SUPPLEMENTAL DATA

SUPPLEMENTAL FIGURES

Figure S1. Experimental strategy to probe selective enrichment of PKA isoforms and their interacting partners using stable isotope labeling.

Following the parallel affinity enrichments using C8 and C2, $C8\_OCH_3$ and EtOH beads, proteins were digested in-solution. The tryptic peptides originating from the pull-down using the C8 beads were chemically labeled using CD_2O ('heavy-label') whereas those originating from C2, $C8\_OCH_3$, EtOH beads were labeled with CH_2O ('light-label'). Each set of CD_2O and CH_2O labeled samples were mixed in a 1:1 ratio and then analyzed by LC-coupled nanospray LTQ-FT-ICR mass spectrometry for protein identification and quantification.

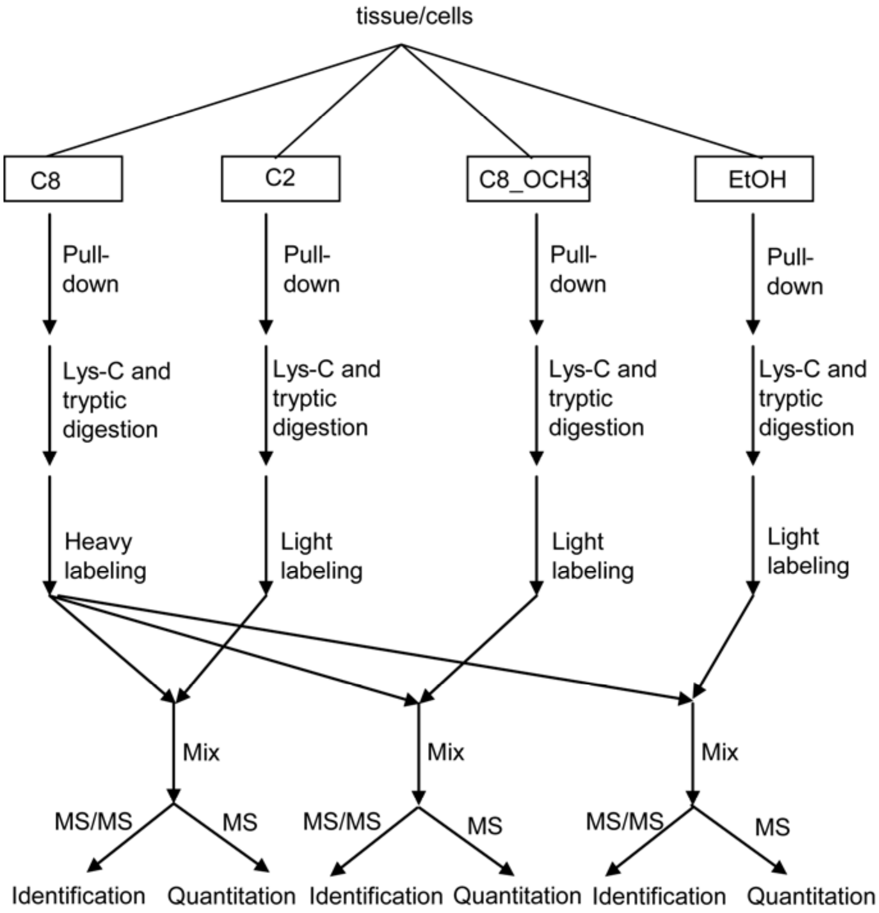

Figure S2. Binding specificity patterns of the ß-type PKA regulatory isoforms and PKG
C2 vs. C8 (white bars) and C8 vs. C8_OCH$_3$ (grey bars) enrichment ratios for (A) PKA RIIβ, (B) PKA RIβ and (C) PKG. For PKG we were unable to unambiguously identify which type I isoform was quantitated, Iα or Iβ due to lack of proteotypic peptides for these isoforms

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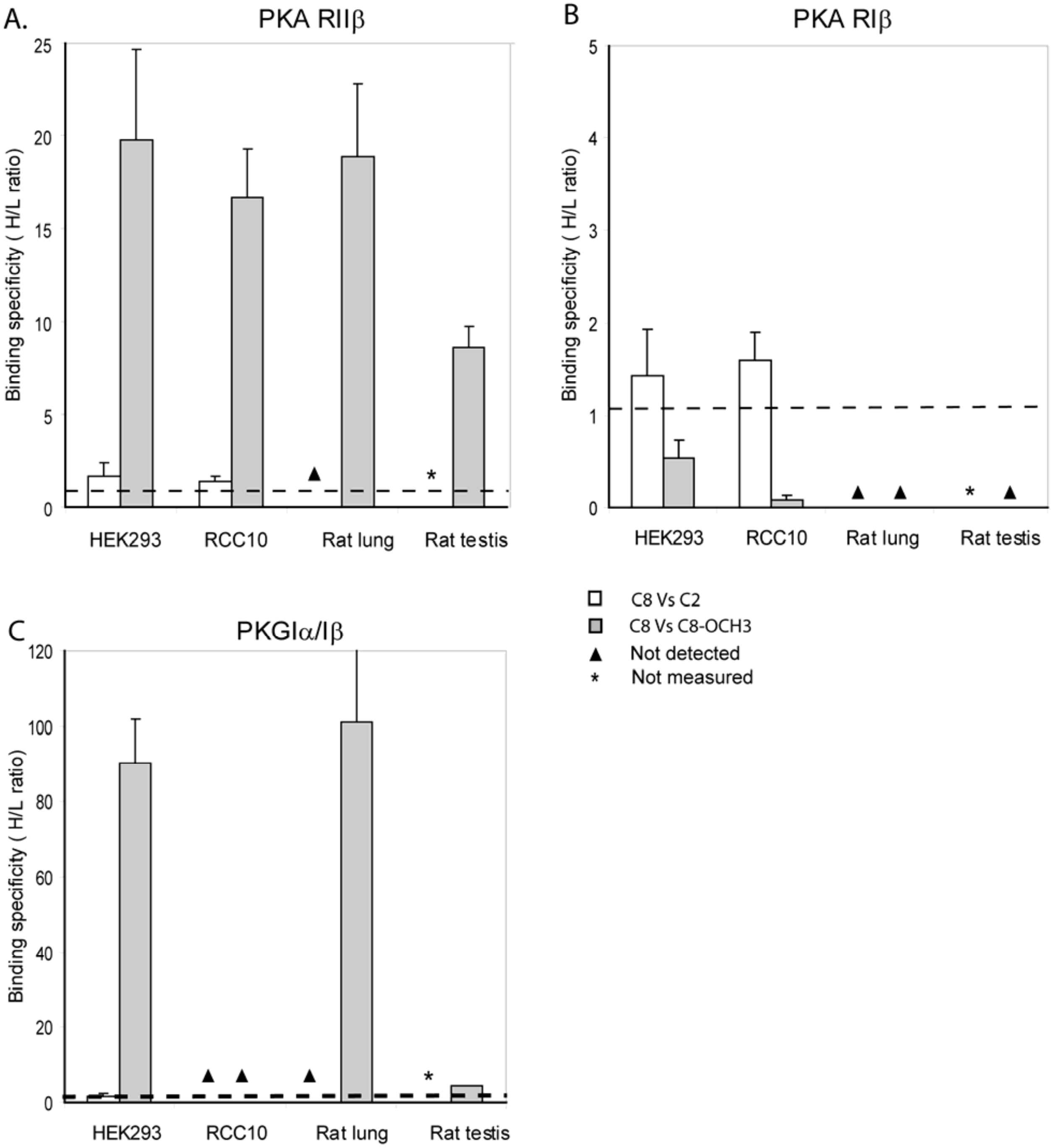


Figure S3. Binding specificity patterns of AKAP7 and AKAP2

Acquired ratios C8 vs. C2 (white) and C8 vs. C8_OCH$_3$ (grey) for AKAP7 (A) and AKAP2 (B) show consistent RII and dual specificity respectively in three different lysates.

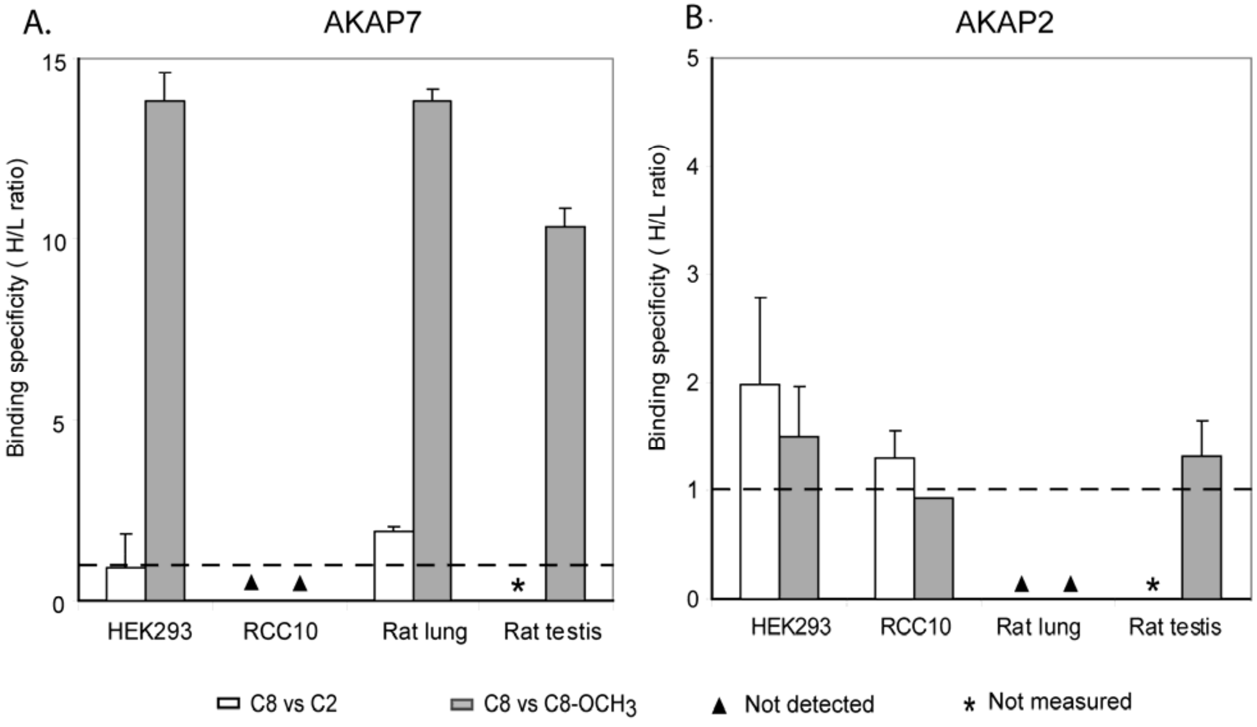
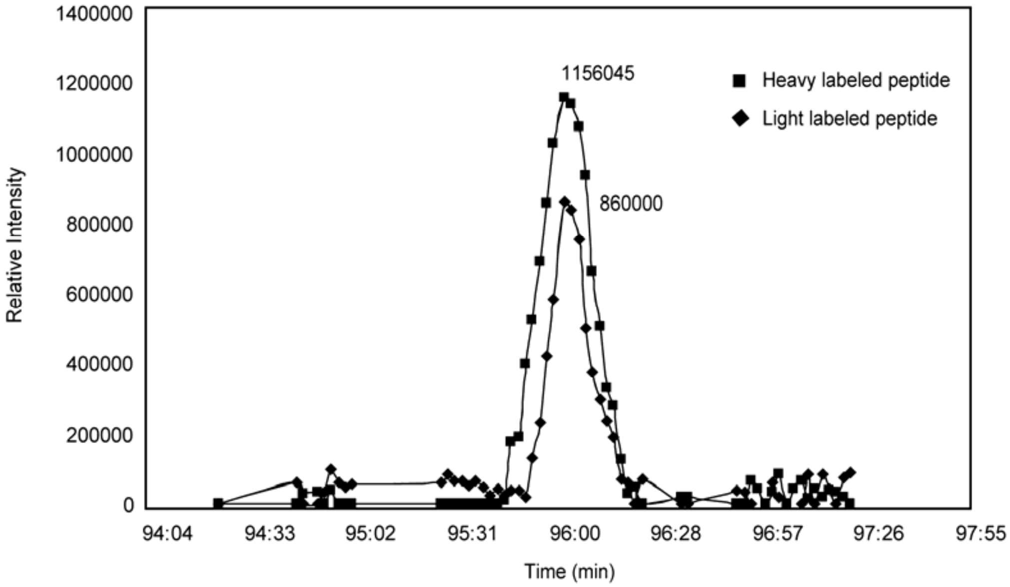
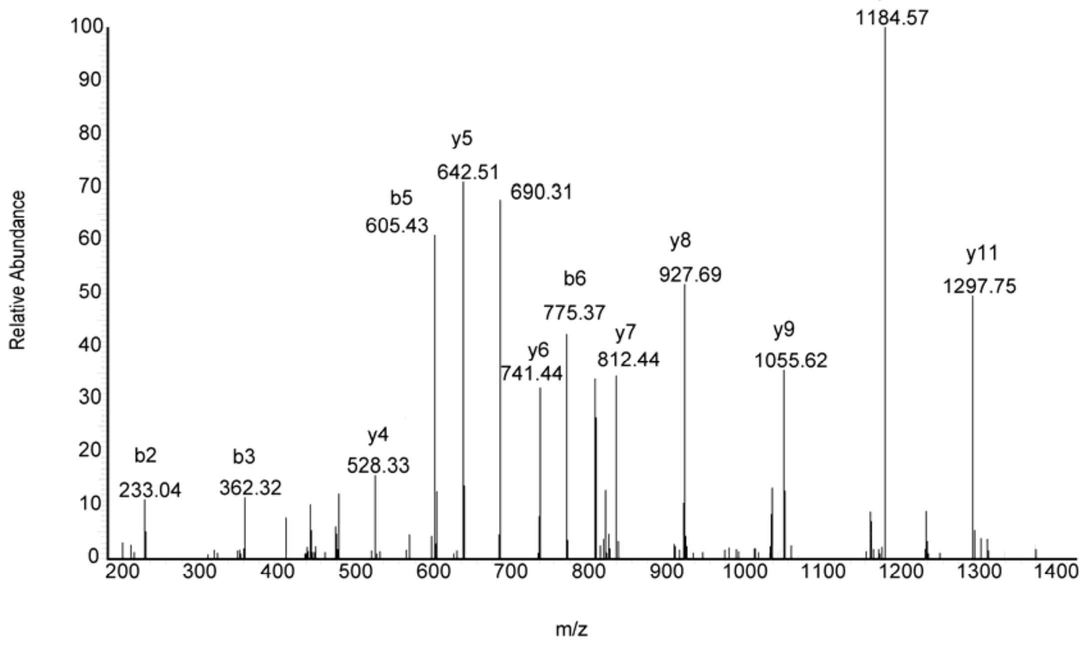


Figure S4. XIC and tandem mass spectrum of single peptide identification AKAP10.

