	Reference	S7-E2B-20				P (pro)	Sf	Score	Coverage	MW	Acsn	Peptide (Hits)
	Scan(s)	Peptide	MH+	DeltaM (ppm)	z	P (pep)	Sf	XC	DeltaCn	Sp	RSp	Ions
1	RFP_UB					8.98E-15	69.49	826.30	83.10	38172.1		83 (81 2 0 0 0)
	1549	K.LDITSHN.E	799.39446	-0.38356	2	2.73E-03	0.83	2.54	0.65	375.4	1	11/18
	1005	D.GALKGEIK.M	815.49853	-0.08418	2	2.67E-03	0.69	3.09	-	670.9	1	14/21
	3449	S.TLHLVLR.L	851.54615	0.76601	2	9.38E-06	0.59	2.41	-	367.0	1	14/18
	1003	G.HYDAEVK.T	861.41011	-0.52675	2	5.10E-02	0.80	2.53	0.61	293.1	1	11/18
	448	K.GEIK#M*R.L	863.44034	-0.33643	2	9.17E-03	0.72	2.01	0.46	387.2	1	10/15
	1289	L.SDYNIQK.E	867.42067	-0.74064	2	1.96E-03	0.81	2.74	0.53	365.4	1	11/18
	991	G.GHYDAEVK.T	918.43157	-0.80383	2	3.21E-02	0.83	2.93	0.54	327.9	1	13/21
	6036	K.LSFPEGFK.W	924.48254	-1.00590	2	1.35E-04	0.84	2.53	0.81	339.4	1	11/21
	1696	M.GWEASTER.M	935.42174	-0.58307	2	6.23E-03	0.80	2.32	0.76	321.5	1	11/21
	3446	E.STLHLVLR.L	938.57818	-1.17483	2	4.97E-05	0.64	2.85	-	606.2	1	14/21
	2179	K.PVQLPGAYK.T	972.55129	-0.54019	2	1.29E-06	0.93	3.15	0.57	835.6	1	17/24
	2138	F.PSDGPVM*QK.K	974.46116	0.38118	2	8.18E-04	0.80	2.85	0.67	242.9	1	12/24
	2281	T.LSDYNIQK.E	980.50474	-0.42514	2	2.91E-04	0.93	3.36	0.70	638.4	1	14/21
	891	H.HASSEDVIK.E	985.49490	-1.09438	2	7.92E-05	0.92	3.13	0.79	434.4	1	15/24
	548	R.PYEGTQTAK.L	994.48400	-1.41775	2	4.37E-05	0.93	3.19	0.74	621.9	1	16/24
	2391	R.MYPEDGALK.G	1023.48156	-0.66059	2	2.21E-06	0.91	2.68	0.71	515.6	1	17/24
	3146	H.PADIPDYLK.L	1031.54079	-1.74499	2	1.31E-03	0.83	2.97	0.62	452.8	1	12/24
	2260	Y.TIVEQYER.A	1037.52620	-1.08780	2	4.38E-01	0.59	2.38	0.39	296.1	1	11/21
	2127	R.M*YPEDGALK.G	1039.47648	-0.10843	2	1.70E-02	0.84	2.36	0.60	391.7	1	16/24
	4455	K.ESTLHLVLR.L	1067.62077	-1.02397	2	1.54E-08	0.65	3.20	-	367.6	1	16/24
	4958	R.TLSDYNIQK.E	1081.55242	-1.35403	2	3.30E-07	0.94	3.36	0.81	478.4	1	17/24
	1941	T.M*GWEASTER.M	1082.45714	-0.73333	2	8.98E-05	0.90	2.30	0.88	498.7	1	15/24
	1314	K.DGGHYDAEVK.T	1090.47998	-0.51447	2	8.40E-06	0.91	2.93	0.75	520.4	1	17/27
	3957	K.KPVQLPGAYK.T	1100.64626	-0.08215	2	4.46E-05	0.84	3.43	0.57	268.2	1	14/27
	2111	N.FPSDGPVM*QK.K	1121.52958	-1.83985	2	1.61E-04	0.84	3.02	0.72	320.3	1	13/27
	489	G.RPYEGTQTAK.L	1150.58511	-1.57567	2	1.29E-05	0.84	2.74	0.46	380.2	1	18/27
	2564	Y.PEDGALKGEIK.M	1156.62083	-0.57451	2	1.97E-04	0.91	4.00	0.46	679.2	1	17/30
	2744	K.TMGWEASTER.M	1167.50990	-0.80509	2	1.62E-07	0.96	3.88	0.84	762.2	1	18/27
	4124	K.HPADIPDYLK.L	1168.59970	-0.35012	2	3.34E-07	0.90	2.95	0.92	218.8	1	15/27
	1913	K.TM*GWEASTER.M	1183.50482	-0.21503	2	1.94E-08	0.96	3.29	0.86	949.7	1	18/27
	3669	S.SLQDGEFIYK.V	1199.59428	-0.19876	2	1.25E-05	0.89	2.84	0.71	570.3	1	15/27
	3075	D.YTIVEQYER.A	1200.58953	-1.73183	2	4.04E-06	0.92	3.33	0.59	677.3	1	16/24
	2309	K.K#PVQLPGAYK.T	1214.68916	-1.82675	2	1.10E-05	0.95	3.67	0.00	966.9	1	18/27
	1102	L.KDGGHYDAEVK.T	1218.57494	-1.15529	2	1.29E-08	0.94	3.34	0.69	883.9	1	18/30

3387	I.FAGK#QLEDGR.T	1234.61745	-0.46891	2	1.43E-04	0.83	3.56	0.23	705.8	1	15/27
3913	R.LIFAGK#QLED.G	1247.66300	0.10623	2	3.16E-05	0.79	2.99	0.22	692.4	1	16/27
3567	D.SSLQDGEFIYK.V	1286.62631	-0.12618	2	2.87E-08	0.94	3.54	0.60	1050.8	1	18/30
2094	K.KTMGWEASTER.M	1295.60486	-0.90799	2	1.23E-07	0.95	3.93	0.75	692.8	1	18/30
1910	L.SSSEHM*QIFVK.T	1308.62527	0.01803	2	1.70E-04	0.89	2.94	0.77	359.9	1	16/30
1502	K.KTM*GWEASTER.M	1311.59978	0.74254	2	1.60E-05	0.93	3.94	0.75	319.9	1	17/30
1178	K.LKDGGHYDAEVK.T	1331.65901	0.25807	2	4.60E-08	0.97	4.11	0.67	1346.5	1	21/33
1377	R.PYEGTQTAK#LK.V	1349.70593	-0.69514	3	1.22E-01	0.42	3.43	0.05	223.0	1	21/60
2687	R.GTNFPSDGPVMQK.K	1377.64673	0.83349	2	3.57E-09	0.94	4.21	0.64	592.9	1	19/36
2306	R.GTNFPSDGPVM*QK.K	1393.64165	-0.26085	2	1.87E-08	0.96	4.70	0.79	657.9	1	19/36
3605	N.EDYTIVEQYER.A	1444.65907	-0.81732	2	7.10E-09	0.94	3.33	0.93	594.2	1	16/30
1216	K.L]KDGGHYDAEVK.T	1445.70191	-1.06572	2	2.49E-04	0.72	3.87	0.01	648.1	1	16/33
1216	K.LK#DGGHYDAEVK.T	1445.70191	-1.06572	2	1.83E-05	0.70	3.83	0.57	648.1	1	16/33
2991	R.MYPEDGALKGEIK.M	1450.72464	-0.49484	2	8.67E-07	0.83	3.11	0.51	355.9	1	19/36
2683	R.HSTGAENLYFQGH.M	1460.65532	-0.41531	2	2.04E-10	0.97	5.16	0.87	602.9	1	20/36
3444	R.LIFAGK#QLEDGR.T	1460.78558	-0.42171	2	3.97E-08	0.93	4.23	0.35	920.9	1	20/33
2568	R.M*YPEDGALKGEIK.M	1466.71956	3.39020	2	1.47E-04	0.94	3.53	0.75	713.2	1	21/36
1362	K.IQDKEGIPPDQQR.L	1523.78125	-0.20652	2	1.50E-08	0.94	4.39	0.52	571.1	1	21/36
3637	T.QDSSLQDGEFIYK.V	1529.71183	0.00686	2	9.46E-07	0.85	3.17	0.79	260.3	1	14/36
3673	N.E]DYTIVEQYER.A	1558.70197	0.46132	2	1.25E-09	0.98	4.19	0.00	1980.3	1	23/30
2699	R.HSTGAENLYFQGHM*.C	1607.69072	0.75897	2	9.90E-10	0.95	4.50	0.87	404.0	1	18/39
2650	K.KPVQLPGAYK#TDIK.L	1671.94280	-1.32702	3	2.21E-05	0.77	4.14	0.16	498.3	1	28/78
3711	T.VTQDSSLQDGEFIYK.V	1729.82792	-0.27822	2	8.23E-10	0.95	3.97	0.77	1022.2	1	20/42
3313	K.AYVK#HPADIPDYLK.L	1743.90642	-1.61735	3	2.15E-03	0.72	3.62	0.30	394.7	1	24/78
3678	K.LDITSHNEDYTIVEQ.Y	1776.82865	-0.47464	2	5.76E-03	0.69	2.23	0.62	364.2	1	16/42
3336	T.SHNEDYTIVEQYER.A	1782.79293	0.66302	2	8.68E-12	0.97	4.32	0.81	1668.6	1	21/39
4173	K.TITLEVEPSDTIENVK.A	1787.92730	3.75096	2	2.16E-06	0.94	3.99	0.65	724.7	1	24/45
2414	K.TTYM*AK#KPVQLPGAYK.T	1926.01532	-0.64942	3	4.31E-05	0.47	2.63	0.20	488.2	1	25/90
1631	F.EIEGEGEGRPYEGTQTAK.L	1950.90394	-2.33367	3	8.39E-02	0.66	2.72	0.71	181.9	1	18/102
3165	R.MEGSVNGHEFEIEGEGEGR.P	2062.87707	-1.10685	3	9.42E-11	0.97	5.38	0.80	1103.3	1	35/108
2864	R.M*EGSVNGHEFEIEGEGEGR.P	2078.87199	-0.88604	3	1.31E-14	0.97	5.23	0.82	1325.6	1	34/108
4281	G.GVVTVTQDSSLQDGEFIYK.V	2086.03389	-2.29675	2	3.33E-12	0.97	4.34	0.77	1433.8	1	24/54
3742	K.TITLEVEPSDTIENVK#AK.I	2101.10228	0.60534	3	5.25E-04	0.29	3.14	0.02	264.4	1	22/102
4077	K.LDITSHNEDYTIVEQYER.A	2225.03568	0.44329	2	8.98E-15	0.97	4.80	0.71	1321.1	1	24/51
2992	H.EFEIEGEGEGRPYEGTQTAK.L	2227.01495	0.15538	3	3.66E-04	0.74	2.63	0.78	243.2	1	21/114
4034	K.TLTGK#TITLEVEPSDTIENVK.A	2402.26605	1.38768	3	4.77E-11	0.94	5.94	0.05	1502.5	1	42/120
2698	N.GHEFEIEGEGEGRPYEGTQTAK.L	2421.09532	0.09569	3	2.50E-07	0.93	4.12	0.89	429.0	1	29/126

3183	R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L	3038.34323	1.26152	4	1.10E-08	0.96	5.35	-	658.5	1	44/243
3033	R.M*EGSVNGHEFEIEGEGEGRPYEGTQTAK.L	3054.33815	0.36029	4	2.02E-07	0.93	4.59	0.88	479.5	1	37/243
5869	H.MCELEELNVPGEIVESLSSSEHM*QIFVK.T	3250.53167	-0.62560	3	3.49E-05	0.77	3.01	0.63	273.2	1	27/162

	Reference	S8-E2B-40				P (pro)	Sf	Score	Coverage	MW	Accession	Peptide (Hits)
	Scan(s)	Peptide	MH+	DeltaM (ppm)	z	P (pep)	Sf	XC	DeltaCn	Sp	RSp	Ions
1	RFP_UB_new					1.10E-10	42.32	484.30	73.59	38172.1		49 (46 3 0 0 0)
	3503	S.TLHLVLR.L	851.54615	-1.59929	2	1.83E-05	0.59	2.38	-	385.6	1	14/18
	4438	K.LSFPEGFK.W	924.48254	-1.99621	2	3.64E-06	0.59	2.08	-	588.8	1	16/21
	3506	E.STLHLVLR.L	938.57818	-1.17483	2	4.34E-06	0.67	2.93	-	665.2	1	14/21
	2290	T.LSDYNIQK.E	980.50474	-2.35485	2	7.29E-06	0.88	2.97	0.65	404.2	1	13/21
	602	H.HASSEDVIK.E	985.49490	-1.96145	2	3.40E-06	0.92	3.06	0.81	473.4	1	15/24
	3151	H.PADIPDYLK.L	1031.54079	-1.03496	2	3.24E-06	0.91	2.94	0.65	710.3	1	15/24
	3684	K.ESTLHLVLR.L	1067.62077	-2.51037	2	3.30E-09	0.41	2.86	-	202.8	1	14/24
	6361	R.TLSDYNIQK.E	1081.55242	-2.03123	2	1.29E-07	0.90	2.48	0.85	385.7	1	15/24
	922	K.DGGHYDAEVK.T	1090.47998	-0.73835	2	3.95E-08	0.92	2.75	0.70	806.6	1	18/27
	6338	K.KPVQLPGAYK.T	1100.64626	-1.63486	2	3.70E-07	0.84	2.95	0.61	319.4	1	15/27
	3726	H.P]ADIPDYLK.L	1145.58369	-1.51126	2	8.30E-06	0.82	3.12	0.47	410.4	1	13/24
	4125	K.HPADIPDYLK.L	1168.59970	-1.60363	2	1.81E-10	0.84	2.53	0.91	187.4	1	13/27
	2097	K.TM*GWEASTER.M	1183.50482	-1.24646	2	4.47E-09	0.96	3.17	0.94	984.7	1	19/27
	3628	S.SLQDGEFIYK.V	1199.59428	-2.74276	2	5.24E-07	0.89	3.12	0.66	508.9	1	15/27
	3073	D.YTIVEQYER.A	1200.58953	-1.02010	2	1.11E-07	0.95	3.64	0.65	830.8	1	17/24
	3362	I.FAGK#QLEDGR.T	1234.61745	0.12432	2	1.68E-06	0.70	3.35	0.08	599.2	1	15/27
	2094	G.RTLSDYNIQK.E	1237.65353	-0.52257	2	2.19E-06	0.90	3.52	0.67	471.6	1	14/27
	3529	D.SSLQDGEFIYK.V	1286.62631	-1.45445	2	2.82E-06	0.95	3.06	0.89	997.6	1	17/30
	2109	K.KTMGWEASTER.M	1295.60486	-1.66174	2	4.17E-07	0.93	3.57	0.76	594.5	1	16/30
	1556	K.KTM*GWEASTER.M	1311.59978	-1.21192	2	5.23E-06	0.92	3.43	0.78	317.1	1	17/30
	816	K.LKDGGHYDAEVK.T	1331.65901	-0.93361	2	9.41E-10	0.94	3.53	0.75	834.7	1	19/33
	2741	R.GTNFPSDGPVMQK.K	1377.64673	-0.31841	2	5.02E-10	0.93	3.64	0.66	605.4	1	20/36
	5727	R.GTNFPSDGPVM*QK.K	1393.64165	-1.57472	2	1.12E-10	0.92	3.16	0.75	674.3	1	19/36
	3578	N.EDYTIVEQYER.A	1444.65907	-1.83129	2	9.37E-08	0.93	2.86	0.78	750.6	1	18/30
	1304	K.LK#DGGHYDAEVK.T	1445.70191	-2.50114	2	1.24E-05	0.74	3.86	0.00	674.6	1	17/33
	2938	R.MYPEDGALKGEIK.M	1450.72464	-1.25214	2	2.33E-10	0.88	2.92	0.69	381.3	1	20/36
	2791	R.HSTGAENLYFQGH.M	1460.65532	-0.83318	2	1.32E-08	0.93	3.55	0.76	556.0	1	19/36
	3358	R.LIFAGK#QLEDGR.T	1460.78558	-0.50527	2	1.45E-07	0.94	4.25	0.37	961.1	1	21/33
	2843	R.M*YPEDGALKGEIK.M	1466.71956	-1.68663	2	4.85E-06	0.91	3.33	0.76	493.2	1	18/36

1617	K.IQDKEGIPPDQQR.L	1523.78125	-1.00762	2	5.26E-10	0.94	4.03	0.61	604.2	1	21/36
3603	T.QDSSLQDGEFIYK.V	1529.71183	-1.90833	2	1.28E-05	0.84	2.98	0.77	268.6	1	15/36
3640	H.NEDYTIVEQYER.A	1558.70199	-0.96596	2	3.41E-09	0.97	3.93	0.89	1511.5	2	22/33
2711	R.HSTGAENLYFQGHM*.C	1607.69072	-1.29112	2	6.60E-09	0.91	3.24	0.90	387.3	1	17/39
2331	K.LRGTNFPSDGPVM*QK.K	1662.82682	-1.17764	3	4.55E-07	0.95	3.65	0.92	816.1	1	33/84
3675	T.VTQDSSLQDGEFIYK.V	1729.82792	-1.68958	2	3.36E-10	0.89	2.69	0.56	1086.8	1	20/42
3282	K.AYVK#HPADIPDYLK.L	1743.90642	-1.72235	3	8.55E-08	0.80	3.96	0.38	370.4	1	24/78
6147	K.TITLEVEPSDTIENVK.A	1787.92730	-1.02827	2	2.25E-10	0.88	3.70	0.55	515.5	1	19/45
2425	K.TTYM*AK#KPVQLPGAYK.T	1926.01532	-1.12477	3	1.24E-07	0.58	2.76	0.35	432.5	1	24/90
3167	R.MEGSVNGHEFEIEGEGEGR.P	2062.87707	-1.99447	3	1.66E-08	0.96	5.34	0.69	857.2	1	33/108
2886	R.M*EGSVNGHEFEIEGEGEGR.P	2078.87199	-0.40982	2	8.55E-10	0.88	2.76	0.87	423.4	1	21/54
4055	K.LDITSHNEDYTIVEQYER.A	2225.03568	-1.53779	3	2.93E-08	0.91	4.06	0.76	548.3	1	24/102
3982	K.TLTGKTITLEVEPSDTIENVK.A	2288.22315	-2.60092	3	2.52E-06	0.94	4.99	0.60	825.3	1	32/120
3990	K.TLTGK#TITLEVEPSDTIENVK.A	2402.26605	-1.66120	3	4.13E-09	0.94	5.91	0.62	1505.1	2	41/120
4718	R.VM*NFEDGGVVTVTQDSSLQDGEFIYK.V	2894.34005	0.95701	2	1.10E-10	0.81	2.56	0.77	371.6	1	20/75
2952	R.M*EGSVNGHEFEIEGEGEGRPYEGTQTAK.L	3054.33815	-0.71440	3	3.85E-07	0.89	4.04	0.84	208.6	1	27/162

