Cys_CAM::::Oxidation_M:::::::::::::::
TTSTTFTTSTTSTRPTTTTTTINVFTTK	12	11.49	0.138	1501	36.3	AY349701	TRUE	FALSE	3	2900.2	-1.9	11of104	1.2396	FALSE	FALSE	::::::::::::::::::::::::::::
KTPRFKIYTELELRPPIGCSNS	14	9.66	0.055	2815	49	AY352649	TRUE	FALSE	3	2608	0.5	10of 84	1.1362	FALSE	FALSE	::::::::::::::::::Cys_CAM::::
PLAGRXXXXKCHPL	15	10.11	0.034	1849	19.8	AY461111	TRUE	FALSE	2	1602	-0.2	10of 26	1.5209	FALSE	FALSE	::::::::::Cys_CAM::::
GTICSDQCNEDGXWGAGTDQCLXCK	10	3.51	0.03	2050	35.9	AY461236	TRUE	FALSE	3	2859.9	-0.5	17of 96	1.708	FALSE	FALSE	::::Cys_CAM:::Cys_CAM::::::::::::Cys_CAM:::Cys_CAM::
NRVFTSKSDVWAFGVTIWELLTFGXXX	2	7.02	0.089	165	81.5	AY461298	TRUE	FALSE	3	3114.7	-1.5	21of104	1.6754	FALSE	FALSE	::::::::::::::::::::::::::::
PMGSPASPVIADILMEELLDKITDK	8	3.85	0.023	2758	71.16	AY484404	TRUE	FALSE	3	2717.2	-0.4	14of 96	1.4514	FALSE	FALSE	::Oxidation_M::::::::::::Oxidation_M:::::::::::
CGDLHDSKQCQINK	7	7.01	0.08	1331	13.8	B32713	TRUE	FALSE	3	1703.8	1.5	25	1.6044	FALSE	FALSE	:Cys_CAM::::::::Cys_CAM:::::
TGDFNGWHPSWGSPTTNTRGKITQR	11	11.33	0.092	1478	32.5	B36186	TRUE	FALSE	3	2803	0.2	21of 96	2.4213	FALSE	FALSE	::::::::::::::::::::::::::::
YYDGWIGGRKYPVDMAGFAVSVK	6	9.36	0.1	2390	58.93	B3GP-DROME	TRUE	FALSE	3	2597	0.4	19of 88	1.7648	FALSE	FALSE	::::::::::::::Oxidation_M:::::::::
GIWPDEHIKGVIKTVVFR	11	9.89	0.028	990	50.7	BAB1-DROME	TRUE	FALSE	3	2095.5	1	11of 68	1.1883	FALSE	FALSE	::::::::::::::::::
NRVHNMLGPSLDGGADPRPKARGR	1	11.95	0.049	1061	28.33	BAB2-DROME	TRUE	FALSE	3	2588.9	1.7	10of 92	1.0831	FALSE	FALSE	:::::Oxidation_M:::::::::::::::::
EIEDQVSAAAAVAAAAAKHQQQQGER	15	4.63	0.022	1853	33.7	BAB2-DROME	TRUE	FALSE	3	2678.9	-0.1	12of100	1.4513	FALSE	FALSE	::::::::::::::::::::::::::::
LAGSALF	4	6.02	0	2774	27.9	BAB2-DROME	TRUE	FALSE	1	678.8	1.1	8of 12	0	FALSE	FALSE	::::::::
TPGMPGLMAGPGAGGMLMNSSGEQHQNK	3	7.82	0.168	2362	42.82	BCL9-DROME	TRUE	FALSE	3	2757.1	0.9	14of108	1.4819	FALSE	FALSE	::::::::::::::::::::::::::::
IPGDLMMGMSGGGGGSIINPTMRQLHMPGNAKS	1	10.09	0.004	2124	66.65	BCL9-DROME	TRUE	FALSE	2	3330.9	-1.4	13of 64	1.9292	FALSE	FALSE	:::::::::::::::::::::::::::Oxidation_M:::::::
RLMDIPVSCQLGRMLIFGILLR	14	10.81	0.102	1706	89.26	BGCN-DROME	TRUE	FALSE	3	2603.2	-0.2	17of 84	1.9713	FALSE	FALSE	::::::::Cys_CAM:::::::::::::
WIWMVMSKATAEMVMRTRYYFFK	12	10.34	0.011	1580	83.02	BGCN-DROME	TRUE	FALSE	3	3009.6	2.5	17of 88	1.4658	FALSE	FALSE	::::::::::::Oxidation_M::Oxidation_M:::::::::
GMDDDEDDLEGLLAEIEDEHQKMQGR	12	3.61	0.034	2626	46.06	BLM-DROME	TRUE	FALSE	2	3022.2	-1.7	8of 50	1.0497	FALSE	FALSE	::Oxidation_M::::::::::::::::::::Oxidation_M::::
AAEATPTAAPEAATKS	10	4.27	0.018	1310	19.7	BNB-DROME	TRUE	FALSE	2	1487.6	-1.9	11of 30	1.3072	FALSE	FALSE	::::::::::::::::
AAVPEQPDVNANPSPSTPAAEPAKEI	9	3.69	0.008	293	41.8	BNB-DROME	TRUE	FALSE	2	2601.8	2.1	11of 50	1.1283	FALSE	FALSE	::::::::::::::::::::::::
VMDLLVTKLSPSSDYFQQSNA	6	3.89	0.011	2767	53.93	BP28-DROME	TRUE	FALSE	3	2360.6	2.4	20of 80	1.5639	FALSE	FALSE	::Oxidation_M:::::::::::::::::
QPVKRRSVQATQL	9	12.42	0.003	1586	19.2	BP28-DROME	TRUE	FALSE	2	1511.8	-0.5	11of 24	1.3735	FALSE	FALSE	::::::::::::
IGSNLQSSNNGGNSGISSLVVGAGK	2	10.1	0.011	825	36.1	BRAT-DROME	TRUE	FALSE	3	2318.5	1.2	20of 96	2.1588	FALSE	FALSE	::::::::::::::::::::::
PASPAVGSNTTTATATTATRSRFMITDILA	3	10.89	0.007	1988	59.93	BRH2-DROME	TRUE	FALSE	3	3025.4	0.6	22of116	1.3943	FALSE	FALSE	::::::::::::::::::::::::::
DLYMWISNTSGSTGPSAKFLIE	2	4.08	0.023	125	60.53	BRIX-DROME	TRUE	FALSE	2	2418.7	0.4	8of 42	1.0295	FALSE	FALSE	::::::::::::::::::::
LIKATAKMPKLPAVGIDLGTTYSCVGVFQHGK	11	9.97	0.382	1128	75.33	BT001361	TRUE	FALSE	3	3419	0	28of124	4.6555	FALSE	FALSE	:::::::Oxidation_M::::::::::::::Cys_CAM:::::::::
LIKATAKMPKLPAVGIDLGTTYSCVGVFQHGK	12	9.97	0.028	1467	75.33	BT001361	TRUE	FALSE	3	3419	-2	26of124	2.4203	FALSE	FALSE	:::::::Oxidation_M::::::::::::::Cys_CAM:::::::::
QVGGGGGGYHASKTSVASRHAAGGGV	11	10.4	0.138	1733	18.8	BT001369	TRUE	FALSE	3	2326.5	-1.8	17of100	1.6085	FALSE	FALSE	::::::::::::::::::::::
IFVHYIFIVNGPTFMGNVLKFNF	11	9.72	0.054	2252	92.03	BT001376	TRUE	FALSE	2	2719.3	2	5of 44	0.8001	FALSE	FALSE	::::::::::::::::::::::
HYADLSARPFFPGLVNYMNSGPVVPMVWEGLNVVQ	8	5.22	0.532	2702	107.16	BT001459	TRUE	FALSE	3	3906.5	1.7	41of136	5.3625	FALSE	FALSE	::::::::::::::::::::::::::::::
IAESFDAFVTK	8	4.08	0.055	3285	32.2	BT001469	TRUE	FALSE	2	1228.4	0.1	4of 20	0.66	FALSE	FALSE	::::::::::
LMLSRESKSKGDPFVTS	11	9.89	0.019	965	32.93	BT001469	TRUE	FALSE	2	1899.2	0.8	6of 32	0.8207	FALSE	FALSE	::Oxidation_M:::::::::::::::
PAPKLLSLPLPQNN	3	10.1	0.102	1537	38.9	BT001493	TRUE	FALSE	2	1502.8	-1.9	9of 26	1.0631	FALSE	FALSE	::::::::::::::
PDNQIVDYNTTYSGITEAMLSNETR	11	3.59	0.053	1711	48.43	BT001493	TRUE	TRUE	3	2834	2.9	19of 96	1.5794	FALSE	FALSE	::::::::::::::::::::::
AAIENILRGCIGLPPISHMTLEQRV	15	7.17	0.093	1385	73.33	BT001560	TRUE	FALSE	3	2806.3	-0.7	11of 96	1.1893	FALSE	FALSE	:::::::::Cys_CAM::::::::Oxidation_M:::::::
KVTFVDSAPMVLKETNINKMHTPSEGMLHINPKDF	8	7.9	0.032	1912	76.19	BT001638	TRUE	FALSE	3	3971.6	-2.4	23of136	2.146	FALSE	FALSE	::::::::::::::::::::::::::::::
MLIGVLSIWLVVLALLLK	14	10.1	0.036	1665	100.33	BT001646	TRUE	FALSE	2	2011.6	-0.3	12of 34	1.9179	FALSE	FALSE	:Oxidation_M:::::::::::::::
KIGAMQFFLALTLILAYS	7	9.72	0.006	1760	77.53	BT001658	TRUE	FALSE	2	2017.5	2	204	1.6486	FALSE	FALSE	:::::Oxidation_M:::::::::::::
ELHIQMHSHILVLIELAGV	10	5.74	0.019	580	67.63	BT001811	TRUE	FALSE	3	2153.6	-0.2	22of 72	2.3501	FALSE	FALSE	::::::::::::::::::
YLYHSQFNSNSPQTRRFTAQR	10	11.16	0.098	1117	32.8	BT001876	TRUE	TRUE	3	2602.8	0.6	20of 80	1.7782	FALSE	FALSE	::::::::::::::::::::
DSQGAMKALMLTVQAAQIK	1	9.89	0.052	1890	43.86	BT003293	TRUE	FALSE	2	2037.4	-0.6	12of 36	1.5548	FALSE	FALSE	:::::Oxidation_M:::Oxidation_M:::::::::
GRQSFRVGTGDSSRSMDM	11	10.8	0.148	1489	21.96	BT003438	TRUE	FALSE	2	1975.2	1.8	10of 34	1.1025	FALSE	FALSE	::::::::::::::::::
QNNAMGFPRILSKNNKIYTKL	8	10.9	0.052	2047	44.03	BT003486	TRUE	FALSE	3	2467.9	2.4	10of 80	1.3364	FALSE	FALSE	:::::Oxidation_M:::::::::::::
ANLDNYAKWYKQNIGEMTYILGTERFQ	3	6.94	0.003	2361	67.53	BT003770	TRUE	FALSE	3	3284.7	1.4	19of104	1.6566	FALSE	FALSE	::::::::::::::::Oxidation_M:::::::::
TLGRKRPSRTKASCESPWNGHR	3	11.97	0.057	2000	17.5	BT009947	TRUE	TRUE	3	2582.9	0.9	13of 84	1.6294	FALSE	FALSE	::::::::::::Cys_CAM:::::::::
SWSMLFASVGYQVVLYDILPEQVS	6	3.01	0.001	1218	87.43	BT009948	TRUE	FALSE	3	2749.2	0.4	21of 92	3.0845	FALSE	FALSE	::::Oxidation_M:::::::::::::::::
GNTPMMVAFNKNANEIATYLESQER	15	4.56	0	719	51.16	BT009959	TRUE	FALSE	3	2846.2	0.5	21of 96	2.2962	FALSE	FALSE	:::::Oxidation_M:::::::::::::::::
DELGSGASQVGGVDPKADAK	14	3.97	0.066	2715	22.4	BT009974	TRUE	FALSE	3	1902	2.5	9of 76	1.1126	FALSE	FALSE	::::::::::::::::::
CEAAAAATHY	13	5.13	0.046	1162	16.7	BT009985	TRUE	FALSE	1	1065.1	-0.4	10of 18	1.7987	FALSE	FALSE	:Cys_CAM:::::::::
IPVPQNVLATAPLLKTPLSQ	9	10.1	0.229	2241	60.1	BT010058	TRUE	FALSE	2	2101.5	0.2	6of 38	0.9349	FALSE	FALSE	::::::::::::::::::
VFLLVFIATHHLVDSAGPLSNIASES	11	5.05	0.204	324	82.5	BT010204	TRUE	FALSE	3	2739.1	-0.3	18of100	1.8201	FALSE	FALSE	::::::::::::::::::::::::
LHPHPGSRGRWR	7	12.71	0.013	3275	14.3	BT010225	TRUE	FALSE	2	1456.7	1.8	468	1.1279	FALSE	FALSE	::::::::::::
LQSAADSAR	8	6.79	0.107	1607	13.3	BT010247	TRUE	FALSE	2	919	0.9	7of 16	1.077	FALSE	FALSE	::::::::
SQSYFDEAVSGARYQNVLR	13	6.9	0.064	391	37.9	BT010247	TRUE	FALSE	2	2191.4	1	6of 36	0.8078	FALSE	FALSE	::::::::::::::::::
APAVEATAEGKVPMVATPVGPMPGILILRQNKKPK	2	10.55	0.043	1452	77.26	BT010297	TRUE	FALSE	3	3611.4	2.6	10of136	1.1896	FALSE	FALSE	::::::::::::::::::::::::::::::
VADEMESYGSIVPIYTMKLYAVSDGPPSLAVR	8	4.07	0.036	2360	86.86	BT011060	TRUE	FALSE	3	3477	-2.4	23of124	1.8942	FALSE	FALSE	::::::::::::::::Oxidation_M:::::::::::::::
EAAKMAGATNADIKRVLSIQSHVVHGY	5	9.63	0.018	1450	49.43	BT011099	TRUE	FALSE	3	2868.3	2.5	20of104	2.2644	FALSE	FALSE	::::::::::::::::::::::::
KNLVDHF	14	7.82	0.09	220	16.6	BT011102	TRUE	FALSE	2	873	-1.4	8of 12	1.6011	FALSE	FALSE	::::::::
KNIWFRKTSLKLLKKNLVDHFSMSVDPLSIDNFTI	4	10.39	0.013	2656	99.33	BT011102	TRUE	FALSE	3	4150.9	-2.9	8of136	1.0016	FALSE	FALSE	::::::::::::::::::::::::::::::
SSCFQKRSARQDAAAAAPECDAR	3	8.3	0.025	2822	26.3	BT011126	TRUE	TRUE	3	2554.7	-2.2	10of 88	1.1053	FALSE	FALSE	:::Cys_CAM::::::::::::::Cys_CAM::::
MACRFLQAKCFELEK	3	8.29	0.071	1693	44.53	BT011179	TRUE	FALSE	2	1932.2	1.6	9of 28	1.2327	FALSE	FALSE	:::Cys_CAM::::::Cys_CAM::::::
EFCEEPVQGQGNGQICLR	12	3.97	0.095	1516	37.3	BT011393	TRUE	FALSE	3	2122.2	0.3	18of 68	1.9905	FALSE	FALSE	:::Cys_CAM::::::::::::Cys_CAM:::
AQIKAAFRFVKREIR	10	12.14	0.136	593	37.1	BT011450	TRUE	FALSE	3	1834.2	-2.6	15of 56	2.0216	FALSE	FALSE	::::::::::::::::
LGVEFDEETLDGR	2	3.51	0.381	857	32.6	BT012432	TRUE	TRUE	2	1480.6	-0.7	17of 24	4.0581	FALSE	FALSE	::::::::::::::
MNKPGVVPMYIFECAAKLKM	3	9.6	0.033	1228	59.29	BT012450	TRUE	FALSE	3	2344.9	-2.5	22of 76	1.8667	FALSE	FALSE	::::::::::::Cys_CAM:::::Oxidation_M:
LHFLNLRRSNGTDERMGQR	6	11.93	0.07	2199	33.53	BT012454	TRUE	FALSE	2	2301.6	-1.4	5of 36	0.9241	FALSE	FALSE	::::::::::::::::::
ISAYTYERTLMMEQRNQMLRALGLNKK	4	10.33	0.081	2736	65.19	BT012491	TRUE	FALSE	3	3260.9	0.9	15of104	1.3662	FALSE	FALSE	::::::::::::::::::::::::::
MLAKIIEAFPVCDE	7	3.83	0.041	1656	50.43	BT012498	TRUE	FALSE	2	1636.9	2	106	1.1458	FALSE	FALSE	::::::::::Cys_CAM:::
KLMSLAKQLPPNVFSLPNSQKEEGASAAKS	3	10.16	0.059	2868	56.43	BT012499	TRUE	FALSE	3	3188.7	2.1	20of116	1.7922	FALSE	FALSE	:::Oxidation_M:::::::::::::::::::::::
LGGGVGGGLGGGGSLGLGGGGGGGGSCTPTSLQPQSSLTTFK	2	8.97	0.075	514	63.8	BTKL-DROME	TRUE	FALSE	3	3606.9	0.6	27of164	2.1878	FALSE	FALSE	::::::::::::::::::::::::::Cys_CAM:::::::::::::::
EQDAMRNKR	11	10.09	0.062	745	4.93	BX088700	TRUE	FALSE	2	1164.3	-2.7	10of 16	1.5231	FALSE	FALSE	:::::Oxidation_M:::::
DGLAAVMVRIAAR	8	10.89	0.189	1665	37.83	BX251410	TRUE	FALSE	2	1343.6	1.2	10of 24	1.2626	FALSE	FALSE	::::::::::::::
CMESGDIPAMAVAPAGAPTGLQLLFP	8	3.01	0.118	2691	77.56	BX284746	TRUE	FALSE	3	2632	2.7	23of100	2.3003	FALSE	FALSE	:Cys_CAM::::::::Oxidation_M:::::::::::::::
MATTMEAK	11	6.95	0.02	1719	15.26	BX294010	TRUE	FALSE	2	915.1	2	5of 14	0.7362	FALSE	FALSE	:Oxidation_M::::Oxidation_M::::

RNTIKQAEEMVAAAVVIYATADSSSPAATATADK	7	4.56	0.021	2022	60.83	BX294016	TRUE	FALSE	3	3453.8	2.3	107	1.8217	FALSE	FALSE	::::::::::::::::::::::::::::::::
STAATATAATASNPASAATTDMPPPSFKRQVKKKK	9	11.1	0.129	2269	35.93	BX294017	TRUE	FALSE	3	3550	3	24of136	2.0918	FALSE	FALSE	::::::::::::::::::::Oxidation_M::::::::::::::
IVWTKDHRTEDLVLS	10	5.28	0.02	1230	40.1	BX294025	TRUE	FALSE	3	1813.1	1.8	17of 56	1.4512	FALSE	FALSE	::::::::::::::::
HHFLSMQGDIDSLQSSRDEVKAESEQLRQ	11	4.74	0.058	140	47.53	BX294133	TRUE	FALSE	3	3372.7	-1.7	12of112	1.0714	FALSE	FALSE	::::::::::::::::::::::::::::
VLEGKLHESAAVMRDLRRKRA	2	11.31	0.037	1962	39.13	BX294133	TRUE	FALSE	3	2436.9	-2.2	8of 80	1.0561	FALSE	FALSE	::::::::::::::::::::
ELERAALKAGYGSTID	10	4.45	0.051	1576	33.8	BX294141	TRUE	FALSE	2	1694.9	1.4	13of 30	2.0632	FALSE	FALSE	::::::::::::::::
VTNMCFATKPNQPPAMVDFQYV	13	6.09	0.072	1208	57.46	BX294144	TRUE	FALSE	3	2575.9	1.8	18of 84	1.8115	FALSE	FALSE	:::::Cys_CAM::::::::::Oxidation_M::::::
TKRFVPDK	5	10.59	0.052	1962	11.1	BX42-DROME	TRUE	FALSE	1	991.2	1	9of 14	1.2971	FALSE	FALSE	::::::::
PPYGQR	4	9.85	0	2813	7.7	BX42-DROME	TRUE	FALSE	1	717.8	-1.4	1of 10	0.2376	FALSE	FALSE	::::::
MQSVNAVLFLEGRKTEESN	13	4.56	0.08	1116	41.23	BX538351	TRUE	FALSE	3	2169.4	1.6	17of 72	1.4111	FALSE	FALSE	:Oxidation_M:::::::::::::::::
KYGGESNRAFEW	7	7.02	0.051	3366	21.7	BX538351	TRUE	FALSE	3	1444.5	2.5	44	1.0924	FALSE	FALSE	::::::::::::
DLLIQSLRNSGRSELDN	10	4.31	0.03	1389	38.1	BX538351	TRUE	FALSE	3	1931.1	-1.5	16of 64	1.8149	FALSE	FALSE	::::::::::::::::
VAPGDR	4	6.79	0.069	2671	8.4	BX842628	TRUE	FALSE	1	614.7	0.1	6of 10	1.2274	FALSE	FALSE	::::::
PIVGSSGYAANSRTAQVNPPSFHLK	9	10.4	0.14	2356	43.5	BX842633	TRUE	FALSE	3	2599.9	1.7	9of 96	1.2179	FALSE	FALSE	::::::::::::::::::::::
LKRHSKLHTGEKPHICPK	15	10.55	0.025	1650	16.2	BX842634	TRUE	FALSE	2	2167.5	-2	7of 34	0.9913	FALSE	FALSE	:::::::::::::::Cys_CAM:::
PPSSLSYPGVLPHGTPMSAPAPPSRGMSMP	8	9.85	0.001	1724	60.39	BX842634	TRUE	FALSE	3	3021.5	-0.4	14of116	1.3619	FALSE	FALSE	:::::::::::::::::::::::::::::Oxidation_M::
SYETFMKIIVMNVLLPFTHNKIFSTLGGFETQK	4	9.56	0.029	2343	100.66	C133-DROME	TRUE	TRUE	3	3868.5	-1.6	17of128	1.6167	FALSE	FALSE	::::::Oxidation_M:::::Oxidation_M::::::::::::::::::::::
FYIMMLKLPGPMGFPFIGL	6	9.72	0.028	2460	87.79	C135-DROME	TRUE	FALSE	2	2189.8	-2.9	12of 36	1.6285	FALSE	FALSE	:::::Oxidation_M:::::::::::::
NYMLSTTFLYKDLRFIDNTTMKLAE	14	6.93	0.005	716	75.76	C135-DROME	TRUE	FALSE	3	3046.5	-0.6	15of 96	1.0959	FALSE	FALSE	::::::::::::::::::Oxidation_M:::::
LPSAKDELSMDALRTDITYTR	13	4.46	0.024	1184	47.53	C302-DROME	TRUE	FALSE	3	2397.7	2.6	19of 80	2.0179	FALSE	FALSE	::::::::::::::::::::
APGPRPWPIIGNLHLLDR	11	10.89	0.141	1486	53.8	C307-DROME	TRUE	FALSE	2	2023.4	-1.3	6of 34	0.9138	FALSE	FALSE	::::::::::::::::::
LVPLFTPSRVRQTLPHVARACQLLR	4	12.41	0.014	1553	72.7	C308-DROME	TRUE	FALSE	3	2930.5	2.7	24of 96	3.0377	FALSE	FALSE	::::::::::::::::::::Cys_CAM:::::
PIFNAEAEVLLQKLELEGVQHGKRLEIYQILK	10	5.53	0.053	1316	94.9	C313-DROME	TRUE	FALSE	3	3721.4	-0.8	24of124	2.2918	FALSE	FALSE	::::::::::::::::::::::::::::::
ISLLNYGVDR	10	6.7	0.058	1116	31.7	C3G-DROME	TRUE	FALSE	2	1150.3	-1.2	8of 18	1.1589	FALSE	FALSE	::::::::::
MAKVGGLIGHPDLLFVFDGDEIRNI	1	4.44	0.044	1021	77.73	C49A-DROME	TRUE	FALSE	3	2728.2	-0.3	21of 96	1.891	FALSE	FALSE	::::::::::::::::::::::
KRGQDVAMM	9	10.09	0.035	454	15.36	C4AA-DROME	TRUE	FALSE	2	1036.3	2.5	7of 16	1.1996	FALSE	FALSE	::::::::::
LAKHTLPAGSNVFICPY	3	8.88	0.008	1504	47.2	C4AA-DROME	TRUE	FALSE	2	1889.2	1.9	7of 32	1.0611	FALSE	FALSE	::::::::::::Cys_CAM:::
FNGPRGLPLMGNAHQMGK	10	11.49	0.103	538	34.56	C4E2-DROME	TRUE	TRUE	3	1942.3	-2.7	19of 68	2.0184	FALSE	FALSE	::::::::::::::Oxidation_M:::
TFDCHDYMSEATVEILLETAM	13	3.51	0.21	1485	62.06	C4GF-DROME	TRUE	FALSE	3	2493.7	1.4	11of 80	1.391	FALSE	FALSE	::::Cys_CAM:::Oxidation_M::::::::::::
KYFIEAGTGVLVSTLGIHHDPEFYPEPEK	2	4.74	0.059	961	70.8	C6AJ-DROME	TRUE	FALSE	3	3275.7	1.7	24of112	2.2404	FALSE	FALSE	::::::::::::::::::::::::::::
LLLFMARRRHGYWQR	11	12.41	0.067	1274	48.53	C6AN-DROME	TRUE	FALSE	2	2004.4	2.5	6of 28	0.8235	FALSE	FALSE	::::::::::::::
SMRHMLSPCFTSGKLKSMFS	4	10.59	0.1	2868	46.09	C6D4-DROME	TRUE	FALSE	3	2365.8	-0.7	14of 76	1.2462	FALSE	FALSE	:::::Oxidation_M::::Cys_CAM::::::::Oxidation_M:::
SLHAKSAEVFTPANMQKLL	6	9.89	0.039	2834	45.33	C6U1-DROME	TRUE	FALSE	3	2086.5	1.8	9of 72	0.9164	FALSE	FALSE	::::::::::::::::::
RKGITEGFNDTSVISKSLLSLR	3	10.58	0.059	1851	47.5	C9C1-DROME	TRUE	FALSE	2	2422.8	1.5	13of 42	1.5781	FALSE	FALSE	::::::::::::::::::
EQLGEKPLDYDTLMGM	11	3.59	0.056	278	42.56	C9C1-DROME	TRUE	FALSE	2	1857.1	-2.7	4of 30	0.6322	FALSE	FALSE	::::::::::::::Oxidation_M:
PWPLIGNIPLKAMIGGMPVLKK	11	10.85	0.103	1703	73.86	C9H1-DROME	TRUE	TRUE	2	2407	1.9	11of 42	1.2993	FALSE	FALSE	::::::::::Oxidation_M:::Oxidation_M:::::
YGAKGPRGEHGLKGEKGASCYGPMK	8	9.81	0.048	2215	22.73	CA14-DROME	TRUE	FALSE	3	2653	1.1	19of 96	1.5918	FALSE	FALSE	::::::::::::::::::Cys_CAM:::Oxidation_M::
EQPVVLDSGIIDEEEEHQDTTTATAD	6	3.2	0.116	1688	45.1	CACT-DROYA	TRUE	FALSE	3	2843.9	0.8	21of100	1.6321	FALSE	FALSE	::::::::::::::::::::::::::
PTIPTTFKAQSYVKYALSFEPDRFSTQVQLRFR	1	10.33	0.221	1589	82.1	CADN-DROME	TRUE	FALSE	3	3924.5	-1.6	13of128	1.7401	FALSE	FALSE	::::::::::::::::::::::::::::
VLEQLSSTSGGNSLGGKYAKEELMR	15	7.09	0.149	984	46.33	CAKI-DROME	TRUE	FALSE	3	2656	2.8	13of 96	1.3896	FALSE	FALSE	::::::::::::::::::::
LVQFQKNTDEPMGIT	15	4.08	0.011	1767	35.73	CAKI-DROME	TRUE	FALSE	2	1738	-2.8	10of 28	1.7446	FALSE	FALSE	::::::::::Oxidation_M::::
FEESVTLLFR	13	4.27	0.006	923	39.4	CAPU-DROME	TRUE	FALSE	2	1241.4	1	8of 18	0.9575	FALSE	FALSE	::::::::::
NFTQVHADFGR	9	7.85	0.338	1280	20.5	CATA-DROME	TRUE	TRUE	2	1292.4	1.4	17of 20	3.0961	FALSE	FALSE	::::::::::
GGGGGGNRRDGGP	14	10.89	0.018	514	-1	CAZ-DROME	TRUE	FALSE	2	1057.1	-0.4	9of 22	1.2084	FALSE	FALSE	::::::::::::
LQLSEMAKLLPVKENFLC	12	6.44	0.054	1288	62.93	CB32-DROME	TRUE	FALSE	3	2150.5	1.5	19of 68	1.9801	FALSE	FALSE	::::::Oxidation_M::::::::::Cys_CAM:
QAHIGIKGLVTDASGFPIAD	11	5.1	0.032	968	47.4	CBPD-DROME	TRUE	FALSE	3	2011.3	-0.1	21of 76	1.877	FALSE	FALSE	::::::::::::::::::