A. Extracted ion chromatogram of peptide SIEQDAVNTFTK (AKAP10) in rat lung tissue. Maximum intensities of $1.2e^6$ and $8.6e^5$ for heavy and light labeled peptide respectively are ample for confident quantitation. B. Annotated tandem MS spectrum of SIEQDAVNTFTK which had a MASCOT score of 59 and a MASCOT delta score of 47, i.e. the next best peptide hit in MASCOT had a score of 12.



A. SIEQDAVNTFTK (AKAP10) annotated spectrum



B. SIEQDAVNTFTK (AKAP10) annotated tamdam MS spectrum

SUPPLEMENTAL TABLES

Table S1. Ratios and peptide counts for PKA R isoforms and AKAPs as observed in a duplicate pull down experiment using C8 vs. $C8\_OCH_3$ beads with rat testis tissue lysate as input.

Table S2. List of proteins identified by in-gel digestion of 1D SDS-PAGE gel shown in Figure 1. For each of the different cAMP-beads (C8-, C2-, C8-OCH3-cAMP-agarose) the amount of unique peptides found for the identification of a protein are shown, as well as their Mascot protein score.

Table S3. All proteins detected and quantified depicted with their identified and quantified peptides, with each of the bead combinations used in this study (i.e. C8, C2, $C8\_OCH_3$, EtOH). Each protein is described with accession number, molecular weight, protein Mascot score, identified peptide sequence(s) and protein specificity ratio with respective standard deviation. For all peptide pairs used ratios are detailed. The protein differential binding ratio was calculated by averaging over all peptide pairs measured for that particular protein. The binding specificity ratio of C8 vs C2 in HEK293 are in **S3A** whereas **S3B** is for the binding specificity ratio of C8 against C8-OCH3. The data of C8 vs Control are in **S3C**. Likewise, for rat lung tissue samples, the binding specificity ratio of C8 vs C2, C8-OCH3 and Control are depicted in **S3D, S3E**, and **S3F** respectively. For RCC10 cells, the data of C8 vs C2 and C8 vs C8-OCH3 are shown in table **S3G** and **S3H**. The data obtained by setting off C8 and C8-OCH3 in rat testis tissue are summarized in table **S3I**.

Supplemental Table S1

Ratios with quantified peptide counts observed in a duplicate pull down experiments

Accession #	MW	Protein Name	#of quantified peptides in Exp1	Protein ratio1	# of quantified peptides in Exp2	Protein ratio2	Stdev
IPI00196684	45797	PKA RIIa	10	10.6	10	7.4	2.3
IPI00764045	44984	PKA RIIb	6	9.6	9	7.2	1.7
IPI00779281	209546	AKAP11	5	8.3	8	8.1	0.2
IPI00231052	49327	MAP2	3	6.2	3	6.0	0.1
IPI00212365	94916	AKAP4	7	3.0	13	3.9	0.6
IPI00201274	96002	AKAP3	3	2.7	8	3.1	0.3
IPI00198250	181514	AKAP12	5	1.7	3	1.9	0.1
IPI00364858	96338	AKAP2	4	1.3	3	1.6	0.2
IPI00471827	74284	AKAP10	1	1.2	1	1.3	0.1
IPI00213479	92660	AKAP1	3	1.1	2	1.1	0.0
IPI00231770	43296	PKA RIa	4	0.7	7	0.6	0.0

Supplemental Table S2

Proteins identified from rat lung tissue pulldown with 3 differently coupled cAMP analogues

▨ Confirmed cyclic nucleotide binding protein or one of its interactors

				C8		C2		C8_OCH3		
	Accession	Protein Name	MW	# of Unique Peptides	ProteinMascot Score	# of Unique Peptides	Protein Mascot Score	# of Unique Peptides	Protein Mascot Score	Total # of Unique Peptides
1	IPI00231770	PKA RIα	42947	32	13163	35	7584	23	1028	90
2	IPI00215470	AKAP5	75941	31	9138	36	9837	16	7550	83
3	IPI00196684	PKA RIIα	45392	34	21665	31	14494	18	12907	83
4	IPI00766097	PKG Iα	76336	39	4852	35	5288	6	1634	80
5	IPI00365600	PKA RIIβ	45974	28	14736	34	10346	13	980	75
6	IPI00360386	similar to heterogeneous nuclear ribonucleoprotein U isoform a	97171	29	2360	17	1575	14	1256	60
7	IPI00779281	AKAP11	206636	25	1288	23	1096	11	975	59
8	IPI00409539	similar to Filamin-A	281264	27	685	23	707	5	650	55
9	IPI00764064	NS1-associated protein 1 isoform 2	62655	17	1234	21	1495	15	1301	53
10	IPI00362975	SKIP	197419	10	323	19	617	18	539	47
11	IPI00769072	similar to AHNAK nucleoprotein isoform 1 isoform 2	588348	13	342	21	616	10	340	44
12	IPI00208697	Rap guanine nucleotide exchange factor 4 (cAMP-regulated guanine	123438	27	938	0	0	15	722	42
13	IPI00210090	SP120	87731	14	364	18	34	10	230	42
14	IPI00191090	Biglycan precursor	41691	17	2515	14	3585	8	1230	39
15	IPI00199861	Decorin precursor	39789	8	280	18	1717	10	1438	36
16	IPI00212868	Laminin subunit beta-2 precursor	196450	0	0	31	1215	0	0	31
17	IPI00211448	EH-domain containing 2	61221	4	113	14	579	12	1009	30
18	IPI00199076	PDE2A3	104648	2	77	25	1574	0	0	27
19	IPI00208205	Heat shock cognate 71 kDa protein	70855	13	507	7	473	6	470	26
20	IPI00200271	Pincher	61452	3	230	10	544	10	357	23
21	IPI00231783	L-lactate dehydrogenase B chain	36463	14	495	0	0	8	560	22
22	IPI00361106	similar to Laminin alpha-4 chain precursor	201509	2	28	19	585	0	0	21
23	IPI00778167	Moesin	67636	5	195	9	248	6	230	20
24	IPI00201347	Histidine-rich glycoprotein 1	59029	12	365	7	465	1	94	20
25	IPI00471584	Heat shock protein HSP 90-beta	83135	12	555	5	204	2	193	19
26	IPI00188885	Isoform 1 of Agrin precursor	208621	0	0	18	1374	0	0	18
27	IPI00396910	ATP synthase subunit alpha, mitochondrial precursor	59737	4	215	7	442	7	346	18
28	IPI00366485	Nitric oxide synthase trafficker	57336	5	189	9	272	4	174	18
29	IPI00362014	Tln1 protein	271021	4	134	9	296	4	149	17
30	IPI00767541	PKG Iβ	77776	6	3128	8	3089	3	1821	17
31	IPI00551812	ATP synthase subunit beta, mitochondrial precursor	56336	4	108	6	236	7	217	17
32	IPI00324102	fibrinogen-like 2	48638	5	152	8	456	4	134	17
33	IPI00212647	GAPDH	35765	10	470	3	153	4	143	17
34	IPI00194728	Integrin-linked protein kinase	51356	5	144	5	205	5	260	15
35	IPI00201032	Isoform 1 of Heterogeneous nuclear ribonucleoprotein D0	38174	13	661	1	87	1	56	15
36	IPI00365769	similar to Ras GTPase-activating-like protein IQGAP1	200475	3	71	7	324	4	298	14
37	IPI00201262	Alpha-1-inhibitor 3 precursor	163756	2	84	11	315	1	78	14
38	IPI00364858	AKAP2	95923	5	235	4	218	5	265	14
39	IPI00326948	Hsd17b4 protein	81072	2	74	9	374	2	56	13
40	IPI00201969	Vesicle amine transport protein 1 homolog	43100	4	156	5	185	4	167	13
41	IPI00364348	AKAP13	303758	4	130	4	99	4	125	12
42	IPI00231136	similar to Nidogen-1 precursor	137020	0	0	12	514	0	0	12
43	IPI00231381	Major vault protein	96806	4	67	6	114	2	98	12
44	IPI00197711	L-lactate dehydrogenase A chain	36433	7	452	0	0	5	398	12
45	IPI00388249	Calpain-2 catalytic subunit precursor	79773	4	91	2	48	5	300	11
46	IPI00195372	Elongation factor 1-alpha 1	50096	4	261	4	167	3	230	11
47	IPI00200225	Fibromodulin precursor	43203	4	72	3	144	4	265	11
48	IPI00421832	Dermcidin	11266	4	862	4	382	3	632	11
49	IPI00190577	similar to Laminin alpha-5 chain precursor	404413	0	0	10	345	0	0	10
50	IPI00480639	Complement C3 precursor	186444	2	240	6	220	2	135	10
51	IPI00326140	Alpha-1-macroglobulin precursor	167108	2	59	6	147	2	137	10
52	IPI00208193	Nucleic acid binding factor pRM10	33798	9	471	0	0	1	69	10
53	IPI00328073	cGMP-specific 3',5'-cyclic phosphodiesterase (PDE10A11)	98326	0	0	9	275	0	0	9
54	IPI00192034	similar to Dihydropyrimidinase-related protein 2	73143	3	138	3	174	3	198	9
55	IPI00194562	Heterogeneous nuclear ribonucleoprotein R	70858	5	541	0	579	4	195	9
56	IPI00767522	similar to sparc/osteonectin, cwcv and kazal-like domains proteoglyca	46801	0	0	9	281	0	0	9
57	IPI00421609	AKAP7	39401	4	346	3	77	2	67	9
58	IPI00200661	Fatty acid synthase	272633	2	66	6	122	0	0	8
59	IPI00210319	Isoform IIBA of Dynamin-2	98232	4	83	0	0	3	211	7
60	IPI00190240	Ribosomal protein S27a	17934	3	173	2	39	2	31	7
61	IPI00214232	Oxysterol-binding protein-related protein 6	108989	0	0	6	156	0	0	6
62	IPI00327185	nucleosome assembly protein 1-like 1	45356	0	0	6	118	0	0	6
63	IPI00200327	PKA RIβ	43133	2	2007	2	1184	2	1268	6
64	IPI00195522	PDE4dip	261914	0	0	5	148	0	0	5
65	IPI00365665	similar to EIB-55kDa associated protein 5 isoform 1 isoform 3	95985	3	46	2	33	0	0	5
66	IPI00231827	Nucleolin	77259	0	0	5	270	0	0	5
67	IPI00551815	Ybx1 protein	36182	0	0	5	159	0	0	5
68	IPI00210566	Heat shock protein HSP 90-alpha	84669	3	318	1	127	0	0	4

69	IPI00362106	Pleckstrin homology domain containing, family C (With FERM domain	77861	3	74	1	39	0	0	4
70	IPI00213019	AKAP14	55736	2	48	1	31	1	30	4
71	IPI00361733	similar to sushi-repeat containing protein	52835	3	64	1	29	0	0	4
72	IPI00366081	similar to desmoplakin isoform I isoform 2	332383	3	119	0	0	0	0	3
73	IPI00363974	Gelsolin	86268	3	113	0	0	0	0	3
74	IPI00206624	78 kDa glucose-regulated protein precursor	72331	3	148	0	0	0	0	3
75	IPI00189074	Polyadenylate-binding protein 1	70683	0	0	3	74	0	0	3
76	IPI00187885	Fibronectin type-III domain-containing protein C4orf31 homolog precu	64584	0	0	3	129	0	0	3
77	IPI00210120	Aa1018	55943	0	0	3	128	0	0	3
78	IPI00358059	Aspartyl aminopeptidase	52538	0	0	3	153	0	0	3
79	IPI00190759	Isoform Gamma-B of Fibrinogen gamma chain precursor	50616	0	0	3	149	0	0	3
80	IPI00204899	Septin-7	50490	0	0	3	87	0	0	3
81	IPI00231615	Annexin A1	38682	3	103	0	71	0	0	3
82	IPI00231865	Cytochrome c, testis-specific	11594	3	48	0	0	0	0	3
Total proteins (Number of uniquie peptide >3 and Mascot score>30)				**56**		**62**		**40**		