	Reference	S9-E2B-80				P (pro)	Sf	Score	Coverage	MW	Accession	Peptide (Hits)
	Scan(s)	Peptide	MH+	DeltaM (ppm)	z	P (pep)	Sf	XC	DeltaCn	Sp	RSp	Ions
1	RFP_UB_new					1.05E-13	48.89	614.30	74.18	38172.1		62 (59 3 0 0 0)
	1645	K.LDITSHN.E	799.39446	-0.99437	2	1.38E-03	0.81	2.42	0.64	329.1	1	11/18
	3555	S.TLHLVLR.L	851.54615	-1.38426	2	1.50E-05	0.61	2.48	-	378.7	1	14/18
	1324	L.SDYNIQK.E	867.42067	-1.86646	2	1.24E-01	0.77	2.44	0.54	307.2	1	11/18
	2666	P.VQLPGAYK.T	875.49853	-1.68185	2	7.67E-04	0.80	2.29	0.84	231.2	1	11/21
	548	G.GHYDAEVK.T	918.43157	-2.33232	2	5.81E-03	0.90	3.17	0.53	470.2	1	15/21
	6568	K.LSFPEGFK.W	924.48254	-1.26998	2	7.40E-04	0.84	2.36	0.99	254.3	1	10/21
	3640	P.ADIPDYLK.L	934.48802	-1.76406	2	1.60E-07	0.50	2.61	-	342.1	1	14/21
	3558	E.STLHLVLR.L	938.57818	-2.41039	2	2.19E-05	0.76	3.21	-	674.5	1	15/21
	2940	K.PVQLPGAYK.T	972.55129	-2.79947	2	1.90E-04	0.84	2.66	0.59	521.5	1	14/24
	2405	T.LSDYNIQK.E	980.50474	-2.60385	2	3.38E-05	0.88	2.68	0.67	380.4	1	14/21
	577	R.PYEGTQTAK.L	994.48400	-2.33836	2	4.62E-06	0.91	3.37	0.54	523.3	1	16/24
	2419	R.MYPEDGALK.G	1023.48156	-1.73402	2	2.24E-02	0.36	2.36	0.42	192.7	1	9/24
	3271	H.PADIPDYLK.L	1031.54079	-2.10000	2	4.66E-04	0.84	2.64	0.64	523.6	1	13/24
	2119	R.M*YPEDGALK.G	1039.47648	-1.98738	2	2.24E-03	0.84	2.33	0.68	370.2	1	15/24
	3818	K.ESTLHLVLR.L	1067.62077	-1.82434	2	1.62E-08	0.47	3.10	-	195.6	1	14/24
	2911	R.TLSDYNIQK.E	1081.55242	-2.48269	2	2.03E-04	0.92	3.03	0.90	304.7	1	14/24
	583	K.DGGHYDAEVK.T	1090.47998	-2.19360	2	1.72E-05	0.87	3.07	0.73	343.2	1	14/27

3742	K.KPVQLPGAYK.T	1100.64626	-0.96941	2	1.30E-04	0.81	3.43	0.64	191.5	1		12/27
2247	N.FPSDGPVM*QK.K	1121.52958	-2.92828	2	3.13E-03	0.65	2.54	0.50	215.0	1		13/27
2768	K.TMGWEASTER.M	1167.50990	-1.43243	2	1.41E-02	0.92	3.80	0.48	758.2	1		17/27
4938	K.HPADIPDYLK.L	1168.59970	-1.81254	2	1.08E-08	0.88	3.08	0.75	229.3	1		15/27
2103	K.TM*GWEASTER.M	1183.50482	-1.65903	2	2.55E-08	0.96	3.14	0.95	816.8	1		18/27
2420	K.K#PVQLPGAYK.T	1214.68916	-1.42477	2	2.35E-04	0.90	3.57	0.00	697.8	1		15/27
1019	L.KDGGHYDAEVK.T	1218.57494	-2.85826	2	4.80E-04	0.87	3.02	0.70	446.1	1		15/30
3682	D.SSLQDGEFIYK.V	1286.62631	-0.50568	2	6.02E-09	0.92	3.18	0.66	870.7	1		16/30
1638	K.KTM*GWEASTER.M	1311.59978	-1.39806	2	6.21E-05	0.93	3.95	0.76	334.6	1		17/30
1141	K.LKDGGHYDAEVK.T	1331.65901	-1.66696	2	9.42E-09	0.96	4.02	0.73	1041.1	1		19/33
1430	R.PYEGTQTAK#LK.V	1349.70593	-1.50912	3	2.92E-02	0.21	2.56	0.09	204.7	1		19/60
2873	R.GTNFPSDGPVMQK.K	1377.64673	-1.11588	2	2.72E-08	0.93	4.11	0.61	564.0	1		19/36
2131	R.GTNFPSDGPVM*QK.K	1393.64165	-1.74990	2	4.75E-10	0.93	4.07	0.76	538.2	1		17/36
1215	K.LK#DGGHYDAEVK.T	1445.70191	-3.26108	2	1.34E-03	0.57	3.63	0.64	457.2	1		15/33
2801	R.HSTGAENLYFQGH.M	1460.65532	-1.00032	2	9.22E-10	0.97	5.06	0.88	762.2	1		22/36
3460	R.LIFAGK#QLEDGR.T	1460.78558	-1.50805	2	4.07E-07	0.81	3.74	0.24	622.7	1		16/33
2659	R.M*YPEDGALKGEIK.M	1466.71956	-1.68663	2	4.97E-06	0.93	3.41	0.77	657.0	1		19/36
2151	K.IQDKEGIPPDQQR.L	1523.78125	-0.84740	2	5.02E-05	0.92	3.87	0.70	432.9	1		17/36
3748	T.QDSSLQDGEFIYK.V	1529.71183	-1.74873	2	6.84E-07	0.87	3.63	0.76	259.1	1		13/36
2805	R.M*YPEDGALK#GEIK.M	1580.76246	-1.95469	3	8.10E-04	0.51	2.82	0.24	337.0	1		24/72
1907	R.GTNFPSDGPVM*QK#K.T	1635.77951	-2.60904	3	5.47E-01	0.18	2.60	0.52	279.2	1		21/78
5272	F.AWDILSPQFQYGSK.A	1639.81148	-2.47767	2	4.72E-10	0.96	4.24	0.86	652.8	1		20/39
2729	K.KPVQLPGAYK#TDIK.L	1671.94280	-3.40784	3	6.43E-08	0.86	4.33	0.25	727.2	1		29/78
3824	T.VTQDSSLQDGEFIYK.V	1729.82792	-2.32469	2	1.16E-05	0.91	3.36	0.70	611.8	1		20/42
3449	T.SHNEDYTIVEQYER.A	1782.79293	1.62162	2	2.30E-11	0.97	4.58	0.78	1611.8	1		21/39
5232	K.TITLEVEPSDTIENVK.A	1787.92730	-1.16482	2	2.13E-06	0.94	4.40	0.72	562.1	1		20/45
2531	K.TTYM*AK#KPVQLPGAYK.T	1926.01532	-2.93109	3	1.27E-04	0.38	2.78	0.07	468.9	1		25/90
3286	R.MEGSVNGHEFEIEGEGEGR.P	2062.87707	-1.37314	3	9.45E-11	0.96	5.37	0.76	868.3	1		32/108
2984	R.M*EGSVNGHEFEIEGEGEGR.P	2078.87199	-1.32644	3	1.05E-13	0.97	5.04	0.84	1635.3	1		37/108
3854	K.TITLEVEPSDTIENVK#AK.I	2101.10228	-1.74764	3	7.26E-05	0.31	3.22	0.01	223.2	1		24/102
4347	K.LDITSHNEDYTIVEQYER.A	2225.03568	-1.29091	3	7.92E-08	0.96	4.69	0.85	883.6	1		30/102
4208	K.TLTGK#TITLEVEPSDTIENVK.A	2402.26605	-2.11853	3	1.25E-08	0.93	5.65	0.04	1317.6	1		40/120
2824	N.GHEFEIEGEGEGRPYEGTQTAK.L	2421.09532	-1.03875	3	2.15E-06	0.90	4.00	0.83	268.7	1		26/126
3291	R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L	3038.34323	0.88427	3	3.22E-09	0.95	5.00	0.79	719.1	1		32/162
3040	R.M*EGSVNGHEFEIEGEGEGRPYEGTQTAK.L	3054.33815	-1.95775	4	1.29E-05	0.88	4.48	0.51	490.5	1		38/243

Reference	**S11-E2C-40**				**P (pro)**	**Sf**	**Score**	**Coverage**	**MW**	**Accession**	**Peptide (Hits)**

	Scan(s)	Peptide	MH+	DeltaM (ppm)	z	P (pep)	Sf	XC	DeltaCn	Sp	RSp	Ions
1	RFP_UB_new					2.10E-14	66.58	814.27	74.80	38172.1		82 (79 3 0 0 0)
	1591	K.LDITSHN.E	799.39446	-2.36870	2	4.30E-02	0.87	2.18	0.69	430.8	1	13/18
	1114	D.GALKGEIK.M	815.49853	-2.55403	2	6.66E-03	0.57	2.96	-	531.0	1	13/21
	3419	S.TLHLVLR.L	851.54615	-2.38772	2	4.44E-05	0.72	2.29	-	501.0	1	16/18
	1033	G.HYDAEVK.T	861.41011	-2.15641	2	6.98E-02	0.83	2.12	0.50	595.0	1	13/18
	1323	L.SDYNIQK.E	867.42067	-3.48484	2	5.89E-01	0.83	2.31	0.59	443.3	1	12/18
	2566	P.VQLPGAYK.T	875.49853	-2.93672	2	5.67E-05	0.67	2.05	0.84	169.6	1	9/21
	606	K.LKDGGHYD.A	904.41592	-2.94812	2	5.22E-02	0.71	2.26	0.79	271.9	1	9/21
	1101	G.GHYDAEVK.T	918.43157	-2.79751	2	1.40E-01	0.93	2.68	0.61	843.9	1	17/21
	5836	K.LSFPEGFK.W	924.48254	-2.59040	2	4.54E-03	0.86	2.54	0.88	377.1	1	11/21
	3567	P.ADIPDYLK.L	934.48802	-2.67846	2	4.09E-01	0.21	2.24	-	291.7	1	11/21
	3514	E.STLHLVLR.L	938.57818	-3.06068	2	8.41E-05	0.63	3.03	-	469.8	1	14/21
	2835	K.PVQLPGAYK.T	972.55129	-3.30153	2	5.80E-05	0.88	2.74	0.61	578.7	1	15/24
	2151	F.PSDGPVM*QK.K	974.46116	-2.75055	2	1.82E-04	0.78	2.92	0.61	243.7	1	12/24
	2309	T.LSDYNIQK.E	980.50474	-2.66610	2	1.30E-05	0.90	2.97	0.67	532.0	1	13/21
	903	H.HASSEDVIK.E	985.49490	-3.69558	2	5.87E-05	0.86	3.19	0.74	313.7	1	12/24
	570	R.PYEGTQTAK.L	994.48400	-2.52248	2	4.56E-04	0.89	2.70	0.68	533.7	1	15/24
	2405	R.MYPEDGALK.G	1023.48156	-3.52307	2	2.51E-04	0.82	2.67	0.68	286.7	1	13/24
	3661	H.PADIPDYLK.L	1031.54079	-2.92837	2	1.23E-03	0.90	3.08	0.65	604.7	1	14/24
	2167	R.M*YPEDGALK.G	1039.47648	-3.51403	2	6.96E-02	0.85	2.25	0.67	400.2	1	16/24
	3623	L.KLSFPEGFK.W	1052.57751	-2.73173	2	5.11E-02	0.60	2.13	0.80	133.5	1	9/24
	4415	K.ESTLHLVLR.L	1067.62077	-3.31074	2	2.03E-07	0.58	3.08	-	364.5	1	15/24
	3737	R.TLSDYNIQK.E	1081.55242	-1.12830	2	4.15E-04	0.95	3.48	0.79	578.9	1	17/24
	1991	T.M*GWEASTER.M	1082.45714	-2.65045	2	7.86E-07	0.50	2.48	-	489.7	1	15/24
	1590	K.DGGHYDAEVK.T	1090.47998	-2.97719	2	1.81E-03	0.87	3.10	0.66	509.9	1	14/27
	2548	K.KPVQLPGAYK.T	1100.64626	-3.40938	2	2.54E-05	0.84	3.27	0.69	220.2	1	13/27
	1831	N.FPSDGPVM*QK.K	1121.52958	-3.36365	2	9.84E-04	0.83	3.08	0.68	282.0	1	13/27
	2581	Y.PEDGALKGEIK.M	1156.62083	-2.89640	2	2.97E-04	0.89	3.73	0.45	585.9	1	17/30
	2659	K.TMGWEASTER.M	1167.50990	-3.31444	2	6.44E-06	0.95	3.72	0.70	731.6	1	18/27
	3924	K.HPADIPDYLK.L	1168.59970	-2.64821	2	7.60E-08	0.90	2.80	0.88	263.0	1	16/27
	2042	K.TM*GWEASTER.M	1183.50482	-1.34960	2	4.61E-07	0.96	3.29	0.95	924.3	1	18/27
	3635	S.SLQDGEFIYK.V	1199.59428	-2.94628	2	7.61E-06	0.88	3.26	0.64	504.3	1	14/27
	3073	D.YTIVEQYER.A	1200.58953	-2.34188	2	4.62E-05	0.95	3.31	0.62	1108.9	1	18/24
	2346	K.K#PVQLPGAYK.T	1214.68916	-3.03269	2	8.84E-05	0.94	3.68	0.00	1097.9	1	16/27
	1134	L.KDGGHYDAEVK.T	1218.57494	-1.44181	3	6.17E-06	0.91	3.54	0.68	786.0	1	25/60
	2294	E.VEPSDTIENVK.A	1230.62122	-1.95120	2	5.89E-01	0.30	2.25	0.48	58.4	1	10/30

3358	I.FAGK#QLEDGR.T	1234.61745	-1.75426	2	3.52E-04	0.83	3.39	0.18	812.5	1	16/27
3867	R.LIFAGK#QLED.G	1247.66300	-2.14407	2	4.18E-05	0.89	3.07	0.48	763.9	1	16/27
3540	D.SSLQDGEFIYK.V	1286.62631	-2.78271	2	1.59E-07	0.96	3.55	0.85	1033.8	1	18/30
2131	K.KTMGWEASTER.M	1295.60486	-1.85017	2	8.65E-07	0.96	3.74	0.80	861.2	1	19/30
1553	K.KTM*GWEASTER.M	1311.59978	-2.14262	2	2.55E-06	0.93	3.35	0.82	382.4	1	18/30
1208	K.LKDGGHYDAEVK.T	1331.65901	-1.94196	2	1.10E-07	0.95	4.20	0.66	986.3	1	18/33
3314	R.LIFAGKQLEDGR.T	1346.74268	-2.82980	3	2.96E-04	0.71	3.05	0.54	248.1	1	22/66
2830	R.GTNFPSDGPVMQK.K	1377.64673	-2.97664	2	8.92E-09	0.91	4.15	0.56	513.0	1	18/36
2141	R.GTNFPSDGPVM*QK.K	1393.64165	-4.55281	2	2.50E-07	0.96	4.43	0.80	647.2	1	19/36
3729	Q.DSSLQDGEFIYK.V	1401.65325	-3.05226	2	2.43E-05	0.86	2.97	0.54	595.4	1	17/33
1567	K.K#TM*GWEASTER.M	1425.64268	-3.53789	3	9.56E-01	0.86	3.44	0.62	374.0	1	24/60
3577	N.EDYTIVEQYER.A	1444.65907	-2.67626	2	1.48E-07	0.94	3.20	0.86	649.5	1	17/30
1248	K.L]KDGGHYDAEVK.T	1445.70191	-3.26108	2	7.14E-03	0.75	3.98	0.05	647.1	1	16/33
1325	K.LK#DGGHYDAEVK.T	1445.70191	-3.50258	3	9.50E-03	0.40	3.06	0.04	429.4	1	22/66
2224	G.T]NFPSDGPVM*QK.K	1450.66308	-2.57359	2	7.66E-06	0.93	3.39	0.82	529.7	1	17/33
2873	R.MYPEDGALKGEIK.M	1450.72464	-2.00944	2	4.08E-04	0.87	3.07	0.71	311.2	1	18/36
2700	R.HSTGAENLYFQGH.M	1460.65532	-2.92248	2	8.39E-08	0.97	4.99	0.89	758.1	1	22/36
3566	R.LIFAGK#QLEDGR.T	1460.78558	-1.50805	2	1.72E-03	0.84	3.71	0.27	643.6	1	17/33
2492	R.M*YPEDGALKGEIK.M	1466.71956	-2.85180	2	3.21E-05	0.95	3.86	0.73	939.1	1	21/36
1392	K.IQDKEGIPPDQQR.L	1523.78125	-1.40817	2	2.31E-08	0.95	4.32	0.64	649.5	1	22/36
3601	T.QDSSLQDGEFIYK.V	1529.71183	-2.46693	2	3.22E-06	0.91	3.65	0.82	342.8	1	15/36
2712	R.HSTGAENLYFQGHM*.C	1607.69072	-1.89855	2	1.20E-08	0.92	3.68	0.85	349.3	1	18/39
3291	K.AYVKHPADIPDYLK.L	1629.86352	-2.82125	3	1.18E-06	0.95	4.41	0.71	1130.6	1	30/78
2758	K.LRGTNFPSDGPVMQK.K	1646.83190	-3.56961	3	9.49E-01	0.87	3.39	0.77	414.8	1	25/84
2335	K.LRGTNFPSDGPVM*QK.K	1662.82682	-2.71928	3	8.75E-07	0.96	4.08	0.94	940.0	1	33/84
2669	K.KPVQLPGAYK#TDIK.L	1671.94280	-2.64122	3	1.85E-06	0.82	4.47	0.20	529.5	1	27/78
3319	K.AYVK#HPADIPDYLK.L	1743.90642	-4.66227	3	9.44E-07	0.50	2.77	0.31	294.6	1	22/78
3857	K.TITLEVEPSDTIENVK.A	1787.92730	-3.07652	2	2.17E-06	0.93	4.11	0.61	658.0	1	22/45
3589	G.KTITLEVEPSDTIENVK.A	1916.02226	-3.19239	3	4.47E-01	0.82	3.74	0.46	527.7	1	26/96
2444	K.TTYM*AK#KPVQLPGAYK.T	1926.01532	-2.93109	3	2.69E-04	0.45	3.14	0.18	324.9	1	22/90
4050	K.LDITSHNEDYTIVEQYER.A	2225.03568	-1.53175	2	2.10E-14	0.97	4.65	0.75	1097.4	1	23/51
2997	H.EFEIEGEGEGRPYEGTQTAK.L	2227.01495	-2.96899	3	1.37E-01	0.74	2.70	0.69	279.6	1	25/114
3985	K.TLTGKTITLEVEPSDTIENVK.A	2288.22315	-2.52090	3	3.42E-10	0.95	4.86	0.65	1134.6	1	36/120
3988	K.TLTGK#TITLEVEPSDTIENVK.A	2402.26605	-1.20387	3	3.79E-10	0.91	5.30	0.05	1240.9	1	40/120
2717	N.GHEFEIEGEGEGRPYEGTQTAK.L	2421.09532	-2.92948	3	8.62E-08	0.94	4.56	0.90	512.5	1	33/126
4765	R.VM*NFEDGGVVTVTQDSSLQDGEFIYK.V	2894.34005	-3.34489	2	9.11E-05	0.83	2.51	0.78	436.6	1	21/75
3034	R.M*EGSVNGHEFEIEGEGEGRPYEGTQTAK.L	3054.33815	-1.55809	4	6.78E-06	0.94	5.02	0.82	595.8	1	44/243

