

Table S1. Protein identification by nUPLC-MS/MS

Hit	Accession	Description	PLGS score	Mass	SeqCov(%)	Peptide sequence	score	m/z	z
1	P02784	Seminal plasma protein PDC 109	1247.399	15480.6561	39.55	CVFPFIYGGK	6.8752	594.2978	2
						HFDCTVHGSLFPWC ^{SLD} ADYVGR	6.7637	913.7476	3
						KHFDCTVHGSLFPWC ^{SLD} ADYVGR	5.8255	717.5912	4
						IGSMW ^{MS} SWC ^{SL} SPNYDKDR	6.3295	789.0105	3
						HFDCTVHGSLFPWC	6.2101	582.256	3
						HFDCTVHGSLFPWC ^{SLD} A	6.1002	710.983	3
						HFDCTVHGSLFPWC ^{SLD} ADYV	6.1378	836.705	3
						HFDCTVHGSLFPWC ^{SLD} ADYVGR	5.2386	681.0652	4
2	P10096	Glyceraldehyde 3 phosphate dehydrogenase	547.1618	35868.188	20.12	IVSNASCTTNC ^L APLAK	7.176	910.4588	2
						LTGMAFR	6.6196	398.2116	2
						VPTPNVSVVDLT ^{CR}	5.3987	778.9051	2
						DGRGAAQNIIPASTGA ^{AK}	5.364	566.6415	3
						LVTRAAFNSGK	5.164	582.3296	2
						GMAFR	5.3488	581.2803	1
						TGMAFR	6.1614	682.3283	1
						LTGMAFR	5.323	389.205	2
3	Q2T9U2	Outer dense fiber protein 2	493.9897	75498.3489	45.05	KEELEVAQELAETEHENTVLR	6.1887	866.102	3
						LSTFEETNR	6.3127	548.7659	2
						VTDLVNQQQTLEEK	5.9407	822.9225	2
						ILKDEMNKEIEAAR	5.9229	553.9646	3
						AEVEAIMEQLK	5.5804	630.8275	2
						LNQAHIEVQQLK	5.6558	474.268	3
						LLLLLQDKDKEVEELLQEIQ ^{CEK}	5.717	942.8506	3
						LAECQDQLQGYER	5.9515	805.3666	2
						MREDRDSLVER	5.5562	469.2315	3
						LEADEVAAQLER	5.4145	672.3435	2
						QMT ^{CS} DINTLTR	5.5146	720.3344	2
						L ^{CM} QIK	5.862	396.7068	2
						QKELLQK	5.9471	500.3117	2
						QFQSQLADLQQLPDILK	5.673	993.0396	2
						LMEQQGTLLK	4.7391	580.8255	2
						DLYVAEALSTLESWR	5.2932	876.9423	2
						GHLQAQLR	5.9492	461.7622	2
						NGVTSLTQK	5.1057	474.2571	2
						EELEEVAQELAETEHENTVLR	5.1502	617.8013	4
						HLQQEKE ^{CL} MSK	4.828	765.8772	2
						QTAEYSAFK	5.1399	522.751	2
						C ^{KEA} ENSR	5.0374	497.2418	2
						HNIER	5.3664	668.3264	1
						FLEERK	4.3665	411.2088	2
						LVSVMR	5.3304	704.396	1
						ASFAPMEDKLNQAHIEVQQLK	6.0054	600.0655	4
						TRLEADEVAAQLER	5.965	800.9085	2

4	Q3ZBU7	Tubulin beta 4A	5211.085	49585.9449	53.83	QTAEYSAFKLENER	5.6075	562.611	3
						RQFQSQLADLQQLPDILK	5.6552	714.3967	3
						KNIDLTAIISDLR	5.7878	736.4296	2
						HLQQEKE <u>C</u> LSK	5.238	773.8705	2
						FAPMEDKLNQAHIEVQQLK	6.0691	747.0613	3
						TRLEADEVA	5.4732	493.2512	2
						NQAHIEVQQLK	5.5833	654.3547	2
						MREDRDS	4.359	445.6989	2
						TRLEADE	5.3016	408.1939	2
						LQK	3.8593	388.2521	1
						<u>C</u> MQIK	5.5855	679.323	1
						AAQLER	6.0498	687.3697	1