Supplemental Table S3 (A)

Hek293_Binding specificity ratio_C8_C2

	Accession	MW	Protein Name	Peptide Sequence	Peptide Score	Peptide C8/C2 ratio	StDev	Protein Score	Protein C8/C2 ratio	StDev
1	IPI00063234	43998	PKA RIIα	AASAYAVGDVK	99	1.2	1.11	905	1.7	0.98
				AATIVATSEGSLWGLDR	127	1.1	0.38			
				CLVMDVQAFER	78	2.2	1.49			
				DGGNQEVEIAR	81	1.1	0.21			
				GSFGELALMYNTPR	94	1.2	0.00			
				IVDVIGEK	42	1.3	0.81			
				MFESFIESVPLLK	51	1.6	0.55			
				NISHYEEQLVK	53	1.0	0.00			
				NLDQEQLSQVLDAMFER	115	1.2	0.20			
				QSLGHPPPEPGPDR	50	1.1	0.60			
2	IPI00021831	43828	PKA RIα	ECELYVQK	45	1.8	1.30	306	1.4	0.31
				HNIQALLK	52	1.2	0.60			
				LTVADALEPVQFEDGQK	138	1.1	0.00			
3	IPI00456775	47317	PKA RIIβ	AASAHAIGTVK	65	2.6	0.82	728	1.7	0.75
				AATITATSPGALWGLDR	61	1.8	0.20			
				ASVCAEAYNPDEEEDDAESR	102	1.3	0.36			
				DILLFK	28	0.7	1.60			
				GTFDIYVK	59	2.4	0.97			
				SEVEENGAVEIAR	69	2.0	0.76			
				TWGDLGAAAGGGTPSK	121	0.8	1.72			
4	IPI00554488	44043	PKA RIβ	SNSQSDSHDEEVSPTPPNPVVK	50	1.4	0.72	70	1.4	0.72
5	IPI00427586	78494	PKG Iα / PKGIβ	AQGISAEPQTYR	71	0.8	0.26	398	1.2	0.58
				GDTFFIISK	76	1.0	0.72			
				GIDMIEFPK	53	1.0	0.37			
				HLIGGLDDVSNK	71	1.0	3.47			
				YEAEAAFFANLK	69	2.2	0.10			
6	IPI00022585	99512	AKAP1	ETGGAEGTGDAVLGEK	104	1.5	0.78	260	1.1	0.37
				VLEEALLSR	48	0.7	0.50			
				VVSTPPSVTEPPEK	32	1.2	0.59			
7	IPI00032064	124528	AKAP2	SPGALETPSAAGSQGNTASQGK	96	1.4	0.86	259	2.0	0.81
				STASLLATQESDVMVGPFK	133	2.6	0.48			
8	IPI00307794	48534	AKAP5	DGDEVCESNVSNSITSGEK	101	1.1	0.50	47	1.1	0.50
9	IPI00422254	38160	AKAP7	IDLCSMLK	37	0.3	0.94	109	0.9	0.91
				LAEGDHVNSLLEIAETANR	72	1.6	0.78			
10	IPI00019223	465228	AKAP9	ACMFEPLPIK	49	3.8	1.20	1650	3.3	1.18
				ALEIDVEEQVSR	82	1.3	1.24			
				ALNEELHLQR	50	3.6	0.10			
				DLELTQCYK	48	2.2	1.38			
				ETEQNYEAEIHCLQK	54	3.6	0.97			
				EVEIDQLNEQVTK	94	4.0	1.41			
				FIELEQEK	43	1.0	0.53			
				HGEISFLNEEVK	35	4.2	1.64			
				LALEQQVETANEEMTFMK	104	3.1	0.80			
				LIEMNGGGTGCNHELEMIR	45	3.4	0.36			
				LMNVAINELNIK	66	3.2	0.56			
				LSQDQIGFQTFETVDVK	117	3.2	0.41			
				MAESQEAELER	54	4.6	0.99			
				MLYDAQLSEEQGR	58	2.5	1.26			
				QAHAVCQQEQHYFNEMK	39	4.4	0.64			
				QSQMLEMQVELSSMK	81	4.6	0.16			
				SIASQTDGTLK	64	3.5	1.63			
				SSIDNENLVSER	63	3.1	1.47			
				SVLLAAFR	56	3.2	1.57			
				TTAAVEETIGR	64	3.4	1.44			
				YEVQDFQENMHTLLNK	50	1.0	0.71			
11	IPI00007411	217039	AKAP11	AAVSVSTDNIK	87	1.2	1.07	499	1.7	0.79
				EFMLLSK	38	1.4	1.04			
				FAADLVEK	40	1.7	1.00			
				FPDSQNQLTHCSLSAAK	30	1.3	0.67			
				NPCLNVQSQR	33	3.6	1.51			
				SISCEVLGSVLR	82	1.9	0.28			
				SQCDAASQTVTGHHLETHDLK	60	0.8	0.78			
				SVIPNIDK	28	1.6	0.99			
12	IPI00304925	71724	Heat shock 70 kDa protein 1	ATAGDTHLGGEDFDNR	73	0.9	0.52	516	1.1	0.24
				DAGVIAGLNVLR	80	1.2	1.22			
				IINEPTAAAIAYGLDR	107	1.3	1.65			
				NQVALNPQNTVFDAK	68	1.6	0.49			
				TTPSYVAFTDTER	49	0.9	1.39			
				VEIIANDQGNR	53	0.9	0.77			
13	IPI00011654	50544	Tubulin beta-2 chain	AILVDLEPGTMDSVR	107	1.3	0.37	466	1.6	0.32

				EAESCDCLQGFQLTHSLGGGTGSGMGTLL	127	1.4	1.55			
				FWEVISDEHGIDPTGTYHGDSDLQLDR	37	2.2	1.18			
				ISEQFTAMFR	31	1.3	1.84			
				LAVNMVPFPR	66	1.6	0.96			
				NSSYFVEWIPNNVK	58	1.8	1.07			
				TAVCDIPPR	40	1.4	0.66			
14	IPI00166768	38214	TUBA6 protein	DVNAAIATIK	74	1.7	0.00	365	1.7	0.19
				EIIDLVLDR	64	1.9	6.69			
				TIGGGDDSFNTFFSETGAGK	139	1.6	1.95			
				VGINYQPPTVVPGGDLAK	88	1.5	0.52			
15	IPI00219217	37526	L-lactate dehydrogenase B chain	FIIPQIVK	26	152.0	0.00	332	113.6	56.01
				LIAPVAEEEATVPNNK	100	49.9	8.82			
				MVVESAYEVIK	70	155.0	11.99			
				VIGSGCNLDSAR	67	135.8	13.64			
16	IPI00337544	131716	phosphodiesterase 4D interacting	ALQQLQEELQNK	90	3.3	23.59	479	2.5	1.33
				DLQMQLVDPEDIPAMER	77	0.2	5.35			
				QCVQFVEAAAHESEQQK	59	3.6	2.74			
				QVLEHEMEIQGLLQSVSTR	60	2.6	2.73			
				VADSDYEAICK	38	2.6	1.93			
17	IPI00301277	72188	Heat shock 70 kDa protein 1L	ATAGDTHLGGEDFDNR	73	0.9	0.52	349	0.8	0.36
				DAGVIAGLNVLR	80	1.2	1.22			
				IINEPTAAAIAYGLDK	64	0.2	0.77			
				TTPSYVAFTDTER	49	0.9	1.39			
				VEIIANDQGNR	53	0.9	0.77			
18	IPI00026781	278233	Fatty acid synthase	AALQEELQLCK	76	1.0	0.67	333	0.9	0.25
				ACLDTAVENMPSLK	78	1.3	0.54			
				LQVVDQPLPVR	45	1.0	0.68			
				SEGVVAVLLTK	38	0.6	2.53			
				VVVQVLAEEPEAVLK	96	0.8	0.52			
19	IPI00339269	72562	Heat shock 70 kDa protein 6	ATAGDTHLGGEDFDNR	73	0.9	0.52	340	1.0	0.16
				IINEPTAAAIAYGLDR	107	1.3	1.65			
				TTPSYVAFTDTER	49	0.9	1.39			
				VEILANDQGNR	53	0.9	0.77			
20	IPI00294398	35210	Isoform 1 of Short chain 3-hydroxy	FIVDGWHEMDAENPLHQPSPSLNK	68	0.2	0.33	135	0.2	0.00
				TFESLVDFSK	67	0.3	0.00			
21	IPI00007752	50704	Tubulin beta-2C chain	EAESCDCLQGFQLTHSLGGGTGSGMGTLL	127	1.4	1.55	358	1.6	0.19
				FWEVISDEHGIDPTGTYHGDSDLQLER	36	1.8	1.52			
				ISEQFTAMFR	31	1.5	3.08			
				LAVNMVPFPR	66	1.6	0.95			
				NSSYFVEWIPNNVK	58	1.8	1.07			
				TAVCDIPPR	40	1.4	0.66			
22	IPI00024317	49086	Isoform Long of Glutaryl-CoA dehy	DMLGGNGISDEYHVIR	46	4.2	0.00	247	4.2	0.02
				GELLGCFGLTEPNSGSDPSSMETR	116	3.9	0.00			
				HAMNLEAVNTYEGTHDIHALILGR	85	4.1	2.50			
23	IPI00013296	18184	40S ribosomal protein S18	IAFAITAIK	72	0.4	0.24	122	0.4	0.00
				VITIMQNPR	50	0.2	0.00			
24	IPI00219018	36827	GAPDH	GALQNIIPASTGAAK	73	10.4	7.43	323	10.6	0.27
				IISNASCTTNCLAPLAK	108	10.8	15.15			
25	IPI00217966	37763	lactate dehydrogenase A	FIIPNVVK	31	223.9	110.23	179	194.9	52.29
				VIGSGCNLDSAR	67	134.5	139.11			
				VTLTSEEEAR	44	226.2	335.73			
26	IPI00444262	67914	CDNA FLJ45706 fis, clone FEBRA	FGYVDFESAEDLEK	75	0.5	0.00	171	0.4	0.04
				GFGFVDFNSEEDAK	71	0.4	7.37			
				NDLAVVDVR	25	0.4	0.35			
27	IPI00292496	50678	Beta-tubulin 4Q	EAESCDCLQGFQLTHSLGGGTGSGMGTLL	127	1.4	1.55	233	1.5	0.13
				LAVNMVPFPR	66	1.6	0.96			
				TAVCDIPPR	40	1.4	0.66			
28	IPI00021439	42612	Actin, cytoplasmic 1	DLYANTVLSGGTTMYPGIADR	98	1.9	1.07	220	1.1	0.96
				EITALAPSTMK	35	0.0	0.52			
				SYELPDGQVITIGNER	97	1.4	0.42			
29	IPI00003865	72624	Isoform 1 of Heat shock cognate 7	CNEIINWLDK	34	1.6	20.49	245	0.9	0.58
				IINEPTAAAIAYGLDK	64	0.2	0.82			
				TTPSYVAFTDTER	49	0.9	1.39			
				VEIIANDQGNR	53	0.9	0.77			
30	IPI00290770	62032	chaperonin containing TCP1, subu	IVLLDSSLEYK	59	0.7	0.39	128	0.7	0.39
				TAVETAVLLLR	69	0.7	0.00			
31	IPI00302925	61488	T-complex protein 1 subunit theta	AIADTGANVVVTGGK	69	1.3	0.00	117	1.3	0.00
				IAVYSCPFDGMITETK	48	1.3	0.85			
32	IPI00018140	71105	Isoform 1 of Heterogeneous nucle	DYAFIHFDER	34	1.0	0.36	160	1.3	0.32
				LMMDPLTGLNR	48	1.6	0.75			
				NLANTVTEEILEK	47	1.2	0.63			
33	IPI00470610	34947	Pyrroline-5-carboxylate reductase	IIASSPEMNLPTVSALR	45	0.1	0.78	119	1.5	1.90
				SLLINAVEASCIR	74	2.8	0.31			
34	IPI00329038	221070	Isoform 1 of CDK5 regulatory subu	EQNLNMQLFSEIHNLQNK	54	2.3	0.00	120	2.4	0.93
				TLEEQISEIR	66	2.4	0.93			
35	IPI00093057	51563	Coproporphyrinogen III oxidase, m	AVVPSYIPLVK	53	0.3	0.15	131	0.9	0.82
				CSSFMAPPVTDLGELR	30	0.0	0.00			
				EAEILEVLR	58	1.4	0.00			