LNMWALSMKMSMPGGKYKNM	6	10.45	0.047	2428	52.85	CCA4-DROME	TRUE	FALSE	2	2335.9	-2.2	11of 38	1.6405	FALSE	FALSE	::::::::::::::::::Oxidation_M:
YWSSLRNLVISLLNSMRSI	4	11.14	0.086	1617	67.63	CCAA-DROME	TRUE	FALSE	3	2269.7	-0.7	22of 72	2.4226	FALSE	FALSE	::::::::::::::Oxidation_M::::
FLQTYDKITEITTAYIDEAI	2	3.59	0.184	1037	61.7	CCB1-DROAC	TRUE	FALSE	3	2349.6	3	24of 76	2.943	FALSE	FALSE	::::::::::::::::::
VAVTMVMDMLMAGIDT	11	2.93	0.18	1353	58.02	CCB2-DROME	TRUE	FALSE	2	1731.1	-2.6	5of 30	1.0799	FALSE	FALSE	::::::Oxidation_M::Oxidation_M:::::::
QTAVIIAMDLLFAG	11	3.1	0.037	422	56.23	CCE1-DROME	TRUE	FALSE	3	1463.8	-2.7	14of 52	1.6016	FALSE	FALSE	::::::::::::::
YDGLTSGNGPAWGK	2	6.68	0.005	2197	22.5	CCE1-DROME	TRUE	FALSE	2	1423.5	2.9	8of 26	0.9108	FALSE	FALSE	::::::::::::::
EIDLEEESLPGNTFVL	11	2.85	0.016	368	51	CD89-DROME	TRUE	FALSE	3	1806	-1.7	21of 60	2.0149	FALSE	FALSE	::::::::::::::::
LYTTSIDMWSAGCILAELADAGRPLFPGSDVLDQ	9	3.37	0.062	2619	103.13	CDK5-DROME	TRUE	FALSE	3	3685.1	-1.6	21of132	2.2012	FALSE	FALSE	::::::::::::Cys_CAM:::::::::::::::::::
WSQLVPRLNSKGRDLLQKLLICRPNQR	2	11.97	0	2289	68.2	CDK5-DROME	TRUE	FALSE	3	3290.9	1.1	9of104	0.9793	FALSE	FALSE	::::::::::::::::::::Cys_CAM:::::::
MVVDFCRTALVSEMED	14	3.59	0.14	323	49.26	CDN2-DROME	TRUE	FALSE	2	1919.1	1.9	5of 30	0.7763	FALSE	FALSE	:Oxidation_M::::Cys_CAM:::::::::::
DTETLGIFSDMVTSPGGLSAT	2	2.88	0.001	1656	48.93	CEB-DROME	TRUE	FALSE	2	2116.3	-0.4	11of 40	1.4879	FALSE	FALSE	::::::::::Oxidation_M:::::::::::
DSIVVKRSIGSALKKALPVAKK	2	11.1	0.003	1282	42.3	CER2	TRUE	FALSE	3	2309.8	3	19of 84	1.7116	FALSE	FALSE	::::::::::::::::::::
SALVHRYLTGSYMQEESP	10	5.3	0.032	734	39.03	CG1A-DROME	TRUE	FALSE	3	2069.3	0	21of 68	2.0927	FALSE	FALSE	::::::::::::::::::
EIPLQYVTVKVPGQKPRGSKSIITNSALTSSLMA	3	10.45	0.024	2579	75.53	CG1A-DROME	TRUE	FALSE	3	3616.3	-0.6	25of132	2.08	FALSE	FALSE	::::::::::::::::::::::::::::::
VKELPPRNDRQRFLEVVQYQMDILEY	13	4.73	0.138	1134	72.53	CG2A-DROME	TRUE	FALSE	3	3296.8	1.4	21of100	2.4971	FALSE	FALSE	::::::::::::::::::Oxidation_M:::::::
GVDILADAVAVTMGPKG	11	3.89	0.089	1318	42.33	CH6B-DROME	TRUE	FALSE	2	1630.9	2	11of 32	2.9457	FALSE	FALSE	::::::::::::Oxidation_M:::::
LEDIKMSDFGRVGEVVVSKDDTM	8	4	0.111	1965	52.66	CH6C-DROME	TRUE	FALSE	3	2587.9	2.3	11of 88	1.0756	FALSE	FALSE	::::::Oxidation_M:::::::::::::::
LRMPCLTIAKNAGVDGAMVVAK	1	9.91	0.024	2078	57.26	CH6C-DROME	TRUE	FALSE	2	2332.8	0.7	10of 42	1.6045	FALSE	FALSE	:::::Cys_CAM::::::::::::Oxidation_M:::::
MQVAKHKMMLTHLVVRPGMGGMTTNFSK	2	11.73	0.155	118	60.25	CHD3-DROME	TRUE	FALSE	3	3132.9	-1.8	17of108	1.8934	FALSE	FALSE	::::::::::::::::::::::::::
WQDIQNDIRFAIINEPFKMDV	7	3.97	0.003	1829	66.93	CHDM-DROME	TRUE	FALSE	3	2594	1.6	443	1.3499	FALSE	FALSE	::::::::::::::::::
TELHTLWLNEEKAAVPGR	15	5.4	0	484	43	CHDM-DROME	TRUE	FALSE	3	2065.3	-2.3	21of 68	2.0329	FALSE	FALSE	::::::::::::::::::
SRLQTKGINSSTIMLCNIPESNRTIGISELNQR	1	10.1	0.017	1742	67.73	CID-DROYA	TRUE	TRUE	3	3733.2	-0.1	10of128	1.1522	FALSE	FALSE	::::::::::::::Cys_CAM:::::::::::::::
QHQQQQQDILYQQHN	15	6.01	0	1483	15.4	CIKB-DROME	TRUE	FALSE	2	1937	-0.6	8of 28	1.398	FALSE	FALSE	::::::::::::::
VMDYVVSTWAMTKGLD	1	3.89	0.082	118	48.56	CIKE-DROME	TRUE	FALSE	2	1849.1	0.9	8of 30	1.0471	FALSE	FALSE	::Oxidation_M::::::::Oxidation_M:::::
LDTACVMIFTAEYLLR	13	4.08	0.141	1387	63.33	CIKL-DROME	TRUE	FALSE	2	1917.2	-0.6	9of 30	1.3526	FALSE	FALSE	:::::Cys_CAM:::::::::::
WLSTAESVDEFGFPDTLPKVPVPALDETMAD	3	3.28	0.104	1797	87.03	CLAT-DROME	TRUE	FALSE	3	3395.8	-0.9	16of120	1.5046	FALSE	FALSE	::::::::::::::::::::::::Oxidation_M:::
LHIIEVGAPPNGNQPFAK	5	7.82	0.376	1475	41.3	CLH-DROME	TRUE	TRUE	2	1903.2	2.7	23of 34	3.702	FALSE	FALSE	::::::::::::::::::
KIVLYAKKVNYTPDYVFLLR	14	10.03	0.17	1203	65.6	CLH-DROME	TRUE	FALSE	3	2445	1.1	18of 76	2.3485	FALSE	FALSE	::::::::::::::::::
MDKSTVLK	2	9.89	0.01	732	15.03	CLOC-DROME	TRUE	TRUE	1	938.1	1.2	10of 14	1.4406	FALSE	FALSE	:Oxidation_M:::::::
IGTENEAISVSGSYR	8	4.27	0.012	2939	26.9	CLP8-DROME	TRUE	FALSE	3	1583.7	-1	19of 56	1.7545	FALSE	FALSE	::::::::::::::
MVIDIVLSTDMSKHMSLLADLKTMVET	12	4.44	0.054	2663	82.92	CNA1-DROME	TRUE	FALSE	2	3055.6	-2.2	5of 52	0.6965	FALSE	FALSE	::::::::::Oxidation_M:::Oxidation_M:::::::::::::
QSMIPPSPPPSGVDENPQEDRIR	14	4.07	0.05	2578	37.33	CNA1-DROME	TRUE	FALSE	2	2563.8	1	9of 44	1.1027	FALSE	FALSE	:::Oxidation_M:::::::::::::::::::
GRISSVEVSNAQR	3	10.89	0.061	1148	17.9	CNN-DROME	TRUE	FALSE	2	1403.5	2	12of 24	1.5053	FALSE	FALSE	::::::::::::::
RFDEAVKADDLAS	14	3.97	0.009	2751	26	COG4-DROME	TRUE	FALSE	2	1437.5	-0.1	7of 24	1.0758	FALSE	FALSE	::::::::::::::
LVERPHPVVLAPHDFCNIK	11	7.32	0.303	865	51.1	COPB-DROME	TRUE	TRUE	2	2242.6	0.3	18of 36	3.2791	FALSE	FALSE	::::::::::::::Cys_CAM::::
TCVQTLEGHAQNISAVCFHPELPIVLTGSEDGTVR	3	4.61	0.298	1744	79.9	COPP-DROME	TRUE	TRUE	3	3838.2	1.1	33of136	4.1433	FALSE	FALSE	::Cys_CAM::::::::::::Cys_CAM:::::::::::::::::
CIAVHPTQPLVLTSSDDMLIKLWNWEKMW	5	5.28	0.143	1724	98.66	COPP-DROME	TRUE	FALSE	3	3514.1	-2.9	20of112	2.5551	FALSE	FALSE	:Cys_CAM:::::::::::::::::::::::::

FVVVCGDGEYIIYTSMA	8	3.01	0.011	2213	58.33	COPP-DROME	TRUE	FALSE	2	1925.2	1.4	9of 32	1.2428	FALSE	FALSE	:::::Cys_CAM:::::::::::
HDKLRQFGMTYMGNGKQQMQK	4	10.45	0.093	2814	27.89	CP18-DROME	TRUE	FALSE	3	2543.9	-1.3	13of 80	1.5615	FALSE	FALSE	::::::::::Oxidation_M:::::::::
DEAKATGGSAAVVPA	13	4.08	0.083	2271	21.2	CPR1-DROME	TRUE	FALSE	2	1344.5	2.8	9of 28	1.3918	FALSE	FALSE	::::::::::::::::
LIKSQQRHEQILGQDNLLMAK	8	9.89	0.076	1728	48.13	CRBA-DROME	TRUE	FALSE	3	2464.9	0.2	7of 80	1.1211	FALSE	FALSE	::::::::::::::::::::
SNITLYQMSRITDLPKVFSQPFSFENASGY	3	6.89	0.027	2045	78.23	CRB-DROME	TRUE	FALSE	3	3442.9	-1.9	20of116	1.6863	FALSE	FALSE	::::::::::::::::::::::::::::
RKLPAYAR	13	11.39	0.056	554	15.3	CRK-DROME	TRUE	FALSE	2	975.2	0.1	10of 14	1.4669	FALSE	FALSE	::::::::
LFDCSLDQTDMHGESPYEIMFGPDICGPGTK	1	3.69	0.406	1433	72.76	CRTC-DROME	TRUE	TRUE	2	3519.8	1.3	17of 60	3.3399	FALSE	FALSE	::::Cys_CAM::::::::::::::::::::Cys_CAM::::::
KWKTRRADVTPGLTMGR	11	12.14	0.006	1493	27.03	CSA5-DROME	TRUE	FALSE	2	1990.3	-0.8	9of 32	0.9471	FALSE	FALSE	::::::::::::::Oxidation_M:::
SFSVLQSAAMPFMGVALPR	14	11.05	0.142	1701	62.06	CSE1-DROME	TRUE	TRUE	2	2010.4	1.8	18of 36	2.8773	FALSE	FALSE	::::::::::::::::::::
LVKTSLHTKYDSLVSHALQFLSVVADR	5	9.63	0.126	2535	68.9	CSE1-DROME	TRUE	FALSE	3	3029.5	0.1	19of104	2.4101	FALSE	FALSE	::::::::::::::::::::::::::::
TKKDLLAYLQRIALYCHQIQITSKVK	5	10.12	0.049	1380	65.3	CTNA-DROME	TRUE	FALSE	3	3133.7	2.4	10of100	1.2495	FALSE	FALSE	::::::::::::::::Cys_CAM:::::::::::
EEDHR	11	4.43	0	2663	-0.3	CYA1-DROME	TRUE	FALSE	1	685.7	-2.6	2of 8	0.3502	FALSE	FALSE	::::::
TSVAQKSEPTWSTEQQTEESSVKSW	11	4.26	0.066	1420	33	CYB5-DROME	TRUE	FALSE	3	2842	-1.4	21of 96	2.0186	FALSE	FALSE	::::::::::::::::::::::::
TFTRAEVAKHNTN	9	10.09	0.032	2764	14	CYB5-DROME	TRUE	FALSE	2	1489.6	-2.7	6of 24	0.9006	FALSE	FALSE	::::::::::::::
RRDKMNTYINELSSMIPMCFAM	6	8.87	0.01	2226	61.22	CYCL-DROME	TRUE	FALSE	2	2710.2	2.3	5of 42	0.9466	FALSE	FALSE	::::::::::::::::::Cys_CAM::::
HTGSGILSMANAGANTNGSQFFICTVK	8	8.97	0.184	1904	52.63	CYPH-DROME	TRUE	TRUE	2	2801.1	1.8	13of 52	1.7105	FALSE	FALSE	::::::::Oxidation_M::::::::::::::Cys_CAM::::
IYMDVKHNKKPVGRITF	8	10.45	0.122	2793	35.93	CYPR-DROME	TRUE	FALSE	2	2063.5	1.5	6of 32	1.1063	FALSE	FALSE	:::Oxidation_M:::::::::::::::
RTTCCIPQHYAARVVAA	8	9.08	0.082	2184	35	D43795	TRUE	FALSE	2	1975.2	-2.3	10of 32	1.7857	FALSE	FALSE	::::Cys_CAM:Cys_CAM::::::::::::
LSLALQMYGCRVIQK	10	9.75	0.087	1001	48.23	D43951	TRUE	FALSE	2	1781.1	-0.3	8of 28	0.9599	FALSE	FALSE	::::::::::Cys_CAM::::::
YRSASSASSLFSPSSTLFSSSRLRY	5	11.16	0.036	1436	52.1	D43951	TRUE	FALSE	3	2746	2.4	8of 96	0.8123	FALSE	FALSE	::::::::::::::::::::::::
LQMYGCRVIQKALEFIPSDQQNEMVR	3	6.47	0.021	2538	69.36	D43951	TRUE	FALSE	2	3187.6	0.5	6of 50	1.0063	FALSE	FALSE	:::Oxidation_M:::Cys_CAM::::::::::::::::::Oxidation_M:::
AVRCHSLTPNFLQMQLQ	11	9.02	0.033	584	46.63	D50922	TRUE	FALSE	3	2044.3	2.3	22of 64	2.1903	FALSE	FALSE	::::Cys_CAM:::::::::::::
RLCETVHNKHLDLENITTGHLAMETLL	13	5.77	0.108	1019	66.63	D87450	TRUE	FALSE	3	3160.6	2.1	7of104	0.9609	FALSE	FALSE	:::Cys_CAM:::::::::::::::::::::::
PTTTSGKLRISGDIDYEQDSEQ	1	3.85	0.083	2381	30.3	DAB-DROME	TRUE	FALSE	2	2441.6	-2.7	8of 42	1.1962	FALSE	FALSE	::::::::::::::::::::::
VVLPSNAVAGPQR	7	11.05	0.061	1185	29.5	DAB-DROME	TRUE	FALSE	2	1308.5	2.7	61	1.1995	FALSE	FALSE	::::::::::::
RYCSSADEDDDA	13	3.37	0.112	895	12	DA-DROME	TRUE	FALSE	2	1404.3	2.4	7of 22	1.1828	FALSE	FALSE	:::Cys_CAM:::::::::
TQLLINPGTDSQRYNPEVPFNAK	9	6.94	0.063	261	46.8	DALY-DROME	TRUE	FALSE	3	2603.9	2	14of 88	1.4781	FALSE	FALSE	::::::::::::::::::::
RVGRTARAGRKGTAVTVLTEQDMTLFK	14	11.97	0.006	2889	47.93	DB73-DROME	TRUE	FALSE	3	2964.5	0.6	15of104	1.3133	FALSE	FALSE	::::::::::::::::::::::
IPKIGKASDEVWVRSPRQAKMPQRPKKSMSKPK	15	11.67	0.021	1463	42.46	DC13-DROME	TRUE	FALSE	3	3823.6	-2.9	26of128	2.2675	FALSE	FALSE	::::::::::::::::::::Oxidation_M::::::::Oxidation_M::::::
SKQEDKPK	1	9.76	0.012	956	-3.2	DC13-DROME	TRUE	FALSE	1	960.1	0.2	9of 14	1.8413	FALSE	FALSE	::::::::
DGQAGHDAVAAAAAVAAAAAAASSHQQQQHK	8	6.31	0.221	3432	27.2	DCO-DROME	TRUE	FALSE	3	2840	1.1	17of116	1.5775	FALSE	FALSE	::::::::::::::::::::::::::::
MRHKLDGRVPLIGFTGAPWTLMGYMIEGGGSK	14	10.18	0.022	1015	81.49	DCUP-DROVI	TRUE	FALSE	3	3494.1	2.6	21of124	1.8928	FALSE	FALSE	::::::::::::::::::::Oxidation_M:::::::::::
HLMKGIETADSFNFNPHK	8	7.95	0.054	2584	33.13	DDC-DROLE	TRUE	TRUE	2	2087.4	1.5	5of 34	0.9289	FALSE	FALSE	::::::::::::::::::
NHEETCRRHSLYVDF	3	6.03	0.043	2698	25.1	DECA-DROPS	TRUE	FALSE	3	1964.1	-1.1	16of 56	1.3242	FALSE	FALSE	::::::Cys_CAM:::::::::
QHSTHKTPTKGGIRFSLDVSR	2	11.47	0.13	1238	22	DHE3-DROME	TRUE	FALSE	3	2353.6	-1.3	19of 80	1.9885	FALSE	FALSE	::::::::::::::::::
DVVSRSMTIEIMEGRGAGPEKDH	10	4.7	0.073	2624	37.76	DHSA-DROME	TRUE	FALSE	3	2531.8	2.4	9of 88	0.9916	FALSE	FALSE	::::::Oxidation_M:::::::::::::::
DVIVPGLYAAGEAASSSVHGANRLGANS	10	5.22	0.021	2146	52.9	DHSA-DROME	TRUE	FALSE	3	2684.9	2.8	22of108	1.518	FALSE	FALSE	::::::::::::::::::::::::
FLEIIEDMNIPK	1	3.83	0.034	580	45.63	DIA-DROME	TRUE	TRUE	2	1462.7	2.3	17of 22	3.0161	FALSE	FALSE	::::::::::::
PPMPGR	12	11.05	0.03	2550	10.73	DIA-DROME	TRUE	FALSE	1	670.8	2	4of 10	0.6849	FALSE	FALSE	:::Oxidation_M::::
YKCEGRTAGSIPGMNSSSETG	3	6.43	0.133	1555	22.53	DIF-DROME	TRUE	FALSE	2	2206.3	2.2	11of 40	1.5007	FALSE	FALSE	:::Cys_CAM::::::::::Oxidation_M:::::::::
TGVLRWRANTSPDHIIFTLLNSK	15	11.33	0.067	1586	59.8	DIP2-DROME	TRUE	FALSE	2	2641	2.3	11of 44	1.8529	FALSE	FALSE	::::::::::::::::::::
RRFLEGSLHPANVLMCPHTCVTNLPKP	9	9.15	0.049	2443	64.43	DIP2-DROME	TRUE	FALSE	3	3146.6	2.8	15of104	1.44	FALSE	FALSE	::::::::::::::Cys_CAM:::Cys_CAM::::::::
AMMER	14	6.98	0	2767	13.56	DOA-DROME	TRUE	FALSE	1	653.8	-1.6	1of 8	0.2405	FALSE	FALSE	:::Oxidation_M:::
HLLVKHKGSRR	4	12.43	0.018	1489	11.2	DOD-DROME	TRUE	FALSE	2	1331.6	2	10of 20	1.5309	FALSE	FALSE	::::::::::::
LKPLVAAPLSQTGGPAFAGSSPATSPPLQLPPVHAAS	1	10.1	0.022	2394	84	DOME-DROME	TRUE	FALSE	3	3535.1	2.7	9of144	0.9957	FALSE	FALSE	::::::::::::::::::::::::::::::::::::
VPSNCTGDLMHLAVSRNWLV	3	7.16	0.105	2020	56.53	DOR-DROME	TRUE	FALSE	2	2270.6	-0.4	8of 38	0.9299	FALSE	FALSE	:::::Cys_CAM:::::::::::::::
ECMLRKWISAVDLALTFDMKLAK	12	8.9	0.035	1894	76.36	DOR-DROME	TRUE	FALSE	3	2757.3	1.3	16of 88	1.588	FALSE	FALSE	::Cys_CAM:Oxidation_M:::::::::::::::::::
VFIQLRRPSDGVTS	9	10.89	0.036	917	34.6	DORS-DROME	TRUE	FALSE	3	1575.8	1.2	19of 52	1.5655	FALSE	FALSE	::::::::::::::
STSLDSALEALRCTLTWGHVAPTAPDTLACY	8	4.3	0.061	2489	79	DPD2-DROME	TRUE	FALSE	3	3379.7	0.6	16of120	1.3225	FALSE	FALSE	::::::::::::Cys_CAM::::::::::::::::Cys_CAM::
VVYGDTDSLMINTNITDYDQVYK	10	3.43	0.049	462	55.83	DPOA-DROME	TRUE	FALSE	2	2684.9	-0.7	5of 44	0.9087	FALSE	FALSE	::::::::::Oxidation_M:::::::::::::
EEPAATSE	9	3.03	0.015	617	9.7	DPOA-DROME	TRUE	FALSE	2	833.8	-2	10of 14	1.4201	FALSE	FALSE	::::::::
NNAVVIYGDTDSVMVNFGVK	13	3.89	0.071	1693	49.03	DPOD-DROME	TRUE	FALSE	3	2159.4	0.6	23of 76	3.1149	FALSE	FALSE	::::::::::::Oxidation_M:::::::
NVSLGNVLANINR	14	11.05	0.245	1196	32.2	DPP3-DROME	TRUE	TRUE	2	1384.6	1	15of 24	2.1765	FALSE	FALSE	::::::::::::::
TQPMHMLNISATDGGNLRSNADAVVFLSI	9	5.1	0.071	1445	72.36	DS-DROME	TRUE	FALSE	3	3090.5	-1.7	21of112	1.9309	FALSE	FALSE	:::::Oxidation_M:::::::::::::::::::::
MDSLTGALSLQAPLDFEAV	14	2.88	0.025	1316	60.53	DS-DROME	TRUE	FALSE	2	1995.3	0.7	15of 36	2.9046	FALSE	FALSE	:Oxidation_M:::::::::::::::::
AHAKKLTRVMLSDADPSLEQYYVNVRTMTQES	1	7.68	0.009	1574	63.06	DX-DROME	TRUE	FALSE	3	3716.2	-1.9	23of124	2.0709	FALSE	FALSE	::::::::Oxidation_M::::::::::::::::Oxidation_M:::::
SLAVKKQELQAKNEAAN	4	9.76	0.008	1594	23.7	DYHC-DROME	TRUE	FALSE	2	1843.1	-2.2	6of 32	1.0587	FALSE	FALSE	::::::::::::::::
NFGSYVTHETR	9	7.77	0.307	1116	16.2	DYL1-DROME	TRUE	TRUE	2	1311.4	0.4	13of 20	2.7579	FALSE	FALSE	::::::::::::
RRLPSDQHVI	4	10.89	0.059	3029	19.2	DYNA-DROME	TRUE	FALSE	2	1221.4	-2.2	5of 18	0.8197	FALSE	FALSE	::::::::::
ESLQDPSLKM	8	4.08	0.044	3351	22.53	DYNA-DROME	TRUE	FALSE	2	1148.3	1.7	5of 18	0.7748	FALSE	FALSE	::::::::::
HSVLAKSLMAEPRMTPEQMK	3	9.89	0.016	2285	41.29	E75A-DROME	TRUE	FALSE	2	2285.7	1	14of 38	1.5391	FALSE	FALSE	::::::::::::::::::
GAADFTAQVIVLNHPGQIANGYTPVLDCHTAHIACK	9	6.3	0.519	1829	79.2	EF11-DROME	TRUE	TRUE	3	3862.3	-0.1	35of140	6.693	FALSE	FALSE	::::::::::::::::::::::::::Cys_CAM::::::Cys_CAM::
SGDAAIVNLVPSKPLCVEAFQEFPPLGR	3	4.45	0.386	1935	77.8	EF11-DROME	TRUE	TRUE	2	3013.4	2.2	20of 54	3.5126	FALSE	FALSE	::::::::::::::Cys_CAM:::::::::::::
GAADFTAQVIVLNHPGQIANGYTPVLDCHTAHIACK	10	6.3	0.281	1457	79.2	EF11-DROME	TRUE	TRUE	3	3862.3	2.5	27of140	3.9991	FALSE	FALSE	::::::::::::::::::::::::::Cys_CAM::::::Cys_CAM::
VETGVLKPGTVVVFAPANITTEVK	1	7.07	0.22	1173	61	EF11-DROME	TRUE	TRUE	2	2470.9	1.6	15of 46	2.2426	FALSE	FALSE	::::::::::::::::::::::
PANITTEVK	7	6.95	0.19	1503	16	EF11-DROME	TRUE	FALSE	1	973.1	0	13	1.6452	FALSE	FALSE	::::::::
DCAVQIDAAGTGEFEAGISK	6	3.59	0.157	1964	38.8	EF11-DROME	TRUE	FALSE	2	2040.2	-0.6	13of 38	2.1578	FALSE	FALSE	::Cys_CAM:::::::::::::::::
KFETAKYYVTIIDAPGHR	10	9.47	0.112	968	38.3	EF11-DROME	TRUE	FALSE	3	2110.4	-1.9	20of 68	2.4494	FALSE	FALSE	::::::::::::::::
YKIGGIGTVPVGRVETGVLKPGTVVVFAPANITTEVK	2	10.05	0.085	1272	89.4	EF11-DROME	TRUE	FALSE	3	3769.5	1.6	24of144	2.4307	FALSE	FALSE	::::::::::::::::::::::::::::::::
KEVSSYIKKIGYNPASVAFVPISGW	10	9.87	0.021	1577	64.1	EF12-DROME	TRUE	FALSE	3	2742.2	-1.6	18of 96	1.6853	FALSE	FALSE	::::::::::::::::::::::
KDYKLCEKALVFDPK	4	8.81	0.025	1626	33.5	EF1G-DROME	TRUE	FALSE	2	1855.2	1.6	11of 28	1.4573	FALSE	FALSE	::::::Cys_CAM:::::::::
GYREMAEKGMLSGHKLSGIRFRL	4	10.69	0.083	2457	50.26	EFGM-DROME	TRUE	FALSE	3	2654.1	2	10of 88	1.2735	FALSE	FALSE	::::::::::Oxidation_M:::::::::::::
FEVILDVQQFSPSEITV	12	2.95	0.033	1724	58.7	EFL2-DROME	TRUE	FALSE	2	1952.2	-0.6	6of 32	0.9096	FALSE	FALSE	::::::::::::::::::
QHFGQGLKRDDLMSSVWNSRPTVLR	2	11.23	0.01	1232	52.13	EFL2-DROME	TRUE	FALSE	3	2929.3	-0.1	9of 96	1.0314	FALSE	FALSE	::::::::::::::::::::::
EMRHVNYQYTAIGPYCAASPPR	11	8.77	0.019	1883	43.43	EGFR-DROME	TRUE	FALSE	3	2582.9	-1.4	14of 84	1.9624	FALSE	FALSE	::::::::::::::::Cys_CAM:::::::
HIDLIYNDG	10	3.88	0.139	2262	24.9	ELF1-DROME	TRUE	FALSE	2	1060.2	-0.3	6of 16	1.1503	FALSE	FALSE	::::::::
PVTDRSEFYGMQDFAKPPVLFSPAEDMEK	13	4.07	0.132	327	69.06	ELF1-DROME	TRUE	FALSE	3	3349.8	1.2	13of112	1.2014	FALSE	FALSE	::::::::::::::::::::::::::Oxidation_M:::
HIADLAGNKEIILPVPAFNVINGGSHAGNK	10	7.95	0.485	1566	65.4	ENO-DROME	TRUE	TRUE	3	3068.5	2	43of116	5.8656	FALSE	FALSE	::::::::::::::::::::::::::::
LANLYKEFIK	7	9.63	0.188	1449	34.5	ENO-DROME	TRUE	TRUE	2	1239.5	0.9	1	3.4003	FALSE	FALSE	::::::::::
AAVPSGASTGVHEALELR	7	5.3	0.139	1096	35.5	ENO-DROME	TRUE	TRUE	2	1766	0.4	8	1.803	FALSE	FALSE	::::::::::::::::
PVPAFNVINGGSHAGNK	10	10.1	0.038	1614	26.7	ENO-DROME	TRUE	FALSE	2	1679.9	2.9	14of 32	1.6091	FALSE	FALSE	::::::::::::::::
YLFGTLDENDRVEI	6	3.59	0.122	1850	43	ENV2-DROME	TRUE	FALSE	2	1684.8	-2	5of 26	0.9487	FALSE	FALSE	::::::::::::::
LIDISCLVYQKSTNTYAPYNK	1	8.73	0.04	235	51.7	ER-DROVI	TRUE	FALSE	3	2492.8	0.3	13of 80	1.3884	FALSE	FALSE	::::::Cys_CAM:::::::::::::::

KTYQYRKVMKPMLERK	14	10.68	0.07	2845	27.26	ESMB-DROME	TRUE	FALSE	2	2132.6	-0.4	7of 30	0.9707	FALSE		FALSE	:::::::::Oxidation_M:::Oxidation_M::::::