						MREDRDSL	4.5426	502.2411	2
						QTAEYSAFK	4.8492	513.7444	2
						LNQAHIEVQQLK	4.3985	468.5904	3
						SGPFGQIFRPDNFVFGQSGAGNNWAK	8.3878	933.4586	3
						IMNTFSVVPSPK	7.9525	660.3533	2
						EIVHLQAGQ <u>C</u> GNQIGAK	8.0789	608.314	3
						AVLVDLEPGTMDSVR	8.0011	801.4095	2
4	Q3ZBU7	Tubulin beta 4A	5211.085	49585.9449	53.83	YLTVAAVFR	7.1075	520.2986	2
						NSSYFVEWIPNNVK	8.0472	848.9231	2
						ALTVPELTQQMFDAK	7.7038	846.4368	2
						LAVNMVPPFR	7.5185	572.3186	2
						LTPTYGDLNHLVSATMSGVTT <u>C</u> LR	7.3618	903.4556	3
						NMMAA <u>C</u> DPR	7.0028	533.2167	2
						LHFFMPGFAPLTSR	7.7404	540.9504	3
						EAE <u>S</u> <u>C</u> D <u>C</u> LQGFQLTHSLGGGTGSGMGTLLISK	7.1082	1104.5308	3
						ISEQTAMFR	5.8605	615.3048	2
						IREEFPR	5.5312	531.2698	2
						ISEQTAMFRR	5.9472	693.361	2
						TAV <u>C</u> DIPPR	6.081	514.7631	2
						FPGQLNADLRK	6.176	420.2324	3
						LHFF <u>M</u> PGFAPLTSR	6.9518	546.2843	3
						<u>M</u> REIVHLQAGQ <u>C</u> GNQIGAK	6.3458	709.3595	3
						LHFFMPGFA	7.0195	524.7567	2
						LHFFMPGF	6.8523	489.2373	2
						LHFF <u>M</u> PGFA	6.3043	532.7555	2
						EIVHLQAGQ <u>C</u>	6.6863	568.7834	2
						<u>C</u> GNQIGAK	7.4888	424.2111	2
						LHFF <u>M</u> PGF	6.3696	497.2348	2
						PLTSR	5.7904	573.3299	1
						A <u>C</u> DPR	6.4292	618.27	1
						PNNVK	6.7504	571.3149	1
						GNQIGAK	7.4421	687.373	1
						AGQ <u>C</u> GNQIGAK	7.1993	552.2748	2
						PGFAPLTSR	7.3768	473.2607	2
						LHFF <u>M</u> PG	6.4822	423.7025	2
						EIVHLQAGQ <u>C</u> GNQI	6.9248	774.8803	2

						PELTQQMFDAK	7.3087	654.3207	2
						MAACDPR	6.1889	820.3438	1
						PSPK	6.7654	428.2469	1
						NSSYFVEWI	7.0353	563.7643	2
						EIVHLQAGQC [~] GNQIGAK	6.1231	602.3079	3
						YLTVAAVFR	7.2622	511.2943	2
5	P19858	L lactate dehydrogenase A	225.0374	36597.7423	25	VIGSGC [~] NLDSAR	5.9348	624.8021	2
						LVIIITAGAR	5.6842	457.2935	2
						NLHPELGTADADKEQWK	4.4101	627.6473	3
						DQLIQNLLKEEHVPQNK	4.5897	682.7076	3
						MATLKDQLIQNLLKEEHVPQNK	4.0932	864.1157	3
						IVSGKDYNVTANSR	4.3566	762.3703	2
						DLADEVALVDVMEDK	4.4995	554.6327	3
						TAGAR	4.0496	475.2584	1
6	Q29438	Outer dense fiber protein 1	275.9544	29435.6936	16.41	CIDELSA [~]	6.0743	482.2303	2
						LYCLRPSLR	5.9152	393.2197	3
						ILASSCCSSNILGSVNV [~] CGFEPDQVK	5.0701	947.7943	3
						YCLRPSLR	5.3585	532.7846	2
						CLRPSLR	5.3259	451.2514	2
7	O77797	A kinase anchor protein 3	421.4077	94672.6034	40.91	SCVETLGEHIIK	5.4656	462.5722	3
						ASGTLQSPPNLK	5.8379	606.8305	2