36	IPI00383046	28933	Carboxymethylenebutenolidase ho	DVSLLTQK	58	117.8	12.18	88	117.8	227.18
				VEYQIK	30	120.0	0.00			
37	IPI00075248	16948	Calmodulin	DGNGYISAAELR	55	2.6	1.25	109	2.3	0.42
				EAFSLFDK	34	2.0	1.21			
38	IPI00011253	27431	40S ribosomal protein S3	FGFPEGSVELYAEK	59	0.1	0.00	88	0.2	0.18
				QGVLGIK	39	0.4	0.17			
39	IPI00025054	93023	Isoform Long of Heterogeneous nu	MCLFAGFQR	36	1.2	0.00	65	1.3	1.35
				SSGPTSLFAVTVAPPGAR	39	1.3	1.35			
40	IPI00003918	49447	60S ribosomal protein L4	AAAAAAALQAK	57	1.4	0.80	78	1.4	0.80
				APIRPDIVNFVHTNLR	31	1.0	0.00			
41	IPI00297779	58728	T-complex protein 1 subunit beta	EALLSSAVDHGSDEVK	44	0.9	0.36	73	0.9	0.05
				ILIANTGMDTDK	30	0.9	0.82			
42	IPI00017596	30665	Microtubule-associated protein RP	LEHEYIQNFK	35	2.1	0.00	84	2.5	0.00
				LTVEDLEK	39	2.5	1.47			
43	IPI00013485	32290	40S ribosomal protein S2	ATFDAISK	32	0.3	0.00	58	0.4	0.20
				LLMMAGIDDCYTSAR	35	0.4	0.20			
44	IPI00302592	287094	Filamin A, alpha	AEAGVPAEFSIWTR	34	0.6	1.52	47	2.8	3.17
				TFSVWYVPEVTGTHK	33	5.1	0.00			

Supplemental Table S3 (B)

Hek293_Binding specificity ratio_C8_O-CH$_3$

	Accession	MW	Protein Name	Peptide Sequence	Peptide Score	Peptide C8/C8-OCH3 ratio	StDev	Protein Score	Protein C8/C8-OCH3 ratio	StDev
1	IPI00063234	43998	PKA RIIα	AATIVATSEGSLWGLDR	142	7.60	5.04	876	13.2	6.34
				APASVLPAATPR	61	8.81	4.04			
				CLVMDVQAFER	66	10.58	7.68			
				DGGNQEVEIAR	75	9.26	9.82			
				DILLFK	56	10.07	17.76			
				GSFGELALMYNTPR	112	7.63	6.07			
				GTYDILVTK	62	8.91	8.93			
				VSVCAETYNPDEEEEDTDPR	102	11.61	7.03			
2	IPI00021831	43828	PKA RIα	EYFER	33	0.35	0.00	447	0.8	0.49
				GAISAEVYTEEDAASYVR	147	0.62	0.00			
				HNIQALLK	35	0.34	0.00			
				LTVADALEPVQFEDGQK	126	0.39	0.35			
				MYEEFLSK	36	0.54	0.00			
				SENEEFVEVGR	51	0.81	0.53			
				VLGPCSDILK	39	0.38	0.00			
3	IPI00456775	47317	PKA RIIβ	ASVCAEAYNPDEEEDDAESR	128	19.87	9.43	543	19.8	12.34
				DILLFK	36	10.07	17.76			
				GSFGELALMYNTPR	112	7.54	6.11			
				SEVEENGAVEIAR	79	22.20	17.34			
				SLEFSER	38	17.13	9.99			
				VVDVIGTK	37	11.90	8.38			
4	IPI00554488	44043	PKA RIβ	MYEEFLSK	36	0.54	0.22	49	0.5	0.21
5	IPI00427586	78494	PKG Iα / PKGIβ	AQGISAEPQTYR	75	103.52	38.70	392	90.1	11.61
				GDTFFIISK	68	83.31	51.96			
				GIDMIEFPK	55	83.52	113.58			
				TLVNVK	30	101.00	0.00			
6	IPI00022585	99512	AKAP1	ETGGAEGTGDAVLGEK	56	1.20	0.00	121	1.2	0.00
7	IPI00032064	124528	AKAP2	SPGALETPSAAGSQGNTASQGK	38	1.18	0.00	186	1.5	0.46
				STASLLATQESDVMVGPFK	115	1.83	5.47			
8	IPI00307794	48543	AKAP5	DGDEVCESNVSNSITSGEK	104	3.60	0.00	135	3.5	0.00
				IIEDSDCSIK	31	3.49	0.00			
9	IPI00422254	38160	AKAP7	AVQQYLEETQNK	72	7.46	1.05	211	13.8	0.76
				IDLCSMLK	30	4.98	0.00			
				ILQNAIIQQDER	63	10.40	0.93			
				LAEGDHVNSLLEIAETANR	56	9.66	1.12			
10	IPI00019223	465228	AKAP9	ACMFEPLPIK	39	11.72	3.64	1695	10.0	1.53
				AEGVIDGYADEK	66	9.73	1.56			
				DLELTQCYK	46	11.64	1.49			
				DNLGIHYK	38	4.35	2.62			
				DSQFETDIVQR	67	3.17	2.69			
				EVEQLANHLK	54	8.90	1.35			
				LALEQQVETANEEMTFMK	109	7.63	1.53			
				LLGELQEQIVQK	68	10.49	0.00			
				LQQELANIGQK	51	8.60	0.00			
				LSDLSEQLK	50	4.82	1.24			
				QQCIQLNEEIEK	44	6.16	1.59			
				QQIDGLQNEMSQK	67	7.84	1.97			
				QSQMLEMQVELSSMK	90	4.88	1.50			
				QYQEQLEEEVAK	67	6.41	3.24			
				SGFAGTEIDPENEELMLNISSR	119	7.04	2.60			
				SIASQTDGTLK	50	6.00	2.41			
				SSIDNENLVSER	71	8.23	2.77			
				SVLLAAFR	50	5.24	0.18			
				SYSNITVNEDQIK	81	3.34	1.37			
				TTAAVEETIGR	34	7.81	3.92			
				VTQTELMR	33	7.43	3.43			
11	IPI00007411	217039	AKAP11	ESLPVSGEESQLTPEK	97	13.75	2.00	436	9.0	0.70
				NPCLNVQSQR	36	7.41	2.87			
				SGYEEDNECHVTPELPK	42	5.43	0.80			
				SISCEVLGSVLR	78	4.44	0.60			
				SLTDSCLFEK	60	10.39	0.00			
				SQCDAASQTVTGHHLETHDLK	31	9.72	2.30			
12	IPI00003842	199539	MAP2	LINQPLPDLK	34	10.85	2.10	106	10.9	1.77
				SAILVPSEK	50	9.62	3.64			
				TPGTPGTPSYPR	32	12.12	3.84			
13	IPI00217966	37763	lactate dehydrogenase A	GEMMDLQHGSLFLR	78	32.50	1.48	350	56.0	22.52
				LVIITAGAR	44	44.56	2.55			
				SADTLWGIQK	49	46.60	10.89			
				VIGSGCNLDSAR	81	89.92	517.86			

				VTLTSEEEAR	70	66.30	131.51			
14	IPI00011654	50704	Tubulin beta-2 chain	AILVDLEPGTMDSVR	76	4.04	2.73	424	5.1	1.94
				EVDEQMLNVQNK	100	5.71	3.64			
				ISEQFTAMFR	31	7.77	5.19			
				ISVYYNEATGGK	33	5.42	7.81			
				LAVNMVPFPR	50	2.59	2.80			
				YLTVAAVFR	30	0.00	0.00			
15	IPI00166768	38214	TUBA6 protein	DVNAAIATIK	40	2.05	3.79	185	3.3	1.72
				TIGGGDDSFNTFFSETGAGK	145	4.48	1.62			
16	IPI00219217	37526	L-lactate dehydrogenase	GEMMDLQHGSLFLQTPK	56	12.84	19.09	307	142.0	189.05
				GLTSVINQK	72	147.20	0.00			
				MVVESAYEVIK	46	0.58	166.95			
				VIGSGCNLDSAR	81	407.55	530.63			
17	IPI00383046	28933	Carboxymethylenebuteno	DSEDIYNLK	59	2.67	1.51	359	10.1	9.58
				DVSLLTQK	46	7.39	3.77			
				EISAILK	38	3.48	12.30			
				EVQVEHIK	52	10.85	17.34			
				LEYGGLGR	37	26.22	7.45			
18	IPI00304925	71724	Heat shock 70 kDa protei	AQIHDLVLVGGSTR	55	0.46	0.00	211	3.5	2.67
				ATAGDTHLGGEDFDNR	69	6.68	5.68			
				DNNLLGR	40	2.36	3.10			
				QTQIFTTYSDNQPGVLIQVYEGER	64	4.39	3.08			
19	IPI00024317	49086	Isoform Long of Glutaryl-	GYGCAGVSSVAYGLLAR	83	27.67	176.30	289	55.6	39.54
				HAMNLEAVNTYEGTHDIHALILGR	66	83.59	0.00			
20	IPI00018511	50678	Tubulin beta-4q chain	EAESCDCLQGFQLTHSLGGGTGSGMGTLL	134	8.22	0.00	184	5.4	4.03
				LAVNMVPFPR	50	2.52	2.78			
21	IPI00219018	36827	GAPDH	LISWYDNEFGYSNR	98	1.45	0.00	157	1.3	0.27
				VIISAPSADAPMFVMGVNHEK	59	1.07	0.00			
22	IPI00026781	278233	Fatty acid synthase	LQVVDQPLPVR	58	1.43	0.00	142	2.0	0.76
				VVVQVLAEEPEAVLK	84	2.51	1.37			
23	IPI00013296	18184	40S ribosomal protein S1	IAFAITAIK	58	1.23	0.61	94	1.2	0.04
				VLNTNIDGR	36	1.18	0.28			
24	IPI00337544	131716	phosphodiesterase 4D int	NSELQALR	34	6.23	2.56	141	11.6	7.65
				VADSDYEAICK	57	17.05	11.51			
25	IPI00444262	67914	CDNA FLJ45706 fis, clon	FGYVDFESAEDLEK	57	1.20	0.00	113	0.8	0.50
				GFGFVDFNSEEDAK	56	0.48	2.60			
26	IPI00018140	71105	Isoform 1 of Heterogeneo	LFVGSIPK	39	0.46	0.00	119	0.4	0.04
				NLANTVTEEILEK	42	0.40	1.94			
27	IPI00221354	53355	Isoform Short of RNA-bin	APKPDGPGGGPGGSHMGGNYGDDR	36	0.51	0.63	51	1.3	1.18
				EFSGNPIK	35	2.18	1.04			
28	IPI00022434	71576	ALB protein	LVTDLTK	39	0.72	0.44	54	0.9	0.33
				YICENQDSISSK	35	1.18	0.80			
29	IPI00093057	51563	Coproporphyrinogen III ox	EAEILEVLR	32	1.17	0.00	54	0.8	0.47
				YFEVEEADGNK	36	0.51	0.23			

Supplemental Table S3 (C)

Hek293_Binding specificity ratio_C8_Control

	Accession	MW	Protein Name	Peptide Sequence	Peptide Score	Peptide C8/Ctl ratio	StDev	Protein Score	Protein C8/Ctl ratio	StDev
1	IPI00063234	43998	PKA RIIα	IVDVIGEK	66	767.3	514.0	1016	169.9	229.08
				GSFGELALMYNTPR	133	197.7	243.2			
				MFESFIESVPLLK	79	113.1	151.3			
				AASAYAVGDVK	98	108.8	87.2			
				AATIVATSEGSLWGLDR	74	70.0	813.5			
				NISHYEEQLVK	47	64.9	91.3			
				LLGPCMDIMK	49	63.5	1144.9			
				CLVMDVQAFER	68	29.0	13.3			
				NLDQEQLSQVLDAMFER	128	0	0.0			
				QQPPDLVEFAVEYFTR	88	0	0.0			
2	IPI00021831	43828	PKA RIα	ECELYVQK	37	97.4	0.0	381	218.6	122.78
				GAISAEVYTEEDAASYVR	38	147.1	15.5			
				HNIQALLK	147	256.2	55.1			
				ILMGSTLR	50	373.6	149.9			
3	IPI00456775	47317	PKA RIIβ	CLAMDVQAFER	43	23.50	0.0	877	83.2	85.75
				VVDVIGTK	33	170.4	0.0			
				MYESFIESLPFLK	85	47.7	0.0			
				NLDPEQMSQVLDAMFEK	98	60.4	0.0			
				GTFDIYVK	56	81.7	0.0			
				DILLFK	28	153.3	0.0			
				GSFGELALMYNTPR	133	237.7	116.4			
4	IPI00554488	44043	PKA RIβ	ILMGSTLR	38	147.1	15.5	119	78.0	97.74
				SNSQSDSHDEEVSPTPPNPVVK	58	8.8	7.1			
5	IPI00427586	78494	PKG Iα / PKGIβ	AQGISAEPQTYR	56	10.4	4.2	545	60.0	82.80
				CQSVLPVPSTHIGPR	57	13.5	0.0			
				EAILDNDFMK	44	16.5	0.0			
				GDTFFIISK	70	19.1	7.9			
				GIDMIEFPK	71	80.1	0.0			
				HLIGGLDDVSNK	58	220.3	0.0			
6	IPI00171217	122975	AKAP2	DALGDSLQVPVSPSSTTSSR	99	11.1	21.6	289	10.2	1.22
				STASLLATQESDVMVGPFK	37	9.3	0.0			
7	IPI00422254	38160	AKAP7	AVQQYLEETQNK	75	7.1	0.0	197	22.3	21.50
				ILQNAIIQQDER	85	37.5	15.1			
8	IPI00019223	465228	AKAP9	HQLDVVIAEK	87	50.9	0.0	2632	138.7	49.65
				TLEDMLK	71	9.32	0.0			
				QQILTHQQQLEEQDHLLEDYQK	66	178.7	0.0			
				NSTHSSTAADLLQAK	64	32.6	0.0			
				LIEMNGGGTGCNHELEMIR	62	101.1	8.7			
				FAQIIQEK	60	143.8	0.0			
				ESDAMSTQDQHVLFGK	51	132.3	0.0			
				QLMGTVEELQK	35	100.4	0.2			
				LQGIMQEFQK	35	114.2	11.9			
				EVEIDQLNEQVTK	35	46.0	14.8			
9	IPI00007411	217039	AKAP11	QEGGNSELIMDQYANR	122	4.1	0.0	1163	74.1	97.68
				SQCDAASQTVTGHHLETHDLK	87	51.2	3.1			
				TPPFSHCDQAVLQCSEASSNK	63	25.1	13.1			
				SISCEVLGSVLR	92	34.6	0.0			
				MFPVPSSQVK	25	54.5	0.0			
				ESLPVSGEESQLTPEK	104	76.3	0.0			
				EFMLLSK	40	78.2	0.0			
				VSMVHGSSLETLPSCPAVTGQK	60	132.2	0.0			
				SFSEDVFQSVK	66	326.3	440.3			
10	IPI00219018	36827	GAPDH	GALQNIIPASTGAAK	72	15.3	6.4	417	26.8	7.78
				GILGYTEHQVVSSDFNSDTHSSTF	72	29.2	5.6			
				IISNASCTTNCLAPLAK	123	31.1	7.5			
				LISWYDNEFGYSNR	92	31.8	0.0			
11	IPI00217966	37763	lactate dehydrogenase A	LLIVSNPVDILTYVAWK	31	14.2	0.0	515	211.9	144.03
				LVIITAGAR	52	150.1	0.0			
				NVNIFK	64	184.6	72.3			
				QVVESAYEVIK	47	219.0	53.6			
				SADTLWGIQK	72	249.29	96.2			
12	IPI00219217	37526	L-lactate dehydrogenase B chain	GEMMDLQHGSLFLQTPK	50	0.4	0.0	427	92.2	75.19
				GLTSVINQK	46	4.8	1.7			
				IVVVTAGVR	107	98.1	31.6			
				LIAPVAEEEATVPNNK	72	119.6	57.0			
				MVVESAYEVIK	68	145.8	71.0			
				VIGSGCNLDSAR	64	184.6	72.3			
13	IPI00011654	50544	Tubulin beta-2 chain	AILVDLEPGTMDSVR	90	1.9	0.3	400	2.6	1.33
				EIVHIQAGQCGNQIGAK	64	5.1	2.4			