	Reference	S12-E2C-80				P (pro)	Sf	Score	Coverage	MW	Accession	Peptide (Hits)
	Scan(s)	Peptide	MH+	DeltaM (ppm)	z	P (pep)	Sf	XC	DeltaCn	Sp	RSp	Ions
1	RFP_UB_new					1.42E-10	43.30	546.24	71.20	38172.1		55 (53 2 0 0 0)
	1040	D.GALKGEIK.M	815.49853	-2.47919	2	1.67E-02	0.53	2.68	-	597.0	1	13/21
	1257	S.DTIENVK.A	818.42542	-1.51886	2	4.96E-02	0.55	2.24	0.31	245.8	1	11/18
	3557	S.TLHLVLR.L	851.54615	-2.38772	2	1.80E-04	0.72	2.30	-	505.0	1	16/18
	826	G.GHYDAEVK.T	918.43157	-2.39877	2	5.93E-03	0.47	2.16	0.56	148.2	1	9/21
	5469	K.LSFPEGFK.W	924.48254	-2.78846	2	3.32E-04	0.84	2.40	0.97	283.4	1	10/21
	3582	P.ADIPDYLK.L	934.48802	-2.02532	2	3.59E-02	0.33	2.17	-	333.4	1	13/21
	3559	E.STLHLVLR.L	938.57818	-2.34536	2	2.05E-05	0.72	2.93	-	706.8	1	15/21
	2396	T.LSDYNIQK.E	980.50474	-2.60385	2	2.26E-05	0.91	3.12	0.66	482.0	1	14/21
	560	R.PYEGTQTAK.L	994.48400	-3.13622	2	1.98E-01	0.81	2.33	0.61	492.5	1	14/24
	2586	R.MYPEDGALK.G	1023.48156	-3.16526	2	5.44E-05	0.73	2.47	0.54	290.3	1	13/24
	3288	H.PADIPDYLK.L	1031.54079	-2.92837	2	1.78E-03	0.86	2.76	0.77	471.9	1	12/24
	2128	R.M*YPEDGALK.G	1039.47648	-1.98738	2	1.27E-03	0.79	2.07	0.63	339.8	1	15/24
	4122	K.ESTLHLVLR.L	1067.62077	-3.53942	2	1.04E-07	0.90	3.14	-	138.7	1	12/24
	2581	R.TLSDYNIQK.E	1081.55242	-2.93415	2	2.20E-05	0.95	3.35	0.87	500.7	1	17/24
	1348	K.DGGHYDAEVK.T	1090.47998	-2.97719	2	2.60E-05	0.87	3.11	0.70	367.7	1	14/27
	5130	K.KPVQLPGAYK.T	1100.64626	-2.41121	2	5.46E-03	0.79	3.29	0.52	275.1	1	13/27
	2664	Y.PEDGALKGEIK.M	1156.62083	-2.79086	2	8.08E-06	0.81	3.28	0.42	492.1	1	15/30
	2754	K.TMGWEASTER.M	1167.50990	-2.68710	2	3.51E-07	0.92	3.69	0.61	546.7	1	16/27
	4276	K.HPADIPDYLK.L	1168.59970	-2.85713	2	5.04E-07	0.85	2.90	0.76	172.4	1	14/27
	2082	K.TM*GWEASTER.M	1183.50482	-2.58732	2	1.35E-08	0.96	3.36	0.92	881.3	1	18/27
	2437	K.K#PVQLPGAYK.T	1214.68916	-2.93219	2	2.13E-06	0.96	3.60	0.00	1611.4	1	19/27
	1199	L.KDGGHYDAEVK.T	1218.57494	-2.25721	2	6.50E-05	0.81	2.95	0.48	470.7	1	16/30
	3493	I.FAGK#QLEDGR.T	1234.61745	-2.54525	2	1.28E-07	0.81	3.48	0.20	692.6	1	15/27
	3656	D.SSLQDGEFIYK.V	1286.62631	-3.44685	2	9.22E-10	0.93	3.52	0.73	710.8	1	16/30
	2197	K.KTMGWEASTER.M	1295.60486	-2.88658	2	6.24E-08	0.95	4.19	0.80	590.3	1	18/30
	1582	K.KTM*GWEASTER.M	1311.59978	-1.86341	2	1.70E-05	0.90	3.54	0.70	318.0	1	16/30
	1232	K.LKDGGHYDAEVK.T	1331.65901	-2.58363	2	3.93E-08	0.96	4.16	0.65	1066.8	1	19/33
	2753	R.GTNFPSDGPVMQK.K	1377.64673	-2.44500	2	4.87E-10	0.92	3.92	0.61	586.3	1	19/36
	2296	R.GTNFPSDGPVM*QK.K	1393.64165	0.79024	2	1.33E-07	0.94	4.19	0.78	585.0	1	18/36
	3839	Q.DSSLQDGEFIYK.V	1401.65325	-2.09427	2	7.97E-07	0.72	2.52	0.61	337.9	1	14/33
	3695	N.EDYTIVEQYER.A	1444.65907	-2.16928	2	2.62E-08	0.89	2.68	0.86	473.2	1	15/30
	2979	R.MYPEDGALKGEIK.M	1450.72464	-2.76674	2	2.70E-02	0.55	2.80	0.58	104.9	1	11/36
	2795	R.HSTGAENLYFQGH.M	1460.65532	-2.17033	2	1.76E-07	0.96	4.18	0.86	646.3	1	20/36

3542	R.LIFAGK#QLEDGR.T	1460.78558	-1.34092	2	3.64E-09	0.85	3.70	0.32	602.8	1	17/33
2779	R.M*YPEDGALKGEIK.M	1466.71956	-2.76858	2	1.91E-06	0.91	3.32	0.78	406.9	1	18/36
3870	R.MEGSVNGHEFEIE.G	1477.62638	-2.63994	2	1.03E-05	0.84	3.02	0.75	364.0	1	14/36
1339	K.IQDKEGIPPDQQR.L	1523.78125	-2.20927	2	1.33E-09	0.94	4.10	0.58	596.0	1	21/36
3714	T.QDSSLQDGEFIYK.V	1529.71183	-1.82853	2	1.34E-06	0.86	3.06	0.78	285.6	1	15/36
928	E.GEGEGRPYEGTQTAK.L	1579.73469	-2.17824	2	9.11E-03	0.75	2.72	0.81	175.0	1	13/42
2868	K.LRGTNFPSDGPVMQK.K	1646.83190	-2.23537	3	1.28E-02	0.91	3.14	0.79	777.7	1	29/84
2424	K.LRGTNFPSDGPVM*QK.K	1662.82682	-2.38893	3	8.72E-08	0.96	4.11	0.91	844.2	1	33/84
2757	K.KPVQLPGAYK#TDIK.L	1671.94280	-2.31267	3	2.81E-04	0.47	3.32	0.11	338.1	1	23/78
3427	K.AYVK#HPADIPDYLK.L	1743.90642	-2.98232	3	1.78E-03	0.50	3.12	0.31	231.7	1	19/78
5840	K.TITLEVEPSDTIENVK.A	1787.92730	-1.84757	2	6.19E-07	0.93	4.21	0.71	427.7	1	19/45
4180	K.LDITSHNEDYTIVEQYER.A	2225.03568	-2.60760	3	1.42E-10	0.91	4.07	0.75	596.1	1	24/102
4127	K.TLTGK#TITLEVEPSDTIENVK.A	2402.26605	-2.34720	3	2.10E-09	0.90	4.81	0.14	1108.0	1	37/120
4848	R.VM*NFEDGGVVTVTQDSSLQDGEFIYK.V	2894.34005	0.61961	2	2.76E-03	0.64	2.24	0.75	174.5	1	14/75

	Reference	S13-c5B-20				P (pro)	Sf	Score	Coverage	MW	Accession	Peptide (Hits)
	Scan(s)	Peptide	MH+	DeltaM (ppm)	z	P (pep)	Sf	XC	DeltaCn	Sp	RSp	Ions
1	RFP_UB_new					4.39E-10	50.41	638.24	70.30	38172.1		65 (59 6 0 0 0)
	1052	D.GALKGEIK.M	815.49853	3.80770	2	1.15E-02	0.62	3.04	-	646.0	1	13/21
	1125	R.HSTGAENL.Y	828.38462	4.06241	2	9.85E-03	0.18	2.08	0.22	186.0	1	9/21
	3355	S.TLHLVLR.L	851.54615	4.34979	2	2.39E-04	0.55	2.13	-	397.6	1	14/18
	1060	G.HYDAEVK.T	861.41011	3.93712	2	1.93E-02	0.85	2.35	0.58	540.8	1	12/18
	1321	L.SDYNIQK.E	867.42067	3.12938	2	2.17E-01	0.69	2.14	0.54	380.4	1	10/18
	907	G.GHYDAEVK.T	918.43157	2.51896	2	5.14E-02	0.79	2.56	0.61	321.2	1	12/21
	4020	K.LSFPEGFK.W	924.48254	3.08740	2	2.32E-05	0.89	2.24	0.81	514.6	1	14/21
	3385	P.ADIPDYLK.L	934.48802	2.87324	2	1.34E-06	0.24	2.16	-	263.6	1	12/21
	3354	E.STLHLVLR.L	938.57818	3.70237	2	2.34E-05	0.67	3.01	-	608.5	1	14/21
	2739	K.PVQLPGAYK.T	972.55129	2.84873	2	2.35E-05	0.82	2.72	0.52	506.9	1	14/24
	2054	F.PSDGPVM*QK.K	974.46116	3.57556	2	9.31E-03	0.84	3.05	0.64	274.4	1	13/24
	2225	T.LSDYNIQK.E	980.50474	2.37605	2	8.29E-05	0.93	2.91	0.78	560.6	1	15/21
	710	R.PYEGTQTAK.L	994.48400	2.08055	2	1.73E-02	0.92	2.55	0.72	763.9	1	17/24
	2370	R.MYPEDGALK.G	1023.48156	2.67896	2	4.43E-05	0.87	2.52	0.71	389.7	1	15/24
	3066	H.PADIPDYLK.L	1031.54079	2.98852	2	4.17E-04	0.88	2.73	0.75	530.5	1	13/24
	2067	R.M*YPEDGALK.G	1039.47648	3.06230	2	5.71E-03	0.86	2.63	0.56	429.0	1	16/24
	1716	K.LDITSHNED.Y	1043.46399	2.26350	2	1.30E-03	0.81	2.22	0.72	409.8	1	13/24
	3437	K.ESTLHLVLR.L	1067.62077	3.66391	2	3.86E-08	0.51	2.74	-	237.8	1	16/24
	2326	R.TLSDYNIQK.E	1081.55242	2.59627	2	5.01E-06	0.95	2.86	0.96	561.0	1	18/24

1892	T.M*GWEASTER.M	1082.45714	2.87536	2	6.69E-04	0.94	2.77	0.86	785.3	1	17/24
1037	K.DGGHYDAEVK.T	1090.47998	3.06767	2	3.93E-06	0.91	3.01	0.76	536.6	1	16/27
2118	K.KPVQLPGAYK.T	1100.64626	2.46873	2	1.58E-06	0.88	3.26	0.61	373.5	1	16/27
2579	Y.PEDGALKGEIK.M	1156.62083	3.75265	2	9.74E-05	0.72	2.98	0.44	373.3	1	14/30
2682	K.TMGWEASTER.M	1167.50990	3.27260	2	4.34E-03	0.93	3.65	0.68	534.1	1	16/27
3255	K.HPADIPDYLK.L	1168.59970	3.30593	2	2.50E-07	0.87	2.81	0.93	155.2	1	13/27
2049	K.TM*GWEASTER.M	1183.50482	3.08555	2	2.42E-05	0.91	2.90	0.85	564.0	1	14/27
2398	R.TLSDYNIQKE.S	1210.59501	-2.00857	2	1.16E-02	0.59	2.21	0.67	120.7	1	11/27
2264	K.K#PVQLPGAYK.T	1214.68916	3.29850	2	4.22E-05	0.88	2.75	0.00	810.1	1	14/27
1265	L.KDGGHYDAEVK.T	1218.57494	4.94433	3	1.45E-02	0.78	3.06	0.64	403.3	1	19/60
3215	R.HSTGAENLYFQ.G	1266.57494	2.84000	2	6.75E-03	0.38	2.02	0.46	295.8	1	11/30
3443	D.SSLQDGEFIYK.V	1286.62631	3.28937	2	5.98E-07	0.90	2.73	0.76	726.4	1	16/30
2833	L.SSSEHMQIFVK.T	1292.63035	3.07651	2	4.52E-05	0.89	2.76	0.80	464.4	1	16/30
2047	K.KTMGWEASTER.M	1295.60486	2.95498	2	2.51E-07	0.91	3.86	0.72	365.0	1	14/30
1822	L.SSSEHM*QIFVK.T	1308.62527	3.37616	2	5.80E-05	0.90	3.02	0.80	323.5	1	17/30
1504	K.KTM*GWEASTER.M	1311.59978	3.31498	3	4.35E-02	0.84	3.56	0.68	250.3	1	21/60
1130	K.LKDGGHYDAEVK.T	1331.65901	3.74145	2	6.77E-09	0.95	4.02	0.65	994.4	1	18/33
2646	R.GTNFPSDGPVMQK.K	1377.64673	4.90946	2	4.39E-10	0.92	4.12	0.60	519.5	1	18/36
2246	R.GTNFPSDGPVM*QK.K	1393.64165	3.94351	2	1.25E-05	0.94	3.59	0.79	654.0	1	19/36
3480	N.EDYTIVEQYER.A	1444.65907	3.91455	2	2.03E-08	0.83	2.82	0.73	373.1	1	13/30
1238	K.LK#DGGHYDAEVK.T	1445.70191	2.81837	2	1.91E-03	0.45	3.34	0.50	412.5	1	14/33
2864	R.MYPEDGALKGEIK.M	1450.72464	3.62824	2	6.50E-08	0.87	2.89	0.71	320.8	1	19/36
2623	R.HSTGAENLYFQGH.M	1460.65532	2.66765	3	2.72E-05	0.91	3.32	0.78	785.6	1	25/72
3275	R.LIFAGK#QLEDGR.T	1460.78558	3.17158	2	6.42E-07	0.88	3.89	0.34	619.0	1	18/33
2564	R.M*YPEDGALKGEIK.M	1466.71956	4.72183	2	5.19E-04	0.95	3.39	0.78	845.8	1	21/36
1986	K.IQDKEGIPPDQQR.L	1523.78125	3.95921	2	1.91E-07	0.95	4.13	0.65	652.3	1	22/36
3508	T.QDSSLQDGEFIYK.V	1529.71183	4.07664	2	2.21E-04	0.65	2.47	0.53	251.5	1	15/36
2619	R.HSTGAENLYFQGHM*.C	1607.69072	3.74980	3	1.32E-03	0.92	3.61	0.88	728.0	1	22/78
2672	K.LRGTNFPSDGPVMQK.K	1646.83190	3.10158	3	9.20E-04	0.92	3.08	0.83	956.8	1	30/84
2144	K.LRGTNFPSDGPVM*QK.K	1662.82682	2.45622	3	6.33E-02	0.84	3.06	0.71	433.7	1	26/84
2551	K.KPVQLPGAYK#TDIK.L	1671.94280	3.05364	3	6.73E-05	0.79	3.56	0.28	681.8	1	28/78
3230	K.AYVK#HPADIPDYLK.L	1743.90642	2.68754	3	6.78E-03	0.62	2.75	0.41	415.7	1	22/78
3883	K.TITLEVEPSDTIENVK.A	1787.92730	2.95828	3	9.11E-09	0.91	3.79	0.62	790.6	1	30/90
3073	R.MEGSVNGHEFEIEGEGEGR.P	2062.87707	3.15374	3	1.21E-04	0.89	3.73	0.85	390.9	1	24/108
3580	K.TITLEVEPSDTIENVK#AK.I	2101.10228	4.00409	3	8.44E-06	0.76	3.20	0.60	269.2	1	24/102
3911	K.LDITSHNEDYTIVEQYER.A	2225.03568	3.31751	3	5.15E-08	0.90	3.38	0.73	748.1	1	27/102

	Reference	S14-c5B-40				P (pro)	Sf	Score	Coverage	MW	Accession	Peptide (Hits)
	Scan(s)	Peptide	MH+	DeltaM (ppm)	z	P (pep)	Sf	XC	DeltaCn	Sp	RSp	Ions
1	RFP_UB_new					9.99E-15	31.88	404.24	60.80	38172.1		41 (38 3 0 0 0)
	5577	K.LSFPEGFK.W	924.48254	4.86996	2	7.09E-05	0.89	2.42	0.95	419.1	1	12/21
	3439	E.STLHLVLR.L	938.57818	4.80787	2	1.15E-06	0.67	2.80	-	579.7	1	15/21
	2194	T.LSDYNIQK.E	980.50474	4.92824	2	2.45E-05	0.90	3.21	0.65	436.9	1	13/21
	910	H.HASSEDVIK.E	985.49490	4.97511	2	1.71E-03	0.89	2.79	0.82	334.5	1	14/24
	708	R.PYEGTQTAK.L	994.48400	4.47412	2	1.70E-04	0.90	2.80	0.61	652.0	1	16/24
	2349	R.MYPEDGALK.G	1023.48156	4.46800	2	1.66E-04	0.85	2.25	0.73	353.5	1	15/24
	3590	H.PADIPDYLK.L	1031.54079	4.52692	2	3.51E-04	0.93	3.08	0.71	673.8	1	16/24
	1854	R.M*YPEDGALK.G	1039.47648	4.70638	2	7.34E-02	0.55	2.01	0.44	229.5	1	13/24
	4621	K.EGIPPDQQR.L	1039.51670	4.76707	2	3.76E-01	0.40	2.08	0.53	81.2	1	10/24
	4311	K.ESTLHLVLR.L	1067.62077	4.80730	2	2.43E-06	0.35	3.07	-	218.5	1	12/24
	5585	R.TLSDYNIQK.E	1081.55242	4.40213	2	4.52E-04	0.86	2.84	0.92	180.1	1	11/24
	1862	T.M*GWEASTER.M	1082.45714	4.90524	2	7.39E-06	0.91	2.40	0.80	600.0	1	16/24
	865	K.DGGHYDAEVK.T	1090.47998	4.85874	2	1.97E-07	0.82	2.59	0.46	622.5	1	16/27
	3753	K.KPVQLPGAYK.T	1100.64626	4.24326	2	5.51E-03	0.80	3.19	0.51	260.9	1	14/27
	1683	N.FPSDGPVM*QK.K	1121.52958	4.03766	2	2.24E-04	0.78	2.75	0.63	319.5	1	13/27
	2572	K.TMGWEASTER.M	1167.50990	4.73638	2	4.19E-07	0.95	3.88	0.73	741.9	1	18/27
	6098 - 6123	K.HPADIPDYLK.L	1168.59970	4.40274	2	3.48E-06	0.82	2.79	0.85	108.6	1	12/27
	1920	K.TM*GWEASTER.M	1183.50482	4.94213	2	1.10E-08	0.96	3.18	0.91	988.7	1	19/27
	3561	S.SLQDGEFIYK.V	1199.59428	4.78746	2	1.66E-03	0.87	3.10	0.63	410.8	1	15/27
	1148	L.KDGGHYDAEVK.T	1218.57494	4.35431	2	6.02E-03	0.70	2.45	0.66	345.1	1	12/30
	1458	K.KTM*GWEASTER.M	1311.59978	4.78083	3	1.13E-01	0.69	2.87	0.57	211.4	1	20/60
	2817	M.YPEDGALKGEIK.M	1319.68416	4.97364	2	6.98E-07	0.70	2.22	0.49	512.3	1	16/33
	1139	K.LKDGGHYDAEVK.T	1331.65901	4.84146	2	1.02E-07	0.96	3.96	0.74	1143.1	1	21/33
	2422	R.GTNFPSDGPVM*QK.K	1393.64165	4.99460	2	5.92E-09	0.92	3.76	0.77	449.1	1	16/36
	1444	K.K#TM*GWEASTER.M	1425.64268	4.81052	3	1.83E-03	0.87	3.07	0.55	744.1	1	25/60
	1169	K.LK#DGGHYDAEVK.T	1445.70191	4.67598	2	4.92E-03	0.70	3.90	0.01	590.4	1	16/33
	2608	R.HSTGAENLYFQGH.M	1460.65532	4.92411	3	2.38E-04	0.88	3.40	0.64	683.9	1	24/72
	3231	R.LIFAGK#QLEDGR.T	1460.78558	3.87267	3	3.30E-04	0.68	2.83	0.38	406.1	1	25/66
	4226	R.M*YPEDGALKGEIK.M	1466.71956	4.85831	3	4.23E-05	0.79	2.64	0.80	295.2	1	22/72
	1511	K.IQDKEGIPPDQQR.L	1523.78125	4.84042	2	8.12E-10	0.95	4.20	0.66	640.0	1	22/36
	2589	R.M*YPEDGALK#GEIK.M	1580.76246	4.87950	3	2.57E-04	0.39	2.83	0.07	410.3	1	24/72
	2658	K.LRGTNFPSDGPVMQK.K	1646.83190	4.99175	3	5.28E-02	0.85	3.14	0.73	514.7	1	25/84
	2622	K.KPVQLPGAYK#TDIK.L	1671.94280	4.47736	3	1.55E-06	0.78	3.85	0.30	516.4	1	25/78
	3198	K.AYVK#HPADIPDYLK.L	1743.90642	4.68249	3	4.00E-05	0.75	3.66	0.32	377.5	1	26/78