RRKNRPAMNYDKLSRSIRQYYKK	8	11.46	0.011	1909	25.73	ETS4-DROME	TRUE	FALSE	3	2989.5	-0.1	8of 88	0.8339	FALSE		FALSE	:::::::Oxidation_M::::::::::::::::
LQADLGDAPPGTSNSK	10	3.89	0.042	844	21.7	EXPA-DROME	TRUE	FALSE	2	1571.7	0.9	11of 30	1.2744	FALSE		FALSE	::::::::::::::::::
LKKPPMPAPSEKPPPI	11	10.32	0.021	1773	31.63	EXPA-DROME	TRUE	FALSE	2	1728.1	1.6	6of 30	0.9139	FALSE		FALSE	::::::::::::::::::
RRIRANGAASSKN	15	12.71	0.158	308	7.7	EXU1-DROPS	TRUE	FALSE	3	1401.6	-0.2	16of 48	1.5325	FALSE		FALSE	::::::::::::::
FANTCPMAKTFLGKHGIKNCGLRKLSMLLAK	5	10.71	0.005	2746	74.36	EXU2-DROPS	TRUE	FALSE	3	3524.2	1.7	14of120	1.2561	FALSE		FALSE	:::::Cys_CAM::Oxidation_M::::::::::::Cys_CAM::::::::::::
EGAQKNEFISEY	7	3.97	0.035	1083	22.2	EZ-DROME	TRUE	FALSE	2	1415.5	0.3	71	1.9876	FALSE		FALSE	::::::::::::::
DNGLTVNSAAVAEINSIMAGMMNITSTQCVWTGADQ	15	2.88	0.029	58	83.59	EZ-DROME	TRUE	FALSE	3	3805.2	-1.9	16of140	1.4161	FALSE		FALSE	:::::::::::::::::::Oxidation_M:::Oxidation_M::::::::Cys_CAM::::::::
GLHKHLLMAPSDIAGWGIFLK	6	9.89	0.024	2351	66.63	EZ-DROME	TRUE	TRUE	2	2321.8	0	7of 40	1.1814	FALSE		FALSE	:::::::Oxidation_M::::::::::::::
SIKSGKGKNKFR	4	11.8	0.087	1449	5.1	FAT2-DROME	TRUE	FALSE	1	1350.6	0.4	9of 22	1.8216	FALSE		FALSE	::::::::::::::
STSKMLPITILDVNDNRP	2	6.9	0.063	2378	42.83	FAT2-DROME	TRUE	FALSE	2	2015.3	-2.3	8of 34	1.1763	FALSE		FALSE	::::::::::::::::::
EQQESHNLIVVAE	5	3.96	0.013	1670	27.9	FAT2-DROME	TRUE	FALSE	2	1496.6	2.6	13of 24	2.2396	FALSE		FALSE	::::::::::::::
GTYANLYYEIVSEEMK	9	3.97	0.013	941	42.33	FAT2-DROME	TRUE	FALSE	3	1911.1	1.9	15of 60	1.528	FALSE		FALSE	::::::::::::::::
AEDCGVPKLHSIATVAVNILDINDNPPEFSMR	1	4.2	0.01	159	77.83	FAT2-DROME	TRUE	TRUE	3	3524.9	0.8	17of124	1.4264	FALSE		FALSE	:::::Cys_CAM:::::::::::::::::::::::::::
PGVPQQQAQQTSMGLT	9	6.02	0.05	2482	25.23	FAT-DROME	TRUE	FALSE	3	1671.9	2.5	8of 60	1.0889	FALSE		FALSE	::::::::::::::::
RLGSDFQCMCPANRDG	7	6.1	0.017	3426	28.93	FAT-DROME	TRUE	FALSE	3	1885	-0.9	41	1.6331	FALSE		FALSE	:::::::Cys_CAM::Cys_CAM:::::::
IRILDENDNSPVFDPK	11	3.97	0.007	138	37.6	FAT-DROME	TRUE	FALSE	2	1873.1	-1.4	8of 30	1.1094	FALSE		FALSE	::::::::::::::::
QVMLQLKGQQAQQVVGI	10	10.1	0.078	2193	43.63	FBP1-DROME	TRUE	FALSE	2	1885.2	1.5	10of 32	1.1813	FALSE		FALSE	:::Oxidation_M:::::::::::::
LMTDDEILEMLQRNRQQRLQK	6	7.17	0.037	2894	49.56	FBP1-DROME	TRUE	TRUE	3	2676.1	1.2	9of 80	1.1182	FALSE		FALSE	::Oxidation_M:::::::::::::::::::
SPYAFDVATVASAAGIPGHRD	4	5.1	0.084	2886	41.5	FD3-DROME	TRUE	FALSE	3	2103.3	-2.4	15of 80	1.4524	FALSE		FALSE	::::::::::::::::::::
HVDTAHR	9	8	0.18	2761	3	FDL-DROME	TRUE	FALSE	2	835.9	0.2	6of 12	1.3543	FALSE		FALSE	::::::::
NTNGRLPIKWMAPESLQEKKYDSQSDVWS	10	7.05	0.042	833	56.33	FGR2-DROME	TRUE	FALSE	3	3425.8	-0.8	20of112	2.0135	FALSE		FALSE	:::::::::::Oxidation_M:::::::::::::::::
LYAEPPPSSAPVSMASSGGGGPPSGGGGGG	14	3.3	0.024	1801	39.03	FKH-DROME	TRUE	FALSE	3	2559.7	-0.3	10of116	1.0809	FALSE		FALSE	:::::::::::::Oxidation_M:::::::::::::::
DEKKEAIRQLHK	12	9.76	0	859	10.9	FKH-DROME	TRUE	TRUE	3	1495.7	-2.7	17of 44	1.9584	FALSE		FALSE	::::::::::::
MDSNFIRFGKS	3	10.09	0.069	2700	25.43	FMRF-DROME	TRUE	FALSE	2	1318.5	-0.6	8of 20	1.4652	FALSE		FALSE	:Oxidation_M:::::::::
RQAEQLPQATGPGYYEC	14	4.27	0.027	1750	29.5	FMRF-DROVI	TRUE	FALSE	2	1969.1	-0.9	6of 32	0.8453	FALSE		FALSE	:::::::::::::::::Cys_CAM:
KMSAELDVFLESGK	14	4.45	0.028	1075	34.43	FNG-DROME	TRUE	FALSE	1	1554.8	1	15of 26	1.5443	FALSE		FALSE	::::::::::::::
IPGGVDLLAAPSDAFST	14	2.93	0.084	1444	46.9	FOG-DROME	TRUE	FALSE	2	1631.8	-1.3	7of 32	1.1871	FALSE		FALSE	::::::::::::::::
FPTGTGEHEEMPLPPDMAAA	10	3.69	0.024	566	43.46	FOG-DROME	TRUE	FALSE	3	2131.3	-1.4	12of 76	1.1173	FALSE		FALSE	:::::::::Oxidation_M:::::Oxidation_M::::
SLQRRACLLSILAAFV	14	10.9	0.085	1088	59.9	FOJO-DROME	TRUE	FALSE	2	1819.2	1	11of 30	1.4141	FALSE		FALSE	:::::::Cys_CAM:::::::::
SRKMLLQPLLLLLMPAL	10	11.49	0.028	2057	78.96	FRIZ-DROVI	TRUE	FALSE	2	1967.6	-1.1	7of 32	1.1128	FALSE		FALSE	:::::::::::::Oxidation_M::::
LPRSGRCAPLCEADILFTPAEK	1	6.33	0.021	2306	56.3	FRZ4-DROME	TRUE	TRUE	3	2502.8	-0.8	8of 84	0.8703	FALSE		FALSE	:::::::Cys_CAM:::Cys_CAM:::::::::::
LQDVTGQLGASKKTAKKDES	9	9.67	0.003	270	18.7	FSH-DROME	TRUE	FALSE	2	2105.4	-2.3	7of 38	0.8962	FALSE		FALSE	::::::::::::::::::
KQIKFETPPKSSQQMRSNGEGDETK	7	9.67	0.022	1255	19.13	FSYA-DROME	TRUE	TRUE	3	2852.1	-1.8	70	2.0716	FALSE		FALSE	::::::::::::::::::::::
KASYDVNSHDDDPMPHYDMTDSNR	9	4.16	0.063	1764	24.16	FUR1-DROME	TRUE	FALSE	3	2811.9	-0.2	9of 92	1.0247	FALSE		FALSE	::::::::::::::::::::
AFIEGTTKGRGGKGSIFIWASGNGGREQDNCNCDG	13	6.36	0.053	1412	50.8	FUR1-DROME	TRUE	FALSE	3	3718.9	-0.4	21of136	1.8917	FALSE		FALSE	:::::::::::::::::::::::::::Cys_CAM::Cys_CAM:::
QWEMSALRRAITRSSPEN	5	10.8	0.025	1314	35.63	G10B-DROME	TRUE	FALSE	3	2133.4	-1.8	20of 68	2.3231	FALSE		FALSE	::::::::::::::::::
LLDLNHRLTAIYDIQVTLFMATLFS	15	5.1	0.104	1232	97.33	G22A-DROME	TRUE	FALSE	3	2926.4	1.2	12of 96	1.3512	FALSE		FALSE	:::::::::::::::::::Oxidation_M:::::::
IINMAISQHYLVILFVR	11	9.85	0.075	717	72.43	G36A-DROME	TRUE	FALSE	3	2031.5	1.3	19of 64	1.9767	FALSE		FALSE	::::::::::::::::::
MIEKFLLKNLR	5	10.59	0.012	2722	41.03	G391-DROME	TRUE	TRUE	2	1405.8	0.3	8of 20	1.5305	FALSE		FALSE	::::::::::::
WMFASLDVTGVIYLTMVIQTK	11	6.68	0.066	1390	79.96	G392-DROME	TRUE	FALSE	3	2417.9	-2.6	16of 80	1.2623	FALSE		FALSE	::::::::::::::::::::
VVSNASCTTNCLAPLAK	15	8.3	0.439	544	36.9	G3P1-DROME	TRUE	TRUE	2	1807	3	18of 32	3.9675	FALSE		FALSE	:::::::Cys_CAM:::Cys_CAM:::::::
DAYSPDMKVVSNASCTTNCLAPLAK	15	6.09	0.303	544	49.03	G3P1-DROME	TRUE	FALSE	3	2715	-0.5	25of 96	3.4762	FALSE		FALSE	:::::::::::::::Cys_CAM:::Cys_CAM:::::::
LISWYDNEFGYSNR	7	4.08	0.298	1445	40.3	G3P1-DROME	TRUE	TRUE	2	1764.9	1.5	1	2.9477	FALSE		FALSE	::::::::::::::
VVSNASCTTNCLAPLAK	14	8.3	0.267	524	36.9	G3P1-DROME	TRUE	TRUE	2	1807	1.2	14of 32	2.0435	FALSE		FALSE	:::::::Cys_CAM:::Cys_CAM:::::::
VVSNASCTTNCLAPLAK	1	8.3	0.241	528	36.9	G3P1-DROME	TRUE	TRUE	2	1807	2.2	17of 32	2.5764	FALSE		FALSE	:::::::Cys_CAM:::Cys_CAM:::::::
SCTTNCLAPLAKVINDNFEIVEGLMTTVHATTATQK	3	5.35	0.239	1931	81.03	G3P1-DROME	TRUE	FALSE	3	3951.4	0.7	23of140	3.2989	FALSE		FALSE	::Cys_CAM:::Cys_CAM:::::::::::::::::::::::::::
APMFVCGVNLDAYSPDMK	9	3.89	0.004	1290	49.66	G3P1-DROME	TRUE	FALSE	3	2048.3	-2.3	17of 68	1.5973	FALSE		FALSE	:::Oxidation_M::Cys_CAM::::::::::Oxidation_M::
KVIISAPSADAPMFVCGVNLDAYKPDMK	7	6.32	0.513	1567	71.26	G3P2-DROME	TRUE	TRUE	3	3039.5	1.3	1	5.7717	FALSE		FALSE	:::::::::::::::Cys_CAM::::::::::::
KVIISAPSADAPMFVCGVNLDAYKPDMK	6	6.32	0.396	1742	71.26	G3P2-DROME	TRUE	TRUE	3	3039.5	0.4	34of108	4.1226	FALSE		FALSE	:::::::::::::::Cys_CAM::::::::::::
IIPASTGAAK	10	10.1	0.15	606	20.9	G3P2-DROME	TRUE	FALSE	2	929.1	1.1	6of 18	1.2491	FALSE		FALSE	::::::::::
AYFLFLELLSK	14	6.87	0.06	1436	53.9	G43A-DROME	TRUE	FALSE	2	1344.6	2.5	10of 20	1.3074	FALSE		FALSE	::::::::::::
LCLRIAYAYGRLTGVINFKIDLKT	11	9.95	0.065	212	78.3	G59D-DROME	TRUE	FALSE	2	2800.3	2.6	6of 46	0.7869	FALSE		FALSE	::Cys_CAM::::::::::::::::::::
DTGNALCYTFVFMS	3	3.1	0.089	1044	44.33	G63A-DROME	TRUE	FALSE	2	1626.8	-0.1	10of 26	1.7908	FALSE		FALSE	:::::::Cys_CAM:::::::
WFLRIIGVLPIVRHGPAR	15	12.71	0.061	1686	67	G63A-DROME	TRUE	FALSE	2	2101.6	2.4	9of 34	1.2396	FALSE		FALSE	::::::::::::::
SLVLAMGTTIITYELMISDV	10	3.01	0.02	1556	76.56	G64B-DROME	TRUE	FALSE	2	2187.6	1	10of 38	1.5293	FALSE		FALSE	:::::Oxidation_M:::::::::::::
SYYALVTILFFGVSSGYMVAFVTSVS	1	5.82	0.098	297	95.73	G64E-DROME	TRUE	FALSE	3	2810.3	1.1	19of100	2.0897	FALSE		FALSE	::::::::::::::::::::::
FCGYARSM	13	8.9	0.029	1362	21.73	G6PD-DROME	TRUE	FALSE	1	1008.1	-0.5	10of 14	1.6023	FALSE		FALSE	::Cys_CAM:::::Oxidation_M:
LNERKAEVRIQYQDVPGDIFEG	4	4.29	0.02	2940	48.9	G6PD-DROYA	TRUE	FALSE	3	2577.9	1.9	9of 84	1.0236	FALSE		FALSE	::::::::::::::::::::
NMVISGVWR	15	11.05	0.047	2180	30.13	G6PI-DROME	TRUE	FALSE	2	1078.3	-1.9	3of 16	0.5149	FALSE		FALSE	::Oxidation_M:::::::
SGKPVKYSTGP	9	10.18	0.009	834	9.1	G6PI-DROME	TRUE	FALSE	2	1121.3	-0.2	9of 20	1.0621	FALSE		FALSE	::::::::::::
YWRDER	9	6.96	0.006	2605	13.4	GAB3-DROME	TRUE	FALSE	2	925	0.5	5of 10	0.9641	FALSE		FALSE	::::::
EINGRMDQL	9	4.08	0.068	416	20.93	GAGJ-DROFU	TRUE	FALSE	1	1076.2	-2.6	6of 16	0.8429	FALSE		FALSE	::::::::
NSVSDTMAQMAGKAARK	8	10.59	0.029	2236	18.86	GAGJ-DROFU	TRUE	FALSE	2	1783	-1.8	6of 32	1.3366	FALSE		FALSE	:::::::Oxidation_M:::::::::::
FYINLKQGPNVKESLKITRLGRYRVTVER	13	10.91	0.153	1437	66.1	GAGJ-DROME	TRUE	FALSE	3	3480.1	2.2	8of112	1.2279	FALSE		FALSE	::::::::::::::::::::::::
AEKAKKLKPRSRLPMT	1	11.63	0.004	2332	21.63	GAGJ-DROME	TRUE	FALSE	2	1855.3	0.4	4of 30	0.8158	FALSE		FALSE	::::::::::::::
YLQPRSMTHSSRSLNATPRSCATPPGTR	1	11.94	0.064	139	36.93	GAP1-DROME	TRUE	FALSE	3	3131.5	0.8	14of108	1.2949	FALSE		FALSE	:::::::::::::::::::Cys_CAM:::::::
RRLTLQSLQSAAKRAGTS	1	12.71	0.07	494	26.8	GATC-DROME	TRUE	FALSE	2	1945.2	2.9	9of 34	0.8768	FALSE		FALSE	::::::::::::::::
DNMCSIYNLKTREGNVR	8	8.87	0.11	2304	29.53	GBB1-DROME	TRUE	FALSE	2	2087.3	-1.4	5of 32	0.9953	FALSE		FALSE	:::Oxidation_M:Cys_CAM:::::::::::
WIHCFEGVTAIIFCVALSGYDLVLAEDEE	4	3.44	0.032	2287	104.9	GBI5-DROME	TRUE	FALSE	3	3358.7	2.8	23of112	2.1246	FALSE		FALSE	:::::Cys_CAM::::::::Cys_CAM:::::::::::::
EEVPLMVLDPK	14	3.83	0.015	1398	36.03	GCL1-DROME	TRUE	FALSE	1	1270.5	1.6	11of 20	2.5372	FALSE		FALSE	::::::::::
TKNVDHVLPMTLENLLGLTLRISSAR	3	10.09	0.082	1565	71.43	GCP2-DROME	TRUE	FALSE	3	2909.4	0.7	24of100	2.1429	FALSE		FALSE	:::::::::Oxidation_M:::::::::::::::
PIISAVGLAKYDTDFDIHTHLDRSL	12	5.1	0.059	1139	64.6	GCP2-DROME	TRUE	FALSE	3	2799.2	1	17of 96	1.6792	FALSE		FALSE	::::::::::::::::::::::
MLPKFVPMDMANKILMTGKSINFLR	11	10.83	0.013	1541	80.72	GCP3-DROME	TRUE	FALSE	3	2929.6	0.3	21of 96	1.9274	FALSE		FALSE	:::::::Oxidation_M::Oxidation_M:::::::::::::::
TANLLQTFAAASAAAAAAAAASSTNSPR	6	11.05	0.023	1162	51.5	GIAN-DROME	TRUE	FALSE	3	2577.8	2	26of108	2.686	FALSE		FALSE	::::::::::::::::::::::::::
HKSLQYTVVYDAKDISGAA	13	7.67	0.273	147	34.6	GIL-DROME	TRUE	FALSE	2	2067.3	0.8	9of 36	1.3515	FALSE		FALSE	::::::::::::::::::
LEPSAKAKARTQGGPNSLPPISAQAALMYD	10	9.63	0.05	1089	57.23	GLK1-DROME	TRUE	FALSE	3	3084.5	-0.6	28of116	2.9294	FALSE		FALSE	::::::::::::::::::::::::::
EGPTLK	15	6.95	0.183	533	9.5	GNA1-DROME	TRUE	FALSE	1	644.7	0.3	6of 10	1.1022	FALSE		FALSE	::::::
LYDQLAPLCPIMLALTAASPIYR	6	6.09	0.352	2604	86.43	GSH1-DROME	TRUE	TRUE	2	2592.1	-0.3	18of 44	3.3739	FALSE		FALSE	:::::::::Cys_CAM:::::::::::::
LNEMSQGMDEEEGSELDED	8	2.66	0.015	1640	33.06	GSR2-DROME	TRUE	FALSE	3	2190.2	-2.9	21of 72	1.6795	FALSE		FALSE	:::::Oxidation_M:::Oxidation_M:::::::::::
VWMTMGLTVMSWIALFCIAIFVGCYTAGVGSLTWVL	12	5.18	0.04	436	155.69	GTR3-DROME	TRUE	FALSE	3	4056.8	0.1	9of140	1.1999	FALSE		FALSE	:::::::::::::::::Cys_CAM::::::Cys_CAM:::::::::::::
FSAIHEFQNLHAVAKEKINEFV	10	6.05	0.026	1132	56.7	GYS-DROME	TRUE	FALSE	3	2572.9	-1.1	26of 84	2.5161	FALSE		FALSE	::::::::::::::::::::::
VTSSAAAAKKKT	15	10.85	0.004	723	7.5	H1-DROHY	TRUE	FALSE	1	1163.4	2.6	10of 22	1.4806	FALSE		FALSE	::::::::::::

PKAKKAVATKKTAENKKTEKA	15	10.75	0.003	993	3.6	H1-DROME	TRUE	FALSE	3	2271.7	2.3	18of 80	2.2068	FALSE	FALSE	::::::::::::::::::::
LLSGVTIAQGGVLPNIQAVLLPK	15	10.1	0.399	1809	75.4	H2A-DROME	TRUE	TRUE	2	2302.8	2.3	21of 44	3.6336	FALSE	FALSE	::::::::::::::::::::
MTHNLLLNYG	8	7.76	0.04	2905	31.43	HDA1-DROME	TRUE	FALSE	2	1176.4	1.5	7of 18	1.4979	FALSE	FALSE	::::::::::
MKEFLALASSSLLRL	8	10.09	0.024	2019	55.93	HEM-DROME	TRUE	FALSE	2	1696.1	-0.4	5of 28	0.6577	FALSE	FALSE	:Oxidation_M:::::::::::::
HQRLLTSALRSLTSIYALR	12	12.11	0.001	1941	53.1	HEM-DROME	TRUE	FALSE	3	2200.6	-0.8	12of 72	1.2138	FALSE	FALSE	::::::::::::::::::::
HLGDLGNGTSGNVVKMMHLSSNTIIAVKQMRR	11	11.47	0.007	1739	61.29	HEP-DROME	TRUE	TRUE	3	3467.1	-1.2	20of124	1.8726	FALSE	FALSE	::::::::::::::::::::::::::::::
RITPMFIPLHEDGPTSLSMNIV	8	5.22	0.02	2585	67.16	HIRA-DROME	TRUE	FALSE	2	2485.9	0.1	9of 42	1.0413	FALSE	FALSE	:::::Oxidation_M:::::::::::::::::
LAAAAVASHGHA	12	8	0.134	1866	20.5	HMAA-DROME	TRUE	FALSE	2	1076.2	2.9	9of 22	1.2066	FALSE	FALSE	::::::::::::
VAMAAHAQHAAALGPGFLPGLPAFQFAAAQVAAGGDGR	1	8	0.077	1833	90.33	HMCU-DROME	TRUE	FALSE	3	3617.1	1.1	24of148	2.1524	FALSE	FALSE	::::::::::::::::::::::::::::::::::::
SEQKLKVINEEKLRMVRVRR	1	11.4	0.061	2197	37.93	HMCU-DROME	TRUE	FALSE	2	2529	-1.9	4of 38	0.7873	FALSE	FALSE	:::::::::::::::Oxidation_M:::::::
YKKMMKAAQGPGTNSG	1	10.45	0.084	1066	14.46	HMDL-DROME	TRUE	FALSE	2	1686	1	9of 30	1.3774	FALSE	FALSE	:::::Oxidation_M:::::::::::
EMTEYKTSGKIAMSAPSMQASMQAQAQKAALLAAAA	8	9.56	0.045	2024	70.32	HMG2-DROME	TRUE	FALSE	3	3704.3	0.7	22of140	2.7834	FALSE	FALSE	:::::::::::::Oxidation_M:::::::::::::::::::::::
PPQQQQVAAPSDMDLERIKLVAAVAAR	2	7.07	0.034	602	60.13	HMN1-DROME	TRUE	FALSE	3	2904.4	1.5	16of104	1.3897	FALSE	FALSE	::::::::::::::::::::::::::::
NFVVANGFMSTIMGQTSYATSAPGTSSAAATAAAM	2	5.93	0.136	1377	74.89	HMRO-DROVI	TRUE	FALSE	3	3402.8	0	9of136	1.1253	FALSE	FALSE	:::::::::Oxidation_M:::::::::::::::::::::::::
AAAAAAAAAAVQGG	11	6.02	0.123	1034	24.6	HMUX-DROME	TRUE	FALSE	2	1071.2	-2.7	11of 26	0.9665	FALSE	FALSE	::::::::::::::::
TDLLHMQMR	5	7.85	0.023	2908	25.36	HOOK-DROME	TRUE	FALSE	2	1145.4	1	7of 16	0.9391	FALSE	FALSE	::::::::::
PNISSSCSFFKLKKLSEESLLQPPEK	4	8.88	0.109	2002	57.7	HPO-DROME	TRUE	FALSE	3	2995.4	0.9	13of100	1.2902	FALSE	FALSE	:::::::Cys_CAM:::::::::::::::::
QCRGAMNCEVTKHHR	9	9.15	0.004	514	11.13	HR78-DROME	TRUE	FALSE	3	1901	0.2	20of 56	1.7506	FALSE	FALSE	::Cys_CAM:::Oxidation_M::Cys_CAM::::::::
MAKKITAF	1	10.6	0.09	772	21.43	HR96-DROME	TRUE	FALSE	1	926.2	0.9	10of 14	1.9259	FALSE	FALSE	:Oxidation_M:::::::
QTLEPVEKALNDAKMDKNQIHVYVLVGG	12	5.39	0	1552	60.93	HS70	TRUE	FALSE	3	3111.6	-2.1	16of108	1.4638	FALSE	FALSE	::::::::::::::::::::::::::::::
IINEPTAAAIAYGLDKQ	7	4.08	0.433	1248	43.8	HS7A-DROME	TRUE	FALSE	2	1789	0.3	1	4.9137	FALSE	FALSE	::::::::::::::::
REIAEVYLGGKVK	2	9.63	0.014	406	29	HS7B-DROME	TRUE	FALSE	2	1462.7	2.3	12of 24	1.4975	FALSE	FALSE	::::::::::::::
NPDDISQEEYGEFYK	2	3.51	0.417	724	27.1	HS83-DROAV	TRUE	TRUE	2	1834.9	0.7	22of 28	3.7325	FALSE	FALSE	::::::::::::::
LGRGTKIVLYIKEDQTDYLEESK	2	4.73	0.239	384	50.5	HS83-DROAV	TRUE	FALSE	3	2700.1	0.7	21of 88	2.0554	FALSE	FALSE	::::::::::::::::::::::
RAKLADFLRFHTSASGDDFCSLADYVSR	2	7.16	0.309	956	63.1	HS83-DROME	TRUE	FALSE	3	3207.5	-2.9	21of108	4.0285	FALSE	FALSE	:::::::::::::::::Cys_CAM:::::::::
VFIMDNCEDLIPEYLNFMK	1	3.59	0.191	1732	71.66	HS83-DROME	TRUE	TRUE	2	2392.8	1.9	18of 36	2.5551	FALSE	FALSE	:::::::Cys_CAM::::::::::::
SEPENSSGLMDLMT	9	2.95	0.049	1437	30.86	HSF-DROME	TRUE	FALSE	2	1527.7	1.4	13of 26	1.4591	FALSE	FALSE	:::::::::::Oxidation_M::
QEPGHHLDGNSVASSPRQSPI	6	6.03	0.012	2360	23.2	HUNB-DROME	TRUE	FALSE	2	2214.4	0.2	10of 40	1.2008	FALSE	FALSE	::::::::::::::::::::
GGPIASGGSGSGSGSGSGR	10	11.05	0.042	488	8	HUNB-DROOR	TRUE	FALSE	2	1435.5	0.7	14of 34	1.8361	FALSE	FALSE	::::::::::::::::::
GSSRDQSTLQRRGSNSKILWRSARER	1	12.41	0.065	2270	28.4	HYD-DROME	TRUE	FALSE	3	3033.3	1.7	21of100	2.6066	FALSE	FALSE	::::::::::::::::::::::::
NAIVSGAATGGILAARNGIR	6	12.41	0.104	1914	42.5	I17D-DROME	TRUE	FALSE	2	1883.2	-2.1	6of 38	0.9866	FALSE	FALSE	::::::::::::::::::
QPRLINSMCNS	10	9.01	0.002	694	23.43	I45713	TRUE	FALSE	2	1336.5	0.6	9of 20	1.0342	FALSE	FALSE	:::::::Oxidation_M:Cys_CAM:::
ESGHDYSILVDAVPGGVK	8	4.3	0.129	2353	35.3	ICCR-DROME	TRUE	FALSE	2	1844	-2.3	6of 34	1.0814	FALSE	FALSE	::::::::::::::::
PMTFLTNSSGGSLTGSIIGSR	12	11.05	0.061	1672	45.43	ICCR-DROME	TRUE	FALSE	2	2100.4	-1.3	5of 40	0.7521	FALSE	FALSE	::Oxidation_M:::::::::::::::::
LALPNSFIPTNFDISDVPADAPK	1	3.6	0.134	1464	63.7	IDE-DROME	TRUE	TRUE	2	2443.8	2	17of 44	2.038	FALSE	FALSE	::::::::::::::::::::
LAPLRKVTDLTQK	12	10.59	0.039	1957	29.9	IDG1-DROME	TRUE	FALSE	2	1483.8	-2.2	10of 24	1.3667	FALSE	FALSE	::::::::::::::
STEELPIRINLIAPPLYVMTTSTTKK	6	9.63	0	2493	68.93	IF2A-DROME	TRUE	FALSE	3	2934.5	1.7	17of100	1.5669	FALSE	FALSE	:::::::::::::::::Oxidation_M:::::::
MLPPDVQVILLSATMPPDVLEVSR	2	3.71	0.333	1740	81.96	IF4A-DROME	TRUE	TRUE	2	2622.2	2.6	18of 46	2.8397	FALSE	FALSE	::::::::::::::::::::::
LREELLRGIYGYGFEKPSAIQQR	15	9.53	0.143	819	58.8	IF4A-DROME	TRUE	FALSE	3	2725.1	-2.9	19of 88	3.1922	FALSE	FALSE	::::::::::::::::::::
PSAIQQRAIIPCVRGRDVIAQAQSGTGKT	4	11.23	0.002	2415	50.7	IF4A-DROME	TRUE	FALSE	3	3080.5	2.7	16of112	1.6805	FALSE	FALSE	:::::::::::Cys_CAM:::::::::::::::