				EVDEQMLNVQNK	85	2.4	1.0			
				ISVYYNEATGGK	49	1.7	0.0			
				LAVNMVPFPR	64	3.1	2.0			
				YLTVAAVFR	48	1.6	0.5			
14	IPI00383046	28933	Carboxymethylenebutenolidase homolog	DSEDIYNLK	75	96.6	27.6	313	335.2	351.53
				DVSLLTQK	49	841.6	0.0			
				TFSGQTHGFVHR	60	97.7	85.1			
15	IPI00304925	71724	Heat shock 70 kDa protein 1	AFYPEEISSMVLTK	74	1.7	0.2	510	3.6	1.96
				ATAGDTHLGGEDFDNR	51	3.3	1.0			
				FGDPVVQSDMK	60	2.1	0.6			
				NQVALNPQNTVFDAK	44	3.7	0.3			
				QTQIFTTYSDNQPGVLIQVYEGER	69	2.2	1.1			
				TTPSYVAFTDTER	79	7.4	0.0			
16	IPI00301277	72188	Heat shock 70 kDa protein 1L	AFYPEEISSMVLTK	74	1.7	0.2	490	3.1	2.50
				ATAGDTHLGGEDFDNR	51	3.3	1.0			
				IINEPTAAAIAYGLDK	45	1.1	0.3			
				QTQIFTTYSDNQPGVLIQVYEGER	69	2.2	1.1			
				TTPSYVAFTDTER	79	7.4	0.0			
17	IPI00007752	50704	Tubulin beta-2C chain	EIVHLQAGQCGNQIGAK	64	5.1	2.4	310	3.0	1.30
				EVDEQMLNVQNK	85	2.4	1.0			
				INVYYNEATGGK	49	3.0	1.2			
				LAVNMVPFPR	64	3.1	2.0			
				YLTVAAVFR	48	1.6	0.5			
18	IPI00018140	71105	Isoform 1 of Heterogeneous nuclear ribonu	GFCFLEYEDHK	57	0.7	0.2	206	0.7	0.02
				NLANTVTEEILEK	66	0.6	0.4			
19	IPI00337544	131716	phosphodiesterase 4D interacting protein i	DSLMSQAPISNQQAEVTPTGCLGK	41	36.0	0.0	345	58.3	31.60
				QCVQFVEAAAHESEQQK	64	80.7	0.0			
20	IPI00003865	72624	Heat shock cognate 71 kDa protein	IINEPTAAAIAYGLDK	45	1.1	0.3	328	2.4	2.22
				MVNHFIAEFK	30	2.2	0.9			
				NQVAMNPTNTVFDAK	42	1.8	0.6			
				SFYPEEVSSMVLTK	42	1.3	0.0			
				SQIHDIVLVGGSTR	49	1.9	0.3			
				STAGDTHLGGEDFDNR	41	1.2	0.5			
				TTPSYVAFTDTER	79	7.4	0.0			
21	IPI00444262	67914	CDNA FLJ45706 fis, clone FEBRA202845	FGYVDFESAEDLEK	90	0.5	0.2	207	0.5	0.14
				GFGFVDFNSEEDAK	72	0.5	0.1			
				NDLAVVDVR	45	0.7	0.0			
22	IPI00456484	259126	Phosphodiesterase 4D interacting protein	DSLMSQAPISNQQAEVTPTGCLGK	41	36.0	0.0	325	58.3	31.60
				QCVQFVEAAAHESEQQK	64	80.7	0.0			
23	IPI00012074	72446	Heterogeneous nuclear ribonucleoprotein	GFCFLEYEDHK	57	0.7	0.2	174	0.7	0.01
				YGGPPPDSVYSGVQPGIGTEVFVG	34	0.7	0.2			
24	IPI00166738	41102	Zinc-binding alcohol dehydrogenase doma	FVGVNASDINYSAGR	81	13.5	0.0	217	7.3	8.81
				SASVQGFFLNHYLSK	64	1.0	0.3			
25	IPI00215719	22165	60S ribosomal protein L18	ILTFDQLALDSPK	85	0.9	0.3	149	1.5	0.78
				TAVVVGTITDDVR	64	2.0	0.7			
26	IPI00472102	62859	Heat shock protein 60	LVQDVANNTNEEAGDGTTTATVLA	134	0.3	0.1	192	0.2	0.05
				NAGVEGSLIVEK	58	0.2	0.1			
27	IPI00093057	51563	Coproporphyrinogen III oxidase, mitochond	AGVSISVVHGNLSEEAAK	71	15.7	0.0	214	10.7	7.01
				CSSFMAPPVTDLGELR	79	5.8	1.9			
28	IPI00013296	18184	40S ribosomal protein S18	IAFAITAIK	63	0.3	0.1	182	0.5	0.24
				VITIMQNPR	60	0.8	0.1			
				YSQVLANGLDNK	59	0.5	0.1			
29	IPI00297779	58728	T-complex protein 1 subunit beta	EALLSSAVDHGSDEVK	62	0.8	0.3	105	1.2	0.53
				GATQQILDEAER	43	1.5	0.3			
30	IPI00645907	278288	fatty acid synthase	FCFTPHTEEGCLSER	41	1.9	0.9	169	2.0	0.83
				GLVQALQTK	51	1.3	0.5			
31	IPI00290770	62032	chaperonin containing TCP1, subunit 3 iso	IVLLDSSLEYK	57	1.6	0.4	188	1.1	0.42
				TAVETAVLLLR	43	1.3	0.4			
32	IPI00302592	287094	Filamin A, alpha	AEAGVPAEFSIWTR	48	1.7	1.1	161	2.2	0.47
				AYGPGIEPTGNMVK	61	2.7	0.0			
33	IPI00302925	61488	T-complex protein 1 subunit theta	HFSGLEEAVYR	47	0.9	0.6	104	1.2	0.34
				IAVYSCPFDGMITETK	36	1.6	0.3			
34	IPI00396485	51797	Elongation factor 1-alpha 1	QLIVGVNK	30	0.4	0.0	74	0.4	0.03
				SGDAAIVDMVPGKPMCVESFSDYP	44	0.3	0.1			

Supplementary Table S3 (D)

Rat Lung Tissue_Binding specificity ratio_C8_C2

	Accession	MW	Protein Name	Peptide Sequence	Peptide Score	Peptide C8/C2 ratio	StDev	Protein Score	Protein C8/C2 ratio	StDev
1	IPI00196684	46367	PKA RIIα	AATIVATSDGSLWGLDR	95	2.3	9.49	912	1.7	0.98
				CLVMDVQAFER	62	1.2	0.33			
				GQYFGELALVTNKPR	112	0.1	0.05			
				GSFGELALMYNTPR	67	1.1	1.27			
				GTYDILVTK	72	1.9	1.32			
				LLGPCMDIMK	61	3.9	3.75			
				MFESFIESVPLFK	105	1.7	1.27			
				NLDQEQLSQVLDAMFEK	128	1.7	1.98			
				TDEHVIDQGDDGDNFYVIER	80	2.0	0.95			
				VSVCAETFNPDEEEDNDPR	82	1.3	0.50			
2	IPI00231770	43782	PKA RIα	MYEEFLSK	43	2.1	2.51	121	1.6	0.67
				VLGPCSDILK	41	0.8	0.22			
				VSILESLDK	37	1.7	1.36			
3	IPI00365600	46979	PKA RIIβ	CLAMDVQAFER	68	2.2	2.63	557	2.8	1.33
				EGEHVIDQGDDGDNFYVIDR	86	4.6	1.15			
				GSFGELALMYNTPR	67	1.1	1.26			
				GTFDIYVK	62	4.0	2.67			
				LLGPCMEIMK	60	2.9	2.17			
				NLDPEQMSQVLDAMFEK	102	1.9	1.21			
4	IPI00766097	78639	PKG Iα / PKGIβ	EAILDNDFMK	65	1.6	29.36	715	1.6	0.63
				EDSPSEDPVFLR	51	1.5	0.32			
				GDTFFIISK	63	1.1	5.46			
				GIDMIEFPK	60	2.6	20.26			
				HTEYMEFLK	66	1.4	1.36			
				LADVLEETHYENGEYIIR	83	0.9	0.53			
				LVDFGFAK	49	1.1	1.39			
				SVPTFQSLPDEILSK	91	1.4	0.77			
				VELVQLK	54	1.7	1.06			
				VFGELAILYNCTR	92	2.8	10.32			
5	IPI00215470	77628	AKAP5	ATMGQAEEATVGHIEK	145	1.7	1.40	613	1.9	0.27
				ATVGQAEEPIVGQAEETVLR	140	1.7	1.44			
				SGETALGQAEEASSVSQADK	142	1.9	0.60			
				SVLSQAEEATVGHTEEATVIQAQSQAK	129	2.3	0.73			
6	IPI00393033	445055	AKAP 9	NAELIDLR	39	3.6	1.82	342	3.0	1.87
				NFEVNYQELQR	54	3.5	9.36			
				SEEMNLQINELQK	101	4.7	2.07			
				VAEVLSDIMSEK	68	0.4	6.19			
7	IPI00213479	92660	AKAP1	VVLSLMGDEAK	61	0.702	0.03	60	1.42	0
8	IPI00766036	216203	AKAP11	TSVTTSISEPWTQR	90	1.3	0.54	90	1.3	0.54
9	IPI00421609	40631	AKA7	DYQPNYFLSIPITNK	63	1.9	0.17	63	1.9	0.17
10	IPI00199076	107567	PDE2A3	AMLCVPVISR	30	0.1	2.37	330	0.2	0.18
				LGGDFFTDEDER	57	0.2	0.17			
				LLHDGIQPVAAIDSNFANFTYTPR	61	0.4	0.19			
				LLQDLFPK	56	0.2	0.18			
11	IPI00196935	130730	Rap guanine nucleotide exchange fact	LGSGEGLIIVK	29	25.0	12.03	88	18.1	9.78
				TFIDNLVNFEK	59	11.2	31.51			
12	IPI00368515	95593	IRAG	SSLGDAPSAVSPNLSSGASPASSR	157	0.6	0.13	157	0.6	0.13
13	IPI00369586	240313	myosin, heavy polypeptide 1skeletal m	ALQEAHQQTLDDLQAEEDK	61	0.3	0.18	639	0.5	0.17
				ANLLQAEIEELR	64	0.7	0.36			
				DLEEATLQHEATAATLR	80	0.8	0.28			
				HADSVAELGEQIDNLQR	35	0.6	0.21			
				IQLELNQVK	30	0.6	0.43			
				LASADIETYLLEK	57	0.3	4.15			
				QAFTQQIEELK	57	0.4	0.29			
				VVESMQSTLDAEIR	40	0.5	0.49			
14	IPI00191090	42780	Biglycan precursor	DLPETLNELHLDHNK	59	0.4	0.23	428	0.6	0.14
				EISPDTTLLDLQNNDISELR	31	0.8	0.25			
				IQAIELEDLLR	66	0.5	0.15			
				LAIQFGNYK	52	0.5	0.41			
				NHLVEIPPNLPSSLVELR	52	0.7	0.22			
				NMNCIEMGGNPLENSGFEPGAFDGLK	94	0.5	0.24			
				VGINDFCPMGFGVK	74	0.7	0.25			
15	IPI00199861	40907	Decorin precursor	DLHTLILVNNK	52	0.2	1.14	275	0.1	0.04
				MIVIELGGNPLK	77	0.1	1.38			
				TSYTAVSLYSNPVR	91	0.1	1.77			
				YWQIHPHTFR	28	0.1	0.34			
16	IPI00231192	16320	Hemoglobin beta-2 subunit	FGDLSSASAIMGNPQVK	110	0.7	0.38	255	0.8	0.25
				LLVVYPWTQR	41	0.6	0.19			
				VINAFNDGLK	40	0.8	0.46			