3960	K.TITLEVEPSDTIENVK.A	1787.92730	4.80170	3	1.75E-05	0.88	3.63	0.69	506.9	1		26/90
4002	K.LDITSHNEDYTIVEQYER.A	2225.03568	4.39337	2	9.99E-15	0.95	4.04	0.67	972.2	1		21/51

Reference	S15-c5B-80				P (pro)	Sf	Score	Coverage	MW	Accession		Peptide (Hits)
Scan(s)	Peptide	MH+	DeltaM (ppm)	z	P (pep)	Sf	XC	DeltaCn	Sp	RSp		Ions
1 RFP_UB_new					5.88E-12	55.91	716.28	68.50	38172.1			73 (66 7 0 0 0)
1102	D.GALKGEIK.M	815.49853	4.85552	2	9.81E-03	0.61	3.07	-	580.9	1		13/21
3420	S.TLHLVLR.L	851.54615	4.70817	2	1.49E-03	0.64	2.21	-	449.5	1		15/18
1384	L.SDYNIQK.E	867.42067	4.46629	2	3.10E-02	0.83	2.53	0.64	393.3	1		11/18
2572	P.VQLPGAYK.T	875.49853	4.73190	2	2.20E-04	0.78	2.19	0.91	199.8	1		10/21
1419	G.WEASTER.M	878.40027	4.21947	2	2.47E-02	0.71	2.06	0.68	191.7	1		10/18
1423	I.F]AGKQLE.D	906.46793	4.79504	2	3.72E-02	0.64	2.09	0.24	502.6	1		12/18
1100	G.GHYDAEVK.T	918.43157	4.11390	2	1.16E-01	0.80	2.89	0.41	463.8	1		13/21
5562	K.LSFPEGFK.W	924.48254	4.27577	2	5.72E-03	0.86	2.76	0.93	291.5	1		10/21
1409	E.DGALKGEIK.M	930.52547	4.62036	2	1.57E-01	0.90	2.94	0.57	689.8	1		16/24
3466	P.ADIPDYLK.L	934.48802	3.98357	2	9.26E-03	0.34	2.27	-	300.4	1		13/21
1752	M.GWEASTER.M	935.42174	3.65810	2	1.83E-04	0.79	2.14	0.65	485.6	1		12/21
3255	E.STLHLVLR.L	938.57818	4.87290	2	3.41E-04	0.49	2.55	-	513.5	1		13/21
2813	K.PVQLPGAYK.T	972.55129	3.85285	2	6.26E-07	0.87	2.81	0.57	578.9	1		15/24
2332	T.LSDYNIQK.E	980.50474	4.86600	2	8.61E-03	0.87	2.82	0.66	332.8	1		13/21
658	R.PYEGTQTAK.L	994.48400	3.49214	2	6.93E-04	0.77	2.23	0.64	413.5	1		13/24
2513	R.MYPEDGALK.G	1023.48156	3.99092	2	1.99E-02	0.71	2.15	0.78	212.1	1		11/24
3643	H.PADIPDYLK.L	1031.54079	3.58021	2	1.33E-03	0.88	3.14	0.66	457.1	1		13/24
2085	R.M*YPEDGALK.G	1039.47648	4.35408	2	7.00E-03	0.80	2.23	0.69	310.9	1		14/24
4396	K.ESTLHLVLR.L	1067.62077	4.46429	2	1.52E-07	0.94	3.30	-	346.7	1		14/24
2269	R.TLSDYNIQK.E	1081.55242	3.83780	2	5.17E-06	0.92	2.86	0.78	457.1	1		16/24
686	F.AGK#QLEDGR.T	1087.54903	4.00755	2	1.20E-04	0.30	2.84	0.05	415.4	1		10/24
1177	K.DGGHYDAEVK.T	1090.47998	4.18709	2	5.31E-07	0.92	3.08	0.80	606.9	1		16/27
2211	K.KPVQLPGAYK.T	1100.64626	4.35417	2	1.09E-06	0.83	3.27	0.59	247.9	1		14/27
1852	N.FPSDGPVM*QK.K	1121.52958	4.79955	2	4.87E-03	0.83	2.97	0.69	294.7	1		13/27
3060	T.GAENLYFQGH.M	1135.51670	4.47155	2	1.61E-03	0.84	3.25	0.74	360.1	1		11/27
2674	Y.PEDGALKGEIK.M	1156.62083	2.59170	2	6.46E-02	0.41	3.01	0.23	194.4	1		12/30
2681	K.TMGWEASTER.M	1167.50990	4.21360	2	4.97E-03	0.95	4.12	0.61	720.0	1		18/27
4613	K.HPADIPDYLK.L	1168.59970	4.66389	2	1.13E-07	0.85	2.83	0.85	187.6	1		13/27
2069	K.TM*GWEASTER.M	1183.50482	4.32327	2	6.92E-07	0.96	3.14	0.93	996.1	1		19/27
3620	S.SLQDGEFIYK.V	1199.59428	3.76986	2	1.04E-05	0.86	3.26	0.53	386.2	1		15/27
2152	K.KTMGWEASTER.M	1295.60486	4.65092	2	8.27E-08	0.85	2.84	0.72	440.8	1		14/30

1592	K.KTM*GWEASTER.M	1311.59978	4.37227	2	6.45E-06	0.92	3.09	0.78	382.5	1		18/30
1281	K.LKDGGHYDAEVK.T	1331.65901	4.38312	2	1.04E-07	0.95	3.64	0.71	1005.3	1		19/33
2709	R.GTNFPSDGPVMQK.K	1377.64673	4.73224	2	5.35E-09	0.87	3.35	0.57	505.8	1		18/36
2344	R.GTNFPSDGPVM*QK.K	1393.64165	4.20628	2	7.01E-08	0.94	4.19	0.80	481.1	1		17/36
2829	V.K#HPADIPDYLK.L	1410.73756	3.60519	3	4.35E-01	0.83	3.12	0.00	585.3	1		22/60
1596	K.K#TM*GWEASTER.M	1425.64268	4.29677	3	3.04E-02	0.89	3.51	0.64	611.7	1		24/60
1305	K.LK#DGGHYDAEVK.T	1445.70191	4.25379	2	7.32E-07	0.67	3.75	0.63	590.0	1		16/33
2954	R.MYPEDGALKGEIK.M	1450.72464	4.89040	2	3.47E-05	0.81	3.18	0.56	254.3	1		17/36
2705	R.HSTGAENLYFQGH.M	1460.65532	3.93044	2	2.36E-09	0.96	4.71	0.85	553.9	1		19/36
3327	R.LIFAGK#QLEDGR.T	1460.78558	4.17436	2	5.06E-06	0.64	3.10	0.22	542.4	1		14/33
2660	R.M*YPEDGALKGEIK.M	1466.71956	4.22247	2	2.21E-04	0.94	3.58	0.76	750.4	1		20/36
3091	T.LEVEPSDTIENVK.A	1472.74788	4.45554	2	1.13E-06	0.95	4.13	0.68	784.4	1		22/36
2089	K.IQDKEGIPPDQQR.L	1523.78125	4.84042	2	2.50E-08	0.95	4.30	0.62	635.7	1		22/36
3596	T.QDSSLQDGEFIYK.V	1529.71183	4.63523	2	4.40E-04	0.79	3.21	0.67	230.4	1		13/36
2699	R.M*YPEDGALK#GEIK.M	1580.76246	3.03467	2	6.71E-05	0.67	2.96	0.32	374.1	1		16/36
3291	K.AYVKHPADIPDYLK.L	1629.86352	3.69471	3	7.76E-04	0.91	4.47	0.66	492.7	1		21/78
2252	K.LRGTNFPSDGPVM*QK.K	1662.82682	2.67645	3	5.87E-03	0.89	3.73	0.68	507.8	1		28/84
2725	K.KPVQLPGAYK#TDIK.L	1671.94280	4.03929	3	4.22E-04	0.53	3.08	0.21	413.6	1		23/78
3911	T.ITLEVEPSDTIENVK.A	1686.87962	4.16249	2	4.59E-08	0.90	3.61	0.63	473.7	1		19/42
3304	T.SHNEDYTIVEQYER.A	1782.79293	4.15506	2	5.88E-12	0.97	4.24	0.80	1507.8	1		21/39
4168	K.TITLEVEPSDTIENVK.A	1787.92730	4.91163	2	1.19E-08	0.93	4.01	0.64	659.2	1		22/45
2440	K.TTYM*AK#KPVQLPGAYK.T	1926.01532	4.10406	3	9.85E-06	0.34	2.66	0.07	443.4	1		25/90
3443	D.ITSHNEDYTIVEQYER.A	1996.92468	4.36763	2	5.93E-12	0.97	4.48	0.85	1001.7	1		21/45
2883	R.M*EGSVNGHEFEIEGEGEGR.P	2078.87199	4.92719	3	1.67E-11	0.97	5.65	0.88	1307.9	1		34/108
3616	T.GK#TITLEVEPSDTIENVK.A	2087.08663	4.13071	3	9.36E-03	0.81	3.89	0.00	1210.7	1		35/102
3683	K.TITLEVEPSDTIENVK#AK.I	2101.10228	4.70126	3	1.09E-05	0.32	2.68	0.07	434.2	1		25/102
4044	K.LDITSHNEDYTIVEQYER.A	2225.03568	4.30503	3	1.76E-07	0.94	4.58	0.82	711.6	1		26/102
3973	K.TLTGKTITLEVEPSDTIENVK.A	2288.22315	4.52094	3	2.62E-04	0.80	3.49	0.57	455.6	1		24/120
3999	K.TLTGK#TITLEVEPSDTIENVK.A	2402.26605	4.11186	2	2.85E-08	0.82	4.94	0.55	689.7	1		20/60
2930	R.M*EGSVNGHEFEIEGEGEGRPYEGTQTAK.L	3054.33815	4.19704	4	3.61E-07	0.93	5.10	0.69	589.8	1		39/243

	Reference	S16-c5C-20				P (pro)	Sf	Score	Coverage	MW	Accession	Peptide (Hits)
	Scan(s)	Peptide	MH+	DeltaM (ppm)	z	P (pep)	Sf	XC	DeltaCn	Sp	RSp	Ions
1	RFP_UB_new					6.56E-09	50.90	634.27	69.70	38172.1		64 (61 3 0 0 0)
	1079	D.GALKGEIK.M	815.49853	3.43348	2	1.32E-02	0.40	2.65	-	459.1	1	12/21
	3539	S.TLHLVLR.L	851.54615	1.84114	2	1.50E-04	0.66	2.37	-	430.8	1	15/18
	455	K.GEIK#M*R.L	863.44034	1.78422	2	3.07E-01	0.66	2.05	0.39	301.7	1	10/15

1360	L.SDYNIQK.E	867.42067	0.24445	2	8.77E-02	0.71	2.51	0.50	321.7	1	10/18
879	G.GHYDAEVK.T	918.43157	2.18668	2	1.80E-02	0.78	2.60	0.66	299.0	1	11/21
5455	K.LSFPEGFK.W	924.48254	1.89902	2	3.96E-04	0.92	2.28	0.98	544.7	1	14/21
3567	P.ADIPDYLK.L	934.48802	0.58724	2	2.10E-05	0.23	2.07	-	274.5	1	12/21
3542	E.STLHLVLR.L	938.57818	1.55640	2	2.10E-05	0.77	3.20	-	730.3	1	15/21
2895	K.PVQLPGAYK.T	972.55129	1.65633	2	1.08E-03	0.85	2.96	0.50	564.5	1	14/24
2214	F.PSDGPVM*QK.K	974.46116	1.50861	2	8.16E-02	0.85	3.27	0.62	294.4	1	13/24
2383	T.LSDYNIQK.E	980.50474	1.25557	2	1.06E-05	0.92	3.35	0.66	525.9	1	14/21
686	R.PYEGTQTAK.L	994.48400	1.52819	2	1.35E-03	0.89	2.61	0.63	657.2	1	16/24
2594	R.MYPEDGALK.G	1023.48156	1.84407	2	8.47E-04	0.80	2.64	0.74	239.2	1	12/24
3250	H.PADIPDYLK.L	1031.54079	0.85844	2	1.98E-04	0.92	3.04	0.73	728.2	1	15/24
2201	R.M*YPEDGALK.G	1039.47648	0.71361	2	9.32E-03	0.72	2.32	0.56	285.5	1	13/24
3623	K.ESTLHLVLR.L	1067.62077	2.52053	2	6.56E-09	0.63	2.99	-	285.4	1	17/24
2583	R.TLSDYNIQK.E	1081.55242	1.69335	2	8.55E-07	0.95	3.14	0.92	543.3	1	18/24
1235	K.DGGHYDAEVK.T	1090.47998	2.17213	2	1.67E-06	0.92	2.92	0.77	646.3	1	17/27
2455	K.KPVQLPGAYK.T	1100.64626	1.58147	2	9.87E-07	0.87	3.37	0.61	313.3	1	15/27
1754	K.IQDKEGIPPD.Q	1111.56298	-1.15778	2	2.56E-02	0.78	2.17	0.69	400.3	1	14/27
1849	N.FPSDGPVM*QK.K	1121.52958	0.66353	2	3.76E-03	0.68	2.68	0.41	298.5	1	14/27
2729	Y.PEDGALKGEIK.M	1156.62083	1.32522	2	2.75E-03	0.93	3.81	0.39	961.7	1	20/30
2728	K.TMGWEASTER.M	1167.50990	1.91337	2	4.28E-06	0.94	3.71	0.66	695.1	1	18/27
5258	K.HPADIPDYLK.L	1168.59970	1.73905	2	4.39E-07	0.86	2.92	0.85	178.0	1	13/27
2072	K.TM*GWEASTER.M	1183.50482	2.67298	2	8.31E-08	0.97	3.33	0.96	1047.3	1	20/27
3727	S.SLQDGEFIYK.V	1199.59428	0.41179	2	7.18E-04	0.83	2.84	0.58	461.2	1	14/27
3146	D.YTIVEQYER.A	1200.58953	1.82681	2	2.11E-04	0.89	3.02	0.65	544.5	1	14/24
2545	R.TLSDYNIQKE.S	1210.59501	-3.52109	2	6.63E-01	0.38	2.60	0.38	116.1	1	10/27
2429	K.K#PVQLPGAYK.T	1214.68916	1.79108	2	1.21E-05	0.96	3.90	0.00	1405.5	1	18/27
1166	L.KDGGHYDAEVK.T	1218.57494	2.35082	2	8.80E-08	0.89	3.37	0.56	587.2	1	17/30
3479	I.FAGK#QLEDGR.T	1234.61745	1.01418	2	8.07E-04	0.75	3.31	0.13	700.6	1	15/27
3629	D.SSLQDGEFIYK.V	1286.62631	3.00474	2	9.38E-08	0.88	3.07	0.76	438.0	1	14/30
2176	K.KTMGWEASTER.M	1295.60486	1.44748	2	1.68E-08	0.96	4.04	0.74	953.1	1	20/30
1974	L.SSSEHM*QIFVK.T	1308.62527	1.88366	2	1.90E-04	0.88	2.91	0.77	302.4	1	16/30
1572	K.KTM*GWEASTER.M	1311.59978	2.32473	2	3.14E-07	0.92	3.71	0.78	310.3	1	16/30
1242	K.LKDGGHYDAEVK.T	1331.65901	2.54977	2	6.11E-08	0.96	4.20	0.63	1097.8	1	19/33
2718	R.GTNFPSDGPVMQK.K	1377.64673	3.22591	2	2.83E-08	0.93	4.13	0.67	510.9	1	18/36
2394	R.GTNFPSDGPVM*QK.K	1393.64165	2.54206	2	1.91E-08	0.93	4.05	0.75	432.8	1	17/36
3666	N.EDYTIVEQYER.A	1444.65907	2.30910	2	7.40E-09	0.90	2.68	0.87	520.6	1	15/30
1352	K.LK#DGGHYDAEVK.T	1445.70191	0.99368	3	2.70E-01	0.26	3.28	0.45	287.7	1	17/66