						SVGEVLQSVLR	5.457	593.8419	2
						GTGTAETLLQNAYQAIHNELR	5.4879	767.3962	3
						SPQVGADPEEVEKK	6.1439	504.9223	3
						LTNLVIAMAR	6.0846	551.3241	2
						QLDEAVGNVTR	5.4676	601.3093	2
						LLQLSAAAVEK	5.5111	571.8406	2
						EDNSPQC [~] ERPVTSPAK	5.7251	637.9681	3
						SLSAQPPEGCTAPK	5.9678	721.8507	2
						LC [~] LIIAK	6.0741	415.7588	2
						SPAVSHESSLR	6.4284	585.2989	2
						NLLSETIFK	5.4028	532.8022	2
						FKPGESSLGR	6.0373	539.2862	2
						EGISA [~] CLQGS [~] PFVTPK	5.5409	845.9258	2
						EGLTLWHNSQQK	4.9477	720.8593	2
						ENPHQGPT [~] CNGSSVDEVSFYANR	5.2467	855.7161	3
						EASHDPIR	5.1218	462.7291	2
						NLHNVTGTLMTD ^T DFVSAVK	4.3483	721.7033	3
						VASELVNETVTA [~] CSK	4.4769	804.3963	2
						LNE [~] CDETGGAFAGLTK	5.1275	841.8916	2
						LQLLDWLMVNL	5.0397	453.2602	3
						LHFEMSHR	4.1847	528.7632	2
						LDGHMNGQMVDHLMDSVMK	4.6695	720.0094	3
						SFFSHGSQK	4.9385	512.7461	2
						STAGFQDIR	4.779	497.7231	2
						VDWLQSQNGV [~] CK	4.7987	717.3244	2

						SPQVGADPEEVEK	4.5584	692.8599	2
						TLPAERK	5.2458	407.7372	2
						DLEKSTAGFQDIR	5.0893	740.3625	2
						PAVSHESLR	6.5012	361.5223	3
						KPGESSLGR	5.7353	465.7529	2
						TLWHNSQQK	4.7634	571.294	2
						LIIAK	4.6951	557.4051	1
						EDNSPQ <u>C</u> ERPVTSPAK	4.7763	631.9703	3
						SC <u>V</u> ETLGEHIK	4.3435	456.5633	3
8	Q32LE5	L asparaginase	501.9153	32050.5254	57.47	VGDTPC <u>V</u> GSGGYADNDIGAVSTTGHGESILK	5.6004	1012.1464	3
						LALFHVEQGK	6.0491	571.3187	2
						AATVGYNILK	5.8719	525.3006	2
						FAAANGIPTIPGQQLVTER	5.8514	992.0324	2
						SLEEAAASLGHMK	6.0377	486.573	3
						TPHC <u>F</u> LTDDQGAAR	5.5294	737.3499	2
						GVGGIIMVNK	5.0982	494.2821	2
						DLSAGAVSAVR	5.732	523.2841	2
						WTSTSMPWAAAKDGK	4.523	546.2412	3
						NLGTVGAVALD <u>C</u> QGNLAYATSTGGIVNK	5.0761	691.8647	4
						LHSGIDFGDTSIIDLS	5.1777	845.4201	2
						ALFHVEQGK	5.9864	514.7789	2
						EEAANASLGHMK	5.7634	629.2985	2
						TVGYNILK	5.9045	454.263	2
						EAANASLGHMK	5.58	564.7772	2
						GGIIMVNK	4.5982	831.4709	1
						AATVGYNILK	5.0469	516.2954	2
9	Q2TBH0	Outer dense fiber protein 3	205.9449	27633.9404	24.41	HVFDSAPSHSISAR	5.7415	504.2514	3
						DLGPAYSILGR	5.0331	581.317	2
						TTLTPGPGDYFPEK	4.8948	761.8728	2
						VTMTRPC <u>A</u> PVVVSFGIK	4.3055	588.3119	3
						GPIMALYSSPGPK	4.0807	659.3207	2
						VEPPGDK	4.6127	371.2129	2
10	Q32KN8	Tubulin alpha 3	3789.191	49925.68	58.22	AVFVDLEPTVVDEV	8.1393	844.4475	2
						IHFPLATYAPVISA	7.651	586.3253	3