				VVAGVASALAHK	36	1.2	0.58			
17	IPI00557424	102069	PREDICTED: similar to NS1-associate	LFVGSIPK	32	0.8	0.23	174	0.9	0.20
				SAFLCGVMK	28	0.8	0.41			
				VTEGLTDVILYHQPDDK	53	0.8	0.65			
				YGGPPPDSVYSGQQPSVGTEIFVGK	23	1.2	1.28			
18	IPI00194562	72377	Heterogeneous nuclear ribonucleoprot	LFVGSIPK	32	0.8	0.23	173	0.7	0.14
				NLATTVTEEILEK	51	0.6	0.32			
				SAFLCGVMK	28	0.8	0.41			
				VTEGLVDVILYHQPDDK	24	0.6	0.43			
19	IPI00230897	16317	Hemoglobin beta-1 subunit	LLVVYPWTQR	41	0.6	0.19	179	0.7	0.31
				VINAFNDGLK	40	0.8	0.46			
				VVAGVASALAHK	36	1.2	0.58			
				YFDSFGDLSSASAIMGNPK	62	0.4	0.50			
20	IPI00400573	50674	Tubulin, beta, 2	ALTVPELTQQMFDAK	61	1.1	0.94	189	0.9	0.29
				AVLVDLEPGTMDSVR	65	0.6	0.57			
				NSSYFVEWIPNNVK	63	1.1	8.59			
21	IPI00362160	51319	Tubulin beta-3 chain	AILVDLEPGTMDSVR	42	8.6	21.42	166	3.8	4.15
				ALTVPELTQQMFDAK	61	1.1	0.94			
				NSSYFVEWIPNNVK	63	1.9	23.43			
22	IPI00191745	50518	Coproporphyrinogen oxidase	AGVNISVVHGNLSEEAANQMR	51	0.1	0.09	163	0.2	0.06
				CSTFMSSPVTELR	58	0.3	0.44			
				TCAEAVVPSYVPIVK	54	0.2	0.10			
23	IPI00197579	50544	Tubulin beta-5 chain	AILVDLEPGTMDSVR	42	8.6	21.20	160	4.1	3.93
				ALTVPELTQQVFDAK	55	1.7	18.52			
				NSSYFVEWIPNNVK	63	2.0	25.21			
24	IPI00205157	35409	Short chain 3-hydroxyacyl-CoA dehydr	FILDGWHEMDPENPLFQPSPSMNNLVA	28	0.9	3.70	133	2.7	1.68
				LLVPYLIEAIR	44	3.1	0.00			
				TFESLVDFCK	61	4.2	11.18			
25	IPI00212647	36813	GAPDH	IVSNASCTTNCLAPLAK	123	3.1	1.25	198	3.3	0.31
				LISWYDNEYGYSNR	75	3.6	3.35			
26	IPI00197711	37525	L-lactate dehydrogenase A chain	GEMMDLQHGSLFLK	58	NaN	0.00	133	134.0	0.00
				SADTLWGIQK	75	134.0	89.56			
27	IPI00360386	99413	PREDICTED: similar to heterogeneous	EVEGDDVPESIMLEMK	88	2.3	1.11	133	2.0	0.42
				VVVVVPNEEDWK	45	1.7	0.75			
28	IPI00205036	15810	Alpha-2-globin chain	AADHVEDLPGALSTLSDLHAHK	45	0.3	2.20	104	0.4	0.16
				MFAAFPTTK	59	0.6	0.50			
29	IPI00189819	42612	Actin, cytoplasmic 1	SYELPDGQVITIGNER	51	NaN	0.00	96	0.8	0.00
				VAPEEHPVLLTEAPLNPK	45	0.8	0.92			
30	IPI00327185	46695	nucleosome assembly protein 1-like 1	NVDLLSDMVQEHDEPILK	40	0.4	0.00	88	0.3	0.19
				YAVLYQPLFDK	48	0.1	1.03			

Supplemental Table S3 (E)

Rat Lung Tissue_Binding specificity ratio_C8_C8-OCH$_3$

	Accession	MW	Protein Name	Peptide Sequence	Peptide Score	Peptide C8/C8-OCH3 ratio	StDev	Protein Score	Protein C8/C8-OCH3 ratio	StDev
1	IPI00196684	46367	PKA RIIα	AATIVATSDGSLWGLDR	143	9.76	3.46	1276	8.7	3.91
				CLVMDVQAFER	73	7.28	4.51			
				DILLFK	28	8.97	0.27			
				GSFGELALMYNTPR	123	7.75	4.20			
				GTYDILVTK	79	9.69	1.13			
				LLGPCMDIMK	66	14.48	6.55			
				MFESFIESVPLFK	113	10.64	11.66			
				NISHYEEQLVK	59	12.86	18.68			
				NLDQEQLSQVLDAMFEK	130	6.78	6.11			
				QQPPDLVDFAVEYFTR	92	9.38	2.96			
				TDEHVIDQGDDGDNFYVIER	84	6.40	10.35			
				VSVCAETFNPDEEEDNDPR	83	10.54	5.11			
2	IPI00231770	43782	PKA RIα	HNIQALLK	52	0.3	0.19	395	0.2	0.07
				LTVADALEPVQFEDGQK	124	0.2	0.15			
				MYEEFLSK	57	0.3	0.28			
				VLGPCSDILK	61	0.4	0.15			
				VSILESLDK	71	0.2	0.08			
3	IPI00365600	46979	PKA RIIβ	AATITATSPGALWGLDR	119	16.8	12.84	954	18.9	9.37
				CLAMDVQAFER	65	14.6	6.99			
				DILLFK	28	16.0	57.17			
				EGEHVIDQGDDGDNFYVIDR	109	19.1	17.98			
				GSFGELALMYNTPR	123	17.7	4.20			
				GTFDIYVK	59	18.9	10.53			
				HQPADLLEFALQHFTR	62	16.1	8.07			
				LLGPCMEIMK	64	17.6	29.45			
				MYESFIESLPFLK	100	18.6	15.24			
				NLDPEQMSQVLDAMFEK	102	23.2	15.67			
4	IPI00766097	78639	PKG Iα / PKGIβ	CQSVLPVPSTHIGPR	80	17.3	13.59	880	101.1	75.48
				EAILDNDFMK	45	18.8	19.78			
				GDTFFIISK	75	175.7	105.26			
				HTEYMEFLK	34	194.0	319.86			
				LADVLEETHYENGEYIIR	101	91.7	112.66			
				LVDFGFAK	48	234.6	136.73			
				LWAIDR	23	28.7	68.21			
				QCFQTIMMR	46	119.2	54.45			
				QIMQGAHSDFIVR	64	45.1	26.66			
				SVPTFQSLPDEILSK	82	141.8	137.44			
				TYNIILR	42	122.8	67.19			
				VFGELAILYNCTR	73	24.0	58.11			
6	IPI00215470	77628	AKAP 5	ATMGQAEEATVGHIEK	119	8.9	7.35	810	11.0	3.88
				ATVGQAEEPIVGQAEETVLR	132	9.6	1.30			
				ETVLSQAEEVK	76	7.1	2.67			
				LSQIEEPAISQAK	82	7.1	2.43			
				SGETALGQAEEASSVSQADK	149	8.1	8.71			
				SVLSQAEEATVGHTEEATVIQAQSQAK	118	9.7	9.47			
				TSEQYETLLIETASSLVK	134	9.9	4.67			
7	IPI00421609	40631	AKAP7	DYQPNYFLSIPITNK	36	13.8	0.33	26	13.8	0.33
				METMQCETDNLITR	66	1.3	3.44			
				NFEVNYQELQR	47	7.0	1.16			
				SEEMNLQINELQK	76	5.2	2.13			
8	IPI00766036	216203	AKAP11	GVSSCTNALCHLAVK	101	6.4	0.15	222	6.3	0.10
				TSVTTSISEPWTQR	77	6.2	0.09			
9	IPI00196935	130730	128 kDa protein (Epac2)	TFIDNLVNFEK	44	3.4	22.53	115	2.7	0.91
				VLLQQFNTGDER	71	2.1	7.43			
10	IPI00213479	92660	AKAP1	VVLSLMGDEAK	29	0.902	0.03	60	1.11	0
11	IPI00368515	95593	IRAG	SSLGDAPSAVSPNLSSGASPASSR	90	4.5	1.31	90	4.5	1.30
12	IPI00189819	42612	Actin, cytoplasmic 1	EITALAPSTMK	57	1.0	1.23	324	1.0	0.56
				SYELPDGQVITIGNER	97	1.6	2.43			
				VAPEEHPVLLTEAPLNPK	94	0.4	50.48			
13	IPI00191090	42780	Biglycan precursor	DLPETLNELHLDHNK	65	0.5	0.34	320	0.6	0.30
				GVFSGLR	39	0.2	0.47			
				IQAIELEDLLR	67	0.6	0.23			
				LAIQFGNYK	39	0.5	0.33			
				VGINDFCPMGFGVK	82	0.6	0.24			
				VPAGLPDLK	28	1.1	0.42			
14	IPI00189813	42927	Actin, alpha skeletal muscle	EITALAPSTMK	57	1.0	1.23	282	1.3	0.38
				SYELPDGQVITIGNER	97	1.5	2.42			
15	IPI00205036	15810	Alpha-2-globin chain	AADHVEDLPGALSTLSDLHAHK	95	1.1	0.55	245	1.1	0.19
				FLASVSTVLTSK	22	0.8	0.43			

				MFAAFPTTK	58	1.2	0.71			
				TYFSHIDVSPGSAQVK	70	1.1	0.74			
16	IPI00230897	16317	Hemoglobin beta-1 subunit	LHVDPENFR	22	0.3	0.13	320	0.6	0.35
				LLVVYPWTQR	42	0.8	0.52			
				VINAFNDGLK	50	1.0	0.32			
				VVAGVASALAHK	24	0.2	0.09			
				YFDSFGDLSSASAIMGNPK	142	0.4	0.23			
17	IPI00369586	240313	myosin, heavy polypeptide 1, skeleta	ALQEAHQQTLDDLQAEEDK	108	0.6	0.22	177	1.7	0.94
				DLEEATLQHEATAATLR	87	2.6	0.00			
				LASADIETYLLEK	53	1.4	3.98			
				SELQAALEEAEASLEHEEGK	44	2.4	2.19			
18	IPI00197711	37525	L-lactate dehydrogenase A chain	DLADELALVDVIEDK	57	99.6	155.95	213	131.5	53.69
				DQLIVNLLK	52	137.0	0.00			
				FIIPNVVK	31	193.5	0.00			
				SADTLWGIQK	73	101.4	208.05			
19	IPI00231192	16320	Hemoglobin beta-2 subunit	FGDLSSASAIMGNPQVK	47	1.1	0.69	225	0.7	0.42
				LHVDPENFR	22	0.3	0.13			
				LLVVYPWTQR	42	0.8	0.52			
				VINAFNDGLK	50	1.0	0.32			
				VVAGVASALAHK	24	0.2	0.09			
20	IPI00212647	36813	GAPDH	IVSNASCTTNCLAPLAK	95	4.3	2.68	176	4.7	0.60
				LISWYDNEYGYSNR	81	5.2	1.53			
21	IPI00201032	39264	Isoform 1 of Heterogeneous nuclear	GFGFVLFK	54	3.0	0.85	151	2.9	0.13
				IFVGGLSPDTPEEK	97	2.8	2.60			
22	IPI00199861	40907	Decorin precursor	MIVIELGGNPLK	54	0.2	0.15	160	0.2	0.11
				TSYTAVSLYSNPVR	106	0.3	0.13			
23	IPI00372601	227048	myosin heavy polypeptide 13	DLEEATLQHEATAATLR	87	2.6	0.00	475	2.0	0.85
				LASADIETYLLEK	53	1.4	3.98			
24	IPI00189795	51348	Tubulin alpha-1 chain	TIGGGDDSFNTFFSETGAGK	37	1.7	0.47	100	1.7	0.00
				VGINYQPPTVVPGGDLAK	63	1.7	0.56			
25	IPI00190348	14470	H2B histone family, member T	AMGIMNSFVNDIFER	80	0.1	0.15	147	0.1	0.02
				LLLPGELAK	46	0.0	0.02			

Supplemental Table S3 (F)