GLVGKIRYAIAGGIMGDSLRVDPMSGL	1	9.72	0.013	368	73.56	IJFFTM	TRUE	FALSE	3	2764.3	1.3	10of104	0.9823	FALSE	FALSE	:::::::::::::::::::::Oxidation_M::::
SDFLMSYNKLSETCFTDCIR	15	4.31	0.029	227	53.83	IM9A-DROME	TRUE	FALSE	3	2488.7	1.6	22of 76	2.1997	FALSE	FALSE	:::::::::::::Cys_CAM::::Cys_CAM:::
QDSRMRRHEVTIELRKSKK	4	11.4	0.083	1870	17.83	IMA-DROME	TRUE	FALSE	3	2414.8	1.9	15of 72	1.6809	FALSE	FALSE	:::::Oxidation_M:::::::::::::::
RESLLGNSDDDE	3	3.43	0.11	1327	17.2	INL1-DROME	TRUE	FALSE	2	1350.3	2.3	14of 22	1.8817	FALSE	FALSE	::::::::::::::
NLSAPQQFR	14	11.05	0.089	252	18.8	INO1-DROME	TRUE	TRUE	2	1061.2	2.4	12of 16	1.9311	FALSE	FALSE	::::::::::
HSFNKSLIHSQR	15	11.49	0.008	1424	15.5	ITA1-DROME	TRUE	TRUE	2	1454.6	1.8	10of 22	2.0963	FALSE	FALSE	::::::::::::::
AFRIDPVGTCFTSHNFEEFYEV	15	4.16	0.05	1272	61.9	ITA2-DROME	TRUE	FALSE	3	2666.9	2.9	8of 84	0.9504	FALSE	FALSE	:::::::::Cys_CAM:::::::::::::
SPKHLKFHINQTR	14	11.64	0.184	2720	16.4	ITA3-DROME	TRUE	FALSE	2	1606.9	2.8	6of 24	1.2449	FALSE	FALSE	::::::::::::::
TDVIVSAPQH	12	4.94	0.038	1100	19.9	ITA3-DROME	TRUE	FALSE	1	1067.2	1.1	9of 18	0.9983	FALSE	FALSE	::::::::::
NLTGNYRLGFGSFADKPTLPMILPQHRENP	10	9.72	0.117	1578	70.53	ITBN-DROME	TRUE	FALSE	3	3401.9	2.4	21of116	2.7155	FALSE	FALSE	:::::::::::::::::::Oxidation_M:::::::::
IEPSTPSLRTSISETSETDGFYRLKKDSQRR	11	9.63	0.036	1172	45.7	JC4673	TRUE	FALSE	3	3586.9	2.9	21of120	2.3943	FALSE	FALSE	::::::::::::::::::::::::::::::
KAQAPAQLGLTFR	9	11.49	0.138	645	30	JC5793	TRUE	FALSE	3	1401.7	0.2	14of 48	1.696	FALSE	FALSE	::::::::::::::
WLGLAILSLFVPCLWCYPPLRACHL	3	8.02	0.002	2673	114	JC5909	TRUE	FALSE	3	3057.6	2.2	17of 96	1.2037	FALSE	FALSE	:::::::::::Cys_CAM:::Cys_CAM::::::Cys_CAM:::
GTYMSTFRTISSSEKMFQGSK	12	10.18	0.047	2808	35.86	JC7896	TRUE	FALSE	3	2374.7	-0.9	14of 80	1.3509	FALSE	FALSE	::::::::::::::::::::
NYSTAKLPTQTNRQRLIHK	10	11.51	0.001	1732	25	JC7896	TRUE	FALSE	2	2270.6	2.8	5of 36	0.7094	FALSE	FALSE	::::::::::::::::::
VRERPGFELVLESPEC	4	4.26	0.104	2800	43.7	JH0827	TRUE	FALSE	3	1918.1	-0.9	7of 60	0.9188	FALSE	FALSE	:::::::::::::::Cys_CAM:
EMLQRPGEGTELLGKVEFVR	1	4.73	0.042	1554	51.03	JIP3-DROME	TRUE	FALSE	2	2289.7	-2.1	10of 38	1.2329	FALSE	FALSE	::::::::::::::::::
EFFEPYGKITKVMSKEDGKSKGFGFVAFE	4	7.12	0.042	2701	65.43	JN0573	TRUE	FALSE	3	3320.8	-2.1	21of112	1.8045	FALSE	FALSE	:::::::::::Oxidation_M:::::::::::::::
NIIGLLNAFTPQR	14	11.05	0.377	1612	41.7	JNK-DROME	TRUE	TRUE	2	1457.7	2.7	17of 24	3.2742	FALSE	FALSE	::::::::::::::
PFQNVTHAKRAYREFKLMKLVNHKNIIG	3	11.02	0.052	2019	59.13	JNK-DROME	TRUE	FALSE	3	3355	-0.6	10of108	1.299	FALSE	FALSE	::::::::::::::::::::::::
RIVRTQNVMAALSISNIVK	9	12.42	0.05	2217	50.53	JT0367	TRUE	TRUE	2	2114.6	-1.1	5of 36	0.6138	FALSE	FALSE	::::::::::::::::::
SVKITDPRGQAVYSIKAVNVLKAHGK	3	10.63	0.006	2641	43.7	JT0367	TRUE	FALSE	2	2781.3	-0.8	5of 50	0.8573	FALSE	FALSE	::::::::::::::::::::
APGKGILAADESGPTHGKR	13	9.89	0.016	1601	19.5	JX0233	TRUE	FALSE	3	1863.1	-2.5	14of 72	1.5022	FALSE	FALSE	::::::::::::::::
CPESLFQPSFLGMEACGLHETTYNSIMK	3	4.54	0.184	1884	73.36	K00670	TRUE	TRUE	3	3249.6	2.1	34of108	3.9895	FALSE	FALSE	:Cys_CAM::::::::::::Cys_CAM:::::::::::
LMMGPPMGPMGPGPRGP	2	11.05	0.016	2374	40.62	K10-DROME	TRUE	FALSE	3	1713.1	-1	23of 64	2.6056	FALSE	FALSE	::Oxidation_M:Oxidation_M:::::::::::::
RLLEGEDAHLSSPHASGQSCSSR	5	6.03	0.07	3100	28.3	K1CP	TRUE	TRUE	3	2482.6	2.5	10of 88	1.1363	FALSE	FALSE	:::::::::::::::::Cys_CAM:::::
DYQELMNTKLALDLEIATYRTLLEGEESRMSG	4	4.02	0.012	2461	83.06	K2C1	TRUE	FALSE	3	3692.1	2	24of124	2.178	FALSE	FALSE	::::::::::::::::::::::::::::::
GGGGGIGGGFGGGTSGFSGGSGFGSISGARYGVSGGGFSS	11	9.85	0.016	137	52.9	K2C3	TRUE	FALSE	3	3319.4	1.3	17of156	1.0989	FALSE	FALSE	::::::::::::::::::::::::::::::::::::
TTGGYAGGLSSAYGDLTD	13	2.93	0.081	2516	30	K2C8	TRUE	FALSE	3	1706.8	1.6	15of 68	1.355	FALSE	FALSE	::::::::::::::::::
AKLAASDSKSLLKKYLTK	14	10.47	0.013	1909	32.6	KARG-DROME	TRUE	FALSE	2	1966.4	-1	10of 34	1.7046	FALSE	FALSE	::::::::::::::::
IGRHCNKLFLIDFGLAKK	11	10.32	0.002	842	50.1	KC1A-DROME	TRUE	FALSE	2	2131.5	2	10of 34	1.4946	FALSE	FALSE	:::::Cys_CAM:::::::::::::
KMGLDMFRKAPNLR	7	11.47	0.228	2069	33.36	KDGE-DROME	TRUE	FALSE	2	1678.1	2.5	129	1.7368	FALSE	FALSE	::::::::::::::
DNCESAAECERSGGHNNK	2	4.63	0.001	1697	5.3	KEN-DROME	TRUE	FALSE	2	2036	-1	4of 34	0.5879	FALSE	FALSE	:::Cys_CAM::::::Cys_CAM:::::::::::
TEDSQKPATAALSKSPGP	8	6.99	0.011	2685	17.6	KG3H-DROME	TRUE	FALSE	2	1785.9	-1.7	10of 34	2.04	FALSE	FALSE	::::::::::::::::::
SSSAGSSFLIEGISALSK	15	6.95	0.128	840	40.3	KGP3-DROME	TRUE	FALSE	2	1741.9	2.5	12of 34	1.4511	FALSE	FALSE	::::::::::::::::::
RTDGRVHM	10	10.89	0.024	505	7.83	KI10-DROME	TRUE	FALSE	2	972.1	2	7of 14	1.2155	FALSE	FALSE	::::::::
QATAPMNLSRNPTQSAIGGNLTSRM	1	12.41	0.011	66	42.46	KI10-DROME	TRUE	FALSE	2	2618	-2.2	5of 48	0.7974	FALSE	FALSE	::::::::::::::::::::::
HKAMLDSMQEKFATIIDSSLQSVEEHAK	2	5.29	0.122	2016	54.16	KL61-DROME	TRUE	TRUE	3	3191.6	-2.1	18of108	1.539	FALSE	FALSE	::::Oxidation_M:::::::::::::::::::::::
LEAPVKVATSNALDLT	4	4.08	0.047	3010	41.9	KNRL-DROME	TRUE	FALSE	3	1642.9	0.7	9of 60	1.2273	FALSE	FALSE	::::::::::::::::
VSSVARGNLSIVSCKSSR	10	11.33	0.067	1617	29.8	KPBA-DROME	TRUE	FALSE	2	1908.1	0	9of 34	1.1124	FALSE	FALSE	:::::::::::::Cys_CAM:::::
RLRKGALKKKNVFNVK	9	12.45	0.085	651	23.2	KPC1-DROME	TRUE	FALSE	3	1900.4	1.2	19of 60	1.6662	FALSE	FALSE	::::::::::::::::
HTKGILYR	14	10.4	0.026	1278	15.6	KPC1-DROME	TRUE	FALSE	1	988.2	1.2	6of 14	1.1565	FALSE	FALSE	::::::::
DANNFDAEFTK	11	3.71	0.017	858	19	KPC3-DROME	TRUE	TRUE	2	1272.3	2.9	9of 20	1.1273	FALSE	FALSE	::::::::::::

KLRRTFPYHHAPTKDVAKN	11	10.89	0.041	774	22.8	KZ-DROME	TRUE	FALSE	3	2280.6	1.3	18of 72	2.3026	FALSE	FALSE	::::::::::::::::::
GPGADLASQLRHPATTDGAGPSVLREH	11	6.03	0.04	54	39.4	L27654	TRUE	FALSE	3	2712	0.5	9of104	0.9871	FALSE	FALSE	::::::::::::::::::::::
CIYSGHTGGPGTPVSQRK	8	9.75	0.06	2339	18.7	L2DT-DROME	TRUE	FALSE	2	1903.1	1.8	12of 34	1.3495	FALSE	FALSE	:Cys_CAM:::::::::::::::
LGIMSPKRKAKEKVDWLTNIRKQK	8	11.17	0.043	2205	41.43	L2DT-DROME	TRUE	FALSE	3	2869.5	2.4	12of 92	1.2607	FALSE	FALSE	::::::::::::::::::::
RLMDQNERTPGSVEKTT	13	7.14	0.04	2378	20.53	L2DT-DROME	TRUE	FALSE	3	1979.2	-0.3	14of 64	1.3708	FALSE	FALSE	:::Oxidation_M:::::::::::::
PLSPDFGHLFLTSSIKIWSLKLP	9	9.89	0.026	285	79.8	L41945	TRUE	FALSE	2	2598.1	0.9	8of 44	0.9955	FALSE	FALSE	::::::::::::::::::::
ADYYVSASAKGNVEIK	2	6.87	0.011	1820	28.3	LAM0-DROME	TRUE	FALSE	2	1715.9	2.5	11of 30	1.2015	FALSE	FALSE	::::::::::::::::
VRAYT	7	9.85	0.004	3660	11.5	LAR-DROME	TRUE	FALSE	1	609.7	2	1	0.2753	FALSE	FALSE	::::::
NTSSVAAVSTSVLGEHGIDKDVFLSLPCVLNANGVTSVVK	6	5.28	0.015	2118	91.9	LDH-DROME	TRUE	TRUE	3	4087.6	1.6	21of156	1.3501	FALSE	FALSE	:::::::::::::::::::::::::::Cys_CAM::::::::::::
YNQIKDPNGAYYKMHEKFARMAGSKK	13	10.14	0.078	2098	34.36	LDS-DROME	TRUE	FALSE	2	3077.5	-1.1	7of 50	1.0602	FALSE	FALSE	::::::::::::::::::::::
TRRGGTLVVCPASLLRQWESEVESK	7	8.97	0.006	1541	54.3	LDS-DROME	TRUE	FALSE	3	2860.2	-1	24	1.4898	FALSE	FALSE	:::::::::Cys_CAM:::::::::::::::
IRAISLYFNSLVGSSIR	1	11.14	0.002	569	55.2	LIP1-DROME	TRUE	FALSE	2	1897.2	-2.4	4of 32	0.6831	FALSE	FALSE	::::::::::::::::
HYMSIEMIDGAIFFNIS	9	4.07	0.039	1328	61.36	LMA-DROME	TRUE	FALSE	3	1989.3	2	20of 64	2.2635	FALSE	FALSE	::::::::::::::::
NLEAAASTKIDAALE	6	3.83	0.023	2898	33.7	LMA-DROME	TRUE	FALSE	2	1517.7	0.1	6of 28	1.047	FALSE	FALSE	::::::::::::::::
SSLYDMNYKSDPKCQN	14	6.23	0.103	1142	21.63	LMB1-DROME	TRUE	FALSE	2	1951.1	2.2	5of 30	0.8401	FALSE	FALSE	:::::::::::::Cys_CAM:::
CLSGTLPFSDEYGTPAAQQIKKGR	11	8.85	0.077	562	43.5	LOK-DROME	TRUE	FALSE	3	2625.9	2.8	21of 92	1.6071	FALSE	FALSE	:Cys_CAM:::::::::::::::::::::
DTSGDVSGSREGSSSPSRRRRKVRR	4	12.28	0.006	1462	5.8	LOLL-DROME	TRUE	FALSE	3	2777	3	19of 96	1.6979	FALSE	FALSE	::::::::::::::::::::::::
TNMLNDKMIFQDGKFVWDMSLFARQMR	13	9.88	0.039	1934	80.02	LP1B-DROME	TRUE	FALSE	3	3356.9	-2.6	16of104	1.5413	FALSE	FALSE	:::::::Oxidation_M::::::::::::::::Oxidation_M::
QKFMYQIL	14	9.72	0.009	2848	31.53	LSP2-DROME	TRUE	FALSE	2	1071.3	-2.3	4of 14	0.5891	FALSE	FALSE	::::::::
EISQQHALEKEKLAK	9	7.78	0.129	2070	22.3	LVA-DROME	TRUE	FALSE	2	1753	2.4	6of 28	0.9546	FALSE	FALSE	::::::::::::::::
LAASAPPPISPPPTIEDLQRNVSDLEK	13	4.07	0.122	1282	61.4	LVA-DROME	TRUE	FALSE	3	2857.2	-2.2	14of104	1.4208	FALSE	FALSE	::::::::::::::::::::::::
ANLVSKELR	9	10.09	0.087	1062	20.8	LVA-DROME	TRUE	FALSE	2	1030.2	1.7	11of 16	1.9798	FALSE	FALSE	::::::::::
QLXXGRTLSDYNIQKESTLHLVLR	3	9.72	0.299	1595	53.3	M33017	TRUE	TRUE	3	2812.3	2.6	30of 92	4.6345	FALSE	FALSE	::::::::::::::::::::::
IDGHTLCDSVAIIHYLEET	15	4.06	0.092	908	51.7	MAA1-DROME	TRUE	FALSE	3	2187.4	-2.9	20of 72	2.5078	FALSE	FALSE	:::::::Cys_CAM:::::::::::::
RQQFYLR	9	11.14	0.045	1470	19.5	MAL1-DROVI	TRUE	FALSE	1	1011.2	1.6	9of 12	1.4413	FALSE	FALSE	::::::::
PRVATRFGPASVDAMNM	1	10.89	0.096	1980	37.76	MAL2-DROVI	TRUE	FALSE	2	1853.1	-1.3	7of 32	0.9424	FALSE	FALSE	:::::::::::::::Oxidation_M::Oxidation_M:
RPVMSSLLSAQTEDFIDWWQHAVFYQIYPRSFK	6	7.69	0.042	3095	101.33	MAL2-DROVI	TRUE	FALSE	3	4048.6	-1.9	7of128	0.853	FALSE	FALSE	::::::::::::::::::::::::::::::
NANLGATGGIAGITGGNGAGGPTNPGAVPTAPGDTMPTK	3	6.76	0.048	2623	52.53	MAM-DROME	TRUE	FALSE	3	3450.8	0.6	23of152	2.0267	FALSE	FALSE	:::::::::::::::::::::::::::::::::Oxidation_M::::
RMTQQPIPPSGPMMRPQHAM	2	12.41	0.016	904	38.42	MAM-DROME	TRUE	FALSE	3	2324.8	1	19of 76	1.719	FALSE	FALSE	:::::::::::::Oxidation_M::::::Oxidation_M:
TTIILGEDILPSKHVVMHNTLPHW	10	6.31	0.098	900	68.53	MAN2-DROME	TRUE	FALSE	3	2753.2	-1.5	22of 92	2.7242	FALSE	FALSE	::::::::::::::::::::::
EVPLQDVVINGHPNFIPYALLALK	5	5.22	0.395	2351	80.5	MCA2-DROME	TRUE	TRUE	2	2662.1	1.8	17of 46	3.4646	FALSE	FALSE	::::::::::::::::::::::
TFQHTTAFQNGGLK	9	10.1	0.305	1200	22.9	MCA2-DROME	TRUE	TRUE	2	1550.7	1.8	20of 26	3.0911	FALSE	FALSE	::::::::::::::
DLVRCSRTCSSWLHADCLERK	8	8.02	0.041	2509	43.4	MES4-DROME	TRUE	FALSE	2	2650.9	0.8	7of 40	0.9701	FALSE	FALSE	:::::Cys_CAM::::Cys_CAM::::::::Cys_CAM:::::
DRKCLLVVMECMEGGELF	15	4.17	0.096	1108	59.06	MKK2-DROME	TRUE	FALSE	3	2219.5	2.3	21of 68	2.4692	FALSE	FALSE	:::::Cys_CAM::::::Oxidation_M::Cys_CAM:Oxidation_M::::::::
PIYQAISK	7	9.72	0.02	2107	21	MLC2-DROME	TRUE	FALSE	1	920.1	1.2	15	1.9911	FALSE	FALSE	::::::::
LPIAAMRSEILTAIND	15	4.08	0.035	1148	52.43	MLE-DROME	TRUE	FALSE	2	1745	2	11of 30	1.9883	FALSE	FALSE	:::::::Oxidation_M:::::::::
MNHTMNAMNMQMRSMNR	1	12.41	0.04	1461	29.88	MLF-DROME	TRUE	FALSE	2	2115.5	0.7	10of 32	1.5543	FALSE	FALSE	:::::::Oxidation_M:::::::::
HNFTVMTRYISEPENLKLMMNMLKEKSRNIQF	14	10.05	0.06	411	81.02	MO25-DROME	TRUE	FALSE	3	3945.7	-1.3	14of124	1.2141	FALSE	FALSE	::::::::::::::::::::::::::::
APDFMFFAPR	8	6.79	0.438	2155	37.43	MOEH-DROME	TRUE	TRUE	2	1199.4	0.6	16of 18	3.5154	FALSE	FALSE	::::::::::
AYALPLMEGRHRDLKSISSETVARLLKGEFSD	1	7.73	0.056	2012	74.03	MPIP-DROME	TRUE	FALSE	3	3608.1	2.5	11of124	0.9796	FALSE	FALSE	:::::::Oxidation_M:::::::::::::::::::::::
AAETTEEEGPVAPK	5	3.8	0.035	1575	18.3	MR15-DROME	TRUE	FALSE	2	1429.5	1	11of 26	1.8742	FALSE	FALSE	::::::::::::::
ILPKWVAFKKKDKEHELVPESPEVPK	4	9.54	0.016	2357	55.2	MSL1-DROME	TRUE	FALSE	3	3073.6	-0.3	14of100	1.4072	FALSE	FALSE	::::::::::::::::::::::
TLNNCSPHTYS	15	7.15	0.003	1445	14.7	MSL1-DROME	TRUE	FALSE	2	1294.3	-1.8	8of 20	0.7321	FALSE	FALSE	:::::Cys_CAM:::::::
HPDMRTGSSAPSDIRK	8	10.09	0.002	1829	13.73	MSL1-DROME	TRUE	FALSE	2	1771.9	-2.2	4of 30	0.7523	FALSE	FALSE	:::::Oxidation_M:::::::::::
MEREYDRVMSTVCMLKEVVDGLRIYFEFHVDD	5	4.29	0.028	2425	92.39	MSL3-DROME	TRUE	FALSE	3	4000.5	2.5	20of124	2.6603	FALSE	FALSE	:::::::::::::Cys_CAM:Oxidation_M:::::::::::::::::
GSKQSGSDKGKKNGKKNDMKN	7	10.66	0.002	3394	-11.97	MST1-DROHY	TRUE	FALSE	3	2237.5	2.5	222	1.3177	FALSE	FALSE	::::::::::::::::::::
RPILRSFNFLNKYIDQSQHSGGLSSF	5	10.39	0.022	1686	62.1	MST2-DROHY	TRUE	FALSE	3	3013.4	-2.2	20of100	2.2485	FALSE	FALSE	::::::::::::::::::::::
KREKEAAEKKKCAEAAKK	11	10.18	0.017	720	1.7	MST2-DROHY	TRUE	FALSE	3	2104.4	1.7	16of 68	1.6921	FALSE	FALSE	:::::::::::Cys_CAM:::::::
GLVIPVQTRTLQPDWRCITC	1	8.3	0.016	112	59.6	MSTA-DROME	TRUE	FALSE	2	2414.7	0.6	6of 38	0.7748	FALSE	FALSE	:::::::::::::::Cys_CAM:::Cys_CAM:
LAIEEMSPPPAAPPRPSPPPTVK	15	7.1	0.046	297	49.73	MTH1-DROME	TRUE	FALSE	2	2380.8	-0.6	4of 44	0.5654	FALSE	FALSE	::::::::::::::::::::::
FFMVITIAAYLWLPK	11	9.72	0.145	1184	75.53	MTHB-DROME	TRUE	FALSE	2	1814.3	-0.9	6of 28	1.128	FALSE	FALSE	::::::::::::::::
YAGQFSMEGFLNLQWPR	10	6.89	0.008	872	54.53	MVL-DROME	TRUE	FALSE	3	2061.3	-0.4	18of 64	1.4221	FALSE	FALSE	:::::::Oxidation_M:::::::::::
KETLSKAGNGIVRSCFPEK	3	9.79	0.119	1032	29.7	MY1B-DROME	TRUE	FALSE	3	2122.4	0.7	20of 72	2.0461	FALSE	FALSE	:::::::::::::::Cys_CAM:::::
VHKSWANHYRLGLPR	14	11.39	0.02	320	30	MYS9-DROME	TRUE	FALSE	2	1835.1	-2.3	5of 28	0.929	FALSE	FALSE	::::::::::::::::
GSGAVPHPAVLIGELEQQLLQANPILEAFGNAK	4	4.54	0.228	2667	86.3	MYSN-DROME	TRUE	TRUE	3	3383.9	1.5	25of128	3.6755	FALSE	FALSE	::::::::::::::::::::::::::::::
KHARRFMLAVSLLDCGEAHK	3	9.91	0.062	2302	42.83	N160-DROME	TRUE	FALSE	2	2340.7	1.8	11of 38	1.4168	FALSE	FALSE	:::::::::::::::Cys_CAM:::::::
QSLLQLVGYINKMLWP	6	9.72	0.02	2471	62.53	N160-DROME	TRUE	FALSE	2	1920.3	2.8	9of 30	1.3966	FALSE	FALSE	:::::::::::::::Oxidation_M::::
LQFAQMYEHYERQRTDNITDPALRQ	2	5.39	0.01	91	51.53	NBEA-DROME	TRUE	FALSE	3	3141.4	-2.9	15of 96	1.7942	FALSE	FALSE	:::::Oxidation_M:::::::::::::::::::
TGSGKTYTMDGVPESVGVIPRTVDLLFDSIR	11	4.46	0.022	1242	72.53	NCD-DROME	TRUE	FALSE	3	3328.8	-1.8	20of120	1.4749	FALSE	FALSE	:::::::::Oxidation_M:::::::::::::::::::::
VAIYVDKRLEELGANRVFELGLGDDDANIEDDFI	2	3.65	0.06	1956	96.8	NCPR-DROME	TRUE	FALSE	3	3826.2	2.6	25of132	1.7949	FALSE	FALSE	::::::::::::::::::::::::::::::
IRGDFCIQVGRNIIHGSDAVESAEKEIALWFNEK	3	4.82	0.077	2048	83.8	NDKA-DROME	TRUE	FALSE	3	3904.3	-2.4	20of132	2.2769	FALSE	FALSE	:::::Cys_CAM:::::::::::::::::::::::::
PFFPGLVNYMNSGPVVPMVWEGLNVVK	8	6.87	0	2867	91.16	NDKA-DROME	TRUE	TRUE	2	2992.6	0.5	14of 52	1.7157	FALSE	FALSE	::::::::::::::::::::::::::
WCDNVVDCSDGSDESACTCADRV	9	3.27	0.059	298	38.9	NDL-DROME	TRUE	FALSE	2	2679.6	2.1	8of 44	1.0706	FALSE	FALSE	::Cys_CAM:::::Cys_CAM::::::::Cys_CAM::Cys_CAM::::
TGRNCHQCK	13	9.15	0	2500	0.2	NETA-DROME	TRUE	FALSE	2	1161.2	-2	3of 16	0.5859	FALSE	FALSE	:::::Cys_CAM::::Cys_CAM:::
LNLNKFCMEDY	5	4.08	0.086	2868	34.93	NETB-DROME	TRUE	FALSE	2	1463.6	-1.1	5of 20	1.0861	FALSE	FALSE	:::::::Cys_CAM:Oxidation_M::::
AIGSSAAGISSNDPCYFEGK	6	4.08	0.084	1224	35.2	NETB-DROME	TRUE	FALSE	3	2032.1	1	20of 76	2.0091	FALSE	FALSE	:::::::::::::Cys_CAM:::::::
DKLSSKKKMHLLKKIKKRFGLVR	7	11.8	0.022	1872	37.93	NEUR-DROME	TRUE	TRUE	3	2799.5	-0.4	424	1.6146	FALSE	FALSE	:::::::::Oxidation_M:::::::::::::::
RRPRVRLEPIQSGGGQERGL	4	12.23	0.091	2286	30.8	NFS1-DROME	TRUE	FALSE	2	2262.6	-2.8	12of 38	1.7905	FALSE	FALSE	::::::::::::::::::::
ACGVSRPIVACSVTTNEGSQLK	15	8.3	0.139	509	39.7	NHPX-DROME	TRUE	TRUE	3	2335.6	2.4	27of 84	2.0494	FALSE	FALSE	::Cys_CAM::::::::Cys_CAM:::::::::::
ASAPTIPLRSRGMPRK	3	12.71	0.131	2238	27.13	NLFA-DROME	TRUE	TRUE	2	1755.1	2.2	8of 30	1.2992	FALSE	FALSE	:::::::::::Oxidation_M::::
HSDLGMLPLEC	15	4.07	0.014	633	33.23	NLFA-DROME	TRUE	FALSE	3	1288.4	-0.9	15of 40	1.6988	FALSE	FALSE	:::::Oxidation_M::::Cys_CAM:
WVTLDLNDANDLKELYTLLNENYVED	13	3.28	0.009	1430	79.2	NMT-DROME	TRUE	FALSE	3	3114.4	-1.3	12of100	1.3131	FALSE	FALSE	::::::::::::::::::::::
PIITMEDAIKAESFRL	9	4.45	0.05	980	50.03	NNOS-DROME	TRUE	FALSE	3	1835.2	-1.1	17of 60	2.0243	FALSE	FALSE	::::::::::::::::
IDQWRMDKFLMLTRRMVRYLLRFLK	6	11.86	0.167	2968	92.79	NNP1-DROME	TRUE	FALSE	3	3363.1	0.8	15of 96	1.8632	FALSE	FALSE	:::::Oxidation_M::::::::Oxidation_M:::::::::
MWLYENHKDESMLRR	1	7.75	0.132	1641	36.76	NO60-DROME	TRUE	FALSE	2	2025.3	-2.5	6of 28	0.9488	FALSE	FALSE	:Oxidation_M:::::::::::::
IKPSSKIAELDTSQWPLLLKNFDKLNIR	10	10.16	0.083	2550	76.9	NO60-DROME	TRUE	FALSE	3	3269.9	0.2	13of108	1.5262	FALSE	FALSE	::::::::::::::::::::::::
LLEGFQCTALAYGQTGTGKSYSMGMTPPGEI	8	4.27	0.076	2981	71.36	NOD-DROME	TRUE	FALSE	3	3299.7	-0.7	22of120	1.6222	FALSE	FALSE	:::::Cys_CAM::::::::::::::Oxidation_M::Oxidation_M:::::::
PCIPEKASARLLQNADKAER	5	8.93	0.023	2252	34.4	NOG1-DROME	TRUE	FALSE	2	2268.5	-2.1	10of 38	1.2956	FALSE	FALSE	::Cys_CAM:::::::::::::::::