						QLFHPEQLITGKEDAANNYAR	7.489	604.554	4
						VGINYQPPTVVP	7.5605	912.9931	2
						QLFHPEQLITGK	7.0103	470.928	3
						DVNAAIATIK	7.414	508.2909	2
						TIQFVDW <u>C</u> PTGFK	7.4285	799.8846	2
						LSVDYGKK	7.5946	455.2536	2
						LIGQIVSSITASLR	7.0161	729.4354	2
						AYHEQLSVAEITNA <u>C</u> FEPANQMVK	6.5074	917.4392	3
						YMA <u>C</u> CMLYR	6.6615	634.2594	2
						TIGGGDDSFNTFFSETGAGK	6.775	1004.4518	2
						FDGALNVDLTEFQTNLVPYPR	6.5742	803.7426	3
						LSVDYGK	7.3015	391.2063	2

					AVC <u>M</u> LSNTTAIAEAWAR	6.3268	932.9584	2	
					LADLCTGLQGFLIFHSFGGGTGSGFASLLMER	5.7064	840.6555	4	
					EIVDLVLDR	5.906	536.3026	2	
					RTIQFVDW <u>C</u> PTGFK	6.1548	585.6332	3	
					AVC <u>M</u> LSNTTAIAEAWAR	6.0758	940.9551	2	
					PVISA <u>E</u> K	7.3036	743.4245	1	
					DIERPTYTNLNR	7.3945	746.3796	2	
					DYGKK	7.3504	610.3145	1	
					NAAIATIK	7.4327	801.4801	1	
					IHFPLATY	6.6264	472.2525	2	
					SVDYGKK	7.5842	398.7116	2	
					APVISA <u>E</u> K	6.991	407.7346	2	
					SVDYGK	7.1313	668.3232	1	
					ERPTYTNLNR	7.0167	632.3234	2	
					VDYGK	6.7176	581.2877	1	
					AIATIK	7.2421	616.4004	1	
					IERPTYTNLNR	7.4522	688.8683	2	
					YGKK	7.174	495.2902	1	
					PYPR	6.4588	532.2849	1	
					TYAPVISA <u>E</u> K	7.0518	539.7899	2	
					FHPEQLITGK	6.8043	585.3175	2	
					NLDI	6.5231	456.2418	1	
					VDYGKK	7.0858	709.3829	1	
					LDIERPTYTNLNR	7.2354	535.6183	3	
					PEQLITGK	6.8701	443.2544	2	
					ATIK	6.5227	432.279	1	
					DVNAA	5.7613	471.2217	1	
					AAIATIK	7.1358	687.4413	1	
					DVNAAIA	5.6801	655.3343	1	
					ITGK	6.455	418.2654	1	
					VGINYQPPTVV	6.675	584.8174	2	
					FVDLEPTVVDEV R	7.5999	759.3944	2	
					QLFHPEQLITGK	6.6958	464.9262	3	
					AVFVDLEPTVVDEV R	5.9683	557.2979	3	
					LSVDYGK	6.0859	382.2027	2	
					DVNAAIATIK	7.1862	499.7802	2	
11	Q3MHM5	Tubulin beta 4B	6649.305	49831.1803	72.58	SGPFGQIFRPDNFVFGQSGAGNNWAK	8.2358	933.4562	3
						INVYYNEATGGK	7.9713	664.8298	2
						EIVHLQAGQ <u>C</u> GNQIGAK	8.0087	608.3147	3
						IMNTFSVVPSPK	7.7736	660.352	2
						FWEVISDEHGIDPTGTYHGDSLQLER	7.7124	779.8678	4
						AVLVDLEPGTMDSVR	8.073	801.412	2
						NSSYFVEWIPNNVK	7.697	848.9151	2
						YLTVAAVFR	7.4002	520.2976	2
						EVDEQMLNVQNK	7.7653	723.846	2
						ALTVPELTQQMFDAK	6.865	846.4344	2
						IREEYPDR	8.1194	539.2683	2
						GHYTEGAELVDSVLDVVRK	7.7003	696.3625	3

GHYTEGAELVDSVLDVVR	8.0572	653.6659	3
EAES <u>C</u> D <u>C</u> LQGFQLTHSLGGTGSGMGTLLISK	7.1352	1104.524	3
LAVNMVFPFR	7.3204	572.3182	2
NMMAA <u>C</u> DPR	6.8998	533.2172	2