Rat Lung tissue_Binding specificity ratio_C8_Control

	Accession	MW	Protein Name	Peptide Sequence	Peptide Score	Peptide C8/Ctl ratio	StDev	Protein Score	Protein C8/Ctl ratio	StDev
1	IPI00196684	46367	PKA RIIα	AATIVATSDGSLWGLDR	157	296.5	118.8	1075	293.6	300.0
				CLVMDVQAFER	63	43.2	9.8			
				GSFGELALMYNTPR	96	118.1	50.6			
				GTYDILVTK	69	989.3	451.6			
				LLGPCMDIMK	52	301.3	37.7			
				NISHYEEQLVK	63	331.8	170.9			
				NLDQEQLSQVLDAMFEK	142	NaN	0.0			
				QQPPDLVDFAVEYFTR	110	144.9	0.0			
				TDEHVIDQGDDGDNFYVIER	97	123.4	47.4			
				VSVCAETFNPDEEEDNDPR	114	NaN	0.0			
5	IPI00231770	43782	PKA RIα	GAISAEVYTEEDAASYVR	146	79.4	43.9	252	103.8	94.5
				MYEEFLSK	47	94.5	18.0			
				VLGPCSDILK	33	7.6	14.8			
3	IPI00365600	46979	PKA RIIβ	CLAMDVQAFER	61	13.5	23.2	558	99.1	88.4
				EGEHVIDQGDDGDNFYVIDR	113	71.8	38.6			
				GSFGELALMYNTPR	96	104.0	61.1			
				GTFDIYVK	45	246.2	0.0			
				LLGPCMEIMK	39	60.0	27.9			
				NLDPEQMSQVLDAMFEK	92	0.0	0.0			
4	IPI00766097	78639	PKG Iα / PKGIβ	EAILDNDFMK	61	450.5	600.2	446	188.5	130.1
				GIDMIEFPK	69	52.8	49.5			
				LADVLEETHYENGEYIIR	93	0.0	0.0			
				LVDFGFAK	25	110.6	812.4			
				LWAIDR	25	139.0	47.5			
				QCFQTIMMR	46	159.3	77.2			
				TYNIILR	43	155.0	70.8			
				VELVQLK	48	251.9	0.0			
2	IPI00215470	77628	AKAP5	ATMGQAEEATVGHIEK	122	118.7	203.5	647	89.9	102.0
				ATVGQAEEPIVGQAEETVLR	125	221.6	142.4			
				ETVLSQAEEVK	79	NaN	0.0			
				LSQIEEPAISQAK	68	NaN	0.0			
				SGETALGQAEEASSVSQADK	125	2.1	55.2			
				SVLSQAEEATVGHTEEATVIQAQSQ	128	17.1	21.1			
6	IPI00393033	445055	AKAP9	NFEVNYQELQR	52	180.0	83.3	99	140.4	83.3
				QLQEFEAAIK	47	100.7	0.0			
7	IPI00210194	128384	AKAP11	SCQPLQNHGLCQNTSSLSGYSCGE	67	124.7	0	67	124.7	0
8	IPI00196935	130730	128 kDa protein (Epac2)	LGSGEGLIIVK	37	108.3	0	37	108.3	0
9	IPI00231192	16320	Hemoglobin beta-2 subunit	ATVSGLWGK	51	0.2	0.1	361	0.1	0.1
				FGDLSSASAIMGNPQVK	77	0.3	0.7			
				GTFAHLSELHCDK	82	0.0	0.1			
				LHVDPENFR	45	0.1	0.1			
				VVAGVASALAHK	106	0.0	0.0			
10	IPI00230897	16317	Hemoglobin beta-1 subunit	GTFAHLSELHCDK	82	0.0	0.1	301	0.1	0.2
				LHVDPENFR	45	0.1	0.1			
				VVAGVASALAHK	106	0.0	0.0			
				YFDSFGDLSSASAIMGNPK	68	0.4	0.2			
11	IPI00205036	15810	Alpha-2-globin chain	AADHVEDLPGALSTLSDLHAHK	99	0.2	0.1	226	0.2	0.0
				FLASVSTVLTSK	66	0.2	0.2			
				MFAAFPTTK	61	0.2	0.1			
12	IPI00369586	240313	myosin, heavy polypeptide 1, skeletal	DLEEATLQHEATAATLR	74	17.7	11.6	461	10.4	4.7
				DSLVSQLSR	58	NaN	0.0			
				HADSVAELGEQIDNLQR	57	8.5	10.4			
				IEELEEEIEAER	88	5.3	5.9			
				NLTEEMAGLDETIAK	70	11.5	7.4			
				TLEDQVSELK	33	NaN	0.0			
				VVESMQSTLDAEIR	81	8.9	8.0			
13	IPI00197711	37525	L-lactate dehydrogenase A chain	QVVDSAYEVIK	57	72.0	44.7	132	112.5	57.2
				SADTLWGIQK	75	152.9	115.5			
14	IPI00561410	36544	36 kDa protein	QVVDSAYEVIK	57	72.0	44.7	132	112.5	57.2
				SADTIWGIQK	75	152.9	115.5			
15	IPI00212647	36813	GAPDH	IVSNASCTTNCLAPLAK	110	4.9	2.3	173	4.5	0.5
				LISWYDNEYGYSNR	63	4.2	1.6			
16	IPI00189813	42927	Actin, alpha skeletal muscle	AVFPSIVGRPR	23	0.0	0.0	202	2.3	0.8
				EITALAPSTMK	61	1.7	0.8			
				SYELPDGQVITIGNER	63	2.9	1.5			
				VAPEEHPTLLTEAPLNPK	55	0.0	0.0			
17	IPI00189819	42612	Actin, cytoplasmic 1	EITALAPSTMK	61	1.7	0.8	197	1.9	0.9
				SYELPDGQVITIGNER	63	2.9	1.4			
				VAPEEHPVLLTEAPLNPK	50	1.0	0.4			

18	IPI00476111	229596	Myosin-4	HADSVAELGEQIDNLQR	57	13.1	9.8	226	9.2	3.9
				IEELEEEIEAER	88	5.3	5.7			
				VVESMQSTLDAEIR	81	9.1	8.0			
19	IPI00363719	36201	Heterogeneous nuclear ribonucleoprote	FGEVVDCTIK	61	0.3	0.5	153	0.3	0.1
				VFVGGLSPDTSEEQIK	92	0.2	0.2			
20	IPI00191090	42780	Biglycan precursor	DLPETLNELHLDHNK	36	0.8	0.5	98	0.6	0.3
				VGINDFCPMGFGVK	62	0.4	0.3			
21	IPI00189809	229943	Myosin heavy chain, cardiac muscle alp	HADSVAELGEQIDNLQR	57	8.5	10.4	145	6.9	2.3
				IEELEEELEAER	88	5.3	5.9			
22	IPI00368874	67742	LOC299458 protein	NVLEGSDEYLVCK	77	1.5	0.5	122	3.6	2.9
				YTATSQVLLSAK	45	5.6	1.2			
23	IPI00382222	60910	Heterogeneous nuclear ribonucleoprote	EQILEEFSK	33	0.6	0.1	61	0.6	0.1
				LFVGSIPK	36	0.6	0.2			

Supplemental Table S3(G)

RCC10_Binding specificity ratio_C8_C2

	Accession	MW	Protein Name	Peptide Sequence	Peptide Score	Peptide C8/C2 ratio	StDev	Protein Score	Protein C8/C2 ratio	StDev
1	IPI00063234	43998	PKA RIIα	AASAYAVGDVK	60	1.0	0.29	605	1.2	0.51
				AATIVATSEGSLWGLDR	51	1.4	0.49			
				CLVMDVQAFER	53	1.7	1.48			
				GQYFGELALVTNKPR	58	0.0	0.04			
				GSFGELALMYNTPR	50	1.0	0.52			
				GTYDILVTK	76	0.9	0.52			
				LLGPCMDIMK	57	1.5	1.39			
				MFESFIESVPLLK	85	1.7	0.79			
				MFGSSVDLGNLGQ	48	0.0	0.00			
				NISHYEEQLVK	38	1.4	0.87			
2	IPI00021831	43828	PKA RIα	GAISAEVYTEEDAASYVR	43	1.5	1.03	262	1.0	0.66
				HNIQALLK	44	1.5	0.25			
				MYEEFLSK	52	0.4	1.37			
				NVLFSHLDDNER	34	1.7	0.00			
				VLGPCSDILK	62	0.2	0.17			
				VSILESLDK	37	0.7	0.70			
	IPI00554488	44043	PKA RIβ	MYEEFLSK	52	1.403886	1.4082		1.40389	0
3	IPI00019223	465228	AKAP9	AYINTISSLK	51	5.4	3.35	942	4.1	1.80
				DMQEQGQFETEMLQK	66	1.5	0.56			
				ESDAMSTQDQHVLFGK	53	2.3	0.98			
				ETIIEELNTK	27	3.5	2.78			
				EVEIDQLNEQVTK	69	6.0	3.24			
				GSIINLETR	38	4.0	1.70			
				HGEISFLNEEVK	54	5.7	4.21			
				IHQLELQTMK	36	2.7	0.96			
				ILLEVVK	48	5.3	4.51			
				IQSIPENSVNVAIDHLSK	71	6.9	6.34			
				LLEAISETSSQLEHAK	54	6.6	8.16			
				LLGELQEQIVQK	48	3.4	3.92			
				LLQLESTVSAK	41	4.2	2.27			
				LMNVAINELNIK	38	0.9	0.00			
				QSIHDEISVSSMDASR	42	4.8	2.22			
				SVLLAAFR	47	2.2	0.00			
				TQLLFSHEEELSK	47	2.5	0.00			
				TSMNAHSLSEEADSLK	49	5.4	2.99			
4	IPI00007411	217039	AKAP11	EFMLLSK	49	1.4	1.04	622	1.2	0.27
				ELLMFSNK	33	1.3	1.29			
				ESLPVSGEESQLTPEK	56	0.5	0.24			
				FPDSQNQLTHCSLSAAK	46	1.1	0.51			
				MFPVPSSQVK	31	1.0	0.88			
				NVIPDTPPSTPLVPSR	36	1.3	0.62			
				SISCEVLGSVLR	67	1.4	0.59			
				SLTDSCLFEK	41	1.3	0.98			
				TSVTTSISEPWTQR	39	1.4	0.78			
				YTLDTFLHQK	45	1.2	0.64			
5	IPI00032064	124528	AKAP2	LWAEDGEFTSAR	34	1.5	3.91	100	1.3	0.25
				WWNPPQEK	30	1.1	0.37			
6	IPI00022585	99512	AKAP1	SIPLECPLSSPK	39	1.4	0.65	39	1.4	0.00
7	IPI00003842	204330	MAP2	LSVEIPCPPAVSEADLATDER	38	1.3	0.00	38	1.3	0.00
8	IPI00337544	131716	PDE4DIP	EQLLQEFR	42	3.1	2.57	235	5.5	2.96
				EVEDLSATLLCK	33	1.8	1.41			
				LNSHETTITQQSVSDSHLAELQEK	36	8.1	3.54			
				QCVQFVEAAAHESEQQK	82	6.2	4.38			
				TLEANEMLLEK	42	8.4	11.71			
9	IPI00219018	36827	GAPDH	GALQNIIPASTGAAK	71	15.3	15.49	219	24.8	8.19
				IISNASCTTNCLAPLAK	116	29.2	26.73			
				LISWYDNEFGYSNR	32	29.8	20.68			
10	IPI00217966	37763	lactate dehydrogenase A	FIIPNVVK	37	36.5	30.21	245	43.1	23.87
				LGVHPLSCHGWVLGEHGDSSVPVW	22	6.2	0.00			
				LVIITAGAR	38	45.6	35.34			
				QVVESAYEVIK	49	60.2	43.04			
				SADTLWGIQK	73	67.0	44.00			
11	IPI00604590	33551	NME1-NME2 protein	GDFCIQVGR	59	1.6	0.76	217	1.4	0.28
				GLVGEIIK	51	1.2	0.52			
12	IPI00025512	23050	Heat-shock protein beta-1	LATQSNEITIPVTFESR	86	1.3	0.68	186	1.3	0.27
				LFDQAFGLPR	45	1.5	0.64			
				VSLDVNHFAPDELTVK	55	1.0	0.00			
13	IPI00019502	233346	Myosin-9	ALELDSNLYR	43	2.1	2.09	471	1.7	0.51
				FLSNGHVTIPGQQDK	36	1.9	0.44			