LLYKSFEIFGPIER	14	7.02	0.021	2717	52.8	NONA-DROME	TRUE	FALSE	3	1713	1.8	9of 52	1.0032	FALSE	FALSE	::::::::::::::
PHNLTRLSEG	7	7.85	0.008	3397	16.2	NOS-DROME	TRUE	FALSE	2	1124.2	-0.8	40	1.2711	FALSE	FALSE	::::::::::
RNMLETVALKMQLDTRTPTSLW	2	10.09	0	1946	60.86	NOS-DROME	TRUE	FALSE	2	2638.1	2.3	5of 42	0.7119	FALSE	FALSE	:::Oxidation_M::::::::Oxidation_M:::::::::::
FLAATAAKHQLRNDFQIHSVRGIK	11	11.47	0.257	2759	50.4	NOTC-DROME	TRUE	FALSE	3	2723.2	-0.8	8of 92	0.9342	FALSE	FALSE	::::::::::::::::::::::
PSLPTSPTHIQAMRHATQQKQFGGSNLNS	12	11.49	0.02	2684	39.73	NOTC-DROME	TRUE	FALSE	2	3151.5	-2.2	5of 56	0.9064	FALSE	FALSE	:::::::::::::Oxidation_M:::::::::::::::

VLGIEMPFPLANPDACVDSGLK	1	3.71	0.12	1529	66.13	NPC2-DROME	TRUE	TRUE	2	2344.7	2	13of 42	1.7652	FALSE	FALSE		::::::::::::::Cys_CAM::::::
VSVLVKWELQDQDGADIICVEIPAKIQ	11	3.85	0.102	1033	81.4	NPC2-DROME	TRUE	FALSE	3	3068.5	-2.6	22of104	2.5867	FALSE	FALSE		::::::::::::::::::::Cys_CAM::::::::
EQANDKPVLVMGATAHEAHTEK	11	5.26	0.111	516	29.13	NRT-DROME	TRUE	TRUE	3	2377.6	-0.9	20of 84	2.5977	FALSE	FALSE		::::::::::::::::::::::
EMLMIGSLVMLAAMTK	14	6.95	0.013	1585	62.02	NU5M-DROME	TRUE	FALSE	2	1756.2	0.1	10of 30	1.2792	FALSE	FALSE		::Oxidation_M::::::::::::::
LTLFSSLILIFMLILSFIMDKTSSSLFLMN	1	6.76	0.004	1941	140.89	NU6M-DROME	TRUE	FALSE	3	3489.3	-2.6	7of116	0.6334	FALSE	FALSE		::::::::::::Oxidation_M::::::::Oxidation_M::::::::::Oxidation_M::
WDFNHAAFVFEKLFK	3	7.8	0.119	1923	52.7	NXF1-DROME	TRUE	FALSE	2	1900.2	1.2	6of 28	1.0566	FALSE	FALSE		::::::::::::::::
IANERLHITNPSKT	13	10.09	0.07	1517	23	NXF2-DROME	TRUE	FALSE	2	1594.8	-2.1	10of 26	1.9232	FALSE	FALSE		::::::::::::::::
ALPLNRMNTSTTYISAR	6	11.14	0.007	2147	38.63	NYR-DROME	TRUE	FALSE	2	1926.2	-0.3	8of 32	1.2306	FALSE	FALSE		::::::Oxidation_M:::::::::::
YLFVHNWRR	12	11.14	0.182	1097	30.6	O30A-DROME	TRUE	FALSE	2	1291.5	1.3	7of 16	1.4872	FALSE	FALSE		::::::::::
PVQLYVVLL	15	5.93	0.098	1199	45.8	O33C-DROME	TRUE	FALSE	1	1044.3	-2.8	7of 16	0.8603	FALSE	FALSE		::::::::::
DFLYSMIFPFDSDPLYIFV	14	2.82	0.098	2157	87.13	O35A-DROME	TRUE	FALSE	3	2330.7	-2.3	20of 72	1.8301	FALSE	FALSE		::::::::::::::::::::
AFLNILSLWPQIERRWRIIHQVNY	13	11.05	0.025	1748	88.9	O46A-DROME	TRUE	FALSE	3	3067.6	-2.1	22of 92	1.8663	FALSE	FALSE		::::::::::::::::::::::
IFYMHLRCD	9	7.16	0.123	2547	33.73	O47B-DROME	TRUE	FALSE	2	1255.4	2.4	6of 16	1.089	FALSE	FALSE		:::::::Cys_CAM::
NDMEKVTACLSVVFTNMLTVIKIST	11	6.36	0.001	1549	72.66	O82A-DROME	TRUE	FALSE	3	2848.3	-2.4	20of 96	1.6424	FALSE	FALSE		:::Oxidation_M:::::Cys_CAM::::::::Oxidation_M::::::::
LTMTIIYFFTGYGTIYWCLRSR	6	9.48	0.004	2238	85.63	O85E-DROME	TRUE	FALSE	2	2780.2	2.3	11of 42	1.4771	FALSE	FALSE		:::Oxidation_M::::::::::::::Cys_CAM:::::
KGDFISSAAMAKLRQK	7	10.83	0.018	1528	27.83	OAF-DROME	TRUE	FALSE	2	1768.1	0.8	297	1.177	FALSE	FALSE		:::::::::Oxidation_M::::::::
RGKGLLNAIVINEKYDAWK	9	10.05	0.003	1796	46.1	OAT-DROAN	TRUE	FALSE	3	2189.6	-0.6	18of 72	1.7556	FALSE	FALSE		::::::::::::::::::::
KQPRRIPPLSTPVATR	3	12.71	0.013	1668	27.6	OP31-DROME	TRUE	FALSE	2	1818.2	2.2	9of 30	0.9471	FALSE	FALSE		::::::::::::::::
NRKAKEALQH	11	10.59	0.026	2703	5.7	OP32-DROME	TRUE	FALSE	2	1195.4	0.6	4of 18	0.7291	FALSE	FALSE		::::::::::
PMNRNMTFTKAIIMN	13	11.49	0.049	2593	40.19	OPS4-DROVI	TRUE	FALSE	2	1799.2	-3	6of 28	0.747	FALSE	FALSE		:::::::::::::Oxidation_M:::
TSVRALLNTPDGEGPVLLSTESATSQEPPLTLDKGNVP	4	3.93	0.005	2001	79	OPT1-DROME	TRUE	FALSE	3	3906.3	1.9	22of148	2.0342	FALSE	FALSE		::::::::::::::::::::::::::::::::::::::
GLNPTQVGNWFKNRR	15	12.42	0.14	1204	27.1	OPT-DROME	TRUE	FALSE	3	1788	-1	19of 56	2.9799	FALSE	FALSE		::::::::::::::::
HKQLQEIVTARLGGSETFKGEAVQLVARK	2	10.32	0.159	2445	54.9	ORC1-DROME	TRUE	FALSE	2	3195.7	-1.2	8of 56	1.2834	FALSE	FALSE		::::::::::::::::::::::::::::
RRRASMAASSSVEFID	1	10.8	0.01	1754	30.73	ORC1-DROME	TRUE	FALSE	2	1784	2.2	6of 30	0.8087	FALSE	FALSE		::::::::::::::::
GDKNTTTQDEILQRISDYCDK	8	4.13	0.033	2275	27.9	ORK1-DROME	TRUE	FALSE	3	2501.6	1.3	22of 80	2.0821	FALSE	FALSE		::::::::::::::::::::Cys_CAM:::
AIYDTFSAFGNILSC	13	3.1	0.073	224	49.8	PABP-DROME	TRUE	FALSE	2	1679.8	-3	5of 28	0.8135	FALSE	FALSE		:::::::::::::Cys_CAM:
TIVHVQDSLSELNAQLAQHPSMLPND	13	4.29	0.069	1396	59.43	PATJ-DROME	TRUE	FALSE	3	2859.2	-1.3	13of100	1.3479	FALSE	FALSE		::::::::::::::::::::::::
HHIVPGDGGR	12	8	0.126	676	9.2	PAX6-DROME	TRUE	FALSE	2	1045.1	2.6	10of 18	1.1901	FALSE	FALSE		::::::::::
VGPNLTKSFDVREVIARIVDGSRFTEFKK	3	10.31	0.012	1268	65.5	PCCB-DROME	TRUE	FALSE	3	3310.8	2.7	21of112	1.4994	FALSE	FALSE		::::::::::::::::::::::::::::
GSCTAGGAYVPAMADESIIVK	12	4.08	0.01	1121	46.23	PCCB-DROME	TRUE	FALSE	2	2114.3	-0.4	14of 40	1.593	FALSE	FALSE		:::Cys_CAM::::::::Oxidation_M::::::::
ALQLAAVTQPGTGGSVTGGGGAAGGGGSAAGMKR	12	11.49	0.001	755	44.03	PCX-DROME	TRUE	FALSE	3	2888.2	-1.1	18of132	1.3712	FALSE	FALSE		:::::::::::::::::::::::::::::Oxidation_M:::
SHLLFFVSR	14	11.05	0.31	1082	34.3	PDI-DROME	TRUE	TRUE	1	1106.3	0.9	10of 16	2.0216	FALSE	FALSE		::::::::::
FLDANGEVADSEPVEETEEEEEAPKKDEL	1	3.42	0.243	870	51.3	PDI-DROME	TRUE	FALSE	3	3250.4	2.6	26of112	2.4128	FALSE	FALSE		::::::::::::::::::::::::
PAPAFAGTAVVNGVFK	8	10.1	0.346	1876	40.7	PDX1-DROME	TRUE	TRUE	2	1546.8	1.7	22of 30	2.9717	FALSE	FALSE		::::::::::::::::
TAWGATADYMSF	11	3.1	0.036	2651	33.93	PEN2-DROME	TRUE	FALSE	2	1321.4	-0.5	6of 22	0.933	FALSE	FALSE		::::::::::::
LKMVEYSGPGPGPGHGHGIKR	3	10.18	0.146	1367	27.23	PER-DROCP	TRUE	FALSE	3	2175.5	-0.9	23of 80	2.0639	FALSE	FALSE		::::::::::::::::::
QQLTLNTSGGGGGGGGGGGGMPLF	15	6.02	0.099	1453	38.13	PER-DROEQ	TRUE	FALSE	2	2037.2	1.6	7of 44	1.1186	FALSE	FALSE		::::::::::::::::::Oxidation_M::::
IEKMPEYSGPGHGQTMKRGGSHSWEGDANK	6	7.86	0.133	2331	28.36	PER-DROVI	TRUE	FALSE	3	3289.6	0.5	24of116	1.6731	FALSE	FALSE		::::::::::::::Oxidation_M:::::::::::::
KKNKGAGQGAGQAGQSLISASTS	9	10.85	0.032	1136	15.4	PER-DROYA	TRUE	FALSE	3	2147.4	-1.7	21of 88	2.0544	FALSE	FALSE		::::::::::::::::::::::
TWEAGGPGKVEPVPGVPGTAAAGT	12	4.27	0.032	1961	40.5	PER-DROYA	TRUE	FALSE	3	2207.4	-0.5	21of 92	2.1331	FALSE	FALSE		::::::::::::::::::::::
PTRCCTDDGR	4	6.1	0.034	1463	7.4	PERO-DROME	TRUE	FALSE	2	1238.2	-0.2	8of 18	1.1031	FALSE	FALSE		::::Cys_CAM:Cys_CAM::::::
AALDSIKLALSKKAK	5	10.56	0.045	1495	31.1	PGK-DROME	TRUE	FALSE	2	1557.9	0.1	10of 28	1.2573	FALSE	FALSE		::::::::::::::::
TKNGTVSIIGGGDTASCCAK	14	8.29	0.019	1475	25	PGK-DROME	TRUE	FALSE	2	1998.1	-2.4	6of 38	1.0175	FALSE	FALSE		::::::::::::::::Cys_CAM:Cys_CAM:::
NEQMKALGIEEQSGGAARDAGK	10	4.65	0.035	1202	26.13	PIPA-DROME	TRUE	FALSE	3	2277.5	-0.9	22of 84	1.9286	FALSE	FALSE		::::Oxidation_M:::::::::::::::::
DAGLPDDKNATMTKEQFTFDKFYALYH	6	4.55	0.027	1158	57.53	PIPA-DROME	TRUE	FALSE	3	3168.5	-2.7	9of104	1.0617	FALSE	FALSE		::::::::::::::::::::::::
NPYMYRSAAEPCMSSSMSSSIATLRLK	3	9.56	0.043	2233	58.19	PIX1-DROME	TRUE	FALSE	3	3040.5	-0.9	17of104	1.5514	FALSE	FALSE		::::::::::::Cys_CAM:::::::::::::::
PFPWPVNPLGSMVAGNHHQNSV	14	8	0.005	94	48.73	PIX1-DROME	TRUE	FALSE	3	2386.7	-2.1	14of 84	1.1663	FALSE	FALSE		::::::::::::::::::::::
SYKDFNLSSMIPA	1	6.68	0.005	1634	34.53	PLU-DROME	TRUE	FALSE	1	1489.7	1.8	3of 24	0.6427	FALSE	FALSE		::::::::::Oxidation_M::::
EEPIHGCKDLCSLSDI	12	4.06	0.099	1729	36	PNT2-DROME	TRUE	FALSE	2	1874	2.9	10of 30	1.2855	FALSE	FALSE		::::::Cys_CAM:::Cys_CAM::::::
KAVKRGFEFTLMVVG	9	10.59	0.109	619	43.33	PNUT-DROME	TRUE	FALSE	3	1683.1	1	20of 56	2.1892	FALSE	FALSE		::::::::::::::::
HFTVKTDHRPL	8	10.09	0	1646	17.7	POL4-DROME	TRUE	FALSE	2	1351.6	-2	10of 20	1.1924	FALSE	FALSE		::::::::::::
KPADVFFDRSSRVNYQGLTDF	2	6.91	0.178	2037	47.6	POL5-DROME	TRUE	FALSE	2	2463.7	0.2	4of 40	0.7072	FALSE	FALSE		::::::::::::::::::::
LVTLFSAPNYCGEFDNAGAMMSVDDTLMCSFQILK	3	3.51	0.156	2563	106.99	PP11-DROME	TRUE	FALSE	3	3948.4	2.7	23of136	2.3756	FALSE	FALSE		::::::::::Cys_CAM::::::::::::::::Cys_CAM::::::
MSVDDTLMCSFQILKPADKR	3	6.33	0.08	1383	50.36	PP11-DROME	TRUE	FALSE	3	2388.7	0.3	19of 76	1.7639	FALSE	FALSE		:Oxidation_M::::::Oxidation_M:Cys_CAM::::::::::::
LTNFVGILSHGLRIAPPEAPPTGYMFGKGI	12	9.72	0.118	1688	85.43	PPOL-DROME	TRUE	FALSE	3	3155.7	0.6	15of116	1.4788	FALSE	FALSE		::::::::::::::::::::::::::::::
LIFDIDSMNKTLME	4	3.71	0	2888	49.36	PPOL-DROME	TRUE	FALSE	2	1671	-2.8	3of 26	0.5085	FALSE	FALSE		::::::::::::::
ITNAAQFKYAADEDLRFIGL	9	4.31	0.13	1184	58.3	PR2-DROME	TRUE	FALSE	3	2257.6	0.3	18of 76	2.6877	FALSE	FALSE		::::::::::::::::::
RASVNMAMNRK	11	12.42	0.034	1037	15.36	PR2-DROME	TRUE	FALSE	2	1294.5	-2.3	8of 20	1.0489	FALSE	FALSE		::::::Oxidation_M:::::::
SKIKRLLQAPGTMVKR	8	12.44	0.004	2669	30.83	PR2-DROME	TRUE	FALSE	3	1843.3	-0.5	10of 60	0.9187	FALSE	FALSE		::::::::::::Oxidation_M::::
RPFGISCLIGGFDADGSAHLFQTEPSGIFYEYK	3	4.54	0.471	2035	87.2	PS71-DROME	TRUE	TRUE	3	3682	1.3	35of128	5.8497	FALSE	FALSE		::::::Cys_CAM::::::::::::::::::::::::
RPFGISCLIGGFDADGSAHLFQTEPSGIFYEYK	4	4.54	0.456	2157	87.2	PS71-DROME	TRUE	TRUE	3	3682	1.6	31of128	4.576	FALSE	FALSE		::::::Cys_CAM::::::::::::::::::::::::
IMINRAQVECQSHRLN	9	9.02	0.081	2054	34.43	PS71-DROME	TRUE	FALSE	2	1970.2	-2.5	9of 30	1.1869	FALSE	FALSE		:::::::::Cys_CAM::::::
RPFGLSCLV	5	9.01	0.024	2587	32.9	PS73-DROME	TRUE	FALSE	2	1049.2	-1.4	3of 16	0.5853	FALSE	FALSE		::::::Cys_CAM:::
LFQTDPSGIYYEWSANTTGR	15	4.08	0.039	1200	46.5	PS73-DROVI	TRUE	TRUE	3	2307.5	0.7	18of 76	2.1411	FALSE	FALSE		::::::::::::::::::
IAQTYYLTYKEPIPVSQLVQR	15	9.4	0.41	1289	59.9	PSA2-DROME	TRUE	TRUE	2	2511.9	1.3	17of 40	4.0243	FALSE	FALSE		::::::::::::::::::
IAQTYYLTYKEPIPVSQLVQR	14	9.4	0.283	1206	59.9	PSA2-DROME	TRUE	TRUE	2	2511.9	0.7	17of 40	3.6934	FALSE	FALSE		::::::::::::::::::
YRLLVKQARKIAQTYYLTYKEPIPVSQLVQR	15	10.39	0.18	1289	82.2	PSA2-DROME	TRUE	FALSE	3	3768.5	0.9	18of120	3.0507	FALSE	FALSE		::::::::::::::::::::::::::::
EMIYNHIGMVYSGMGPDYR	1	5.22	0.06	1882	49.09	PSA2-DROME	TRUE	FALSE	2	2250.6	3	4of 36	0.6646	FALSE	FALSE		::::::::::::Oxidation_M:::::::
QSGGVR	4	11.05	0.009	2806	3.8	PSA2-DROME	TRUE	FALSE	1	603.7	-2.4	6of 10	0.8147	FALSE	FALSE		::::::::
TDPAGYFSGFK	6	6.68	0.396	1404	22.8	PSA6-DROME	TRUE	TRUE	1	1190.3	0.7	11of 20	2.0391	FALSE	FALSE		::::::::::::
HITIFSPEGR	9	7.85	0.331	1417	23.5	PSA6-DROME	TRUE	TRUE	2	1157.3	1.4	14of 18	2.7994	FALSE	FALSE		::::::::::::
NIVPETVTHLFR	5	7.85	0.055	1759	34.6	PSA6-DROME	TRUE	TRUE	2	1426.7	1.2	15of 22	2.1471	FALSE	FALSE		::::::::::::
ARYEAANFR	9	9.85	0.015	2395	17.9	PSA6-DROME	TRUE	TRUE	1	1098.2	0.8	7of 16	1.6286	FALSE	FALSE		::::::::::
STASSTTGTSVLGIR	14	11.05	0.387	547	23.1	PSB4-DROME	TRUE	FALSE	2	1438.6	1.9	15of 28	2.6231	FALSE	FALSE		::::::::::::::::
KIRLPVTNGNSSGTASPK	12	11.64	0.06	2187	20.7	PSC-DROME	TRUE	FALSE	3	1828.1	1.5	10of 68	1.1816	FALSE	FALSE		::::::::::::::::::
TLNNRAITPPSP	9	11.05	0.052	664	22.7	PSC-DROME	TRUE	FALSE	2	1281.5	0.9	10of 22	1.521	FALSE	FALSE		::::::::::::
ETKMGPPALPATTPSQGNKNVGK	5	10.32	0.013	2086	25.23	PSC-DROME	TRUE	FALSE	2	2340.7	-1.4	11of 44	1.5702	FALSE	FALSE		::::Oxidation_M:::::::::::::::::
KVEPVSLAEDQKAEASIK	10	4.65	0.004	288	30.3	PSC-DROME	TRUE	FALSE	2	1943.2	-0.5	7of 34	1.373	FALSE	FALSE		::::::::::::::::::
QGKNHKMRIVVFVGSPINHEEGDLVK	3	9.76	0.258	1475	47.83	PSD4-DROME	TRUE	TRUE	3	2933.4	-2.8	22of100	3.6963	FALSE	FALSE		::::::::::::::::::::::::
PCWSSSTPSPRIWACPQR	9	9.2	0.003	615	38.8	PSD7-DROME	TRUE	FALSE	2	2174.4	0.4	4of 34	0.5892	FALSE	FALSE		::Cys_CAM::::::::::Cys_CAM::::
QDQPDAAILAVPNVVMREPCGSR	1	4.31	0.031	150	49.93	PSN-DROME	TRUE	FALSE	2	2524.8	1.6	9of 44	1.3002	FALSE	FALSE		::::::::::::::::::Cys_CAM::::
KIGYCNGPLKSGTTYRVKVR	8	10.54	0.192	1787	31.4	PTP1-DROME	TRUE	FALSE	2	2298.7	1.2	7of 38	1.2971	FALSE	FALSE		:::::Cys_CAM:::::::::::::::
VGRSITPPNALA	5	11.05	0.148	2525	27.5	PU68-DROME	TRUE	FALSE	2	1196.4	-0.2	5of 22	0.8587	FALSE	FALSE		::::::::::::

ASDTSNSGNAGILSPRDSTCAK	13	6.24	0.09	926	22.4	PUM-DROME	TRUE	FALSE	3	2210.3	-1.9	23of 84	2.1172	FALSE	FALSE	:::::::::::::::::Cys_CAM:::
DPDVALLHNKSQR	10	7.82	0.007	2457	20	PUR4-DROME	TRUE	FALSE	3	1493.7	1.3	12of 48	1.3266	FALSE	FALSE	::::::::::::
GPMGNMGPMGGGPMGGPMGGPMGVGPKPMTMGGGK	4	10.6	0.116	2006	48.91	PYGO-DROME	TRUE	FALSE	3	2896.4	-2.6	7of120	0.9503	FALSE	FALSE	:::Oxidation_M:::Oxidation_M:::::::Oxidation_M:::Oxidation_M::::::::::::
MGHPHGPHPHMGGPPPMR	13	11.05	0.105	1792	18.79	PYGO-DROME	TRUE	FALSE	3	1944.3	1.9	10of 68	1.1367	FALSE	FALSE	:::::::::::::::Oxidation_M:::
GPMGNMGPMGGGPMGGPMGGPMGVGPK	5	10.1	0.098	2356	37.95	PYGO-DROME	TRUE	FALSE	2	2104.5	1.2	14of 44	2.2826	FALSE	FALSE	:::Oxidation_M:::::::::Oxidation_M:::::::::
RHYCGKCNLTFVFSKPEEK	6	9.01	0.117	1348	33.8	R27A-DROME	TRUE	FALSE	3	2401.7	-2.1	18of 72	2.8052	FALSE	FALSE	::::Cys_CAM:::Cys_CAM::::::::::
HIQKSTCAQCGYPAAKLR	10	9.69	0.013	1950	26.5	R37A-DROME	TRUE	FALSE	2	2090.3	-2.2	6of 34	0.7844	FALSE	FALSE	::::::Cys_CAM:::Cys_CAM::::::::
QIMSSFFQASTIYGNK	4	9.72	0.125	1882	40.13	RBF-DROME	TRUE	TRUE	2	1839.1	1.7	11of 30	1.3243	FALSE	FALSE	:::Oxidation_M:::::::::::
MDNQCTVYDVNNRDASGVAK	7	4.18	0.044	3312	27.93	RGFFB	TRUE	FALSE	3	2258.4	1.6	243	1.1937	FALSE	FALSE	:::::Cys_CAM:::::::::::::
APAAAAPKKDAKAAAAPAPAKAA	6	10.56	0.149	3049	27.8	RL22-DROME	TRUE	FALSE	3	2030.4	-1.5	10of 88	1.3607	FALSE	FALSE	::::::::::::::::::::::
GHGRIGK	14	11.49	0.003	1540	2	RL2A-DROME	TRUE	FALSE	1	724.8	-1.4	4of 12	0.6703	FALSE	FALSE	::::::::
MIKGVTFGFQYKMR	1	10.71	0.05	136	39.56	RL9-DROME	TRUE	FALSE	2	1707.1	1.4	7of 26	1.2356	FALSE	FALSE	::::::::::::::
FQQGVANLAAVCLSVGYPTIASAPHSIANGFK	14	8.88	0.387	1471	79.3	RLA0-DROME	TRUE	TRUE	2	3290.7	0.5	15of 62	3.2506	FALSE	FALSE	::::::::::Cys_CAM::::::::::::::::::
FQQGVANLAAVCLSVGYPTIASAPHSIANGFK	9	8.88	0.18	2029	79.3	RLA0-DROME	TRUE	TRUE	3	3290.7	1.8	29of124	2.9965	FALSE	FALSE	::::::::::Cys_CAM::::::::::::::::::
RYVAAYLLAVLGGK	4	10.05	0.137	1683	46.2	RLA2-DROME	TRUE	FALSE	2	1494.8	-1.5	12of 26	1.5436	FALSE	FALSE	::::::::::::::
DMLDRRKQIDLPEFYVGSVLAVTSSDPHAAGK	14	5.38	0.042	1464	68.83	RM19-DROME	TRUE	FALSE	3	3534	1.9	25of124	2.9087	FALSE	FALSE	::Oxidation_M::::::::::::::::::::::::::::
NVIDHQGMEVVYELYDPTI	11	3.59	0.018	602	54.73	RM19-DROME	TRUE	FALSE	3	2252.5	1.4	18of 72	1.9783	FALSE	FALSE	:::::::Oxidation_M:::::::::::
LPSDEDMQRVAIAFDNME	15	3.43	0.052	1912	47.06	RNZ-DROME	TRUE	FALSE	2	2114.3	-0.8	10of 34	1.6274	FALSE	FALSE	::::::Oxidation_M::::::::Oxidation_M::
SYQNYVDKLCRVEQDLAMGTDAEG	4	3.85	0.011	2752	46.83	ROP-DROME	TRUE	FALSE	2	2780	0.5	7of 46	0.9621	FALSE	FALSE	:::::::::Cys_CAM:::::::Oxidation_M:::::::
SRGHFRLPNC	1	10.9	0	219	16.5	ROR2-DROME	TRUE	FALSE	1	1244.4	-2.8	1of 18	0.0271	FALSE	FALSE	:::::::::Cys_CAM:
THVEMLKERDYNNYS	7	5.35	0.133	1696	24.43	RPB2-DROME	TRUE	FALSE	2	1900.1	-1.9	65	1.1296	FALSE	FALSE	::::::::::::::
EPTPAPDEVTSSPPKGRAKAEKPTNAQ	6	7.16	0.141	2935	22.2	RRP1-DROME	TRUE	FALSE	3	2805.1	2.3	9of104	1.1412	FALSE	FALSE	::::::::::::::::::::::::::
VYVPNSGRKLVNLEPRMRWEK	5	10.69	0.06	1826	48.63	RRP1-DROME	TRUE	FALSE	3	2573	0.5	9of 80	1.1505	FALSE	FALSE	::::::::::::::::::
VAIYEYLFK	8	6.81	0.177	2163	38.6	RS10-DROME	TRUE	TRUE	2	1146.4	1.2	13of 16	2.7021	FALSE	FALSE	::::::::::
SSMKIGRIED	14	7.02	0.063	738	18.33	RS14-DROME	TRUE	FALSE	2	1136.3	-1.7	9of 18	1.1607	FALSE	FALSE	::::::::::
AFVAIGDNNGHIGLGVK	5	7.82	0.128	1535	39	RS2-DROME	TRUE	TRUE	1	1682.9	0	11of 32	1.6078	FALSE	FALSE	::::::::::::::
PNSANRKCVLVRLSTGKEMVAYIP	10	10.18	0.041	1814	53.73	RT12-DROME	TRUE	FALSE	2	2721.2	1.3	10of 46	1.5511	FALSE	FALSE	::::::Cys_CAM::::::::::Oxidation_M::::::
MLEIDGSYLEGGGQALRNALSLSCILGK	1	4.45	0.072	1701	77.53	RTC1-DROME	TRUE	TRUE	3	2967.4	-1.7	12of108	1.2805	FALSE	FALSE	:::::::::::::::::::::Cys_CAM:::::
QQNVESSRQLQLPPIVASLIRLKRK	15	12.14	0.096	1444	57.1	RTJK-DROFU	TRUE	FALSE	3	2903.4	2.7	24of 96	1.9296	FALSE	FALSE	::::::::::::::::::::::
LFYGLQVYGIAAK	7	9.53	0.011	3439	47.2	RTJK-DROME	TRUE	FALSE	2	1443.7	2.3	221	0.8932	FALSE	FALSE	::::::::::::::
EVRLVPNRHDIAFVEFTT	11	5.35	0.048	480	50.4	RU1A-DROME	TRUE	FALSE	3	2144.4	-2.5	18of 68	1.9313	FALSE	FALSE	::::::::::::::::::
NYREYMAYKFPQLRLLDFR	11	9.84	0.035	1417	60.33	RU2A-DROME	TRUE	FALSE	3	2524.9	1.8	16of 72	1.854	FALSE	FALSE	::::::::::::::::::
GSTRRQSKPQINEFQNEGSPFNYNPH	6	9.72	0.259	2090	28.1	RY44-DROME	TRUE	FALSE	3	3034.2	2.2	8of100	1.3007	FALSE	FALSE	::::::::::::::::::::::
IAFSHDFVGDLQTDQLRRYIEIK	2	5.33	0.238	2230	62.6	RY44-DROME	TRUE	FALSE	3	2766.1	2.9	12of 88	1.1748	FALSE	FALSE	::::::::::::::::::::