3031	R.MYPEDGALKGEIK.M	1450.72464	2.28193	2	4.35E-08	0.87	3.08	0.72	304.6	1	18/36
2774	R.HSTGAENLYFQGH.M	1460.65532	1.35139	3	1.35E-05	0.86	2.94	0.74	603.7	1	25/72
3528	R.LIFAGK#QLEDGR.T	1460.78558	3.25514	2	1.79E-07	0.90	4.05	0.25	801.5	1	19/33
2656	R.M*YPEDGALKGEIK.M	1466.71956	3.97279	2	5.85E-06	0.95	3.76	0.79	832.7	1	21/36
2065	K.IQDKEGIPPDQQR.L	1523.78125	2.83767	2	3.21E-08	0.93	4.14	0.65	451.5	1	19/36
3692	T.QDSSLQDGEFIYK.V	1529.71183	2.32105	2	1.30E-05	0.87	3.26	0.66	385.8	1	17/36
2780	R.HSTGAENLYFQGHM*.C	1607.69072	1.67011	2	4.76E-06	0.95	4.27	0.90	355.0	1	19/39
2840	K.LRGTNFPSDGPVMQK.K	1646.83190	1.65616	3	1.28E-04	0.86	2.97	0.67	748.6	1	27/84
2407	K.LRGTNFPSDGPVM*QK.K	1662.82682	2.34610	3	1.69E-07	0.96	4.31	0.83	884.3	1	34/84
2716	K.KPVQLPGAYK#TDIK.L	1671.94280	1.52041	3	1.27E-08	0.77	3.64	0.23	648.7	1	28/78
3958	K.TITLEVEPSDTIENVK.A	1787.92730	3.34131	2	3.67E-07	0.92	4.05	0.61	499.7	1	20/45
2932	R.M*EGSVNGHEFEIEGEGEGR.P	2078.87199	2.72521	3	3.73E-07	0.97	5.35	0.82	1278.5	1	34/108
3813	K.TITLEVEPSDTIENVK#AK.I	2101.10228	2.69688	3	8.11E-04	0.28	2.91	0.37	330.2	1	25/102
4144	K.LDITSHNEDYTIVEQYER.A	2225.03568	1.01330	3	5.76E-08	0.93	4.21	0.65	808.5	1	28/102
4101	K.TLTGK#TITLEVEPSDTIENVK.A	2402.26605	2.68346	3	1.53E-07	0.71	3.86	0.03	840.2	1	32/120

Reference	S17-c5C-40				P (pro)	Sf	Score	Coverage	MW	Accession	Peptide (Hits)
Scan(s)	Peptide	MH+	DeltaM (ppm)	z	P (pep)	Sf	XC	DeltaCn	Sp	RSp	Ions
1 RFP_UB_new					9.43E-15	52.15	632.29	71.20	38172.1		64 (60 4 0 0 0)
1138	D.GALKGEIK.M	815.49853	1.48754	2	2.68E-03	0.53	2.78	-	546.8	1	13/21
3509	S.TLHLVLR.L	851.54615	0.69433	2	2.81E-04	0.69	2.55	-	418.5	1	15/18
1421	L.SDYNIQK.E	867.42067	0.94809	2	4.35E-02	0.79	2.38	0.62	299.1	1	11/18
1444	I.F]AGKQLE.D	906.46793	1.49572	2	1.24E-01	0.51	2.32	0.25	374.1	1	10/18
1134	G.GHYDAEVK.T	918.43157	0.72465	2	3.19E-02	0.75	2.53	0.34	425.2	1	14/21
4247	K.LSFPEGFK.W	924.48254	0.44656	2	5.27E-05	0.95	2.52	0.93	711.5	1	16/21
3514	E.STLHLVLR.L	938.57818	0.71102	2	1.45E-04	0.63	2.89	-	535.9	1	14/21
2920	K.PVQLPGAYK.T	972.55129	0.90324	2	1.89E-04	0.79	2.86	0.48	503.0	1	13/24
2353	F.PSDGPVM*QK.K	974.46116	-1.30995	2	3.38E-03	0.83	3.10	0.58	313.9	1	13/24
2392	T.LSDYNIQK.E	980.50474	0.50859	2	1.35E-02	0.86	2.82	0.64	358.7	1	13/21
675	R.PYEGTQTAK.L	994.48400	0.30071	2	3.79E-01	0.61	2.41	0.45	311.1	1	12/24
3238	H.PADIPDYLK.L	1031.54079	2.04182	2	1.19E-04	0.89	2.94	0.72	555.8	1	13/24
2135	R.M*YPEDGALK.G	1039.47648	-0.10843	2	5.75E-03	0.76	2.57	0.66	222.7	1	12/24
4400	K.ESTLHLVLR.L	1067.62077	0.00508	2	4.39E-09	0.44	3.54	-	174.6	1	12/24
2623	R.TLSDYNIQK.E	1081.55242	0.00036	2	1.09E-04	0.95	3.50	0.87	474.1	1	17/24
1321	K.DGGHYDAEVK.T	1090.47998	0.38106	2	3.71E-07	0.90	3.08	0.72	498.5	1	15/27
2463	K.KPVQLPGAYK.T	1100.64626	1.02693	2	1.56E-05	0.90	3.51	0.67	339.4	1	15/27
1778	K.IQDKEGIPPD.Q	1111.56298	0.37968	2	1.16E-03	0.63	2.10	0.64	284.8	1	12/27

1886	N.FPSDGPVM*QK.K	1121.52958	-0.42490	2	2.45E-03	0.72	2.67	0.57	220.3	1	13/27
2661	Y.PEDGALKGEIK.M	1156.62083	-0.04681	2	3.37E-03	0.90	3.75	0.48	608.1	1	17/30
2750	K.TMGWEASTER.M	1167.50990	-0.07320	2	1.34E-02	0.94	3.70	0.54	873.1	1	18/27
5061	K.HPADIPDYLK.L	1168.59970	-0.03675	2	2.01E-07	0.87	2.83	0.83	207.2	1	14/27
2181	K.TM*GWEASTER.M	1183.50482	0.50697	2	5.81E-08	0.93	2.96	0.79	729.5	1	17/27
2429	K.K#PVQLPGAYK.T	1214.68916	0.48464	2	2.15E-03	0.94	3.65	0.00	1062.5	1	16/27
1218	L.KDGGHYDAEVK.T	1218.57494	1.14873	2	1.38E-08	0.94	3.29	0.65	960.1	1	18/30
3616	D.SSLQDGEFIYK.V	1286.62631	0.25333	2	2.48E-07	0.94	3.58	0.76	824.0	1	16/30
1605	K.KTM*GWEASTER.M	1311.59978	0.74254	2	2.82E-07	0.92	3.21	0.83	331.2	1	17/30
1301	K.LKDGGHYDAEVK.T	1331.65901	1.63309	2	1.87E-07	0.96	4.12	0.71	1014.4	1	18/33
2790	R.GTNFPSDGPVMQK.K	1377.64673	1.01071	2	3.06E-09	0.90	3.60	0.70	411.2	1	17/36
6393	R.GTNFPSDGPVM*QK.K	1393.64165	-0.43603	2	9.22E-05	0.89	3.73	0.68	383.2	1	16/36
1340	I.QDKEGIPPDQQR.L	1410.69718	1.73704	2	1.40E-02	0.36	2.06	0.60	109.1	1	10/33
1620	K.K#TM*GWEASTER.M	1425.64268	-0.19853	3	7.94E-01	0.77	2.58	0.00	524.0	1	25/60
3647	N.EDYTIVEQYER.A	1444.65907	0.95713	2	3.41E-09	0.95	3.51	0.85	702.0	1	18/30
1322	K.LK#DGGHYDAEVK.T	1445.70191	0.70745	2	2.80E-05	0.85	3.47	0.00	490.8	1	15/33
3050	R.MYPEDGALKGEIK.M	1450.72464	0.85147	2	2.24E-05	0.69	2.73	0.67	141.5	1	13/36
2796	R.HSTGAENLYFQGH.M	1460.65532	1.00541	2	4.63E-11	0.96	4.28	0.83	708.3	1	22/36
3446	R.LIFAGK#QLEDGR.T	1460.78558	1.16602	2	2.61E-07	0.91	3.81	0.35	845.9	1	20/33
2669	R.M*YPEDGALKGEIK.M	1466.71956	2.39148	2	4.70E-04	0.95	3.55	0.76	904.0	1	23/36
1736	K.IQDKEGIPPDQQR.L	1523.78125	0.67469	2	3.54E-09	0.95	4.43	0.60	695.0	1	22/36
3674	T.QDSSLQDGEFIYK.V	1529.71183	1.60285	2	6.55E-06	0.81	2.86	0.80	257.7	1	13/36
1937	R.LKLKDGGHYDAEVK.T	1572.83803	-0.45665	3	2.56E-05	0.79	3.07	0.52	561.7	1	25/78
3406	K.AYVKHPADIPDYLK.L	1629.86352	0.32439	3	1.52E-07	0.97	4.78	0.78	1413.9	1	35/78
2876	K.LRGTNFPSDGPVMQK.K	1646.83190	0.43311	3	1.26E-04	0.91	3.12	0.84	723.7	1	29/84
2407	K.LRGTNFPSDGPVM*QK.K	1662.82682	2.67645	3	5.25E-09	0.96	4.47	0.89	946.4	1	33/84
2738	K.KPVQLPGAYK#TDIK.L	1671.94280	1.30138	3	2.11E-06	0.79	4.09	0.16	581.8	1	29/78
1616	K.AKIQDKEGIPPDQQR.L	1722.91332	0.41370	3	6.59E-04	0.87	3.90	0.64	401.3	1	24/84
3101	K.QLEDGRTLSDYNIQK.E	1779.88717	-0.02728	3	7.99E-02	0.85	3.81	0.66	330.6	1	21/84
5085	K.TITLEVEPSDTIENVK.A	1787.92730	1.15652	2	3.28E-05	0.92	4.41	0.61	460.9	1	19/45
2049	K.LRGTNFPSDGPVM*QKK.T	1790.92178	0.92163	3	4.93E-03	0.87	3.55	0.65	560.0	1	27/90
2965	R.M*EGSVNGHEFEIEGEGEGR.P	2078.87199	1.84442	3	2.94E-11	0.96	4.84	0.67	1475.8	1	36/108
3792	K.TITLEVEPSDTIENVK#AK.I	2101.10228	0.16960	3	5.30E-04	0.34	3.59	0.01	207.5	1	21/102
4123	K.LDITSHNEDYTIVEQYER.A	2225.03568	3.29612	2	9.43E-15	0.97	4.52	0.81	1268.2	1	22/51
4055	K.TLTGKTITLEVEPSDTIENVK.A	2288.22315	0.51989	3	4.79E-05	0.92	4.48	0.61	680.4	1	29/120
4072	K.TLTGK#TITLEVEPSDTIENVK.A	2402.26605	0.32057	3	1.33E-08	0.85	5.08	0.02	901.8	1	34/120
4790	R.VM*NFEDGGVVTVTQDSSLQDGEFIYK.V	2894.34005	0.02915	2	9.43E-07	0.84	2.69	0.80	376.7	1	20/75

	3028	R.M*EGSVNGHEFEIEGEGEGRPYEGTQTAK.L	3054.33815	0.12049	4	1.82E-10	0.95	5.87	0.76	541.9	1		38/243
	Reference	**S18-c5c-40**				**P (pro)**	**Sf**	**Score**	**Coverage**	**MW**	**Accession**		**Peptide (Hits)**
	Scan(s)	**Peptide**	**MH+**	**DeltaM (ppm)**	**z**	**P (pep)**	**Sf**	**XC**	**DeltaCn**	**Sp**	**RSp**		**Ions**
1	RFP_UB_new					4.99E-10	40.66	540.22	56.70	38172.1			55 (50 5 0 0 0)
	3352	P.ADIPDYLK.L	934.48802	-0.39247	2	4.32E-04	0.50	2.60	-	351.2	1		14/21
	1112	K.AKIQDKEGIPPDQQR.L	1722.91332	-1.07418	3	1.48E-02	0.83	3.80	0.61	272.3	1		22/84
	1140	K.DGGHYDAEVK.T	1090.47998	-0.62641	2	2.50E-08	0.81	2.32	0.71	423.0	1		14/27
	3423	N.EDYTIVEQYER.A	1444.65907	0.11216	2	4.01E-07	0.77	2.10	0.86	320.3	1		12/30
	3408	K.ESTLHLVLR.L	1067.62077	-1.13831	2	1.55E-09	0.67	2.96	-	292.6	1		18/24
	1665	N.FPSDGPVM*QK.K	1121.52958	0.11932	2	2.63E-03	0.61	2.16	0.59	287.1	1		12/27
	975	D.GALKGEIK.M	815.49853	-0.08418	2	8.03E-03	0.22	2.19	-	401.5	1		11/21
	967	D.GGHYDAEVK.T	975.45304	-0.54795	2	6.59E-04	0.11	2.32	0.36	218.1	2		10/24
	970	G.GHYDAEVK.T	918.43157	-0.20573	2	2.13E-02	0.49	2.26	0.46	167.9	1		10/21
	2348	R.GTNFPSDGPVM*QK.K	1393.64165	0.61506	2	1.56E-08	0.85	2.67	0.81	432.0	1		15/36
	2625	R.GTNFPSDGPVMQK.K	1377.64673	-0.14119	2	1.39E-08	0.92	3.65	0.63	590.7	1		19/36
	4447	K.HPADIPDYLK.L	1168.59970	0.79892	2	4.99E-10	0.80	2.39	0.84	174.6	1		13/27
	2586	R.HSTGAENLYFQGH.M	1460.65532	0.50398	2	9.48E-10	0.96	4.35	0.86	532.5	1		20/36
	2587	R.HSTGAENLYFQGHM*.C	1607.69072	-0.35037	3	2.29E-03	0.89	3.53	0.94	312.9	1		20/78
	1799	K.IQDKEGIPPDQQR.L	1523.78125	0.67469	2	6.04E-10	0.89	3.67	0.65	363.6	1		17/36
	1087	L.KDGGHYDAEVK.T	1218.57494	-0.35389	2	1.19E-06	0.85	2.97	0.60	513.9	1		15/30
	2098	K.KPVQLPGAYK.T	1100.64626	0.02876	2	2.78E-07	0.78	3.06	0.52	250.1	1		14/27
	2231	K.K#PVQLPGAYK.T	1214.68916	0.18316	2	6.89E-04	0.91	3.35	0.00	670.3	1		15/27
	2534	K.KPVQLPGAYK#TDIK.L	1671.94280	0.42524	3	1.70E-03	0.75	4.01	0.16	539.6	1		27/78
	2001	K.KTMGWEASTER.M	1295.60486	0.12842	2	7.08E-08	0.88	3.03	0.72	446.2	1		15/30
	1442	K.K#TM*GWEASTER.M	1425.64268	0.38887	2	8.24E-04	0.85	2.61	0.80	400.9	1		14/30
	1411	K.KTM*GWEASTER.M	1311.59978	0.09106	2	2.76E-05	0.91	3.26	0.84	309.7	1		16/30
	3244	R.LIFAGK#QLEDGR.T	1460.78558	-0.17102	2	1.22E-06	0.83	3.30	0.32	564.0	1		18/33
	1128	K.LKDGGHYDAEVK.T	1331.65901	-0.01693	2	7.36E-09	0.92	3.28	0.73	780.8	1		17/33
	2125	K.LRGTNFPSDGPVM*QK.K	1662.82682	0.47411	3	3.38E-09	0.95	3.68	0.92	877.1	1		32/84
	2708	K.LRGTNFPSDGPVMQK.K	1646.83190	-0.90113	3	1.25E-02	0.95	3.47	0.76	1287.8	1		33/84
	2191	T.LSDYNIQK.E	980.50474	-0.61189	2	1.66E-04	0.79	2.94	0.67	226.1	1		10/21
	3792	K.LSFPEGFK.W	924.48254	-0.41171	2	3.64E-06	0.91	2.00	-	549.0	1		14/21
	1929	R.M*YPEDGALK.G	1039.47648	-0.34330	2	3.50E-05	0.80	2.11	0.62	373.2	1		15/24
	2377	R.MYPEDGALK.G	1023.48156	-0.42206	2	6.45E-02	0.62	2.04	0.57	281.0	1		12/24
	2458	R.M*YPEDGALKGEIK.M	1466.71956	0.64372	2	4.89E-06	0.95	3.36	0.78	848.4	1		21/36
	2837	R.MYPEDGALKGEIK.M	1450.72464	1.10390	2	5.29E-07	0.81	2.92	0.69	222.2	1		16/36

2552	R.M*YPEDGALK#GEIK.M	1580.76246	-1.14385	3	8.87E-05	0.58	3.18	0.21	404.3	2	24/72
3072	H.PADIPDYLK.L	1031.54079	-1.98167	2	1.16E-04	0.89	2.70	0.71	671.8	1	14/24
3564	H.P]ADIPDYLK.L	1145.58369	-0.65880	2	6.46E-02	0.58	2.58	0.54	149.3	1	10/24
2450	Y.PEDGALKGEIK.M	1156.62083	-0.68005	2	3.56E-02	0.86	3.86	0.47	425.8	1	15/30
2110	K.PVQLPGAYK.T	972.55129	0.46393	2	1.08E-04	0.53	2.40	0.40	357.3	1	11/24
626	R.PYEGTQTAK.L	994.48400	-1.17226	2	1.13E-04	0.82	2.49	0.57	509.6	1	14/24
3449	T.QDSSLQDGEFIYK.V	1529.71183	-0.15274	2	1.22E-05	0.86	3.24	0.80	268.9	1	14/36
3387	D.SSLQDGEFIYK.V	1286.62631	-0.50568	2	3.34E-06	0.75	2.41	0.62	497.7	1	13/30
3334	E.STLHLVLR.L	938.57818	-0.52454	2	1.82E-07	0.72	2.75	-	781.8	1	15/21
3690	K.TITLEVEPSDTIENVK.A	1787.92730	1.42962	2	1.81E-07	0.87	3.44	0.73	300.7	1	17/45
3332	S.TLHLVLR.L	851.54615	-0.38080	2	7.88E-05	0.57	2.66	-	345.2	1	13/18
2472	R.TLSDYNIQK.E	1081.55242	-1.24117	2	1.82E-06	0.88	2.21	0.95	333.3	1	14/24
1897	K.TM*GWEASTER.M	1183.50482	-0.62760	2	2.42E-08	0.96	3.22	0.93	857.1	1	18/27
2640	K.TMGWEASTER.M	1167.50990	-0.59598	2	7.61E-04	0.84	2.79	0.67	407.8	1	14/27
2953	D.YTIVEQYER.A	1200.58953	-0.81675	2	2.98E-05	0.87	2.66	0.69	422.2	1	14/24