KEAES <u>C</u> D <u>C</u> LQGFQLTHSLGGTGSGMGTLLISK	6.631	860.6688	4
LTTPTYGDLNHLVSATMSGVTT <u>C</u> LR	7.2236	903.4562	3
LHFFMPGFAPLTSR	7.9627	540.9489	3
ISEQFTAMFRR	5.8481	462.5742	3
MSATFIGNSTAIQELFKR	6.3194	672.0202	3
MSMKEVDEQMLNVQNK	5.9444	641.9562	3
FPGQLNADLR	5.9744	565.785	2
INVYYNEATGGKYVPR	5.6941	615.3218	3
LHFF <u>M</u> PGFAPLTSR	6.9633	546.2801	3
IREE	6.6912	528.2712	1
PDR	5.5282	387.1948	1
LHFFMPGFA	7.1438	524.7553	2
REEYPDR	7.8395	482.7276	2
GHYTEGAELVDSV	7.0146	679.8142	2
YPDR	6.6696	550.2554	1
GHYTEGAELV	7.3787	529.2503	2
EIVHLQAGQ <u>C</u>	6.5676	568.7834	2
IREEY	7.1122	691.338	1
LDVVR	7.1799	601.3617	1
VDSVLDVVRK	7.2052	565.3279	2
<u>C</u> GNQIGAK	7.6331	424.2115	2
PNNVK	7.5058	571.3123	1
LHFFMPGF	7.3156	489.2361	2
DVVR	7.2441	488.2807	1
GHYTEGAELVDSVL	7.1472	736.3573	2
LVDSVLDVVRK	7.2833	621.8631	2
PLTSR	5.4737	573.3246	1
GHYTEGAELVD	6.7696	586.7672	2
GQ <u>C</u> GNQIGAK	7.2056	516.7527	2
GNQIGAK	7.6038	687.3737	1
EIVHLQAGQ <u>C</u> GNQI	6.9	774.8842	2
MAA <u>C</u> DPR	6.0676	820.3442	1
GHYTEGAEL	6.9939	479.7164	2
PELTQQMFDAK	6.5817	654.3179	2
DSVLDVVRK	7.5406	515.7956	2
PGFAPLTSR	7.393	473.2586	2
IRE	5.7505	399.2331	1
NSSYFVEWI	7.0566	563.7699	2
AVFR	6.8251	492.2854	1
EIVHLQAGQ <u>C</u> GNQIGA	6.7878	838.9128	2
PSPK	6.9926	428.2494	1
PGTMDSVR	7.2239	431.7063	2
PFPR	5.7383	516.2896	1
GHYTEGAELVDS	6.8566	630.2823	2
GHYTEGAELVDSVLDV	6.9572	843.4047	2

						VDSVLDVVR	7.4849	501.2821	2
						YLTV	5.8561	477.2693	1
						EIVHLQAGQCGNQIGAK	6.0216	602.3057	3
						YLTVAAVFR	7.1643	511.2936	2
						IMNTFSVVPSPK	5.5529	651.3517	2
						GHYTEGAELVDSVLDVVR	7.402	647.663	3
12	Q2KJE5	Glyceraldehyde 3 phosphate dehydrogenase testis specific	2672.647	43288.0852	58.48	AGIALNDNFVK	7.4797	581.315	2
						LAQPTPYSAIK	7.0985	594.8313	2
						VPTPDVSVVDLTGR	7.5163	779.3998	2
						FGILEGLMTTVHSYTATQK	6.7391	699.6949	3
						VEAEPEPPAQPPQPEPIKEEVPPPPPPPPAPK	7.4264	1170.9553	3
						LAQPTPYSAIKDAIK	6.7068	539.3067	3
						IVSNASC ^T TNCLAPLAK	7.3021	910.4545	2
						ELIVGINGFGR	6.8776	587.8308	2
						LISWYDNEYGYSNR	6.8871	890.4034	2
						GP ^M MAGILAYTEDEVVSTDFLS ^D THSSIFDAK	6.3648	1106.2015	3
						VVIC ^A PSPDAPMFV ^M MGVNEK	6.2306	1081.0317	2
						LTGMAFR	7.0487	398.2107	2
						EYNPSSMK	6.4987	478.2138	2
						GAHQNIIPASTGAAK	5.6404	718.3841	2
						GQLVVDNNEISVFQCK	5.4694	617.2782	3
						PPPPPPPPAPK	7.2522	546.315	2
						GMAFR	6.1537	581.282	1
						PTPYSAIKDAIK	6.4934	652.3661	2
						PSSMK	6.0893	549.2672	1
						TGMAFR	6.3231	682.3329	1