GDVIGVAIDLSVPIIT	8	2.93	0.173	1899	57.1	RY44-DROME	TRUE	FALSE	2	1582.9	0	11of 30	2.0439	FALSE	FALSE	::::::::::::::
ILAALYHLGTDGTLTHD	7	4.94	0.088	1927	45.9	RY44-DROME	TRUE	FALSE	2	1812	-2.6	58	0.9069	FALSE	FALSE	::::::::::::::::
FLFGGDHGR	6	7.85	0.067	2928	21.2	RY44-DROME	TRUE	TRUE	2	1006.1	2.2	13of 16	1.8895	FALSE	FALSE	::::::::
GGDHGR	14	7.85	0.058	2588	-3.1	RY44-DROME	TRUE	FALSE	1	598.6	1.4	8of 10	1.2513	FALSE	FALSE	::::::
FLFGGDHGR	4	7.85	0.038	2952	21.2	RY44-DROME	TRUE	TRUE	2	1006.1	2.1	13of 16	1.7435	FALSE	FALSE	::::::::
RLTMLLFSNIFDSLSN	7	6.79	0.007	3652	59.93	RY44-DROME	TRUE	FALSE	3	1888.2	2.4	330	1.7817	FALSE	FALSE	::::Oxidation_M:::::::::::
WPSLAAAGVAGDLFIQLMAA	11	3.1	0.074	1048	72.73	S00670	TRUE	FALSE	3	2003.4	-1	21of 76	2.3369	FALSE	FALSE	::::::::::::::::::
KQYNVLGVLMASDVEIP	11	4.08	0.015	2767	50.83	S00954	TRUE	FALSE	2	1893.2	2.4	7of 32	1.1695	FALSE	FALSE	:::::::::Oxidation_M:::::::
GSKLITALSNCMEGTAS	15	6.29	0.004	2669	34.33	S02021	TRUE	FALSE	2	1740.9	2	7of 32	1.2282	FALSE	FALSE	:::::::::Cys_CAM::::::
TELNPKNLKATVK	6	10.32	0.003	1139	20	S09506	TRUE	FALSE	2	1456.7	1.7	10of 24	1.5909	FALSE	FALSE	::::::::::::::
PRTVKELRSFLGTAGWYRR	11	11.96	0.037	1808	43.8	S18211	TRUE	FALSE	2	2294.7	-2.9	15of 36	1.7126	FALSE	FALSE	::::::::::::::::::
RIFGERQLEGMTLATRRMVK	2	11.95	0.029	822	48.26	S18211	TRUE	FALSE	2	2409.9	-1.3	6of 38	0.8477	FALSE	FALSE	:::::::::Oxidation_M:::::::::
DLVHDAPSGDLDMALGGGGYHTSS	11	3.87	0.075	241	40.93	S19095	TRUE	FALSE	2	2373.5	0.3	7of 46	1.211	FALSE	FALSE	::::::::::::::::::::::
LCVLAFDEMKVAAAFEYDSSAD	8	3.43	0.038	2507	65.33	S22802	TRUE	FALSE	2	2453.7	2.7	6of 42	0.8453	FALSE	FALSE	::Cys_CAM:::::::::::::::::
NFRSYMKAVSAAFIEIRTTK	5	10.7	0.04	1899	47.93	S24577	TRUE	FALSE	2	2334.7	-0.5	5of 38	0.87	FALSE	FALSE	::::::::::::::::::
SQPHSLNVMGNSGAANAAATSMVTLQQR	6	11.05	0.032	1902	44.76	S24577	TRUE	FALSE	2	2859.2	2.5	13of 54	1.5811	FALSE	FALSE	:::::::Oxidation_M:::::::::::::::::
HRMLNYSPK	10	10.4	0.002	1081	14.53	S24577	TRUE	FALSE	1	1162.4	0.3	10of 16	1.3831	FALSE	FALSE	:::Oxidation_M:::::::
QSFTFDCKVSGEPAPQTKWLLK	2	8.9	0.058	2154	50.4	S24600	TRUE	FALSE	2	2568.9	2.1	7of 42	1.0986	FALSE	FALSE	::::::Cys_CAM:::::::::::::::
PTQRSDS	3	6.79	0.025	2879	1.8	S24600	TRUE	FALSE	1	790.8	0.3	5of 12	1.0179	FALSE	FALSE	::::::::
TVDNEPVYSRYPSLMGDSD	6	3.51	0.066	1120	36.93	S26840	TRUE	FALSE	2	2162.3	0	11of 36	1.468	FALSE	FALSE	:::::::::::::Oxidation_M:::::
KKGTDSYGNPKKRLVIDFR	4	10.62	0.043	2213	25.3	S26840	TRUE	FALSE	2	2223.6	3	10of 36	2.1659	FALSE	FALSE	::::::::::::::::::
RQARRHAGVLSQFVE	11	12.11	0.099	1849	27	S29964	TRUE	FALSE	2	1755	2	6of 28	0.97	FALSE	FALSE	::::::::::::::::
PARSGFRGGFGSRPPRGGR	6	13.01	0.042	1496	19.6	S30395	TRUE	FALSE	3	1973.2	3	16of 72	1.4154	FALSE	FALSE	::::::::::::::::
RSMILDTQHPDALEKIQKLE	12	5.39	0.059	1192	44.73	S35341	TRUE	FALSE	3	2382.7	-2.3	18of 76	1.7876	FALSE	FALSE	:::Oxidation_M:::::::::::::::::
LSAIYGGTYMLDKPIDEIVLGEGGK	2	4.07	0.374	1324	67.83	S36746	TRUE	TRUE	2	2641.1	-0.1	23of 48	5.0344	FALSE	FALSE	::::::::::::::::::::::::
PDCQSLITTSAGVVATRRR	2	10.81	0.004	2102	33.7	S37766	TRUE	FALSE	2	2089.3	2.3	11of 36	1.3114	FALSE	FALSE	:::Cys_CAM:::::::::::::::
DPHTMKSKGYAF	6	9.63	0.05	1316	16.23	S41644	TRUE	FALSE	2	1382.6	-2.2	10of 22	1.8317	FALSE	FALSE	::::::::::::
SISPHKRNTSLRHSAQRDLNSKPNSSAMPTVGNL	2	12.14	0.071	1910	39.43	S42805	TRUE	FALSE	3	3703.1	-2.8	9of132	1.0363	FALSE	FALSE	::::::::::::::::::::::::::
GLLGGFLVCLSLLAVAVMLVKR	4	10.11	0.039	2390	93.43	S42989	TRUE	FALSE	2	2346.9	-0.5	10of 42	1.3499	FALSE	FALSE	::::::::Cys_CAM::::::::Oxidation_M:::::
GNLANVYRYFPTQALNFAFKDKYKQVFLGG	1	10.03	0.108	1472	79.7	S43651	TRUE	FALSE	3	3472	-1.7	23of116	2.3078	FALSE	FALSE	::::::::::::::::::::::::::
CIDVVRSSAICGSGMTS	10	5.95	0.109	1186	36.53	S46224	TRUE	FALSE	2	1801	1.6	8of 32	1.2786	FALSE	FALSE	:Cys_CAM::::::::Cys_CAM::::::
LYLKALCDTALEKVEEMGHSVEKSIVVSHLKR	2	7.32	0.039	1800	75.73	S52154	TRUE	FALSE	3	3685.3	2.9	20of124	2.5241	FALSE	FALSE	::::::Cys_CAM::::::::::::::::::::
PPKCKPMKSCAKPRRKAACAK	7	10.82	0.069	1957	15.33	S52158	TRUE	FALSE	3	2471.9	-2.6	5	1.7859	FALSE	FALSE	::::Cys_CAM::::::Cys_CAM::::::::Cys_CAM:::
CWDEALPELTLAVNSSVSA	5	2.95	0.067	2758	55.5	S52564	TRUE	FALSE	2	2063.2	1.9	16of 36	2.0911	FALSE	FALSE	:Cys_CAM:::::::::::::::
ERTQRLVVFAELVFHRRRC	12	11.81	0.034	1451	49.7	S54987	TRUE	FALSE	3	2473.9	-0.6	6of 72	0.9324	FALSE	FALSE	:::::::::::::::::Cys_CAM:
GGGVGGGGGGGARLGR	8	12.41	0.071	1951	11.7	S55051	TRUE	FALSE	1	1242.3	-2.9	12of 30	1.2584	FALSE	FALSE	::::::::::::::::
APRPLAAGAHAAAAAHAQ	13	11.05	0	1657	27.1	S55392	TRUE	FALSE	2	1652.9	-2.4	7of 34	1.0509	FALSE	FALSE	::::::::::::::::
PTWPANLLQAIGRYCFQTGNGLCFGDNIPWR	6	8.29	0.09	1426	90.2	S55695	TRUE	FALSE	3	3625	0.8	25of120	2.8561	FALSE	FALSE	::::::::::::Cys_CAM::::::::Cys_CAM::::::::
LGMGMGMGMGMSMGLGISRKNSDALYSQQSR	3	10.39	0.02	2166	65.28	S57238	TRUE	FALSE	3	3285.8	1.3	24of120	1.7457	FALSE	FALSE	:::Oxidation_M::Oxidation_M:::::::::::::::::::::::
AIPDWKRQMMAKKAAERAKKDFEERMAQEAESRR	5	10.37	0.013	2359	49.09	S57238	TRUE	FALSE	3	4126.7	1.2	9of132	0.9542	FALSE	FALSE	:::::::::Oxidation_M::::::::::::::Oxidation_M:::::::::
EEPEKSAAPPADSAAAPAAAPAVEK	14	4.01	0.009	835	35	S58776	TRUE	FALSE	3	2376.6	2.2	25of 96	2.9891	FALSE	FALSE	::::::::::::::::::::::::
VDVVFNHMAAGGGTYGTGGSTASPSSK	1	7.74	0.087	717	36.33	S58958	TRUE	FALSE	2	2572.8	-1.9	10of 52	1.1488	FALSE	FALSE	::::::Oxidation_M:::::::::::::::::
MLLTYVNTHRIEGFRGFKAEFDVVC	2	7.16	0.023	901	74.73	S58984	TRUE	FALSE	3	3020.4	1.3	7of 96	0.8577	FALSE	FALSE	:Oxidation_M::::::::::::::::::::::Cys_CAM:
HQHLEHRQ	9	8.09	0.011	2527	2.3	S58984	TRUE	FALSE	2	1085.2	-2.3	7of 14	1.1694	FALSE	FALSE	::::::::
SELLDNLLRGYDNSIR	4	4.31	0.025	2393	42.8	S60749	TRUE	FALSE	2	1879.1	1.5	7of 30	0.9243	FALSE	FALSE	::::::::::::::::
MNCVVIADVAKMRRVTPR	4	11.23	0.088	2079	43.36	S62337	TRUE	FALSE	2	2133.5	-1.4	5of 34	0.9288	FALSE	FALSE	:Oxidation_M::Cys_CAM:::::::::::::::
QRFKEKSSGSLKPDR	4	10.82	0.115	1482	11.2	S64682	TRUE	FALSE	2	1764	-2.4	6of 28	0.9361	FALSE	FALSE	::::::::::::::::
DDFQHELNEYGYDFVGDKPVVLAR	2	4	0.505	1208	57.6	S68280	TRUE	TRUE	3	2828.1	1.3	39of 92	6.6069	FALSE	FALSE	::::::::::::::::::::::
ARNQTATPTQGGSPGHVAVQPSAT	10	11.05	0.059	1414	22.1	S69205	TRUE	FALSE	3	2334.5	0.8	24of 92	2.3446	FALSE	FALSE	::::::::::::::::::::::

AFPPSRK	14	11.49	0.004	135	11.2	S70554	TRUE	FALSE	1	803	-0.4	4of 12	0.6856	FALSE	FALSE	::::::::
AQAGKELGQKISESEFVSDDFQASSE	4	3.82	0.104	2786	41.9	SA47-DROME	TRUE	FALSE	3	2788.9	-2.6	10of100	1.2645	FALSE	FALSE	::::::::::::::::::::::::
HQGHLAVPSGSGGGSLSGSGR	2	11.05	0.062	158	18	SAV-DROME	TRUE	FALSE	2	1906	0	7of 40	1.1811	FALSE	FALSE	::::::::::::::::::
KDGSSASVEEESGSQEANQ	3	3.59	0.156	1440	9.5	SCA-DROME	TRUE	FALSE	2	1939.9	0.1	13of 36	1.8455	FALSE	FALSE	::::::::::::::::::
LRRQVNGLRFHHIDERVR	6	12.23	0.017	1726	35	SCA-DROME	TRUE	FALSE	3	2302.7	-1.7	18of 68	1.6167	FALSE	FALSE	::::::::::::::::::
PNLYPNTPQPTTPIRRLADR	9	11.05	0.086	1830	39.1	SCR-DROME	TRUE	FALSE	3	2321.6	-2.2	21of 76	2.4501	FALSE	FALSE	::::::::::::::::::
HLATSFEDLKAGLSYLKRKVESQK	2	9.96	0.032	989	45.1	SEC5-DROME	TRUE	FALSE	3	2750.2	1.6	14of 92	1.3053	FALSE	FALSE	::::::::::::::::::
TGLGKSTLMDTLFNTSFESTPSPHTLPSVKLK	11	9.76	0.098	1132	67.73	SEP2-DROME	TRUE	FALSE	3	3452.9	-1	20of124	3.1518	FALSE	FALSE	::::::::Oxidation_M::::::::::::::::::::::
KAHTYELQESNVRLK	11	9.63	0.047	1477	22.8	SEP2-DROME	TRUE	FALSE	2	1817.1	-2.5	9of 28	1.3287	FALSE	FALSE	::::::::::::::::
HCDFVKLREMLIRTNMEDMR	2	7.17	0.001	1688	52.49	SEP2-DROME	TRUE	FALSE	3	2612	1	9of 76	1.1108	FALSE	FALSE	::Cys_CAM::::::::::::::Oxidation_M::
EGDKLIGITSFVSAYGCQ	5	4.08	0.142	2940	43.9	SER3-DROME	TRUE	FALSE	2	1946.1	1.1	9of 34	1.2425	FALSE	FALSE	::::::::::::::::Cys_CAM::
VGGIRASLYNAVTLAETQQLANLMLAFYK	6	9.53	0.024	2526	88.33	SERC-DROME	TRUE	FALSE	3	3157.7	-0.9	17of112	1.3833	FALSE	FALSE	::::::::::::::::::::::::::::
SLDHLRPEGQALNGSSSSGLVSLGSLQLQQQLAP	9	5.22	0.019	2004	73.6	SERR-DROME	TRUE	FALSE	3	3489.9	2	25of132	2.6543	FALSE	FALSE	::::::::::::::::::::::::::::
RQRPAKEAASSSSGGASSGS	2	11.33	0.089	536	5.8	SET8-DROME	TRUE	FALSE	3	1879	2.2	15of 76	1.7964	FALSE	FALSE	::::::::::::::::::
VVAEFPIPAPCGCNRK	15	8.3	0.039	603	38.3	SGS5-DROME	TRUE	FALSE	3	1816	-1.2	20of 60	2.0136	FALSE	FALSE	::::::::::Cys_CAM::Cys_CAM::::
KLLVVAVIACIMLIGFADPASGCK	10	8.29	0.018	1320	85.73	SGS8-DROME	TRUE	FALSE	3	2564.1	-2.7	9of 92	1.1132	FALSE	FALSE	::::::::::Cys_CAM::Oxidation_M::::::::::Cys_CAM::
FSGSRSSHEI	15	7.85	0.051	160	12.9	SIF1-DROME	TRUE	FALSE	2	1107.2	1.1	10of 18	1.4608	FALSE	FALSE	::::::::::
FKFSRKASSSYSLKLDPPGKGKVK	1	10.86	0.043	59	33.5	SIF1-DROME	TRUE	FALSE	3	2657.1	-0.3	16of 92	1.5764	FALSE	FALSE	::::::::::::::::::::::::
QNFITELPPKSFSSFR	7	10.09	0.128	2243	41.6	SLIT-DROME	TRUE	FALSE	3	1899.2	-0.2	13	1.6774	FALSE	FALSE	::::::::::::::::
IMNRSPSISQATQYEGGGTR	12	9.85	0.047	1929	28.13	SLY1-DROVI	TRUE	FALSE	3	2154.4	1.7	15of 76	1.6357	FALSE	FALSE	::::::::::::::::::
RIIYGGSTLTNARQ	9	11.14	0.016	425	28.2	SLY1-DROVI	TRUE	FALSE	2	1550.8	1.5	15of 26	2.0481	FALSE	FALSE	::::::::::::::
KCRSHGAPR	5	11.33	0.057	2620	0.8	SM1A-DROME	TRUE	FALSE	2	1069.2	-1.9	5of 16	0.8578	FALSE	FALSE	::Cys_CAM:::::::
YFILPDSLPLETLLIDDTPK	1	3.51	0.117	1930	74.5	SMD1-DROME	TRUE	TRUE	2	2304.7	0.8	15of 38	2.2906	FALSE	FALSE	::::::::::::::::::
GRGTGGPPGAPGGSGGGR	3	12.41	0.103	1093	5.4	SMD3-DROME	TRUE	FALSE	2	1395.5	0.7	11of 32	1.3198	FALSE	FALSE	::::::::::::::::
KQIDREKTCPMLLR	2	9.9	0.025	1098	30.23	SP18-DROME	TRUE	FALSE	2	1805.1	-1.9	10of 26	1.5686	FALSE	FALSE	::::::::Cys_CAM::Oxidation_M::::
QWNTLKEKSSQR	8	10.59	0.082	1788	12.8	SPCA-DROME	TRUE	FALSE	2	1505.7	0.9	10of 22	1.3433	FALSE	FALSE	::::::::::::
RQEENDKLRK	4	9.88	0.002	2801	4.5	SPCA-DROME	TRUE	TRUE	2	1316.5	0.7	6of 18	0.6903	FALSE	FALSE	::::::::::
TPTIANSSTLSTQSAETPVSSGTVISSSALATTP	3	3.3	0.103	2195	58.3	SPEN-DROME	TRUE	FALSE	3	3266.5	1.3	21of132	1.823	FALSE	FALSE	::::::::::::::::::::::::::::::
NGSASVQGGGINSSNTTT	11	6.02	0.009	633	12.8	SPEN-DROME	TRUE	FALSE	3	1652.7	-2.6	16of 68	1.4253	FALSE	FALSE	::::::::::::::::::
REERELR	9	7.21	0.003	896	9.6	SPEN-DROME	TRUE	FALSE	2	988.1	1	11of 12	1.7715	FALSE	FALSE	::::::::
LPDLNLPELVRCSTPPQTA	12	4.08	0.092	689	51.1	SPRI-DROME	TRUE	FALSE	2	2122.4	1	9of 36	1.3184	FALSE	FALSE	::::::::::Cys_CAM:::::::
VQLMLPR	11	11.05	0.018	1456	28.13	SPRI-DROME	TRUE	FALSE	1	873.1	0.9	6of 12	0.8831	FALSE	FALSE	:::Oxidation_M::::
STHSRSKSRSRS	11	12.71	0.143	1717	-6.6	SR55-DROME	TRUE	FALSE	2	1376.5	1.6	8of 22	1.2747	FALSE	FALSE	::::::::::::
TTPDATGEADAANAATPTTPRGNHNNNNSANGR	6	5.28	0.026	2630	16.8	SRA-DROME	TRUE	FALSE	3	3280.3	0.8	14of128	1.2688	FALSE	FALSE	::::::::::::::::::::::::::::
SSHSGGGGGGTLPA	5	7.85	0.17	2921	8.8	SRP-DROME	TRUE	FALSE	2	1142.2	-0.8	9of 26	1.0012	FALSE	FALSE	::::::::::::
EFVDEEEEEDDDDDD	14	2.51	0.054	1515	21.1	SRYD-DROME	TRUE	FALSE	2	1845.6	-2	8of 28	1.0873	FALSE	FALSE	::::::::::::::
PKRATTAFMLWLNDTR	12	11.33	0.135	2052	42.73	SSRP-DROME	TRUE	TRUE	3	1922.3	-2.8	21of 60	2.4031	FALSE	FALSE	::::::::::::::
RATTAFMLWLND	9	6.79	0.033	2532	42.83	SSRP-DROME	TRUE	FALSE	3	1455.7	0.4	16of 44	1.816	FALSE	FALSE	::::::Oxidation_M::::::
NSSHNVNAAARPSNFLASGYDTTTRR	13	11.05	0.087	1550	30.4	STAN-DROME	TRUE	FALSE	3	2809	-0.7	19of100	1.6839	FALSE	FALSE	::::::::::::::::::::::
MAAYYE	10	3.3	0.018	1160	19.63	STAT-DROME	TRUE	FALSE	1	763.8	-0.1	7of 10	1.3647	FALSE	FALSE	:Oxidation_M::::::
LLERNRRLAAALSSGNSDTKQKCLTK	8	10.81	0.064	1795	41.5	STC-DROME	TRUE	TRUE	3	2932.3	0.8	20of100	2.3708	FALSE	FALSE	::::::::::::::::::::::::Cys_CAM::::
PAHPHQCGSKCHLGQCPPCPKQTGVKC	8	8.48	0.04	2630	25.3	STC-DROME	TRUE	FALSE	3	3128.3	-2.4	21of104	1.935	FALSE	FALSE	::::::Cys_CAM::::Cys_CAM::::::Cys_CAM::::Cys_CAM::::::::Cys_CAM:
RTRTIKFQPPDANYIELLRFR	15	11.22	0.105	1976	55.1	STNB-DROME	TRUE	FALSE	3	2636.1	-1.1	13of 80	1.2094	FALSE	FALSE	::::::::::::::::::::
EISDSSIPDAGALGR	15	3.71	0.068	519	28.8	STUB-DROME	TRUE	FALSE	3	1488.6	0.6	13of 56	1.3679	FALSE	FALSE	::::::::::::::::
HVGMCVDSFMFGSCCTHNYTD	11	4.94	0.051	262	45.56	STUB-DROME	TRUE	FALSE	2	2542.7	-1.6	7of 40	1.0482	FALSE	FALSE	::::Oxidation_M:Cys_CAM::::::::Cys_CAM:Cys_CAM::::::
VKTISAARSECGVPTLARPETRIVGGKSAA	9	10.57	0.009	2000	51.3	STUB-DROME	TRUE	FALSE	3	3084.5	-0.1	23of116	1.7464	FALSE	FALSE	::::::::::Cys_CAM::::::::::::::::::
PYIERGVAKK	15	10.18	0.007	1464	17	STUB-DROME	TRUE	FALSE	1	1161.4	1.3	12of 18	1.8255	FALSE	FALSE	::::::::::
GDQRENICQWLTKVGLAKPDQLK	5	8.9	0.011	2271	46.3	SUI1-DROME	TRUE	FALSE	3	2699	1.3	19of 88	2.1434	FALSE	FALSE	::::::::Cys_CAM::::::::::::::
RNDQSVLDSGAGPEFNMSYFTEIS	11	3.59	0.023	1900	50.93	SUL1-DROME	TRUE	FALSE	3	2665.8	-1.5	15of 92	1.8024	FALSE	FALSE	::::::::::::::::::::::
GVNNRKRRDRDRLEGG	6	11.83	0.119	39	7.7	SUS-DROME	TRUE	FALSE	2	1899.1	2	4of 30	0.7503	FALSE	FALSE	::::::::::::::::
PRMRSSNQDTSDQSLEGSGEGLATANPLLQSTR	10	4.56	0.094	2571	45.53	SUS-DROME	TRUE	FALSE	3	3521.8	-1.5	9of128	1.0935	FALSE	FALSE	:::Oxidation_M:::::::::::::::::::::::::::
LLRVSLDALSTPTPSGATTAIITPKTE	11	7.02	0.014	1458	65.6	SUUR-DROER	TRUE	FALSE	3	2755.2	-1.4	24of104	1.9159	FALSE	FALSE	::::::::::::::::::::::::::
TARADNKLFVKPIP	7	10.59	0.028	1597	32	SUV3-DROME	TRUE	FALSE	2	1570.9	-0.9	80	1.4107	FALSE	FALSE	::::::::::::::
AEQRRQQDRRRTPTKKSHKRHKRRR	11	12.71	0.088	230	-11.7	SUWA-DROME	TRUE	FALSE	3	3297.8	1.4	11of 96	1.222	FALSE	FALSE	::::::::::::::::::::::::
QLIPWMGD	14	3.1	0.013	922	31.83	SUWA-DROME	TRUE	FALSE	1	976.1	3	7of 14	1.3101	FALSE	FALSE	:::::Oxidation_M:::
SSNPPR	14	11.05	0.01	2723	2.4	SUWA-DROME	TRUE	FALSE	1	657.7	0.1	2of 10	0.2418	FALSE	FALSE	::::::
ALRNYLGLNAELVQNHMR	4	9.85	0.103	2121	47.23	SWS-DROME	TRUE	FALSE	2	2129.4	-2.6	6of 34	0.9686	FALSE	FALSE	::::::::::::::Oxidation_M::
FCVYFDNIISKAVLGKDEDFK	11	4.46	0.081	1758	60.7	SYEP-DROME	TRUE	FALSE	3	2509.8	2.5	12of 80	1.3854	FALSE	FALSE	::Cys_CAM:::::::::::::::::
DLPIRLNQWNNVV	2	6.79	0.08	630	42.2	SYEP-DROME	TRUE	FALSE	3	1581.8	-2.6	15of 48	2.1071	FALSE	FALSE	::::::::::::::
LGKGDQLPAKEVADFK	10	7.02	0.142	2508	30.1	SYFA-DROME	TRUE	FALSE	2	1717	-1.8	7of 30	1.2567	FALSE	FALSE	::::::::::::::
TDRFGASKSMSMTSGGVGSGNGSG	2	10.09	0.141	1484	21.66	SYN-DROME	TRUE	FALSE	3	2252.4	-2.2	24of 92	2.1018	FALSE	FALSE	::::::::::Oxidation_M::::::::::::
AESPTDEGVAPTPPLPAGPRPAP	6	3.83	0.101	2236	39.5	SYN-DROME	TRUE	FALSE	2	2225.5	0	12of 44	1.9742	FALSE	FALSE	::::::::::::::::::::::
TMPYRQKFPRLESK	8	10.7	0.003	1808	26.33	T00117	TRUE	FALSE	2	1798.1	-2.9	5of 26	1.1292	FALSE	FALSE	::Oxidation_M::::::::::::
KSKRSKTNEQNINMKKSFSKFDDLQK	14	10.65	0.003	1777	21.43	T03217	TRUE	FALSE	3	3147.6	0.3	10of100	1.1737	FALSE	FALSE	::::::::::::Oxidation_M::::::::::::
QPSSAAATPPPTGMGFASST	5	6.02	0.178	2260	30.23	T03743	TRUE	FALSE	2	1864	-0.8	11of 38	1.5189	FALSE	FALSE	::::::::::::::::::
PNTPPVSPPERQGSSPDSMQKHIR	4	10.09	0.086	1413	24.83	T08431	TRUE	FALSE	3	2659.9	2	15of 92	1.5037	FALSE	FALSE	::::::::::::::::::Oxidation_M::::::
KTATYALPLIQKILNSK	11	10.45	0.01	1939	43.7	T08433	TRUE	FALSE	2	1903.3	1.5	9of 32	1.109	FALSE	FALSE	::::::::::::::::
NGNATRSHGSGYMGREK	1	10.39	0.153	689	5.93	T08619	TRUE	FALSE	2	1823	-1	5of 32	0.7687	FALSE	FALSE	::::::::::::::::
QLANKSKIPRSPSLASS	14	11.64	0.074	2813	25.2	T09144	TRUE	FALSE	2	1785.1	0.3	5of 32	0.9801	FALSE	FALSE	::::::::::::::::
STDNSPSNAKSKRSKIKTKA	13	11.1	0.019	1030	1.5	T09144	TRUE	FALSE	3	2149.4	2.6	25of 76	2.6149	FALSE	FALSE	::::::::::::::::::
KLNQRSSVVELSVKVLT	6	10.59	0.09	2912	40	T12678	TRUE	FALSE	2	1901.3	-1.2	8of 32	0.9836	FALSE	FALSE	::::::::::::::
LIVCAGHHYRSK	10	9.75	0.024	637	22.3	T12681	TRUE	FALSE	3	1441.6	2.3	14of 44	1.744	FALSE	FALSE	::::Cys_CAM:::::::::
SISTKQAAPKELQMKPK	7	10.56	0.041	1295	21.93	T12687	TRUE	FALSE	2	1902.3	-1.6	46	1.4057	FALSE	FALSE	::::::::::::Oxidation_M::::
ASGAALGGENAQQEQL	15	3.13	0.01	1241	25	T13055	TRUE	FALSE	2	1544.6	2.4	12of 30	1.7011	FALSE	FALSE	::::::::::::::::
IVQKNTDRIGSSMDFRNLCQRIDVDGLKAK	11	9.78	0.015	1764	57.93	T13065	TRUE	TRUE	3	3495.9	0.7	21of116	2.6889	FALSE	FALSE	::::::::::::Oxidation_M::::::Cys_CAM::::::::::::
EDSSGDGETKDGTEAKEGTGTGTGPLAVPK	14	3.96	0.054	2616	21	T13153	TRUE	FALSE	2	2893	-2.3	6of 58	1.0221	FALSE	FALSE	::::::::::::::::::::::::::::
DTEKPVAATESGR	15	4.45	0.007	1480	11.5	T13154	TRUE	FALSE	2	1361.5	1.8	8of 24	1.0864	FALSE	FALSE	::::::::::::