	Reference	S19-E2D4-20				P (pro)	Sf	Score	Coverage	MW	Accession	Peptide (Hits)
	Scan(s)	Peptide	MH+	DeltaM (ppm)	z	P (pep)	Sf	XC	DeltaCn	Sp	RSp	Ions
1	RFP_UB_new					9.90E-11	57.61	712.24	66.80	38172.1		72 (68 4 0 0 0)
	3048	S.TLHLVLR.L	851.54615	-0.38080	2	4.20E-05	0.61	2.47	-	376.6	1	14/18
	1996	L.SDYNIQK.E	867.42067	0.10373	2	6.12E-04	0.88	2.68	0.63	470.5	1	12/18
	2217	P.VQLPGAYK.T	875.49853	0.27016	2	2.53E-03	0.77	2.07	0.81	284.9	1	11/21
	625	G.GHYDAEVK.T	918.43157	-0.73738	2	1.05E-02	0.91	2.86	0.59	741.1	1	15/21
	3527	K.LSFPEGFK.W	924.48254	-0.47773	2	5.49E-04	0.90	2.15	0.83	509.4	1	15/21
	3003	P.ADIPDYLK.L	934.48802	0.06473	2	9.92E-07	0.52	2.67	-	350.1	1	14/21
	3047	E.STLHLVLR.L	938.57818	-0.58957	2	9.96E-06	0.75	2.90	-	651.3	1	16/21
	1901	K.PVQLPGAYK.T	972.55129	-0.60295	2	4.14E-05	0.89	2.81	0.64	609.3	1	15/24
	1825	F.PSDGPVM*QK.K	974.46116	-0.80888	2	4.98E-03	0.83	3.12	0.55	378.7	1	13/24
	529	G.H]YDAEVK.T	975.45301	-2.08410	2	1.80E-02	0.74	2.60	0.57	721.8	1	14/18
	1988	T.LSDYNIQK.E	980.50474	-0.11390	2	1.43E-03	0.74	2.53	0.68	243.0	1	10/21
	486	R.PYEGTQTAK.L	994.48400	-1.84737	2	2.61E-04	0.94	3.06	0.73	745.3	1	18/24
	2155	R.MYPEDGALK.G	1023.48156	-0.42206	2	4.06E-06	0.84	2.41	0.64	409.8	1	15/24
	2726	H.PADIPDYLK.L	1031.54079	-0.56161	2	6.97E-04	0.92	3.16	0.63	709.9	1	15/24
	1737	R.M*YPEDGALK.G	1039.47648	-0.34330	2	1.31E-04	0.86	2.54	0.68	369.4	1	15/24
	3720	K.ESTLHLVLR.L	1067.62077	-0.33794	2	1.51E-07	0.42	3.00	-	277.0	1	13/24
	2132	R.TLSDYNIQK.E	1081.55242	-0.67684	2	4.71E-07	0.95	3.13	0.85	600.9	1	18/24
	1676	T.M*GWEASTER.M	1082.45714	-0.28224	2	2.19E-03	0.92	2.59	0.84	604.4	1	15/24

552	K.DGGHYDAEVK.T	1090.47998	-0.85030	2	8.60E-07	0.94	3.22	0.81	772.7	1	17/27
2291	K.KPVQLPGAYK.T	1100.64626	-1.74576	2	2.14E-05	0.88	3.39	0.66	276.0	1	15/27
1563	F.PSDGPVM*QKK.T	1102.55613	-0.59720	2	3.38E-03	0.57	2.45	0.65	150.2	1	10/27
1491	K.IQDKEGIPPD.Q	1111.56298	-0.49887	2	2.01E-01	0.59	2.18	0.63	253.6	1	11/27
1858	N.FPSDGPVM*QK.K	1121.52958	0.01048	2	4.17E-03	0.84	3.18	0.74	302.6	1	12/27
2236	Y.PEDGALKGEIK.M	1156.62083	-0.46897	2	2.61E-04	0.91	3.93	0.51	604.0	1	17/30
2326	K.TMGWEASTER.M	1167.50990	0.13591	2	4.76E-04	0.92	3.33	0.72	502.9	1	16/27
496	D.KEGIPPDQQR.L	1167.61166	-0.55848	2	1.20E-04	0.69	2.47	0.76	214.7	1	10/27
3635	K.HPADIPDYLK.L	1168.59970	-0.24566	2	4.74E-08	0.86	2.78	0.90	164.9	1	13/27
1724	K.TM*GWEASTER.M	1183.50482	0.91955	2	9.54E-08	0.96	3.34	0.93	994.5	1	19/27
2671	D.YTIVEQYER.A	1200.58953	-0.71507	2	5.54E-07	0.94	3.33	0.62	829.6	1	16/24
2158	R.TLSDYNIQKE.S	1210.59501	2.22650	2	1.99E-01	0.53	2.35	0.58	211.1	1	10/27
2014	K.K#PVQLPGAYK.T	1214.68916	-1.32427	2	1.15E-03	0.79	2.72	0.00	529.3	1	14/27
686	L.KDGGHYDAEVK.T	1218.57494	-0.55424	2	2.05E-06	0.86	2.93	0.57	629.2	1	16/30
2924	I.FAGK#QLEDGR.T	1234.61745	-0.66666	2	5.49E-06	0.80	3.38	0.23	658.3	1	15/27
1804	G.RTLSDYNIQK.E	1237.65353	-0.81847	2	1.16E-03	0.76	2.60	0.52	381.5	1	14/27
3305	R.LIFAGK#QLED.G	1247.66300	0.10623	2	7.92E-05	0.72	2.22	0.42	653.5	1	14/27
1511	N.FPSDGPVM*QKK.T	1249.62454	-1.15666	2	5.27E-05	0.77	2.93	0.79	151.8	1	11/30
3068	D.SSLQDGEFIYK.V	1286.62631	0.91746	2	2.36E-07	0.84	3.00	0.59	573.5	1	14/30
1815	K.KTMGWEASTER.M	1295.60486	-0.06002	2	2.19E-06	0.91	3.30	0.77	446.4	1	16/30
1364	K.KTM*GWEASTER.M	1311.59978	0.09106	2	1.01E-08	0.93	3.51	0.84	326.0	1	17/30
2520	M.YPEDGALKGEIK.M	1319.68416	-0.57634	2	1.52E-08	0.93	3.34	0.71	813.4	1	18/33
1166	K.LKDGGHYDAEVK.T	1331.65901	-0.56694	2	3.60E-08	0.94	3.76	0.70	936.7	1	17/33
2380	R.GTNFPSDGPVMQK.K	1377.64673	1.18793	2	1.18E-10	0.94	3.87	0.68	665.7	1	20/36
1959	R.GTNFPSDGPVM*QK.K	1393.64165	0.70265	2	1.19E-09	0.95	4.22	0.80	583.2	1	18/36
3225	Q.DSSLQDGEFIYK.V	1401.65325	0.77971	2	4.80E-05	0.76	2.34	0.69	431.5	1	14/33
1216	I.QDKEGIPPDQQR.L	1410.69718	0.35253	2	1.55E-03	0.55	2.43	0.58	147.0	1	12/33
3108	N.EDYTIVEQYER.A	1444.65907	-0.14133	2	8.24E-07	0.93	2.73	0.97	592.7	1	16/30
1153	K.LK#DGGHYDAEVK.T	1445.70191	-0.39953	3	1.19E-01	0.38	2.95	0.67	486.9	1	23/66
2479	R.MYPEDGALKGEIK.M	1450.72464	-0.57898	2	1.91E-04	0.67	2.36	0.62	223.8	1	15/36
2375	R.HSTGAENLYFQGH.M	1460.65532	0.16969	2	7.81E-10	0.95	4.29	0.81	411.6	1	19/36
2893	R.LIFAGK#QLEDGR.T	1460.78558	-0.17102	2	3.68E-08	0.77	3.59	0.24	482.7	1	16/33
2148	R.M*YPEDGALKGEIK.M	1466.71956	-0.18855	2	4.43E-04	0.95	3.56	0.79	838.9	1	21/36
2020	R.GTNFPSDGPVMQKK.T	1505.74169	-0.78155	3	4.27E-04	0.62	2.54	0.57	315.3	1	21/78
1155	K.IQDKEGIPPDQQR.L	1523.78125	0.11392	2	1.37E-09	0.95	4.18	0.64	625.6	1	22/36
3120	T.QDSSLQDGEFIYK.V	1529.71183	0.00686	2	1.30E-04	0.72	2.41	0.76	243.5	1	13/36
523	E.GEGEGRPYEGTQTAK.L	1579.73469	-0.78733	2	5.70E-05	0.89	3.60	0.84	329.4	1	15/42

3057	R.VM*NFEDGGVVTVTQD.S	1626.73158	-0.80619	2	1.01E-03	0.89	2.77	0.73	669.2	1	20/42
2911	K.AYVKHPADIPDYLK.L	1629.86352	-1.13608	3	6.25E-07	0.96	4.82	0.75	1070.6	1	29/78
2382	K.LRGTNFPSDGPVMQK.K	1646.83190	-0.56757	3	5.30E-06	0.93	3.62	0.77	891.5	1	29/84
2134	K.LRGTNFPSDGPVM*QK.K	1662.82682	-0.29670	3	2.92E-07	0.95	4.39	0.80	841.6	1	32/84
2331	K.KPVQLPGAYK#TDIK.L	1671.94280	-0.56041	3	1.16E-03	0.42	3.00	0.21	304.4	1	20/78
656	K.AKIQDKEGIPPDQQR.L	1722.91332	-0.64907	3	8.52E-07	0.93	4.27	0.80	468.1	1	26/84
2484	K.QLEDGRTLSDYNIQK.E	1779.88717	-0.74741	3	2.86E-02	0.70	3.34	0.58	202.1	1	17/84
3393	K.TITLEVEPSDTIENVK.A	1787.92730	-0.11408	3	2.46E-09	0.96	4.22	0.79	1056.8	1	36/90
1690	K.LRGTNFPSDGPVM*QKK.T	1790.92178	0.41042	3	6.29E-03	0.90	4.11	0.76	409.0	1	24/90
3448	K.LDITSHNEDYTIVEQYER.A	2225.03568	0.76642	3	9.90E-11	0.91	3.65	0.74	718.5	1	26/102
3382	K.TLTGK#TITLEVEPSDTIENVK.A	2402.26605	-0.21298	3	3.74E-08	0.76	3.84	0.47	1040.9	1	35/120
3867	R.VM*NFEDGGVVTVTQDSSLQDGEFIYK.V	2894.34005	0.69931	3	1.13E-05	0.89	3.60	0.73	600.8	1	30/150

Reference	S20-E2D4-40				P (pro)	Sf	Score	Coverage	MW	Accession	Peptide (Hits)
Scan(s)	Peptide	MH+	DeltaM (ppm)	z	P (pep)	Sf	XC	DeltaCn	Sp	RSp	Ions
1 RFP_UB_new					1.08E-14	71.91	930.27	75.40	38172.1		94 (89 5 0 0 0)
1042	D.GALKGEIK.M	815.49853	0.14035	2	2.48E-02	0.52	3.15	-	464.5	1	12/21
3189	S.TLHLVLR.L	851.54615	0.47931	2	1.81E-03	0.47	2.16	-	365.6	1	13/18
1064	G.HYDAEVK.T	861.41011	0.67779	2	1.04E-01	0.82	2.50	0.58	447.9	1	11/18
1338	L.SDYNIQK.E	867.42067	-0.74064	2	7.48E-02	0.78	2.30	0.48	419.0	1	12/18
2503	P.VQLPGAYK.T	875.49853	-0.56642	2	1.98E-03	0.82	2.40	0.86	232.0	1	11/21
843	G.GHYDAEVK.T	918.43157	-0.40510	2	6.94E-02	0.88	2.70	0.66	421.2	1	14/21
5029	K.LSFPEGFK.W	924.48254	0.18248	2	5.59E-03	0.32	2.62	-	387.2	1	11/21
3387	P.ADIPDYLK.L	934.48802	-0.32715	2	2.62E-04	0.21	2.33	-	218.9	1	11/21
3412	E.STLHLVLR.L	938.57818	-0.32945	2	4.96E-06	0.77	2.91	-	775.0	1	16/21
2130	K.PVQLPGAYK.T	972.55129	0.15015	2	5.51E-04	0.88	2.90	0.57	592.3	1	15/24
2294	F.PSDGPVM*QK.K	974.46116	-0.24516	2	5.40E-02	0.80	3.05	0.58	312.7	1	12/24
2243	T.LSDYNIQK.E	980.50474	-0.36290	2	1.43E-04	0.90	3.12	0.67	426.1	1	13/21
938	H.HASSEDVIK.E	985.49490	-0.90858	2	2.17E-06	0.88	2.21	0.72	535.9	1	16/24
619	R.PYEGTQTAK.L	994.48400	-1.29500	2	1.52E-01	0.87	2.39	0.67	602.7	1	15/24
3079	H.PADIPDYLK.L	1031.54079	0.26675	2	4.26E-04	0.93	3.06	0.75	785.4	1	15/24
902	G.G]HYDAEVK.T	1032.47447	-0.29376	2	1.65E-02	0.88	2.83	0.52	577.7	1	14/21
2225	Y.TIVEQYER.A	1037.52620	-0.26422	2	1.13E-02	0.80	2.64	0.48	392.7	1	13/21
2016	R.M*YPEDGALK.G	1039.47648	-0.46073	2	1.52E-03	0.86	2.19	0.62	455.7	1	17/24
1452	K.EGIPPDQQR.L	1039.51670	-0.51728	2	3.77E-03	0.69	2.01	0.84	93.5	1	11/24
4267	K.ESTLHLVLR.L	1067.62077	-1.82434	2	1.25E-07	0.60	3.33	-	275.2	1	15/24
2488	R.TLSDYNIQK.E	1081.55242	-0.78970	2	5.08E-06	0.95	3.50	0.79	582.9	1	18/24

1044	K.DGGHYDAEVK.T	1090.47998	-0.51447	2	5.00E-08	0.90	2.94	0.76	519.2	1	15/27
4708	K.KPVQLPGAYK.T	1100.64626	0.02876	2	6.75E-04	0.84	3.55	0.60	218.2	1	13/27
2092	N.FPSDGPVM*QK.K	1121.52958	0.77237	2	7.20E-03	0.81	3.13	0.52	369.9	1	14/27
2510	Y.PEDGALKGEIK.M	1156.62083	0.16427	2	1.02E-03	0.90	3.86	0.53	528.5	1	16/30
4790	K.HPADIPDYLK.L	1168.59970	-0.45458	2	1.49E-07	0.89	2.80	0.95	179.9	1	14/27
4431	K.TM*GWEASTER.M	1183.50482	0.19755	2	1.35E-05	0.84	3.04	0.69	318.9	1	13/27
3559	S.SLQDGEFIYK.V	1199.59428	-0.91108	2	1.92E-03	0.77	3.04	0.61	254.7	1	12/27
2304	K.K#PVQLPGAYK.T	1214.68916	-0.41981	2	1.45E-05	0.94	3.89	0.00	1045.0	1	15/27
1163	L.KDGGHYDAEVK.T	1218.57494	-0.35389	2	7.06E-07	0.90	3.26	0.62	691.9	1	16/30
3287	I.FAGK#QLEDGR.T	1234.61745	-0.86440	2	4.63E-03	0.74	3.45	0.18	577.4	1	14/27
3790	R.LIFAGK#QLED.G	1247.66300	0.10623	2	1.10E-04	0.82	3.11	0.29	785.5	1	15/27
3464	D.SSLQDGEFIYK.V	1286.62631	0.15845	2	3.25E-07	0.93	3.06	0.69	896.9	1	17/30
1540	K.KTM*GWEASTER.M	1311.59978	-0.17514	3	3.26E-01	0.76	3.25	0.51	286.4	1	22/60
1242	K.LKDGGHYDAEVK.T	1331.65901	-0.20027	2	5.72E-07	0.95	4.25	0.68	927.3	1	17/33
3224	R.LIFAGKQLEDGR.T	1346.74268	-0.50847	2	2.78E-05	0.96	3.66	0.65	1260.3	1	20/33
2256	R.GTNFPSDGPVM*QK.K	1393.64165	-0.43603	2	1.74E-07	0.93	3.98	0.70	597.1	1	18/36
2943	Y.VKHPADIPDYLK.L	1395.76308	-1.05785	3	7.97E-01	0.68	3.13	0.53	362.0	1	17/66
1268	I.QDKEGIPPDQQR.L	1410.69718	0.09294	2	5.76E-02	0.55	2.36	0.46	223.0	1	14/33
1543	K.K#TM*GWEASTER.M	1425.64268	0.81699	2	1.56E-05	0.92	3.23	0.00	550.0	1	16/30
3505	N.EDYTIVEQYER.A	1444.65907	-0.31033	2	3.34E-08	0.94	3.69	0.77	572.1	1	16/30
1284	K.LK#DGGHYDAEVK.T	1445.70191	-0.58951	3	2.78E-01	0.42	3.01	0.47	495.4	1	24/66
2871	R.MYPEDGALKGEIK.M	1450.72464	-0.57898	2	1.75E-02	0.49	2.59	0.40	167.1	1	14/36
2658	R.HSTGAENLYFQGH.M	1460.65532	0.25326	2	5.61E-07	0.95	3.91	0.88	470.2	1	19/36
3354	R.LIFAGK#QLEDGR.T	1460.78558	-0.17102	2	1.58E-07	0.86	3.79	0.37	464.5	1	17/33
2516	R.M*YPEDGALKGEIK.M	1466.71956	3.14052	2	6.63E-04	0.93	3.51	0.77	611.4	1	19/36
2441	Q.LEDGRTLSDYNIQ.K	1523.73363	2.28450	2	1.84E-01	0.06	2.01	0.21	59.9	1	8/36
1715	K.IQDKEGIPPDQQR.L	1523.78125	0.19403	2	7.48E-08	0.93	4.22	0.56	525.6	1	20/36
3519	T.QDSSLQDGEFIYK.V	1529.71183	0.64526	2	1.04E-04	0.92	3.38	0.84	460.4	1	17/36
2514	K.KPVQLPGAYKTDIK.L	1557.89990	-0.12762	2	1.82E-06	0.91	3.47	0.73	476.1	1	18/39
2588	R.M*YPEDGALK#GEIK.M	1580.76246	-1.83035	2	3.58E-02	0.40	2.97	0.03	315.2	1	16/36
2659	R.HSTGAENLYFQGHM*.C	1607.69072	0.07561	2	8.80E-11	0.89	3.32	0.77	391.0	1	17/39
3237	K.AYVKHPADIPDYLK.L	1629.86352	-0.79905	3	4.05E-08	0.97	4.62	0.74	1695.6	1	36/78
1311	K.IQDK#EGIPPDQQR.L	1637.82415	-0.29923	2	6.20E-05	0.60	3.40	0.59	424.6	1	18/36
2152	K.LRGTNFPSDGPVM*QK.K	1662.82682	-1.50799	3	9.49E-04	0.95	4.37	0.86	775.7	1	30/84
2592	K.KPVQLPGAYK#TDIK.L	1671.94280	-0.56041	3	1.25E-07	0.59	3.84	0.12	288.5	1	24/78
1236	K.AKIQDKEGIPPDQQR.L	1722.91332	1.09459	2	6.28E-09	0.95	4.08	0.84	596.8	1	20/42
3596	T.VTQDSSLQDGEFIYK.V	1729.82792	-1.19561	2	8.43E-08	0.94	4.10	0.64	869.7	1	18/42