						PQPQPEPIKEEVPPPPPPPPAPK	6.6206	821.7812	3
						IALNDNFVK	6.9671	517.2859	2
						EYNPSSMK	5.4527	469.2089	2
						LTGMAFR	5.3628	389.2083	2
13	Q2YDG7	Sperm acrosome membrane associated protein 1	1611.784	30938.9255	44.09	GPVDCGWGRPISELEHVR	7.652	538.5156	4
						EVILTS ^G CPGGESK	7.7601	717.349	2
						LA ^C VHTSPENR	7.7709	428.5419	3
						ASTTEIQSELSSMR	6.524	770.3678	2
						AFE ^C ETLDNNEIVASIR	6.4834	990.9724	2
						YKDSTSLDQSPTDIPGHEDDALSEWNE	5.9616	1017.1257	3
						AC ^V VHTSPENR	7.3662	585.7717	2
						^C VHTSPENR	7.8373	550.2482	2
						D ^C GWGRPISELEHVR	7.3078	633.3064	3
						VHTSPENR	7.3772	470.2339	2
						PENR	6.3621	515.2491	1
						HTSPENR	7.4504	420.7	2
						TSPENR	7.0356	703.3334	1
						LA ^C VHTS	6.5537	385.186	2
						LA ^C VHTSPENR	5.8077	422.5387	3
14	P62157	Calmodulin	5654.477	16837.6523	71.81	VFDKDGNGYISAAELR	7.9781	585.6291	3

						EAFSLFDKDGDTITTK	8.0551	615.6358	3
						DTDSEEEIREAFR	6.9187	532.9091	3
						MKDTDSEEEIREAFR	7.7841	619.2894	3
						MKDTDSEEEIR	7.1763	676.8034	2
						DNGYISAAELR	6.974	633.3094	2
						MADQLTEEQIAEFKEAFSLFDKDGDTITTKELGTVMR	5.572	1067.0128	4
						SLGQNPTAEALQDMINEVDADGNGTIDFPEFLTMMARK	6.0991	1062.2431	4
						SAAELR	7.7791	646.3458	1
						VFDKDGNGY	6.5729	498.7247	2
						DSEEEIREAFR	6.6267	690.8226	2
						FDKDGDTITTK	7.6354	649.3172	2
						AELR	6.8311	488.2801	1
						EEIREAFR	6.3656	525.2768	2
						FSLFDKDGDTITTK	7.4256	822.9074	2
						SEEEIREAFR	6.6314	633.3103	2
						AAELR	7.3967	559.317	1
						ELR	5.1535	417.2447	1
						KDTDSEEEIREAFR	7.5384	575.6116	3
						VFDKDGNGYISAA	6.1178	669.8265	2
						ITTK	6.8265	462.2898	1
						EIR	5.3893	417.2429	1
						MKDTDSE	6.5124	404.1619	2
						EAFSLFDKDGDTITTK	6.237	609.6308	3
						DTDSEEEIREAFR	5.7906	526.9062	3
						MKDTDSEEEIR	5.9843	445.535	3
15	Q5E956	Triosephosphate isomerase	859.6281	26689.5607	68.67	SNVSDAVAQ SAR	6.1992	602.799	2
						I AVAAQN CYK	6.1217	569.2891	2
						ELASQPDVDGFLVGGASLKPEFVDIINAK	6.418	1010.542	3
						TATPQQAQEVHEK	6.5123	489.5793	3
						DLGATWVVLGH SER	5.8908	770.399	2
						VANGAFTGEISPGMIK	5.8747	796.4096	2
						VAHALAEG LGVIA IG EK	5.3623	603.3265	3
						I IYGGSVTGAT CK	5.2586	663.8406	2
						HVFGESDELIGQK	5.4519	729.8622	2
						VIADNVKDWSK	4.6718	637.8328	2
						VPADTEVV CAPPTAYIDFARQK	5.2706	612.8134	4
						GATWVVLGH SER	5.785	656.3468	2
						TPQQAQEVHEK	6.2738	647.824	2
						PQQAQEVHEK	6.496	597.2987	2
						TATPQQAQEVHEK	5.1115	483.5767	3