NLQDSFMCDLSFVPETQPEAVAKSGAIQK	2	4.07	0.101	179	65.53	T13157	TRUE	FALSE	2	3212.6	1	7of 56	0.9176	FALSE	FALSE	::::::::Cys_CAM:::::::::::::::::::
EPVAWNKANAKRHKHGK	7	10.99	0.013	2001	8.3	T13157	TRUE	TRUE	2	1972.3	1	36	0.8745	FALSE	FALSE	::::::::::::::::
LLVTILVLHTLDRQGEYVARTDFLWK	13	7.75	0.065	2264	92.1	T13158	TRUE	FALSE	3	3101.7	2.2	16of100	1.6861	FALSE	FALSE	::::::::::::::::::::::::
KMTKYVECWGADR	8	8.85	0.005	2284	25.33	T13158	TRUE	FALSE	2	1660.9	2.7	10of 24	1.3881	FALSE	FALSE	::Oxidation_M:::::Cys_CAM::::::
TKGQDLPLAEAINMPLLQQGRRGR	12	11.23	0.002	2872	50.13	T13160	TRUE	FALSE	3	2664.1	1.9	11of 92	1.0714	FALSE	FALSE	::::::::::::::::::::::
SSETNKDFVS	10	4.08	0.015	2398	11.7	T13164	TRUE	FALSE	2	1114.2	-0.1	7of 18	1.0683	FALSE	FALSE	::::::::::

HGRGGH	4	11.05	0.008	2609	-5.4	T13164	TRUE	FALSE	1	620.6	-1.9	7of 10	1.2082	FALSE	FALSE	::::::
TQDMLADLPPEPPVFK	5	3.71	0.009	2836	44.83	T13165	TRUE	FALSE	3	1815.1	2.4	18of 60	1.5211	FALSE	FALSE	::::Oxidation_M::::::::::::
FGILLSCSSELIPLHRRHCLLDEAIER	2	6.04	0.056	94	84.8	T13166	TRUE	TRUE	3	3236.7	-1.8	18of104	1.6464	FALSE	FALSE	::::::Cys_CAM::::::::::Cys_CAM::::::::
SRLILPHYGVFKGIWDW	5	9.72	0.021	2154	63	T13168	TRUE	FALSE	3	2088.5	0.6	18of 64	2.3326	FALSE	FALSE	::::::::::::::::
YQALLGQYQSRVQ	4	9.59	0.088	2914	31.2	T13169	TRUE	FALSE	2	1554.7	-2.8	5of 24	0.7487	FALSE	FALSE	::::::::::::::
IGNLAREQLLEQRR	10	10.8	0.049	1536	33.3	T13169	TRUE	FALSE	3	1697	2.4	24of 52	2.4406	FALSE	FALSE	::::::::::::::
NLTDVGLAIINPDTFVGNK	7	3.89	0.245	3441	50.4	T13174	TRUE	FALSE	3	2002.3	-2	107	1.3251	FALSE	FALSE	::::::::::::::::::
SSSIEELDFSRNNLMELNPK	6	4.17	0.183	2038	45.53	T13174	TRUE	TRUE	3	2324.6	1.4	23of 76	2.4432	FALSE	FALSE	::::::::::::::::::::
SFNSIVQVHHSMFDK	13	7.97	0.003	1223	31.83	T13174	TRUE	FALSE	2	1777	-0.4	7of 28	0.9571	FALSE	FALSE	::::::::::::::
MDALARSGIWENCRAAYEDIVK	1	4.56	0.14	298	55.63	T13230	TRUE	FALSE	3	2585.9	0	13of 84	1.4483	FALSE	FALSE	:Oxidation_M::::::::::Cys_CAM::::::::
HLVGGLHTVYTKLKRLDIV	4	10.18	0.077	2972	51.3	T13230	TRUE	FALSE	2	2163.6	1.7	9of 36	1.064	FALSE	FALSE	::::::::::::::::::
LDSDTRQAWAQCA	12	3.89	0.038	1749	25.7	T13250	TRUE	FALSE	1	1522.6	-2	4of 24	0.6858	FALSE	FALSE	::::::::::Cys_CAM::
IGQLVSAMRVR	8	12.41	0.088	2552	31.43	T13288	TRUE	FALSE	1	1230.5	-0.2	9of 20	1.1574	FALSE	FALSE	::::::::::::
IEFDSLLDGMR	11	3.71	0.044	729	37.73	T13288	TRUE	TRUE	2	1296.5	2.3	11of 20	2.032	FALSE	FALSE	::::::::::::
SLVAQEAVLAA	8	3.3	0.037	2830	35.1	T13288	TRUE	FALSE	2	1072.2	-0.1	9of 20	1.1804	FALSE	FALSE	::::::::::::
RHFLK	14	11.49	0.034	830	11.4	T13288	TRUE	FALSE	1	700.9	0.8	5of 8	1.114	FALSE	FALSE	::::::
VNLMLLRSVEKQTALYDR	1	9.72	0.039	801	52.23	T13350	TRUE	FALSE	2	2150.5	-2.9	6of 34	0.66	FALSE	FALSE	::::::::::::::::::
FQDHIVKHALFEYDIQKTPEDERPK	1	5.32	0.016	1885	48	T13382	TRUE	FALSE	3	3085.4	-2.4	21of 96	1.4786	FALSE	FALSE	::::::::::::::::::::::::
KTFNIKKDFSPAEEEQVR	15	7.16	0.131	1595	29	T13390	TRUE	TRUE	3	2167.4	-1.6	19of 68	1.519	FALSE	FALSE	::::::::::::::::::
GRPQNRNSSSPATTTRATRLS	4	12.88	0.086	2210	13.9	T13412	TRUE	FALSE	2	2259.4	0.7	8of 40	1.1149	FALSE	FALSE	::::::::::::::::::::
IPKSLTVIPQQMGGNTGGDMGGSS	1	6.76	0.045	2378	39.86	T13412	TRUE	FALSE	2	2349.6	1.5	8of 46	0.9818	FALSE	FALSE	::::::::::::::::::::Oxidation_M::::::
IPLVDLNDDDEGEDGAGGAGERESTNR	8	3.49	0.04	2119	37	T13412	TRUE	FALSE	3	2802.8	-2.1	9of104	0.9549	FALSE	FALSE	::::::::::::::::::::
LSELLCLIPTSSTVGWSFY	1	3.3	0.054	1858	72.1	T13415	TRUE	FALSE	2	2174.5	0	12of 36	1.492	FALSE	FALSE	::::::Cys_CAM::::::::::::
SRLYRSMLMQEVGWFDTKGTG	1	9.72	0.046	2070	51.86	T13416	TRUE	FALSE	2	2479.8	-0.3	7of 40	0.9061	FALSE	FALSE	::::::Oxidation_M::::::::::::::
KFVNEIDAGQVGVNVPIPVPLPMFSFTGTR	7	7.02	0.268	2034	85.53	T13418	TRUE	TRUE	3	3231.8	1	1	4.3242	FALSE	FALSE	::::::::::::::::::::::::::::
PALRLKLASVGKDAPLVSLCLALGLLARRSLATASHSALTG	4	11.38	0.036	2255	113.4	T13423	TRUE	FALSE	3	4170.9	1.3	22of160	1.7549	FALSE	FALSE	::::::::::::::::::::Cys_CAM:::::::::::::::::::::
TQNLSMMSQKYKKDAKLLNRKSMYV	2	10.53	0	98	44.79	T13477	TRUE	FALSE	2	3023.6	-1.6	6of 48	1.2933	FALSE	FALSE	::::::Oxidation_M:::::::::::::::::
VKVSKSTASGGGSYGLR	3	10.71	0.018	1560	19	T13483	TRUE	FALSE	2	1597.8	2.2	12of 30	1.2578	FALSE	FALSE	::::::::::::::::
KCESSAASIVSSSGPMSPK	1	8.94	0.075	2330	23.83	T13564	TRUE	FALSE	2	1927.1	2.7	6of 36	0.9148	FALSE	FALSE	::Cys_CAM::::::::::::Oxidation_M::::
KNILQQSNSLITLHEEMQRDLP	1	5.35	0.087	1868	51.33	T13576	TRUE	FALSE	3	2625	-2.1	11of 84	1.175	FALSE	FALSE	::::::::::::::::Oxidation_M:::::::
RSSPQGKPHPMTDYQSIR	12	10.39	0.184	2874	18.03	T13577	TRUE	FALSE	3	2102.3	2.4	15of 68	1.8089	FALSE	FALSE	::::::::::Oxidation_M::::::::
NKKTQTLESVHK	10	10.32	0.086	981	6.2	T13593	TRUE	FALSE	2	1413.6	2.6	7of 22	0.8825	FALSE	FALSE	::::::::::::
TRCETTTRQYDDVACQRVRRGHKETRMNAER	2	9.76	0.005	1301	26.73	T13593	TRUE	FALSE	3	3899.2	-2.4	12of120	1.371	FALSE	FALSE	::::Cys_CAM::::::::::::Cys_CAM::::::::::::Oxidation_M::::
LTTQSLSCEDEGRGR	10	4.45	0.115	122	20.4	T13603	TRUE	TRUE	2	1709.8	-1.6	9of 28	1.4705	FALSE	FALSE	::::::::Cys_CAM::::::::
FGSSVNGFGRMGCDLDLILRFDSDMGAK	10	4.35	0.065	1030	71.96	T13616	TRUE	FALSE	3	3083.4	2.9	23of108	2.4415	FALSE	FALSE	::::::::::Oxidation_M::Cys_CAM:::::::::::::::
LINVFGVIVFLR	12	11.05	0.004	1061	60.8	T13617	TRUE	FALSE	2	1390.8	1.3	10of 22	1.2865	FALSE	FALSE	::::::::::::
NELQTKHMDDSIIQVNLDCFQKK	3	5.33	0.085	2669	44.73	T13645	TRUE	FALSE	3	2806.1	-2.7	14of 88	1.2334	FALSE	FALSE	::::::::::::::::Cys_CAM:::::
QLSNNIGKGTSDQK	9	9.89	0.144	392	10.1	T13669	TRUE	FALSE	3	1490.6	-0.4	20of 52	1.76	FALSE	FALSE	::::::::::::::
WYANSTLLKELPDC	10	4.08	0.005	556	43.2	T13669	TRUE	FALSE	3	1710.9	1.8	17of 52	1.6563	FALSE	FALSE	:::::::::::::Cys_CAM:
TNYSC	7	5.33	0.004	3281	6.9	T13669	TRUE	FALSE	1	644.6	-2.1	24	0.7386	FALSE	FALSE	:::::Cys_CAM:
PSPMLGRPAGATADMQRYVQR	3	11.05	0.016	2293	39.06	T13675	TRUE	FALSE	2	2335.7	1.6	12of 40	1.6257	FALSE	FALSE	::::Oxidation_M::::::::::Oxidation_M:::::::
KQPASVPQGKATGTASKSTPQGAG	1	10.85	0.084	2301	13.1	T13687	TRUE	FALSE	3	2255.5	2.4	25of 92	2.1755	FALSE	FALSE	::::::::::::::::::::::
PIGGGPGGGGG	9	6.02	0.055	2701	9.8	T13690	TRUE	FALSE	1	782.8	1.8	11of 20	1.0961	FALSE	FALSE	::::::::::::
DAQGQQQGGGRGGGGGGGGGPGMGFNNFNNGNG	7	6.79	0.018	1276	19.33	T13690	TRUE	FALSE	3	2822.9	2.9	9	2.4802	FALSE	FALSE	::::::::::::::::::::::::::::
TATEDMDALTFGSTKLLRYLTYSEARKMPVK	5	9.43	0.075	2236	71.06	T13692	TRUE	FALSE	3	3539.1	-3	9of120	0.8552	FALSE	FALSE	::::::::::::::::::::::::::::
ITTMYLLLNGLDVMVTSQADLLKDPRFQRVFETK	1	7.02	0.122	43	104.46	T13694	TRUE	FALSE	3	3974.7	1.6	18of132	1.5603	FALSE	FALSE	::::::::::::Oxidation_M:::::::::::::::::::
CRIVRLSNIRDVMDRGKHA	4	11.16	0.035	2387	35.83	T13703	TRUE	FALSE	2	2297.7	-2.6	11of 36	1.5696	FALSE	FALSE	:Cys_CAM:::::::::::::::
ICDFGMSIDLDAERMRKE	9	4.21	0.013	2741	45.76	T13710	TRUE	FALSE	3	2203.5	-0.3	9of 68	0.7119	FALSE	FALSE	::Cys_CAM::::::::::::Oxidation_M::::
VKTVSLPR	11	11.49	0.07	510	17.8	T13711	TRUE	FALSE	2	900.1	1	10of 14	1.496	FALSE	FALSE	::::::::
VIHGGAASRDGR	6	10.89	0.165	2998	12.5	T13716	TRUE	FALSE	2	1196.3	3	15of 22	2.39	FALSE	FALSE	::::::::::::
LTGGICSSNSAQPSSQQSHQQQPHPS	12	7.32	0.054	1855	20.1	T13716	TRUE	FALSE	3	2749.8	0.6	16of100	2.0797	FALSE	FALSE	::::::Cys_CAM:::::::::::::::::::
QSDGVR	4	6.79	0.01	2854	4.2	T13716	TRUE	FALSE	1	661.7	-2.6	6of 10	0.9142	FALSE	FALSE	::::::
VGNYDETPAQLHLVD	9	3.7	0.081	2760	33.9	T13717	TRUE	FALSE	2	1671.8	-0.6	5of 28	0.6755	FALSE	FALSE	::::::::::::::::
SPLEVDSGVGTPLSPPSTA	3	3.01	0.075	1972	37.5	T13718	TRUE	FALSE	2	1812	2.3	8of 36	1.0691	FALSE	FALSE	::::::::::::::::::
GYYLESEPCLVCNNPEVPMANIKLPSVK	11	4.56	0.107	2133	73.13	T13719	TRUE	FALSE	3	3239.6	0.6	22of108	2.0603	FALSE	FALSE	::::::::Cys_CAM:::Cys_CAM::::::Oxidation_M:::::::::
SNGGMSRSSSIPALTGFGFKPIRRNISGSSTPSGMQTPRK	11	12.89	0.147	1398	58.56	T13734	TRUE	FALSE	3	4154.7	-1.9	26of156	2.7643	FALSE	FALSE	::::::::::::::::::::::::::::
PVLDKMLIELKEQWTRV	15	7.11	0.062	1491	56.23	T13734	TRUE	FALSE	2	2115.5	1.7	13of 32	2.5431	FALSE	FALSE	:::::Oxidation_M:::::::::::
DFRTSLPERLPHVEPLSSAESPIR	9	5.44	0.036	1164	54.2	T13734	TRUE	FALSE	3	2735.1	1.1	20of 92	2.4195	FALSE	FALSE	::::::::::::::::::::::
MELIPTDEEKIQQRIR	6	4.65	0.016	2453	38.63	T13734	TRUE	FALSE	2	2016.3	0.2	8of 30	1.0252	FALSE	FALSE	:Oxidation_M:::::::::::::::
KNNHCYTNSGFNSSTPSPS	12	8.88	0.109	1236	12.6	T13739	TRUE	FALSE	3	2100.1	1.2	21of 72	2.431	FALSE	FALSE	:::::Cys_CAM:::::::::::::
KSHYASMGNTSNASSIYPGRMSAK	7	10.34	0.016	1101	26.36	T13740	TRUE	TRUE	3	2546.8	1.5	28	2.346	FALSE	FALSE	::::::::::::::::::::::
RMLVLEPTRRYTIDQIKRH	7	11.22	0.081	1171	43.93	T13741	TRUE	FALSE	3	2426.9	-2.8	96	1.0106	FALSE	FALSE	::::::::::::::::::
FIALEAAAGLVSKVQSVTVVGR	1	10.09	0.047	1430	62.9	T13744	TRUE	FALSE	2	2216.6	1.7	10of 42	1.7331	FALSE	FALSE	::::::::::::::::::::
NNVLSIRDVEVLVERW	9	4.45	0.014	1280	52.2	T13749	TRUE	FALSE	3	1942.2	-2.1	19of 60	2.3984	FALSE	FALSE	::::::::::::::::
RIEAVKSQQQLQVEVEVSYFEIYN	13	4.26	0.034	1546	62.7	T13796	TRUE	FALSE	3	2901.2	-1	19of 92	2.4073	FALSE	FALSE	::::::::::::::::::::::
PDYQKSAFIWDDYISEVGGMAASKELFTPR	12	4.21	0.076	2632	75.03	T13797	TRUE	FALSE	2	3439.8	-2	9of 58	1.0221	FALSE	FALSE	::::::::::::::::::Oxidation_M:::::::::::
RSFVKDYGPQFLPNYR	11	10.04	0.001	122	38.2	T13797	TRUE	FALSE	2	1988.3	-2.6	6of 30	0.7803	FALSE	FALSE	::::::::::::::
MNEKTVFTKLDLK	3	9.76	0.01	2160	30.43	T13798	TRUE	TRUE	2	1583.9	-0.9	6of 24	0.9756	FALSE	FALSE	:Oxidation_M:::::::::::
PAPHYDFASLDANLQE	4	3.7	0.005	2769	37.4	T13801	TRUE	FALSE	3	1788.9	-2.7	8of 60	1.1346	FALSE	FALSE	::::::::::::::
GNQGTGANPPANTAAAQKR	15	11.49	0.054	793	10.1	T13802	TRUE	FALSE	3	1825	0.1	17of 72	1.5748	FALSE	FALSE	::::::::::::::::
ATSDEAASVDK	14	3.71	0.023	743	10.6	T13802	TRUE	FALSE	2	1094.1	2.3	10of 20	1.3495	FALSE	FALSE	::::::::::::
GPEEATEEKASEESVTSADDAVDAVPN	3	3.24	0.019	1817	33.9	T13802	TRUE	FALSE	3	2748.8	2.8	13of104	1.2913	FALSE	FALSE	::::::::::::::::::::::::
EKSHSPVECVKTPKEVKTDA	9	7.17	0.004	2057	17.4	T13805	TRUE	FALSE	2	2270.5	2.7	14of 38	2.9289	FALSE	FALSE	::::::::Cys_CAM:::::::::::
RTTTVLKKYFSPKSSASANAVMSSPCDMTS	6	10.06	0.098	2040	48.06	T13806	TRUE	FALSE	3	3270.7	-0.4	8of116	1.1282	FALSE	FALSE	::::::::::::::::::::::::::Cys_CAM::Oxidation_M:::
LTSLAPDKTNMK	14	9.89	0.035	1514	22.13	T13806	TRUE	FALSE	1	1335.6	0.1	6of 22	0.8333	FALSE	FALSE	:::::::::Oxidation_M::
HLKSENTIEKLKFSTK	8	10.16	0.069	2121	23.6	T13812	TRUE	FALSE	2	1904.2	-1.4	7of 30	1.0702	FALSE	FALSE	::::::::::::::::
QTYVLNAQYGAQYV	11	5.82	0.034	1580	35.4	T13812	TRUE	FALSE	3	1618.8	-3	11of 52	1.1128	FALSE	FALSE	::::::::::::::::
DKSYGLDTTFYHSAHKK	1	9.43	0.009	1013	17.7	T13812	TRUE	FALSE	2	1999.2	1.5	12of 32	1.8275	FALSE	FALSE	::::::::::::::::
LAFNFITLDSRPYR	14	9.85	0.003	2655	47.1	T13812	TRUE	FALSE	3	1714	0.9	7of 52	1.1012	FALSE	FALSE	::::::::::::::::
YDHLIRSASASDAHRKVKPK	4	10.44	0.07	2619	21.1	T13825	TRUE	FALSE	2	2280.6	-1.7	12of 38	1.3991	FALSE	FALSE	::::::::::::::::::
QNVAVKELETAHGQPLSMR	9	7.83	0.05	2569	34.73	T13827	TRUE	TRUE	2	2125.4	0.3	8of 36	1.0519	FALSE	FALSE	::::::::::::::::Oxidation_M::
MTEGNKSRTVAATNMNAESSR	6	10.09	0.045	2176	20.16	T13827	TRUE	FALSE	2	2256.5	2.4	14of 40	1.5878	FALSE	FALSE	::::::::::::::::::
CASGLPLSLSNFVF	1	5.33	0.031	886	50.7	T13827	TRUE	FALSE	2	1512.7	-0.7	9of 26	1.0664	FALSE	FALSE	:Cys_CAM:::::::::::::

QNVAVKELETAHGQPLSMRKTVSVPNFSQQ	1	9.89	0.004	1906	52.33	T13827	TRUE	FALSE	3	3325.8	-1.2	19of116	1.5798	FALSE	FALSE	::::::::::::::::::::::::::::::
RISAAAADAIGPLVAA	14	6.79	0.101	1641	43.1	T13828	TRUE	FALSE	2	1467.7	0.8	10of 30	1.6141	FALSE	FALSE	::::::::::::::
GGMTSPHPHQPGIGMK	6	10.1	0.072	2070	17.76	T13828	TRUE	FALSE	1	1648.9	-0.6	12of 30	1.4088	FALSE	FALSE	:::Oxidation_M::::::::::::
MLQSLPPNMSPGVSTQGGMVPNQNWNKMR	10	11.49	0.056	1305	59.42	T13828	TRUE	FALSE	3	3233.7	-0.1	26of112	2.5049	FALSE	FALSE	:Oxidation_M::::::::::::::::::::::::Oxidation_M::
LLMSGGTAGGGTGATTTTTSTSSSSSR	14	11.05	0.054	1492	26.93	T13828	TRUE	FALSE	2	2263.4	2	15of 48	2.8486	FALSE	FALSE	:::Oxidation_M::::::::::::::::::::
GPHLMGASGGAGGPGNGPGGGGPRMQNPNMQMTQLNSL	1	11.05	0.009	1352	53.12	T13828	TRUE	FALSE	3	3669	2.7	16of148	1.492	FALSE	FALSE	:::::Oxidation_M::::::::::::::::::Oxidation_M:::::Oxidation_M::Oxidation_M:::::::
QARQEFVQLRTIAVHLQQKFRGKRLMI	1	12.42	0.059	54	67.63	T13845	TRUE	FALSE	2	3297	-0.1	4of 52	0.4421	FALSE	FALSE	::::::::::::::::::::::::::::
HAQKSMRFMR	3	12.42	0.006	2792	15.56	T13845	TRUE	FALSE	2	1324.6	-1.3	4of 18	0.5749	FALSE	FALSE	::::::Oxidation_M:::Oxidation_M::
GGPDNVAEMTGR	13	4.08	0.092	2189	14.63	T13847	TRUE	FALSE	2	1220.3	0.9	6of 22	0.9522	FALSE	FALSE	::::::::Oxidation_M::::
IRRLWNYLVRQEPAQEVFIKSIFVK	12	10.69	0.014	1879	82.3	T13853	TRUE	FALSE	3	3134.7	2.6	9of 96	1.4511	FALSE	FALSE	::::::::::::::::::::::::::
SSSGPFGKLLFGDQKEPE	14	4.45	0.019	1424	33.4	T13855	TRUE	FALSE	2	1924.1	-2.3	11of 34	1.2866	FALSE	FALSE	::::::::::::::::::
PHPHHMHRGSIGNIGLGLSSASPRAH	5	12.41	0.042	2210	32.63	T13856	TRUE	FALSE	2	2725.1	2.6	13of 50	1.7313	FALSE	FALSE	::::::::::::::::::::::::::
FTPASGTASASGTPQR	9	11.05	0.024	1181	18.3	T13856	TRUE	FALSE	2	1536.6	2.2	10of 30	1.3609	FALSE	FALSE	::::::::::::::::
CTLLPMQLMRLMPR	10	10.9	0.152	473	54.99	T13889	TRUE	FALSE	2	1793.2	3	9of 26	1.2585	FALSE	FALSE	:Cys_CAM::::Oxidation_M:::Oxidation_M::::::
HSMLR	13	11.05	0.108	1107	10.73	T13893	TRUE	TRUE	1	659.8	-0.2	5of 8	1.1134	FALSE	FALSE	:::Oxidation_M:::
SDDEAPNGGGNRGKYPDYSNRKVICAFCLR	14	8.26	0.105	1715	43.5	T13893	TRUE	FALSE	3	3418.6	2.7	21of116	2.2874	FALSE	FALSE	:::::::::::::::::::::::::Cys_CAM:::Cys_CAM:::
DYIVQIAAYNNMGVG	2	3.1	0.07	582	41.93	T13924	TRUE	FALSE	2	1644.8	-1.9	5of 28	0.6487	FALSE	FALSE	::::::::::Oxidation_M::::
SAPITVKTLPGVPSAPLHLRFS	3	11.49	0.023	1815	57.4	T13924	TRUE	FALSE	2	2289.7	-2.8	10of 42	1.2462	FALSE	FALSE	::::::::::::::::::::::
MFFFVTFVR	13	11.05	0.076	1821	47.93	T13927	TRUE	FALSE	2	1210.5	2.6	5of 16	1.0522	FALSE	FALSE	:Oxidation_M::::::::
MGINHGPITAGVIGARKPHYD	9	9.72	0.06	2225	37.73	T13927	TRUE	FALSE	2	2205.5	2.2	11of 40	1.3101	FALSE	FALSE	::::::::::::::::::::::
TGGGVVILPQHVLNELYHNYSIKQRR	8	10.04	0.024	2863	57.3	T13927	TRUE	FALSE	3	2993.4	1	20of100	2.1125	FALSE	FALSE	::::::::::::::::::::::::::
MLFDANKALVATGDAHSHTSFTK	11	7.94	0.173	364	43.53	T13930	TRUE	FALSE	3	2463.8	2.9	20of 88	3.2164	FALSE	FALSE	::::::::::::::::::::::
WRKPKDDG	13	9.89	0.124	1150	6.2	T13931	TRUE	FALSE	2	1002.1	2	8of 14	1.3087	FALSE	FALSE	::::::::
RPGKPEPTNWDK	8	9.89	0.056	3408	11.1	T13931	TRUE	FALSE	2	1425.6	-2.9	6of 22	1.1082	FALSE	FALSE	::::::::::::
KLLVRNK	15	11.64	0.03	463	15.8	T13931	TRUE	TRUE	2	871.1	2.2	7of 12	1.4626	FALSE	FALSE	::::::::
VENKLTKFETILYTYNHKTKHKTTNR	4	10.29	0.034	2708	34.4	T13933	TRUE	FALSE	3	3209.7	-1.5	21of100	1.5542	FALSE	FALSE	::::::::::::::::::::::::
YRAVQIQRFVRGALARRAYQKRRR	6	12.63	0.05	2546	43.5	T13939	TRUE	FALSE	2	3020.6	0.8	6of 46	1.0806	FALSE	FALSE	::::::::::::::::::::::
RISQTEAKF	15	10.09	0.001	2318	16.3	T13940	TRUE	FALSE	2	1080.2	-2.5	6of 16	1.1045	FALSE	FALSE	::::::::::
RYPSGLPPHPYSSHYLPPNYYGLPNGAVPGL	2	9.24	0.071	1678	70.5	T13944	TRUE	FALSE	3	3382.8	-1.1	11of120	1.2011	FALSE	FALSE	::::::::::::::::::::::::::::::
QALDHFNAEGSQDFCFLLSTRAGGLGINLAT	3	4.3	0.028	2029	80.4	T13944	TRUE	FALSE	3	3325.6	2.6	21of120	1.6678	FALSE	FALSE	::::::::::::Cys_CAM::::::::::::::
DVPGTLLNMALLNLGSCDPNLRTAAYNLLCALTATFD	5	3.6	0.17	2435	114.63	T13945	TRUE	FALSE	3	4011.5	-1.3	11of144	1.3238	FALSE	FALSE	::::::::::::::Cys_CAM::::::::::::Cys_CAM::::::::
QERGSRSSVSNESNVLLDPEVLPDLSIQA	12	3.93	0.07	683	60.7	T13945	TRUE	FALSE	3	3141.4	-1.4	20of112	1.8974	FALSE	FALSE	::::::::::::::::::::::::::::
LLLREISQFVDVQSDSNPNAAQLKALAS	4	4.31	0.01	1854	72.8	T13945	TRUE	FALSE	3	3029.4	-2.7	7of108	0.6923	FALSE	FALSE	::::::::::::::::::::::::::
LSLPSLEVITDALLEIMEACM	8	2.89	0.002	1980	83.66	T13945	TRUE	FALSE	3	2349.8	2.6	19of 80	1.7076	FALSE	FALSE	:::::::::::::::::::Cys_CAM::
LGVRRERVPFVLTHDFVYVIN	1	9.84	0.064	2125	68.5	T13950	TRUE	FALSE	2	2531	2.3	7of 40	1.0941	FALSE	FALSE	::::::::::::::::::
AAAATAVTSHQHIGGNSSMSSLVGLKSSA	7	10.1	0.034	1811	43.43	T2AA-DROME	TRUE	FALSE	3	2742	-1.8	71	1.8283	FALSE	FALSE	::::::::::::::::::::::::::
RLFWKSRDNPRRIRMDDIK	12	11.85	0.08	1447	39.93	T2D1-DROME	TRUE	FALSE	3	2503.9	-0.6	19of 72	1.9594	FALSE	FALSE	::::::::::::::::::
DRGNNTMQRRVMEESSRLSADDSR	8	7.23	0.101	3460	24.36	T2D6-DROME	TRUE	FALSE	3	2812	-2.6	9of 92	1.0745	FALSE	FALSE	::::::::::::::::::::