3256	K.AYVK#HPADIPDYLK.L	1743.90642	-0.46238	3	5.60E-06	0.85	4.61	0.34	391.9	1	25/78
2942	K.QLEDGRTLSDYNIQK.E	1779.88717	-1.57041	3	3.37E-02	0.26	2.65	0.29	142.5	1	15/84
3248	T.SHNEDYTIVEQYER.A	1782.79293	0.86843	2	1.51E-09	0.97	4.73	0.79	1346.5	1	20/39
3916	K.TITLEVEPSDTIENVK.A	1787.92730	-0.93338	3	7.96E-06	0.94	4.20	0.77	824.2	1	32/90
1911	K.LRGTNFPSDGPVM*QKK.T	1790.92178	1.02387	3	2.88E-02	0.88	3.76	0.73	386.0	1	24/90
2307	K.TTYM*AKKPVQLPGAYK.T	1811.97242	0.34967	3	6.62E-05	0.68	3.16	0.56	233.5	1	19/90
3386	D.ITSHNEDYTIVEQYER.A	1996.92468	-1.59919	3	5.84E-06	0.82	3.43	0.66	418.0	1	20/90
2828	R.M*EGSVNGHEFEIEGEGEGR.P	2078.87199	-0.70988	3	7.54E-10	0.95	4.76	0.74	945.0	1	33/108
3605	K.TITLEVEPSDTIENVK#AK.I	2101.10228	0.08246	3	2.27E-02	0.35	2.77	0.69	610.4	1	25/102
4135	G.V]VTVTQDSSLQDGEFIYK.V	2143.05533	-0.96006	2	4.47E-09	0.97	4.29	0.00	1454.7	1	26/51
3981	K.LDITSHNEDYTIVEQYER.A	2225.03568	0.88219	2	1.08E-14	0.94	3.69	0.68	903.8	1	22/51
3895	K.TLTGKTITLEVEPSDTIENVK.A	2288.22315	-1.00050	3	4.01E-06	0.94	4.71	0.60	943.0	1	34/120
3900	K.TLTGK#TITLEVEPSDTIENVK.A	2402.26605	-0.06054	3	1.40E-12	0.94	5.37	0.03	1608.3	1	44/120
4588	R.VM*NFEDGGVVTVTQDSSLQDGEFIYK.V	2894.34005	-0.24964	3	2.88E-08	0.85	3.11	0.80	397.8	1	26/150
2889	R.M*EGSVNGHEFEIEGEGEGRPYEGTQTAK.L	3054.33815	-1.39823	4	3.96E-07	0.80	3.46	0.55	379.5	1	35/243

Reference	S21-E2D4-40				P (pro)	Sf	Score	Coverage	MW	Accession	Peptide (Hits)
Scan(s)	Peptide	MH+	DeltaM (ppm)	z	P (pep)	Sf	XC	DeltaCn	Sp	RSp	Ions
1 RFP_UB_new					3.09E-13	58.16	690.29	71.50	38172.1		70 (65 5 0 0 0)
3636	P.ADIPDYLK.L	934.48802	-2.09063	2	3.02E-06	0.35	2.32	-	299.3	1	13/21
3438	K.AYVK#HPADIPDYLK.L	1743.90642	-2.24734	3	1.32E-06	0.63	3.70	0.28	227.1	1	21/78
1213	K.DGGHYDAEVK.T	1090.47998	-0.62641	2	1.99E-07	0.94	2.94	0.74	908.4	1	19/27
3788	N.E]DYTIVEQYER.A	1558.70197	-0.16520	2	2.12E-09	0.98	4.14	0.00	1938.8	1	23/30
3723	N.EDYTIVEQYER.A	1444.65907	-1.49330	2	1.13E-06	0.94	3.55	0.84	559.0	1	16/30
4660	K.ESTLHLVLR.L	1067.62077	-2.05302	2	5.27E-09	0.47	3.34	-	213.5	1	13/24
3512	I.FAGK#QLEDGR.T	1234.61745	-0.66666	2	2.27E-04	0.70	3.35	0.18	582.6	1	13/27
1880	N.FPSDGPVM*QK.K	1121.52958	-2.27522	2	6.09E-02	0.88	3.01	0.65	441.9	1	16/27
1124	D.GALKGEIK.M	815.49853	-1.35653	2	1.46E-02	0.36	2.46	-	463.8	1	12/21
915	G.GHYDAEVK.T	918.43157	-1.33548	2	5.70E-02	0.86	2.65	0.67	400.4	1	13/21
2429	R.GTNFPSDGPVM*QK.K	1393.64165	-0.69881	2	2.12E-06	0.94	4.35	0.71	507.2	1	18/36
2811	R.GTNFPSDGPVMQK.K	1377.64673	-0.31841	2	1.39E-09	0.92	3.76	0.69	522.1	1	18/36
1896	R.GTNFPSDGPVM*QK#K.T	1635.77951	-1.93741	3	9.01E-02	0.20	2.54	0.73	337.4	1	22/78
1014	H.HASSEDVIK.E	985.49490	-1.52791	2	2.43E-03	0.81	2.81	0.78	212.7	1	11/24
6782	K.HPADIPDYLK.L	1168.59970	-1.49917	2	1.53E-07	0.89	2.96	0.92	190.1	1	14/27
2912	R.HSTGAENLYFQGH.M	1460.65532	-0.16460	2	4.29E-07	0.93	4.20	0.74	349.5	1	18/36
1123	G.HYDAEVK.T	861.41011	-0.03076	2	6.71E-03	0.73	2.05	0.55	381.4	1	11/18
1483	K.IQDKEGIPPDQQR.L	1523.78125	-0.84740	2	2.12E-07	0.95	4.23	0.63	745.8	1	23/36

1240	L.KDGGHYDAEVK.T	1218.57494	-1.21641	3	9.85E-04	0.81	3.23	0.79	271.8	1	17/60
2440	K.K]PVQLPGAYK.T	1214.68916	-1.22378	2	1.67E-06	0.95	3.59	0.55	1359.9	1	16/27
2440	K.K#PVQLPGAYK.T	1214.68916	-1.22378	2	1.67E-06	0.95	3.59	0.00	1359.9	1	16/27
3757	K.KPVQLPGAYK.T	1100.64626	-1.85667	2	9.29E-04	0.67	3.22	0.55	159.7	1	10/27
2210	K.KTMGWEASTER.M	1295.60486	-0.53111	2	5.07E-06	0.93	3.64	0.71	576.6	1	17/30
1623	K.KTM*GWEASTER.M	1311.59978	-0.65350	2	6.25E-05	0.93	3.91	0.79	279.7	1	16/30
1648	K.K#TM*GWEASTER.M	1425.64268	-0.80988	2	1.28E-03	0.92	3.35	0.72	653.2	1	15/30
1687	K.LDITSHN.E	799.39446	-0.23085	2	4.70E-03	0.85	2.13	0.68	502.0	1	12/18
4183	K.LDITSHNEDYTIVEQYER.A	2225.03568	-1.12633	3	9.68E-08	0.96	5.01	0.87	796.0	1	27/102
3497	R.LIFAGK#QLEDGR.T	1460.78558	-1.17379	2	4.07E-06	0.75	3.62	0.25	459.9	1	15/33
1346	K.LK#DGGHYDAEVK.T	1445.70191	-1.31903	2	1.36E-05	0.93	3.95	0.00	676.0	1	16/33
1346	K.L]KDGGHYDAEVK.T	1445.70191	-1.31903	2	1.92E-04	0.93	3.95	0.71	676.0	1	16/33
1230	K.LKDGGHYDAEVK.T	1331.65901	-1.48362	2	2.42E-08	0.95	3.90	0.62	1081.8	1	19/33
2367	K.LRGTNFPSDGPVM*QK.K	1662.82682	-1.28776	3	9.11E-06	0.90	3.07	0.79	705.8	1	30/84
2412	T.LSDYNIQK.E	980.50474	-0.67414	2	1.90E-03	0.79	2.99	0.57	257.4	1	11/21
4609	K.LSFPEGFK.W	924.48254	-1.99621	2	7.34E-04	0.91	2.38	0.86	482.0	1	14/21
2995	R.M*EGSVNGHEFEIEGEGEGR.P	2078.87199	-1.23836	3	3.09E-13	0.98	5.80	0.81	1458.2	1	35/108
3303	R.MEGSVNGHEFEIEGEGEGR.P	2062.87707	-0.92933	3	1.70E-05	0.95	4.58	0.77	835.0	1	31/108
3050	R.M*EGSVNGHEFEIEGEGEGRPYEGTQTAK.L	3054.33815	-2.43735	4	1.71E-07	0.95	5.05	0.92	624.6	1	41/243
3708	R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L	3038.34323	-1.30978	4	3.61E-09	0.89	3.84	0.84	338.3	1	35/243
2230	R.M*YPEDGALK.G	1039.47648	-1.40021	2	7.15E-03	0.80	2.34	0.65	308.7	1	14/24
2560	R.MYPEDGALK.G	1023.48156	-1.85329	2	1.35E-05	0.87	2.63	0.79	331.6	1	14/24
2578	R.M*YPEDGALKGEIK.M	1466.71956	-1.10404	2	4.50E-06	0.88	3.55	0.64	449.2	1	16/36
3061	R.MYPEDGALKGEIK.M	1450.72464	-0.66313	2	1.60E-09	0.91	3.86	0.69	223.7	1	18/36
3300	H.PADIPDYLK.L	1031.54079	-1.03496	2	2.60E-04	0.84	3.14	0.71	380.7	1	11/24
2305	K.PVQLPGAYK.T	972.55129	-3.36429	2	8.52E-05	0.83	2.40	0.53	601.7	1	15/24
853	R.PYEGTQTAK.L	994.48400	-1.78599	2	1.23E-02	0.74	2.56	0.59	337.2	1	12/24
3734	T.QDSSLQDGEFIYK.V	1529.71183	-1.03053	2	7.76E-06	0.91	3.17	0.83	461.2	1	17/36
1412	L.SDYNIQK.E	867.42067	-1.23319	2	3.65E-02	0.86	2.47	0.65	399.0	1	12/18
3443	T.SHNEDYTIVEQYER.A	1782.79293	-1.87042	2	3.82E-13	0.98	5.15	0.84	1443.3	1	21/39
3773	S.SLQDGEFIYK.V	1199.59428	-2.13220	2	1.34E-03	0.90	3.20	0.64	568.2	1	15/27
3674	D.SSLQDGEFIYK.V	1286.62631	-1.35957	2	2.84E-08	0.92	3.01	0.70	805.0	1	17/30
3591	E.STLHLVLR.L	938.57818	-1.30489	2	2.67E-05	0.72	2.98	-	664.1	1	15/21
4166	K.TITLEVEPSDTIENVK.A	1787.92730	-1.34303	3	2.04E-08	0.92	4.21	0.73	530.3	1	25/90
3590	S.TLHLVLR.L	851.54615	-1.52761	2	8.14E-04	0.64	2.20	-	454.6	1	15/18
5410	R.TLSDYNIQK.E	1081.55242	-2.14409	2	3.55E-01	0.92	2.95	0.88	425.8	1	15/24
4148	K.T]LTGKTITLEVEPSDTIENVK.A	2402.26605	-1.68101	2	1.11E-07	0.87	5.16	0.03	794.8	1	21/60

4390	K.TLTGK#TITLEVEPSDTIENVK.A	2402.26605	-0.97520	3	1.50E-03	0.84	5.31	0.62	752.5	1	31/120
2879	K.TMGWEASTER.M	1167.50990	-1.32787	2	1.27E-04	0.91	3.34	0.44	878.3	1	17/27
2117	K.TM*GWEASTER.M	1183.50482	-1.24646	2	5.05E-07	0.97	3.53	0.97	1005.1	1	19/27
2294	G.T]NFPSDGPVM*QK.K	1450.66308	-1.05893	2	3.11E-07	0.89	3.24	0.64	520.1	1	17/33
4890	R.VM*NFEDGGVVTVTQDSSLQDGEFIYK.V	2894.34005	-0.88227	3	8.23E-12	0.96	5.52	0.82	850.3	1	32/150
5246	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V	2878.34513	-3.60163	2	4.09E-09	0.78	2.62	0.75	303.6	1	18/75
2675	P.VQLPGAYK.T	875.49853	-0.49670	2	5.07E-04	0.79	2.19	0.94	201.8	1	10/21
3823	T.VTQDSSLQDGEFIYK.V	1729.82792	-1.05447	2	9.12E-11	0.91	3.38	0.64	703.5	1	19/42
2628	M.YPEDGALKGEIK.M	1319.68416	-0.23966	3	1.18E-03	0.76	2.60	0.67	397.9	1	23/66

Reference	S22-E2T-20				P (pro)	Sf	Score	Coverage	MW	Accession	Peptide (Hits)
Scan(s)	Peptide	MH+	DeltaM (ppm)	z	P (pep)	Sf	XC	DeltaCn	Sp	RSp	Ions
1 RFP_UB_new					1.08E-14	63.71	768.26	77.40	38172.1		77 (76 1 0 0 0)
3431	P.ADIPDYLK.L	934.48802	-2.61314	2	4.61E-02	0.58	2.60	-	389.5	1	15/21
1836	K.AKIQDKEGIPPDQQR.L	1722.91332	-2.56205	3	5.27E-03	0.67	2.76	0.55	342.7	1	22/84
3242	K.AYVKHPADIPDYLK.L	1629.86352	-2.03484	3	4.37E-07	0.96	4.73	0.72	1255.2	1	31/78
1073	K.DGGHYDAEVK.T	1090.47998	-2.64137	2	7.66E-07	0.96	2.91	0.80	1082.1	1	20/27
3521	N.EDYTIVEQYER.A	1444.65907	-2.08478	2	8.71E-07	0.93	2.93	0.85	618.2	1	17/30
3589	N.E]DYTIVEQYER.A	1558.70197	-0.32183	2	4.44E-09	0.97	3.65	0.00	1635.9	1	21/30
1592	F.EIEGEGEGRPYEGTQTAK.L	1950.90394	-3.74152	3	4.08E-04	0.73	2.88	0.55	412.6	1	26/102
4456	K.ESTLHLVLR.L	1067.62077	-2.62471	2	2.24E-08	0.66	3.41	-	288.6	1	16/24
3343	I.FAGK#QLEDGR.T	1234.61745	-1.85313	2	1.83E-03	0.51	3.04	0.02	466.0	1	14/27
1747	N.FPSDGPVM*QK.K	1121.52958	-2.38406	2	5.39E-03	0.87	2.76	0.66	520.1	1	15/27
1010	D.GALKGEIK.M	815.49853	-2.25466	2	3.78E-03	0.35	2.38	-	474.1	1	12/21
825	G.GHYDAEVK.T	918.43157	-2.99688	2	3.13E-02	0.78	2.44	0.61	319.7	1	12/21
2773	R.GTNFPSDGPVMQK.K	1377.64673	-2.17917	2	5.70E-11	0.95	4.58	0.70	586.6	1	19/36
2800	R.GTNFPSDGPVM*QK.K	1393.64165	-1.92508	2	5.09E-08	0.95	4.49	0.59	788.9	1	20/36
903	H.HASSEDVIK.E	985.49490	-3.57172	2	6.08E-05	0.94	3.31	0.72	626.2	1	17/24
5936	K.HPADIPDYLK.L	1168.59970	-2.96159	2	1.05E-05	0.78	2.87	0.74	113.3	1	12/27
3291	K.H]PADIPDYLK.L	1282.64260	-3.02535	2	3.54E-01	0.38	2.17	0.61	141.2	1	8/27
2644	R.HSTGAENLYFQGH.M	1460.65532	-2.25390	2	2.76E-08	0.95	3.86	0.83	594.7	1	20/36
2633	R.HSTGAENLYFQGHM*.C	1607.69072	-3.53938	3	4.82E-03	0.79	3.20	0.70	325.4	1	19/78
1013	G.HYDAEVK.T	861.41011	-1.58957	2	1.76E-02	0.89	2.68	0.42	772.2	1	14/18
1961	K.IQDKEGIPPDQQR.L	1523.78125	-1.96894	2	6.98E-09	0.94	4.27	0.55	568.1	1	21/36
1121	L.KDGGHYDAEVK.T	1218.57494	-2.85826	2	8.40E-08	0.93	3.19	0.84	714.9	1	16/30
2965	K.KPVQLPGAYK.T	1100.64626	-2.52212	2	6.63E-04	0.88	3.33	0.65	302.0	1	15/27
2255	K.K#PVQLPGAYK.T	1214.68916	-3.13318	2	1.33E-04	0.94	3.40	0.00	865.2	1	19/27

476	G.KQLEDGR.T	845.44756	-3.10317	2	1.36E-03	0.52	2.25	0.33	298.7	1	10/18
2066	K.KTMGWEASTER.M	1295.60486	-2.14321	3	7.11E-02	0.88	3.44	0.67	402.2	1	25/60
1479	K.KTM*GWEASTER.M	1311.59978	-1.02578	2	7.67E-06	0.92	3.50	0.76	337.6	1	17/30
1527	K.LDITSHN.E	799.39446	-2.13965	2	6.87E-03	0.82	2.39	0.55	449.5	1	12/18
4603	K.LDITSHNEDYTIVEQYER.A	2225.03568	-1.12633	3	1.57E-08	0.95	4.70	0.85	765.5	1	27/102
3324	R.LIFAGK#QLEDGR.T	1460.78558	-2.59440	2	1.67E-08	0.94	4.15	0.41	851.1	1	21/33
1188	K.LKDGGHYDAEVK.T	1331.65901	-2.03363	2	2.48E-08	0.95	4.10	0.66	995.3	1	18/33
2435	K.LRGTNFPSDGPVM*QK.K	1662.82682	-3.60021	3	1.83E-04	0.95	4.96	0.76	581.8	1	28/84
2709	K.LRGTNFPSDGPVMQK.K	1646.83190	-3.12486	3	5.86E-06	0.94	3.32	0.79	1150.2	1	33/84
5947	K.LSFPEGFK.W	924.48254	-2.59040	2	1.29E-03	0.91	2.65	-	441.8	1	12/21
2826	R.M*EGSVNGHEFEIEGEGEGR.P	2078.87199	-2.29531	3	1.83E-09	0.97	4.89	0.81	1303.9	1	34/108
3138	R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L	3038.34323	-2.49056	3	1.08E-14	0.95	5.19	0.86	692.1	1	33/162
2890	R.M*EGSVNGHEFEIEGEGEGRPYEGTQTAK.L	3054.33815	-2.35742	4	3.20E-09	0.94	5.16	0.81	602.4	1	39/243
2404	R.MYPEDGALK.G	1023.48156	-3.64234	2	3.30E-01	0.73	2.06	0.75	259.7	1	12/24
2094	R.M*YPEDGALK.G	1039.47648	-3.04429	2	9.26E-04	0.82	2.30	0.70	331.5	1	14/24
2366	R.M*YPEDGALKGEIK.M	1466.71956	-2.43567	2	4.37E-03	0.95	3.56	0.75	768.6	1	21/36
2819	R.MYPEDGALKGEIK.M	1450.72464	-1.75700	2	8.10E-04	0.73	3.12	0.61	174.4	1	13/36
3614	H.PADIPDYLK.L	1031.54079	-3.28338	2	1.31E-06	0.93	3.14	0.60	901.1	1	16/24
2602	Y.PEDGALKGEIK.M	1156.62083	-1.73545	2	9.68E-05	0.94	3.91	0.48	986.7	1	20/30
2102	F.PSDGPVM*QK.K	974.46116	-1.81103	2	9.13E-04	0.76	3.28	0.56	198.3	1	11/24
2762	K.PVQLPGAYK.T	972.55129	-2.48568	2	3.46E-04	0.89	3.02	0.59	635.1	1	15/24
598	R.PYEGTQTAK.L	994.48400	-4.36369	2	1.79E-03	0.89	2.28	0.69	669.6	1	16/24
1324	I.QDKEGIPPDQQR.L	1410.69718	-1.98383	2	1.70E-02	0.51	2.50	0.49	185.8	1	12/33
3554	T.QDSSLQDGEFIYK.V	1529.71183	-1.74873	2	2.24E-07	0.90	3.57	0.80	383.3	1	15/36
519	G.RPYEGTQTAK.L	1150.58511	-2.95490	2	1.97E-04	0.65	2.40	0.48	220.4	1	14/27
1277	L.SDYNIQK.E	867.42067	-2.28865	2	4.67E-03	0.90	2.92	0.66	508.4	1	12/18
3264	T.SHNEDYTIVEQYER.A	1782.79293	-1.80195	2	8.38E-13	0.96	4.35	0.78	1150.2	1	18/39
3492	D.SSLQDGEFIYK.V	1286.62631	-2.02370	2	4.28E-09	0.94	3.42	0.86	792.8	1	16/30
1867	L.SSSEHM*QIFVK.T	1308.62527	-1.84760	2	9.27E-05	0.87	2.75	0.85	291.4	1	15/30
2882	L.SSSEHMQIFVK.T	1292.63035	-2.77849	2	2.54E-06	0.80	2.68	0.72	338.1	1	13/30
3390	E.STLHLVLR.L	938.57818	-2.54045	2	2.06E-04	0.70	3.28	-	538.9	1	14/21
5174	K.TDIKLDITSHNEDYTIVEQYER.A	2682.28933	-3.59656	4	4.35E-08	0.82	3.55	0.66	308.9	1	26/189
4972	K.TITLEVEPSDTIENVK.A	1787.92730	-1.50620	2	3.70E-11	0.95	4.33	0.68	792.3	1	24/45
3650	K.TITLEVEPSDTIENVKAK#.I	2101.10228	-1.92193	3	6.66E-05	0.45	3.20	0.01	498.8	1	28/102
3576	S.TLHLVLR.L	851.54615	-1.88599	2	1.69E-04	0.40	2.40	-	247.8	1	12/18
6025	R.TLSDYNIQK.E	1081.55242	-2.48269	2	3.34E-03	0.92	2.92	0.78	460.6	1	16/24
3952	K.TLTGK#TITLEVEPSDTIENVK.A	2402.26605	-2.04231	3	2.83E-07	0.86	4.98	0.01	1008.8	1	36/120