16	Q2HJB8	Tubulin alpha 8	1463.448	50053.6829	32.96	NLDIERPTYTNLNR	7.7182	573.6324	3
						VGINYQPPTVVPGGDLAK	7.713	912.9941	2
						TIQFVDW CPTGFK	7.4309	799.8857	2
						ESIDLVLDR	5.602	530.281	2
						FDLMYAK	6.8953	444.2181	2
						YMA C CMLYR	6.6492	634.2596	2
						AV CMLSNTTAIAEAWAR	6.2905	932.9621	2

						FDGALNVDLTEFQTNLVYPYR	6.8905	803.7443	3
						EDLAALEK	6.6349	444.7339	2
						EDAANNYAR	5.6227	512.2324	2
						GDVVPKDVNVAIAAIK	4.9484	804.9343	2
						LDHKFDLMYAK	7.2466	460.9022	3
						VGINYQPPTVVPGGDLAKVQR	5.7208	552.8108	4
						AVC <u>ML</u> SNTTAIAEAWAR	6.2707	940.9532	2
						DIERPTYTNLNR	7.7194	746.3791	2
						IERPTYTNLNR	7.5021	688.8658	2
						ERPTYTNLNR	7.2011	632.3173	2
						PYPR	6.0825	532.2844	1
						PGGDLAK	6.6381	329.1779	2
						LDIERPTYTNLNR	7.4718	535.6163	3
						ALEK	5.4139	460.2712	1
17	Q6B856	Tubulin beta 2B	4087.631	49953.2415	52.58	SGPFGQIFRPDNFVFGQSGAGNNWAK	8.2358	933.4562	3
						NSSYFVEWIPNNVK	7.697	848.9151	2
						EVDEQMLNVQNK	7.7653	723.846	2
						IREEYPDR	8.1194	539.2683	2
						GHYTEGAELVDSVLDVVRK	7.7003	696.3625	3
						GHYTEGAELVDSVLDVVR	8.0572	653.6659	3
						LAVNMVFPFR	7.3204	572.3182	2
						NMMAA <u>C</u> DPR	6.8998	533.2172	2
						LTTPTYGDLNHLVSATMSGVTT <u>C</u> LR	7.2236	903.4562	3
						LHFFMPGFAPLTSR	7.9627	540.9489	3
						ALTVPELTQQMFDSK	5.9737	854.4365	2
						IMNTFSVMPSPK	6.3122	676.3416	2
						ISEQFTAMFRR	5.8481	462.5742	3
						MSATFIGNSTAIQELFKR	6.3194	672.0202	3
						MSMKEVDEQMLNVQNK	5.9444	641.9562	3
						FPGQLNADLR	5.9744	565.785	2
						FWEVISDEHGIDPTGSYHGSDLQLER	5.7153	1034.8149	3
						LHFF <u>M</u> PGFAPLTSR	6.9633	546.2801	3
						IREE	6.6912	528.2712	1
						PDR	5.5282	387.1948	1
						LHFFMPGFA	7.1438	524.7553	2
						REEYPDR	7.8395	482.7276	2
						GHYTEGAELVDSV	7.0146	679.8142	2
						YPDR	6.6696	550.2554	1
						GHYTEGAELV	7.3787	529.2503	2
						IREEY	7.1122	691.338	1
						LDVVR	7.1799	601.3617	1
						VDSVLDVVRK	7.2052	565.3279	2
						PNNVK	7.5058	571.3123	1
						LHFFMPGF	7.3156	489.2361	2
						DVVR	7.2441	488.2807	1
						GHYTEGAELVDSVL	7.1472	736.3573	2
						LVDSVLDVVRK	7.2833	621.8631	2
						PLTSR	5.4737	573.3246	1

GHYTEGAELVD	6.7696	586.7672	2
MAA <u>C</u> DPR	6.0676	820.3442	1
GHYTEGAEL	6.9939	479.7164	2
DSVLDVVRK	7.5406	515.7956	2
PGFAPLTSR	7.393	473.2586	2
IRE	5.7505	399.2331	1
NSSYFVEWI	7.0566	563.7699	2
PFPR	5.7383	516.2896	1
GHYTEGAELVDS	6.8566	630.2823	2
GHYTEGAELVDSVLDV	6.9572	843.4047	2
VDSVLDVVR	7.4849	501.2821	2
GHYTEGAELVDSVLDVVR	7.402	647.663	3