DRLVETMTKILK	3	9.89	0.031	2011	31.83	T2FA-DROME	TRUE	FALSE	2	1463.8	2.8	8of 22	1.1192	FALSE	FALSE	::::::Oxidation_M::::::
DKKKKKPTKDDKKGKSNGSGDSS	5	10.44	0.02	2904	-17.5	T2FA-DROME	TRUE	FALSE	3	2464.7	-1.7	19of 88	1.6081	FALSE	FALSE	::::::::::::::::::::
LHVFVDASQAAFAAVAYWR	5	7.76	0.066	1444	61.9	T31674	TRUE	FALSE	2	2123.4	-1.3	5of 36	0.6443	FALSE	FALSE	::::::::::::::::::
PGDLVGVNK	10	6.76	0.013	888	17.2	T44596	TRUE	TRUE	1	899	-0.2	7of 16	1.501	FALSE	FALSE	::::::::::
PGDLVGVNK	15	6.76	0.008	711	17.2	T44596	TRUE	TRUE	1	899	-1.2	8of 16	1.7213	FALSE	FALSE	::::::::::
RAYLRKGMVMVSQDLKPQACWEFEGEILVLHHPT	4	7.32	0.015	2627	91.76	T44681	TRUE	FALSE	3	4073.7	2	14of132	1.2514	FALSE	FALSE	:::::::Oxidation_M::Oxidation_M::::::::Cys_CAM::::::::::::::
YMACCMLYR	14	8.27	0.402	526	34.76	TBA1-DROME	TRUE	TRUE	2	1284.5	2.2	13of 16	2.1258	FALSE	FALSE	::Oxidation_M::Cys_CAM:Cys_CAM:::::
LIGQIVSSITASLR	12	11.05	0.389	1888	44.6	TBA1-DROME	TRUE	TRUE	2	1458.7	0.2	20of 26	4.3005	FALSE	FALSE	::::::::::::::
TIQFVDWCPTGFK	10	6.1	0.309	1570	41.1	TBA1-DROME	TRUE	TRUE	2	1599.8	-0.2	14of 24	2.8004	FALSE	FALSE	:::::::Cys_CAM::::::
LIGQIVSSITASLR	13	11.05	0.304	1670	44.6	TBA1-DROME	TRUE	TRUE	2	1458.7	2.6	20of 26	3.961	FALSE	FALSE	::::::::::::::
LADQCTGLQGFLIFHSFGGGTGSGFTSLLMER	6	5.22	0.194	2334	88.83	TBA1-DROME	TRUE	TRUE	3	3406.8	-1	23of124	2.17	FALSE	FALSE	:::::Cys_CAM:::::::::::::::::::::::::
PVISAEK	10	6.95	0.19	1524	15.2	TBA1-DROME	TRUE	FALSE	1	743.9	0.5	9of 12	1.73	FALSE	FALSE	::::::::
ACCMLYR	14	8.29	0.148	739	24.73	TBA1-DROME	TRUE	FALSE	1	974.1	0.6	9of 12	1.3732	FALSE	FALSE	::Cys_CAM:Cys_CAM:::::
PVISAEK	9	6.95	0.099	1918	15.2	TBA1-DROME	TRUE	FALSE	1	743.9	0.4	8of 12	1.3268	FALSE	FALSE	::::::::
KLADQCTGLQGFLIFHSFGGGTGSGFTSLLMER	10	7.16	0.09	1876	86.73	TBA1-DROME	TRUE	TRUE	3	3551	1.3	29of128	2.5969	FALSE	FALSE	::::::Cys_CAM::::::::::::::::::::::::Oxidation_M:::
IERPTYTNLNR	6	9.85	0.074	1175	21.9	TBA1-DROME	TRUE	FALSE	2	1377.5	2.5	9of 20	1.6663	FALSE	FALSE	::::::::::::
FMACCMLYR	15	8.29	0.391	768	38.36	TBA4-DROME	TRUE	TRUE	2	1268.5	2.1	13of 16	3.0637	FALSE	FALSE	::Oxidation_M::Cys_CAM:Cys_CAM:::::
FMACCMLYR	14	8.29	0.353	726	38.36	TBA4-DROME	TRUE	TRUE	2	1268.5	1.8	13of 16	3.003	FALSE	FALSE	::Oxidation_M::Cys_CAM:Cys_CAM:::::
ISEQFTAMFR	8	6.98	0.334	1891	32.03	TBB1-DROME	TRUE	TRUE	2	1230.4	-0.1	17of 18	3.4255	FALSE	FALSE	::::::::::::
LHFFMPGFAPLTSR	14	11.05	0.044	1412	49.53	TBB1-DROME	TRUE	TRUE	2	1621.9	0.7	13of 26	1.8995	FALSE	FALSE	::::::::::::::
LLTAAGIFRGRMSPREVDQ	9	10.8	0.065	1094	47.73	TBBP-DROME	TRUE	FALSE	3	2134.5	-0.2	22of 72	2.19	FALSE	FALSE	::::::::::::Oxidation_M:::::::
NVLKAHGKSARESVLIPGYALNCTIASQQMPK	7	10.06	0.006	1539	64.23	TCPA-DROME	TRUE	FALSE	3	3484	-1.4	483	2.5671	FALSE	FALSE	::::::::::::::::::::::Cys_CAM:::::::::
ICADIIAVKPDLVFTEK	2	4.31	0.066	1089	54.9	TCPG-DROME	TRUE	TRUE	2	1933.3	0.8	12of 32	2.0229	FALSE	FALSE	::Cys_CAM:::::::::::::
MADRINLPKTIVDRANNLFK	8	10.58	0.064	1740	49.43	TF2B-DROME	TRUE	FALSE	3	2330.8	-2.8	22of 76	2.241	FALSE	FALSE	::::::::::::::::::
KGSTSSSQTSFPSGGMTDAVRIKC	10	9.91	0.079	990	28.03	TFS2-DROME	TRUE	FALSE	3	2490.7	0.7	22of 92	1.7201	FALSE	FALSE	:::::::::::::::::::::Cys_CAM:
CRRHYSAIQSSAALLSVR	5	11.05	0.102	1407	37	TID-DROVI	TRUE	FALSE	3	2076.3	-2.4	19of 68	2.3442	FALSE	FALSE	:Cys_CAM:::::::::::::::
DNGSNGGGSSGKK	9	9.89	0.05	936	-6.8	TIM-DROHY	TRUE	FALSE	2	1165.2	-2	9of 24	1.1418	FALSE	FALSE	::::::::::::
ECAYGKPSDDVQILLD	4	3.51	0.01	2641	38.9	TIM-DROME	TRUE	FALSE	2	1824	0.3	9of 30	1.174	FALSE	FALSE	::Cys_CAM:::::::::::::
ETMPLPRKLVR	7	11.33	0	3248	29.13	TIPT-DROME	TRUE	TRUE	2	1340.7	1.5	36	0.64	FALSE	FALSE	::::::::::
PRDGR	2	10.89	0	1974	0.8	TKR-DROME	TRUE	FALSE	1	600.7	-0.3	3of 8	0.5886	FALSE	FALSE	:::::
RRKQSHKSQNKAALRLPPPFL	6	12.72	0.101	2063	31.2	TLD-DROME	TRUE	FALSE	3	2473.9	1.5	10of 80	1.3325	FALSE	FALSE	::::::::::::::::::
ETAAEHLFKNVNW	11	5.3	0.061	1148	31.4	TLL-DROME	TRUE	FALSE	2	1559.7	2.1	8of 24	1.7454	FALSE	FALSE	::::::::::::
ATRALPPTPPLMAAEHIK	11	10.09	0.029	1288	42.63	TLL-DROME	TRUE	FALSE	2	1915.3	2.8	13of 34	1.253	FALSE	FALSE	::::::::::::::::
MLQTQINSPFGYMHGLLTLNLR	13	9.85	0.022	392	70.26	TOLL-DROME	TRUE	FALSE	3	2565	1.3	18of 84	1.5729	FALSE	FALSE	:::::::::::Oxidation_M:::::::::
TDVKKFDYLLGMSMWMLTEEKK	3	7.04	0.057	2251	62.29	TOP2-DROME	TRUE	FALSE	2	2711.2	-2.8	5of 42	0.8184	FALSE	FALSE	::::::::::::::Oxidation_M::::::
IVNLAQNFVGANNINLLEPR	1	6.98	0.041	300	60.5	TOP2-DROME	TRUE	FALSE	2	2210.5	2.7	9of 38	1.3727	FALSE	FALSE	::::::::::::::::::
NWRTVDPRSLFDAPVKKGVGSDYEPIKRTLE	4	9.56	0.096	2413	62.5	TP3A-DROME	TRUE	FALSE	3	3576	-2.7	19of120	1.7725	FALSE	FALSE	::::::::::::::::::::::::::::
KANQRVEEFK	10	9.89	0.063	1045	11.9	TPM2-DROME	TRUE	FALSE	3	1249.4	2.2	18of 36	2.084	FALSE	FALSE	::::::::::
YEIQHQAVLIIFTLMESDDQWIPTRQDI	9	3.84	0.047	2216	90.23	TRA1-DROME	TRUE	FALSE	3	3404.9	-0.2	21of108	2.1988	FALSE	FALSE	::::::::::::::::::::::::::::
GLSLCIIHQNTRIVRLMHMFLTRIM	2	12.11	0	170	88.49	TRA1-DROME	TRUE	FALSE	3	3071.7	2.5	19of 96	1.564	FALSE	FALSE	:::::Cys_CAM::::::::::Oxidation_M:::::::::
KTLFVIGFLLPCLVIIVSYSCIYI	8	8.27	0.011	2557	114.7	TRE1-DROME	TRUE	FALSE	3	2833.4	-2.3	22of 92	1.9082	FALSE	FALSE	::::::::::::Cys_CAM::::::::Cys_CAM::::
SLPLPMDSYMDLEITVIK	7	3.71	0.092	3320	63.26	TRE2	TRUE	FALSE	3	2098.5	2	383	1.321	FALSE	FALSE	:::::Oxidation_M::::Oxidation_M:::::::::
QRGQTPSKLELIVVMYVIGFV	3	9.72	0.044	1288	69.53	TRPL-DROME	TRUE	FALSE	3	2378.9	0.8	18of 80	2.6734	FALSE	FALSE	::::::::::::::::::::::
VYGLHYIGPVAGEVIQGFAAALK	11	7.69	0.341	1723	69.2	TRX1-DROME	TRUE	TRUE	2	2374.8	2.3	23of 44	4.9109	FALSE	FALSE	::::::::::::::::::::::
WGVGGTCVNVGCIPK	15	8.3	0.219	1057	35.5	TRX1-DROME	TRUE	TRUE	2	1604.8	1.5	19of 28	2.8283	FALSE	FALSE	::::::Cys_CAM:::::Cys_CAM::::

SIVLRGFDQQMAEL	12	4.08	0.017	1307	44.53	TRX1-DROME	TRUE	FALSE	2	1623.9	-3	8of 26	1.1797	FALSE		FALSE		::::::::::Oxidation_M::::
LKAVAEVSGDQKILGLHYIGPVAGEVIQGFAAALK	10	7.71	0.363	2006	94	TRX2-DROME	TRUE	FALSE	3	3565.2	-2	29of136	3.4846	FALSE		FALSE		::::::::::::::::::::::::::::::::
MKKDSLNRPLNYSR	13	10.7	0.119	1797	21.43	TRX-DROME	TRUE	FALSE	2	1739	1	6of 26	1.0534	FALSE		FALSE		:Oxidation_M::::::::::::
SSDGASSGISCGKSTAK	8	8.94	0.005	3468	8.8	TRX-DROME	TRUE	FALSE	3	1600.6	-2.6	15of 64	1.5245	FALSE		FALSE		::::::::::Cys_CAM::::::
KRNGNVSTAAGGGHAR	10	12.42	0.014	1156	4	TRX-DROVI	TRUE	FALSE	2	1553.7	-2.8	11of 30	1.4006	FALSE		FALSE		::::::::::::::::
ESSSSTTNLFGSGLSR	13	6.98	0.01	2174	23.8	TRX-DROVI	TRUE	FALSE	3	1630.7	-0.1	12of 60	1.6915	FALSE		FALSE		::::::::::::::::
NLSILNGSSEAVLMATTSTTLDAGK	2	4.08	0.042	1068	55.53	TUBE-DROVI	TRUE	FALSE	3	2495.8	-0.5	11of 96	1.077	FALSE		FALSE		::::::::::::::::::::::::
ATNKEQEAHSSSSK	8	7.8	0.111	1860	-0.9	TYDP-DROME	TRUE	FALSE	2	1504.6	-2.5	10of 26	1.4315	FALSE		FALSE		::::::::::::::
GHPWGHARLASLLAKHA	9	11.49	0.031	66	33.5	TYDP-DROME	TRUE	FALSE	3	1823.1	-2.5	14of 64	1.402	FALSE		FALSE		::::::::::::::::
MRSAFGMGLAVKLAER	14	11.33	0.032	295	43.56	U140-DROME	TRUE	FALSE	2	1754.1	-0.7	5of 30	0.9393	FALSE		FALSE		:Oxidation_M:::::::::::::::
HTNLEDGPVAS	7	4.07	0.026	1187	15.9	U202-DROME	TRUE	FALSE	2	1140.2	-0.6	2	1.2539	FALSE		FALSE		::::::::::::
NTPNDLQMMSDAPAHHLFC	10	4.94	0.02	2562	41.36	U202-DROME	TRUE	FALSE	2	2200.4	-2.6	9of 36	1.0004	FALSE		FALSE		:::::::::::::::::::Cys_CAM:
AVVGVLSDDTDPMVTMMK	8	3.6	0.005	2820	47.99	U39303	TRUE	FALSE	2	1942.3	0.1	15of 34	2.3919	FALSE		FALSE		:::::::::::::::Oxidation_M:Oxidation_M::
MRWASEQFNR	1	10.89	0.078	2230	23.53	U41449	TRUE	FALSE	2	1341.5	2.4	4of 18	0.7538	FALSE		FALSE		:Oxidation_M:::::::::
SDENMLLCAPTGAGKTNVALLTMMR	3	6.36	0.062	1187	63.19	U520-DROME	TRUE	FALSE	3	2696.1	-1.6	21of 96	2.0647	FALSE		FALSE		:::::::Cys_CAM::::::::::::::::
PNKLTGPNETAPK	13	9.89	0.015	1364	12.8	U520-DROME	TRUE	FALSE	2	1367.5	2.7	10of 24	1.8419	FALSE		FALSE		::::::::::::
ENLQKLPQLAAIH	3	7.82	0.065	2823	34	U54996	TRUE	FALSE	2	1475.7	-2.6	7of 24	0.9061	FALSE		FALSE		::::::::::::::
LPTKASPAAESPK	3	9.89	0.054	2706	17.2	U63386	TRUE	FALSE	2	1297.5	-1.4	4of 24	0.6174	FALSE		FALSE		::::::::::::
AATHTYTDASQKENIFTSATCTNAAAPTHTDA	1	5.12	0.017	2369	39	U63755	TRUE	FALSE	3	3369.5	2.4	14of124	1.3672	FALSE		FALSE		:::::::::::::::::::::Cys_CAM:::::::::::
KLSPAKAMRPVLPVRPPLPAPAPAWI	5	12.43	0.087	2338	76.43	U65493	TRUE	FALSE	3	2775.5	1.1	16of100	1.4522	FALSE		FALSE		::::::::::::::::::::::::::
GRLFPMGHGYPAEYQHMVHAHWR	13	9.59	0.079	330	48.96	U80667	TRUE	FALSE	2	2795.2	0.4	4of 44	0.8618	FALSE		FALSE		:::::::::::::::::Oxidation_M::::::::
AAAAANASSLFARSR	6	12.41	0.04	2102	27.8	U86339	TRUE	FALSE	2	1464.6	2.8	9of 28	1.3273	FALSE		FALSE		::::::::::::::::
IKLVVSEKNVRKAYHRAM	8	10.89	0.009	1711	35.23	U91994	TRUE	FALSE	2	2143.6	2.2	4of 34	0.6708	FALSE		FALSE		::::::::::::::::::
NPNTPTIEITTNMSSSSTSMSK	13	6.95	0.095	1158	28.86	UAS3-DROME	TRUE	FALSE	3	2329.6	-2.5	24of 84	2.0493	FALSE		FALSE		::::::::::::::::::::
PNVGANGEICVNVLKR	8	8.97	0.01	2588	33.3	UBCE	TRUE	FALSE	2	1741	2.3	5of 30	0.9012	FALSE		FALSE		::::::::Cys_CAM::::::
PEDLFYMRQFTHNACGTVALIHSVANNK	14	7.32	0.044	1042	63.83	UBL-DROME	TRUE	FALSE	3	3251.6	-2.9	22of108	2.6256	FALSE		FALSE		:::::::Oxidation_M:::::::Cys_CAM::::::::::::::
PPIVIPDDSK	15	3.89	0.004	2955	23.9	UBP3	TRUE	FALSE	2	1081.3	0.8	11of 18	1.9653	FALSE		FALSE		::::::::::
DEGIDMSSSTSK	14	3.71	0.051	1657	11.93	UBPE-DROME	TRUE	FALSE	2	1257.3	0.5	12of 22	1.3602	FALSE		FALSE		::::::::::::
MDGPLVTQQGERK	3	7.02	0.021	1003	19.43	UBPE-DROME	TRUE	FALSE	2	1459.7	1.9	11of 24	1.5651	FALSE		FALSE		::::::::::::
RNSCEGEDEEEMEHQEEGK	9	3.91	0.083	2209	11.13	UBPN	TRUE	FALSE	2	2323.3	1.9	10of 36	1.3683	FALSE		FALSE		:::Cys_CAM:::::::::::::::
SAPPSTPPTHKAKPQIPAERDREPSK	5	10.32	0.084	2739	20.8	UBPY	TRUE	FALSE	3	2824.2	-0.3	15of100	1.6048	FALSE		FALSE		::::::::::::::::::::::::
ADFALLARFSSLQYSDKVR	1	9.72	0.036	2265	52.5	UGGG-DROME	TRUE	FALSE	3	2188.5	1.5	13of 72	1.3871	FALSE		FALSE		::::::::::::::::::
EDPKWQDTNYVLANYKTEPCK	11	4.56	0.141	1623	35.8	UNK-DROME	TRUE	FALSE	3	2600.8	0.3	18of 80	1.805	FALSE		FALSE		:::::::::::::::::::Cys_CAM:::
EPMDYLSPKMMRKLSSK	3	10.05	0.24	2584	35.09	URP-DROME	TRUE	FALSE	2	2074.5	-2.2	6of 32	1.1326	FALSE		FALSE		:::Oxidation_M::::::Oxidation_M:::::::
SGAGGSGATAGDAAGLTGGSTEPPAKMARTGK	3	9.89	0.143	2298	28.13	USH-DROME	TRUE	TRUE	3	2807	-0.1	22of124	1.6557	FALSE		FALSE		:::::::::::::::::::::::::::::::Oxidation_M::::::
NVTLRGNYVTLEAPYSGK	8	9.53	0.211	3437	37	UZIP-DROME	TRUE	FALSE	3	1983.2	1.1	7of 68	1.2158	FALSE		FALSE		::::::::::::::::::
TGKPLSVELGPGIMGSIFDGIQRPLK	14	9.89	0.182	1555	66.83	VAA2-DROME	TRUE	TRUE	3	2712.2	0.7	28of100	3.3121	FALSE		FALSE		::::::::::::::::::::::::
ISYSKYMRALDDFYDKNFPEFVPLR	2	6.93	0.126	1276	73.23	VAA2-DROME	TRUE	FALSE	3	3132.6	3	21of 96	2.9772	FALSE		FALSE		::::::Oxidation_M:::::::::::::::::
GGERGERGDGGFARRRRN	2	12.11	0.022	1808	7.1	VASA-DROME	TRUE	FALSE	2	2004.1	-2.6	8of 34	0.8943	FALSE		FALSE		::::::::::::::::::
AVVGEEALTPDDLLYLEFLTK	1	3.51	0.24	1712	71.7	VATB-DROME	TRUE	TRUE	2	2337.7	0.8	17of 40	3.1832	FALSE		FALSE		::::::::::::::::::::
KNQIIDQLVQKC	2	8.94	0.009	476	25.9	VAV-DROME	TRUE	FALSE	2	1487.7	2.5	8of 22	1.4509	FALSE		FALSE		::::::::::Cys_CAM:
TPIRSGDVDFYPNGPAAGVPGASNVVEAAMR	7	4.31	0.027	1836	62.03	VIT1-DROME	TRUE	FALSE	2	3117.5	-1.4	79	1.8357	FALSE		FALSE		::::::::::::::::::::::::::::::
NFLYTNGNSVIIR	5	9.85	0.096	1626	38.3	WDR1-DROME	TRUE	TRUE	2	1511.7	2.1	13of 24	2.0559	FALSE		FALSE		::::::::::::::
NFLYTNGNSVIIR	4	9.85	0.023	1617	38.3	WDR1-DROME	TRUE	TRUE	2	1511.7	1.3	15of 24	2.5493	FALSE		FALSE		::::::::::::::
PNYTLKFTLAGHTKAVSAVKFSPNGEW	11	10.05	0.136	472	58.2	WDS-DROME	TRUE	FALSE	3	2965.4	1.4	17of104	1.65	FALSE		FALSE		::::::::::::::::::::::::::
RAKKQEKESGRQPKAPAPGVLVMPPSTCPPPK	5	10.7	0.103	1287	38.53	WIBG-DROME	TRUE	FALSE	2	3485.1	1.3	7of 62	0.9492	FALSE		FALSE		:::::::::::::::::::::Oxidation_M::::Cys_CAM::::
YQKAKTVQAVKGKRGLRLVL	8	11.65	0.093	2265	38.4	WNT2-DROME	TRUE	FALSE	2	2257.8	0	9of 38	1.2455	FALSE		FALSE		::::::::::::::::::
QLCSHSVFVTSDFKL	15	7.16	0.065	1072	41	WSCK-DROME	TRUE	FALSE	2	1769	0.1	12of 28	1.9781	FALSE		FALSE		:::Cys_CAM:::::::::::
AQYCGGVGVH	5	7.15	0.006	2779	16.4	WSCK-DROME	TRUE	FALSE	2	1048.1	2.8	5of 18	0.7331	FALSE		FALSE		::::Cys_CAM::::::
MCFIGLGRYMGIRNPLGSRHRSTKR	7	12.24	0.104	1540	50.86	X81835	TRUE	FALSE	3	2997.5	1.5	153	1.826	FALSE		FALSE		:Oxidation_M:Cys_CAM::::::Oxidation_M:::::::::::::::
RITRMGKRIGRWTNPIQR	15	13.01	0.073	2906	33.63	X98402	TRUE	FALSE	3	2256.7	2.4	12of 68	1.4075	FALSE		FALSE		:::::Oxidation_M:::::::::::::
LGCAEGGCGACTVMISRMDRGQHKI	1	8.02	0.047	2144	46.06	XDH-DROSU	TRUE	FALSE	3	2766.1	1.1	16of 96	2.0405	FALSE		FALSE		:::Cys_CAM:::::Cys_CAM:::Cys_CAM:::::::::::::
LCGTKLGCAEGGCGACTVMISRMDRGQHKIR	1	8.74	0.025	605	54.46	XDH-DROSU	TRUE	TRUE	3	3513.9	-2.8	18of120	1.4952	FALSE		FALSE		::Cys_CAM:::::Cys_CAM:::::Cys_CAM:::Cys_CAM:::Oxidation_M::::Oxidation_M:::::::::
MVLDEVHTIPAKMFRRVLTIVQSHCK	5	9.91	0.026	1704	69.46	XPB-DROME	TRUE	FALSE	3	3126.7	3	23of100	2.2558	FALSE		FALSE		:::::::::::::Oxidation_M::::::::::::Cys_CAM::
EYGAKDYRSQMQLR	15	9.53	0.026	1588	22.23	XPB-DROME	TRUE	FALSE	2	1762	2.3	8of 26	1.2467	FALSE		FALSE		::::::::::Oxidation_M::::
RIHSDKPLPKSISEFKDHPLYVL	1	9.56	0.062	2318	52.5	XPC-DROME	TRUE	FALSE	3	2721.2	-1.5	12of 88	1.2403	FALSE		FALSE		::::::::::::::::::::::
TSLAAMAAALHKQSPLRQTSVRTR	15	12.71	0.013	1479	42.03	Y08362	TRUE	FALSE	3	2596	1	15of 92	1.3108	FALSE		FALSE		::::::::::::::::::::::
NSFIST	15	6.02	0.001	205	15.1	Y105-DROME	TRUE	FALSE	1	668.7	2.8	5of 10	0.7911	FALSE		FALSE		::::::
IKTKTRLATDHIPILYGKDDK	8	9.96	0.153	1672	38	Y18628	TRUE	FALSE	3	2427.8	0.4	12of 80	1.2975	FALSE		FALSE		::::::::::::::::::::
HNMDITIEGFHSWMW	14	5.05	0.076	2703	48.26	Y33B-DROME	TRUE	FALSE	3	1937.2	-2.5	11of 56	1.3097	FALSE		FALSE		:::Oxidation_M::::::::::Oxidation_M:::
LFCTKTFRQRGDR	12	11.23	0.039	692	24.2	Y484-DROME	TRUE	FALSE	3	1685.9	2.5	17of 48	1.7803	FALSE		FALSE		:::Cys_CAM:::::::::::
GPNECTMCDRKFVHAS	12	7.01	0.011	1779	23.93	Y484-DROME	TRUE	FALSE	3	1926	2	14of 60	1.7358	FALSE		FALSE		:::::Cys_CAM::Oxidation_M:Cys_CAM:::::::::
RCFFLDEASRKLLYAMQANMDR	5	8.87	0.173	1308	61.46	Y799-DROME	TRUE	FALSE	3	2753.1	0.2	16of 84	1.8405	FALSE		FALSE		::Cys_CAM::::::::::::::::Oxidation_M:::
KYEVTLNFLHEVDPEKVTSK	7	5.44	0.362	1372	41.3	YC17-DROME	TRUE	TRUE	3	2377.7	1.2	1	3.6404	FALSE		FALSE		::::::::::::::::::
QQNALLRQILMEKEKLENAYTQHEVA	1	5.48	0.048	1393	57.73	YCDA-DROME	TRUE	FALSE	3	3099.5	-2.4	19of100	1.7958	FALSE		FALSE		::::::::::::::::::::::::
LWVLDTGTVGIGNTTTNP	7	3.1	0.038	1884	45.8	YELL-DROER	TRUE	FALSE	2	1860.1	0	247	0.8294	FALSE		FALSE		::::::::::::::::
NVWVLSDRMP	2	6.79	0.024	1662	33.23	YELL-DROER	TRUE	FALSE	1	1217.4	-0.6	4of 18	0.6416	FALSE		FALSE		::::::::::
YGRRGRYDRYNNSSR	11	11.12	0.135	1094	8.7	Z54163	TRUE	TRUE	2	1921	-1.7	5of 28	0.8409	FALSE		FALSE		::::::::::::::
LVPATPSSSGHGK	11	10.1	0.02	616	14.5	Z600-DROME	TRUE	FALSE	2	1238.4	2.8	8of 24	1.0698	FALSE		FALSE		::::::::::::::
YSVRDTWDKIVRDFNSHPHV	15	7.89	0.008	107	38.5	ZEST-DROVI	TRUE	FALSE	2	2472.7	-1.8	5of 38	0.7906	FALSE		FALSE		::::::::::::::::::
KRFSHSGSFSSHMTSKK	1	11.73	0.053	1820	9.83	ZFH1-DROME	TRUE	FALSE	2	1956.2	1.7	7of 32	1.2803	FALSE		FALSE		:::::::::::Oxidation_M::::::
VNNLGSGVPTTVFK	11	10.1	0.099	457	30.5	ZFH2-DROME	TRUE	FALSE	3	1433.6	-2.1	16of 52	1.6472	FALSE		FALSE		::::::::::::::
DQHTSSSKMAAPSAYIPLSSPKVAGKLTVK	5	10.3	0.035	1846	47.13	ZFH2-DROME	TRUE	FALSE	3	3101.6	-2.9	22of116	3.0197	FALSE		FALSE		::::::::::::::::::::::::::::
KALKKESTDIACPTDK	3	8.88	0.004	1985	18.2	ZFH2-DROME	TRUE	FALSE	2	1806	-1.7	10of 30	1.1588	FALSE		FALSE		::::::::::Cys_CAM::::
IMEMSQKANLPMKVVKHWFR	7	10.83	0.002	1429	54.29	ZFH2-DROME	TRUE	FALSE	3	2507	-2.6	5	1.7828	FALSE		FALSE		::Oxidation_M::Oxidation_M:::::::::::::::
VHQVRSWMKLQQLKTMMNASLKEITELWCK	6	10.17	0.062	2469	79.89	ZW10-DROPS	TRUE	FALSE	3	3735.4	0.5	22of116	1.9996	FALSE		FALSE		:::::::::::::::Oxidation_M::::::::::Cys_CAM::
PGEDEADPLAGVIGMMLQTYIDEVPKVHKKLLE	8	4.22	0.026	2756	84.36	ZW10-DROPS	TRUE	FALSE	3	3638.2	-2.7	26of128	2.135	FALSE		FALSE		::::::::::::::::::::::::::::::
IITHPNFNGNTLDNDIMLIKLSSPATLNSR	10	7.82	0.395	1692	75.23		TRUE	TRUE	3	3327.8	-0.4	32of116	5.5006	FALSE		FALSE		:::::::::::::::Oxidation_M::::::::::::