2621	K.TMGWEASTER.M	1167.50990	-2.26888	2	3.31E-08	0.96	3.87	0.77	813.2	1	19/27
1959	K.TM*GWEASTER.M	1183.50482	-2.07160	2	2.28E-07	0.96	3.01	0.96	961.3	1	19/27
2063	G.TNFPSDGPVM*QK.K	1336.62018	-4.57983	2	6.16E-04	0.80	3.22	0.66	256.0	1	13/33
5007	R.VMNFEDGGVVTVTQDSSLQDGEFIYK.V	2878.34513	-1.61304	3	1.34E-03	0.82	3.16	0.60	550.1	1	28/150
4894	R.VM*NFEDGGVVTVTQDSSLQDGEFIYK.V	2894.34005	-2.02101	3	2.85E-07	0.95	5.20	0.77	635.4	1	31/150
2528	P.VQLPGAYK.T	875.49853	-1.68185	2	3.08E-04	0.83	2.16	0.95	234.7	1	11/21
2802	K.VRM*EGSVNGHEFEIEGEGEGRPYEGTQTAK.L	3309.50768	-1.76063	4	3.19E-06	0.82	3.14	0.77	263.1	1	33/261
3629	T.VTQDSSLQDGEFIYK.V	1729.82792	-2.74810	2	1.01E-05	0.94	3.91	0.66	1018.5	1	19/42
2536	M.YPEDGALKGEIK.M	1319.68416	-2.14883	2	3.70E-07	0.95	3.87	0.61	1041.9	1	20/33
3032	D.YTIVEQYER.A	1200.58953	-3.35863	2	1.01E-01	0.91	3.07	0.62	711.4	1	15/24

	Reference	S23-E2T-40				P (pro)	Sf	Score	Coverage	MW	Accession	Peptide (Hits)
	Scan(s)	Peptide	MH+	DeltaM (ppm)	z	P (pep)	Sf	XC	DeltaCn	Sp	RSp	Ions
1	RFP_UB_new					4.93E-11	39.46	488.21	63.50	38172.1		49 (48 1 0 0 0)
	1363	K.AKIQDKEGIPPDQQR.L	1722.91332	-1.60556	3	7.58E-08	0.77	3.34	0.62	239.8	1	21/84
	3143	K.AYVKHPADIPDYLK.L	1629.86352	-1.02374	3	1.81E-06	0.90	3.73	0.71	640.1	1	25/78
	1052	K.DGGHYDAEVK.T	1090.47998	-1.96971	2	3.61E-07	0.90	2.74	0.78	524.7	1	16/27
	3539	Q.DSSLQDGEFIYK.V	1401.65325	-1.57173	2	3.66E-05	0.72	2.46	0.61	469.2	1	13/33
	3415	N.EDYTIVEQYER.A	1444.65907	-2.08478	2	2.61E-03	0.78	2.31	0.85	257.0	1	12/30
	4293	K.ESTLHLVLR.L	1067.62077	-2.39603	2	1.34E-09	0.90	2.17	0.98	295.1	1	15/24
	956	D.GALKGEIK.M	815.49853	-1.28169	2	5.91E-03	0.56	2.40	-	669.6	1	14/21
	861	E.GEGEGRPYEGTQTAK.L	1579.73469	-1.25097	2	1.28E-04	0.78	2.62	0.81	252.4	1	15/42
	866	E.GEGRPYEGTQTAK.L	1393.67063	-1.70236	2	1.08E-03	0.52	2.26	0.63	165.0	1	12/36
	945	D.GGHYDAEVK.T	975.45304	-2.23737	2	2.22E-02	0.42	2.44	0.50	522.2	2	14/24
	948	G.GHYDAEVK.T	918.43157	-1.80067	2	1.41E-02	0.71	2.50	0.42	426.2	1	12/21
	1893	R.GTNFPSDGPVM*QK.K	1393.64165	1.31578	2	2.99E-10	0.95	4.11	0.76	659.3	1	19/36
	2524	R.GTNFPSDGPVMQK.K	1377.64673	-0.49562	2	1.45E-08	0.93	4.03	0.69	466.7	1	18/36
	4612	K.HPADIPDYLK.L	1168.59970	-1.70808	2	3.19E-10	0.84	2.58	0.83	206.8	1	14/27
	1799	K.IQDKEGIPPDQQR.L	1523.78125	-1.40817	2	4.93E-11	0.95	4.11	0.63	670.0	1	22/36
	1070	L.KDGGHYDAEVK.T	1218.57494	-1.65616	2	2.13E-04	0.83	3.02	0.66	466.2	1	13/30
	2175	K.KPVQLPGAYK.T	1100.64626	-2.63303	2	1.65E-06	0.84	3.03	0.61	312.2	1	15/27
	1905	K.KTMGWEASTER.M	1295.60486	-1.00221	2	1.50E-06	0.83	2.54	0.86	315.3	1	13/30
	1374	K.KTM*GWEASTER.M	1311.59978	-1.30499	2	2.43E-05	0.90	3.12	0.75	317.1	1	17/30
	3874	K.LDITSHNEDYTIVEQYER.A	2225.03568	-0.96174	3	2.97E-08	0.92	3.98	0.82	612.7	1	26/102
	2913	T.LEVEPSDTIENVK.A	1472.74788	-0.68339	2	2.52E-09	0.90	3.19	0.57	635.6	1	21/36
	1114	K.LKDGGHYDAEVK.T	1331.65901	-1.48362	2	2.01E-07	0.96	4.04	0.69	1298.8	1	21/33
	2545	K.LRGTNFPSDGPVMQK.K	1646.83190	-1.81952	2	4.89E-09	0.82	2.93	0.77	311.2	1	15/42

2109	K.LRGTNFPSDGPVM*QK.K	1662.82682	-0.94932	2	2.77E-07	0.83	2.39	0.82	330.3	1	18/42
2096	T.LSDYNIQK.E	980.50474	-0.98538	2	4.41E-03	0.83	2.74	0.56	350.8	1	13/21
4024	K.LSFPEGFK.W	924.48254	-1.13794	2	7.76E-05	0.65	2.08	0.88	172.4	1	8/21
3568	R.MEGSVNGHEFEIE.G	1477.62638	-1.48337	2	7.42E-08	0.91	3.38	0.81	557.4	1	16/36
3168	R.M*EGSVNGHEFEIE.G	1493.62130	-1.58064	2	4.32E-05	0.92	3.50	-	334.2	1	15/36
2667	R.M*EGSVNGHEFEIEGEGEGR.P	2078.87199	-0.62180	3	7.78E-06	0.90	3.60	0.63	843.8	1	29/108
1820	R.M*YPEDGALK.G	1039.47648	-2.10481	2	8.33E-04	0.82	2.30	0.64	349.3	1	15/24
2345	R.M*YPEDGALKGEIK.M	1466.71956	-1.52018	2	6.34E-06	0.88	2.84	0.77	457.3	1	17/36
2750	R.MYPEDGALKGEIK.M	1450.72464	-1.25214	2	2.97E-06	0.74	2.63	0.74	144.6	1	14/36
3017	H.PADIPDYLK.L	1031.54079	-1.98167	2	1.58E-03	0.87	2.95	0.67	517.7	1	13/24
2352	Y.PEDGALKGEIK.M	1156.62083	-4.37397	2	1.19E-03	0.71	3.22	0.42	327.6	1	13/30
2007	K.PVQLPGAYK.T	972.55129	-1.73259	2	3.17E-04	0.86	2.63	0.64	557.8	1	14/24
3432	T.QDSSLQDGEFIYK.V	1529.71183	-1.34973	2	5.48E-06	0.78	2.69	0.81	229.5	1	13/36
2806	K.QLEDGRTLSDYNIQK.E	1779.88717	-0.95316	3	4.56E-02	0.74	3.49	0.64	184.9	1	16/84
3474	S.SLQDGEFIYK.V	1199.59428	-2.13220	2	1.28E-05	0.74	2.59	0.61	355.5	1	12/27
3377	D.SSLQDGEFIYK.V	1286.62631	-1.45445	2	8.57E-07	0.87	2.56	0.60	792.9	1	16/30
3309	E.STLHLVLR.L	938.57818	-0.97974	2	1.79E-05	0.59	2.60	-	599.4	1	14/21
3932	K.TITLEVEPSDTIENVK.A	1787.92730	0.33722	2	9.91E-08	0.94	3.36	0.71	834.9	1	25/45
3308	S.TLHLVLR.L	851.54615	-1.31259	2	5.61E-04	0.39	2.26	-	299.5	1	12/18
2260	R.TLSDYNIQK.E	1081.55242	-1.91836	2	1.69E-07	0.91	2.94	0.84	362.5	1	15/24
1798	K.TM*GWEASTER.M	1183.50482	-1.65903	2	1.54E-08	0.96	3.10	0.92	881.6	1	18/27
2460	K.TMGWEASTER.M	1167.50990	-1.11876	2	2.96E-07	0.94	3.54	0.73	671.5	1	17/27
4478	R.VM*NFEDGGVVTVTQDSSLQDGEFIYK.V	2894.34005	-0.31290	3	2.73E-08	0.88	3.45	0.74	537.0	1	31/150
2885	D.YTIVEQYER.A	1200.58953	-2.24020	2	2.50E-05	0.87	2.80	0.69	448.1	1	13/24

	Reference	S24-E2T-80				P (pro)	Sf	Score	Coverage	MW	Accession	Peptide (Hits)
	Scan(s)	Peptide	MH+	DeltaM (ppm)	z	P (pep)	Sf	XC	DeltaCn	Sp	RSp	Ions
1	RFP_UB_new					1.89E-14	42.45	538.28	62.90	38172.1		54 (53 1 0 0 0)
	3838	P.ADIPDYLK.L	934.48802	-0.91498	2	3.78E-07	0.21	2.31	-	231.9	1	11/21
	1394	K.AKIQDKEGIPPDQQR.L	1722.91332	-0.75535	3	1.20E-06	0.79	3.16	0.66	284.4	1	24/84
	1255	K.DGGHYDAEVK.T	1090.47998	-1.18612	2	6.09E-08	0.93	2.88	0.73	762.1	1	18/27
	3905	N.EDYTIVEQYER.A	1444.65907	-1.32430	2	6.03E-08	0.91	2.81	0.78	614.2	1	16/30
	4704	K.ESTLHLVLR.L	1067.62077	-1.48132	2	2.59E-09	0.35	2.85	-	199.0	1	13/24
	1224	D.GALKGEIK.M	815.49853	-0.30872	2	4.23E-03	0.24	2.69	-	325.2	1	10/21
	1070	G.GHYDAEVK.T	918.43157	-1.60130	2	4.88E-04	0.88	2.05	0.65	695.5	1	15/21
	2602	R.GTNFPSDGPVM*QK.K	1393.64165	-0.43603	2	7.08E-09	0.94	3.77	0.83	623.1	1	18/36
	2910	R.GTNFPSDGPVMQK.K	1377.64673	-1.02727	2	2.32E-08	0.90	3.88	0.62	450.8	1	17/36

3581	K.HPADIPDYLK.L	1168.59970	0.59000	2	5.61E-11	0.92	2.43	0.94	320.8	1	18/27
2291	K.IQDKEGIPPDQQR.L	1523.78125	-1.00762	2	2.27E-10	0.77	3.08	0.61	235.1	1	14/36
1297	L.KDGGHYDAEVK.T	1218.57494	-1.15529	2	4.07E-06	0.87	2.87	0.62	555.5	1	16/30
2838	K.KPVQLPGAYK.T	1100.64626	-1.19122	2	1.12E-07	0.77	2.82	0.57	247.2	1	14/27
2537	K.K]PVQLPGAYK.T	1214.68916	-2.22873	2	2.39E-05	0.88	3.14	0.62	599.1	1	14/27
2537	K.K#PVQLPGAYK.T	1214.68916	-2.22873	2	2.39E-05	0.88	3.14	0.00	599.1	1	14/27
2304	K.KTMGWEASTER.M	1295.60486	-0.81377	2	1.87E-06	0.74	2.68	0.64	253.0	1	13/30
1753	K.KTM*GWEASTER.M	1311.59978	-1.30499	2	4.98E-08	0.91	3.24	0.81	336.3	1	16/30
4324	K.LDITSHNEDYTIVEQYER.A	2225.03568	-1.31230	2	1.89E-14	0.96	3.85	0.80	1174.5	1	24/51
1295	K.LKDGGHYDAEVK.T	1331.65901	-1.02528	2	6.34E-09	0.94	3.95	0.66	869.0	1	17/33
2976	K.LRGTNFPSDGPVMQK.K	1646.83190	-0.78995	3	1.55E-02	0.94	3.25	0.84	1190.4	1	30/84
2460	K.LRGTNFPSDGPVM*QK.K	1662.82682	-0.40682	3	1.63E-09	0.96	4.46	0.91	1041.9	1	34/84
2499	T.LSDYNIQK.E	980.50474	-0.73639	2	1.85E-04	0.85	2.63	0.61	444.5	1	13/21
4740	K.LSFPEGFK.W	924.48254	-1.07192	2	8.73E-06	0.86	2.02	0.94	339.8	1	12/21
3130	R.M*EGSVNGHEFEIEGEGEGR.P	2078.87199	-1.50260	3	3.57E-08	0.93	3.85	0.88	720.3	1	26/108
3430	R.MEGSVNGHEFEIEGEGEGRPYEGTQTAK.L	3038.34323	-2.06871	3	6.16E-09	0.90	3.29	-	370.8	1	27/162
3266	R.M*EGSVNGHEFEIEGEGEGRPYEGTQTAK.L	3054.33815	-1.71796	4	8.58E-11	0.94	4.94	0.82	514.8	1	39/243
2194	R.M*YPEDGALK.G	1039.47648	-0.81303	2	3.80E-03	0.83	2.47	0.69	308.3	1	14/24
3119	R.MYPEDGALKGEIK.M	1450.72464	-0.66313	2	1.74E-08	0.89	3.01	0.64	454.2	1	21/36
2640	R.M*YPEDGALKGEIK.M	1466.71956	-0.43823	2	1.34E-04	0.92	3.36	0.68	722.7	1	19/36
3490	H.PADIPDYLK.L	1031.54079	-1.03496	2	2.40E-04	0.88	2.74	0.73	570.4	1	13/24
2759	Y.PEDGALKGEIK.M	1156.62083	-1.31329	2	4.47E-03	0.80	3.56	0.45	356.3	1	14/30
2432	F.PSDGPVM*QK.K	974.46116	-1.37259	2	9.55E-04	0.87	2.22	0.80	461.6	1	15/24
3081	K.PVQLPGAYK.T	972.55129	-2.17189	2	2.87E-04	0.74	2.52	0.64	395.0	1	11/24
910	R.PYEGTQTAK.L	994.48400	-2.39973	2	1.27E-04	0.83	2.47	0.64	442.5	1	14/24
1383	I.QDKEGIPPDQQR.L	1410.69718	0.00641	2	7.43E-03	0.31	2.03	0.50	86.8	1	11/33
3931	T.QDSSLQDGEFIYK.V	1529.71183	-0.71134	2	3.82E-06	0.90	3.69	0.70	412.3	1	16/36
1493	L.SDYNIQK.E	867.42067	-1.23319	2	1.57E-03	0.86	2.61	0.69	411.7	1	11/18
3871	D.SSLQDGEFIYK.V	1286.62631	-1.64420	2	6.66E-07	0.93	3.01	0.69	1046.0	1	17/30
3911	E.STLHLVLR.L	938.57818	-0.71962	2	2.99E-06	0.26	2.44	-	307.8	1	11/21
5814	K.TITLEVEPSDTIENVK.A	1787.92730	-1.09655	2	1.79E-10	0.83	3.07	0.58	494.4	1	18/45
3906	S.TLHLVLR.L	851.54615	-1.45594	2	1.35E-03	0.25	2.07	-	224.1	1	11/18
2562	R.TLSDYNIQK.E	1081.55242	-1.24117	2	2.67E-06	0.94	2.84	0.89	565.1	1	18/24
4260	K.TLTGK#TITLEVEPSDTIENVK.A	2402.26605	-0.59409	3	8.64E-05	0.71	4.18	0.12	484.4	1	29/120
2199	K.TM*GWEASTER.M	1183.50482	-0.73074	2	1.09E-07	0.96	3.37	0.87	885.1	1	18/27
2951	K.TMGWEASTER.M	1167.50990	-1.43243	2	1.95E-07	0.96	3.88	0.70	782.3	1	19/27
4801	R.VM*NFEDGGVVTVTQDSSLQDGEFIYK.V	2894.34005	-0.50269	3	4.39E-10	0.88	3.75	0.72	467.1	1	28/150

2799	P.VQLPGAYK.T	875.49853	-0.84528	2	1.73E-04	0.82	2.58	0.78	252.4	1	11/21
2706	M.YPEDGALKGEIK.M	1319.68416	-1.21090	3	1.33E-03	0.77	2.52	0.59	547.8	1	25/66
3374	D.YTIVEQYER.A	1200.58953	-1.02010	2	5.48E-03	0.91	3.29	0.73	454.1	1	14/24

Modifications:
M* oxidized Met
K# glygly Lys