				GDLPFVVPR	57	2.2	1.37			
				IAQLEEQLDNETK	86	1.0	0.67			
				IMGIPEEEQMGLLR	31	1.2	0.78			
				NFINNPLAQADWAAK	38	2.1	2.04			
				VIQYLAYVASSHK	63	2.1	1.60			
				VSHLLGINVTDFTR	43	2.3	1.41			
14	IPI00479217	91572	HNRP isoform b	GYFEYIEENK	45	81.8	63.61	327	114.2	26.32
				MCLFAGFQR	44	127.4	49.01			
				NFILDQTNVSAAAQR	37	93.0	61.49			
				SSGPTSLFAVTVAPPGAR	87	146.2	63.23			
				YNILGTNTIMDK	71	122.7	149.63			
15	IPI00013485	32290	40S ribosomal protein S2	LSIVPVR	70	47.4	26.32	159	47.4	0.00
				SPYQEFTDHLVK	63	0.0	0.00			
16	IPI00550689	56613	UPF0027 protein C22orf28	LMFEELR	46	4.3	0.00	352	3.6	3.22
				QIGNVAALPGIVHR	54	6.4	4.30			
17	IPI00294398	35210	Isoform 1 of Hydroxyacyl-coenzyme A dehy	FIVDGWHEMDAENPLHQPSPSLNK	49	1.2	0.00	102	0.8	0.56
				LLVPYLMEAIR	53	0.4	0.29			
18	IPI00039626	119985	Isoform D of UPF0318 protein FAM120A	NIQDTSDLDAIAK	79	0.0	0.38	171	2.7	2.93
				QSVLEGLSFSR	26	2.2	0.00			
				SLTTSQYLMHEVAK	31	5.8	5.64			
19	IPI00093057	51563	Coproporphyrinogen III oxidase, mitochond	AGVSISVVHGNLSEEAAK	62	0.1	0.11	125	0.2	0.08
				EGGGGISCVLQDGCVFEK	32	0.2	0.11			
				NPHAPTIHFNYR	31	0.2	0.08			
20	IPI00000874	22885	Peroxiredoxin-1	GLFIIDDK	52	0.6	0.00	111	0.6	0.03
				LVQAFQFTDK	59	0.7	0.74			
21	IPI00011253	27431	40S ribosomal protein S3	AELNEFLTR	35	3.4	0.00	166	5.6	2.38
				FVADGIFK	32	3.6	2.16			
				GGKPEPPAMPQPVPTA	41	5.0	2.55			
				LLGGLAVR	24	8.3	4.30			
22	IPI00009342	193545	Ras GTPase-activating-like protein IQGAP	FLSAIVSSVDK	45	1.2	0.00	102	1.2	0.00
				ITLQDVVSHSK	57	1.1	0.00			
23	IPI00219217	37526	L-lactate dehydrogenase B chain	IVVVTAGVR	41	45.3	0.00	102	46.3	0.00
				SADTLWDIQK	61	46.3	43.20			
24	IPI00465361	24901	60S ribosomal protein L13	GFSLEELR	53	3.8	1.61	105	3.8	0.00
				LATQLTGPVMPVR	52	0.4	0.00			
25	IPI00013070	97287	HNRP U-like protein 1	EALGGQALYPHVLVK	69	0.7	0.00	93	1.7	1.40
				WMGIAFR	34	2.6	0.00			
26	IPI00219330	76585	Isoform 5 of Interleukin enhancer-binding fa	AYAALAALEK	53	2.3	1.24	108	1.9	0.50
				VLGMDPLPSK	31	1.6	0.80			
27	IPI00021439	42612	Actin, cytoplasmic 1	AVFPSIVGRPR	45	0.0	0.00	83	0.5	0.58
				VAPEEHPVLLTEAPLNPK	38	0.9	0.38			
28	IPI00166768	38214	TUBA6 protein	TIGGGDDSFNTFFSETGAGK	38	0.7	0.54	72	0.6	0.02
				VGINYQPPTVVPGGDLAK	34	0.6	0.35			
29	IPI00012074	72446	Heterogeneous nuclear ribonucleoprotein	ENILEEFSK	35	2.3	1.30	94	1.5	0.72
				GYAFITFCGK	31	1.2	0.65			

Supplemental Table S3 (H)

RCC10_binding specificity ratio_C8_C8-OCH$_3$

	Accession	MW	Protein Name	Peptide Sequence	Peptide Score	Peptide C8/C8-OCH3 ratio	StDev	Protein Score	Protein C8/C8-OCH3 ratio	StDev
1	IPI00063234	43998	PKA RIIα	AASAYAVGDVK	52	6.09	0.46	799	5.60	0.47
				AATIVATSEGSLWGLDR	142	6.40	5.71			
				CLVMDVQAFER	39	9.44	3.18			
				DILLFK	29	7.24	0.27			
				GQYFGELALVTNKPR	86	5.25	0.05			
				GSFGELALMYNTPR	94	9.01	0.42			
2	IPI00021831	43828	PKA RIα	GAISAEVYTEEDAASYVR	106	1.01	0.33	359	0.23	0.44
				HNIQALLK	24	1.20	0.00			
				LTVADALEPVQFEDGQK	90	0.51	0.05			
				MYEEFLSK	57	0.39	0.32			
				VLGPCSDILK	34	0.22	0.73			
				VSILESLDK	48	0.62	0.59			
3	IPI00787996	44027	PKA RIβ	IVVQGEPGDDFYIITEGTASVLQR	52	0.61	0.00	260	0.08	0.06
				MYEEFLSK	57	0.61	0.09			
				VLGPCSEILK	27	0.40	0.00			
				VSILESLEK	29	0.81	0.08			
4	IPI00019223	465228	AKAP9	EVEIDQLNEQVTK	88	4.14	1.21	1550	4.60	1.18
				GSIINLETR	45	3.24	2.71			
				HVLGILDR	41	4.18	3.05			
				IQEQGVEYQAAMECLQK	52	5.37	1.20			
				IQSIPENSVNVAIDHLSK	56	4.36	1.39			
				IVELLNETEK	43	6.61	6.18			
5	IPI00007411	217039	AKAP11	EFMLLSK	51	3.40	0.66	736	3.50	0.38
				ESLPVSGEESQLTPEK	97	4.10	0.26			
				GVSSCTNALYHLAIK	62	2.90	0.69			
				SFSEDVFQSVK	77	3.80	0.83			
6	IPI00032064	124528	AKAP2	NLMQTLMEDYETHK	55	0.93	0.79	104	0.93	0.00
7	IPI00022585	99512	AKAP1	SIPLECPLSSPK	51	1.05	0.44	98	1.05	0.00
8	IPI00019502	233346	Myosin-9	ANLQIDQINTDLNLER	100	0.65	0.37	875	0.77	0.25
				DMFQETMEAMR	77	0.75	0.87			
				FLSNGHVTIPGQQDK	34	0.78	0.46			
				GDLPFVVPR	63	1.05	0.82			
				HSQAVEELAEQLEQTK	59	0.46	2.58			
				IAEFTTNLTEEEEK	83	0.84	0.59			
				IAQLEEQLDNETK	108	0.74	0.90			
				IMGIPEEEQMGLLR	43	0.51	0.27			
				NLPIYSEEIVEMYK	53	1.03	0.78			
				NMDPLNDNIATLLHQSSDK	44	0.62	0.63			
				QIATLHAQVADMK	32	1.37	0.84			
				TDLLLEPYNK	53	0.79	0.60			
				VIQYLAYVASSHK	59	0.75	0.74			
				VSHLLGINVTDFTR	42	0.40	0.85			
				VVFQEFR	25	0.74	0.24			
9	IPI00479217	91572	heterogeneous nuclear ribonucleopro	DCEVVMMIGLPGAGK	97	26.40	35.13	589	21.07	7.36
				GYFEYIEENK	51	10.83	10.04			
				MCLFAGFQR	44	22.10	17.95			
				NFILDQTNVSAAAQR	92	28.44	27.87			
				SPQPPVEEEDEHFDDTVVCLDTYN	32	0.00	0.00			
				SSGPTSLFAVTVAPPGAR	68	28.92	15.48			
				YNILGTNTIMDK	77	13.08	20.28			
10	IPI00337544	131716	phosphodiesterase 4D interacting pro	ALQQLQEELQNK	51	1.12	0.57	550	1.80	1.11
				EQLLQEFR	54	1.34	0.71			
				LGPGQSEIAEELCQR	74	1.41	0.74			
				LNSHETTITQQSVSDSHLAELQEK	53	1.56	0.47			
				QCVQFVEAAAHESEQQK	61	2.06	0.79			
				SSLPGAKPGPSMTDGVSSGFLNR	63	0.34	0.00			
				STLGDLDTVAGLEK	86	3.95	1.48			
				TLEANEMLLEK	59	3.48	2.46			
11	IPI00217966	37763	lactate dehydrogenase A	DLADELALVDVIEDK	116	106.05	0.00	478	76.42	42.21
				DQLIYNLLK	39	49.64	0.00			
				LLIVSNPVDILTYVAWK	126	14.03	0.00			
				LVIITAGAR	38	134.92	64.86			
				QVVESAYEVIK	66	76.58	25.80			
				SADTLWGIQK	71	77.30	36.25			
12	IPI00093057	51563	Coproporphyrinogen III oxidase, mitoc	AGVSISVVHGNLSEEAAK	90	0.01	0.00	0.078181	0.08	0.08
				AVVPSYIPLVK	33	0.01	0.00			
				EGGGGISCVLQDGCVFEK	101	0.08	0.03			
				FGLFTPGSR	30	0.02	0.01			

				LPFCAMGVSSVIHPK	42	0.18	0.00			
				NPHAPTIHFNYR	41	0.16	0.00			
13	IPI00219757	23802	Glutathione S-transferase P	DQQEAALVDMVNDGVEDLR	124	0.11	0.12	357	0.06	0.07
				FQDGDLTLYQSNTILR	114	0.02	0.00			
14	IPI00219018	36827	GAPDH	GALQNIIPASTGAAK	55	26.77	5.90	439	34.29	32.10
				IISNASCTTNCLAPLAK	120	79.04	0.00			
				VIHDNFGIVEGLMTTVHAITATQK	71	2.67	1.70			
				WGDAGAEYVVESTGVFTTMEK	76	28.67	0.00			
15	IPI00215965	39370	heterogeneous nuclear ribonucleopro	GFAFVTFDDHDSVDK	85	0.41	0.22	319	0.29	0.17
				LFIGGLSFETTDESLR	113	0.17	0.21			
				SSGPYGGGGQYFAKPR	38	0.21	0.00			
16	IPI00013485	32290	40S ribosomal protein S2	AFVAIGDYNGHVGLGVK	68	3.52	0.87	185	3.52	0.00
				SPYQEFTDHLVK	58	3.12	0.00			
				TYSYLTPDLWK	59	2.91	0.00			
17	IPI00021439	42612	Actin, cytoplasmic 1	DLYANTVLSGGTTMYPGIADR	79	0.66	0.43	340	0.43	0.24
				IWHHTFYNELR	43	0.19	0.17			
				SYELPDGQVITIGNER	73	0.20	0.00			
				TTGIVMDSGDGVTHTVPIYEGYALP	57	0.51	0.22			
18	IPI00219217	37526	L-lactate dehydrogenase B chain	LIAPVAEEEATVPNNK	61	15.93	13.78	282	43.86	56.75
				MVVESAYEVIK	50	109.17	0.00			
				SLADELALVDVLEDK	87	6.49	4.23			
19	IPI00217030	30461	40S ribosomal protein S4, X isoform	FDTGNLCMVTGGANLGR	129	3.51	0.97	281	3.91	2.82
				LSNIFVIGK	35	6.91	2.89			
				VNDTIQIDLETGK	82	1.30	0.46			
20	IPI00009342	193545	Ras GTPase-activating-like protein IQ	ATFYGEQVDYYK	58	1.31	0.88	267	2.65	1.77
				EQLSDMMMINK	70	1.91	1.08			
				FLSAIVSSVDK	35	1.91	2.40			
				LIFQMPQNK	35	2.36	0.00			
				SNQQLENDLNLMDIK	69	5.75	0.00			
21	IPI00011253	27431	40S ribosomal protein S3	GLCAIAQAESLR	82	2.05	0.79	258	1.75	0.61
				IMLPWDPTGK	52	1.58	0.48			
				LLGGLAVR	40	2.39	0.89			
				TEIIILATR	56	0.98	0.67			
22	IPI00003865	72624	Isoform 1 of Heat shock cognate 71 k	DAGTIAGLNVLR	63	0.32	0.30	219	0.32	0.06
				IINEPTAAAIAYGLDK	108	0.39	0.15			
				SQIHDIVLVGGSTR	48	0.26	0.00			
23	IPI00011654	50544	Tubulin beta chain	AILVDLEPGTMDSVR	69	0.59	0.00	237	0.39	0.14
				LHFFMPGFAPLTSR	52	0.30	0.12			
				NSSYFVEWIPNNVK	77	0.31	0.22			
				YLTVAAVFR	39	0.35	0.34			
24	IPI00550689	56613	UPF0027 protein C22orf28	LADMGIAIR	41	6.45	4.53	274	5.67	1.10
				NLDFQDVLDK	42	4.90	2.73			
25	IPI00334775	87319	85 kDa protein	ADLINNLGTIAK	49	0.28	0.00	198	0.43	0.31
				HLEINPDHPIVETLR	42	0.79	0.00			
				TLTLVDTGIGMTK	68	0.21	0.00			
26	IPI00180675	51348	Tubulin alpha-3 chain	AVFVDLEPTVIDEVR	70	0.42	0.24	163	0.39	0.34
				NLDIERPTYTNLNR	36	0.03	0.00			
				VGINYQPPTVVPGGDLAK	57	0.72	0.23			
27	IPI00465361	24901	60S ribosomal protein L13	GFSLEELR	51	3.11	1.18	150	14.81	18.97
				LATQLTGPVMPVR	77	36.69	11.47			
28	IPI00293655	85115	ATP-dependent RNA helicase DDX1	FLICTDVAAR	32	3.95	0.00	216	2.83	1.12
				FNFGEEEFK	30	2.95	0.00			
				GIDIHGVPYVINVTLPDEK	44	3.14	1.47			
				VGWSTMQASLDLGTDK	66	1.29	0.00			
29	IPI00028888	39506	Isoform 1 of Heterogeneous nuclear r	GFGFVLFK	47	0.13	0.06	112	0.18	0.07
				IFVGGLSPDTPEEK	65	0.22	0.13			
30	IPI00221089	17613	40S ribosomal protein S13	GLAPDLPEDLYHLIK	67	5.65	0.00	120	7.44	6.44
				LILIESR	26	2.08	1.11			
				SVPTWLK	37	14.58	10.06			
31	IPI00026260	17793	Nucleoside diphosphate kinase B	GDFCIQVGR	52	3.44	1.18	178	2.58	1.21
				GLVGEIIK	40	1.72	0.83			
32	IPI00396485	51797	Elongation factor 1-alpha 1	SGDAAIVDMVPGKPMCVESFSDYP	54	0.37	0.30	158	0.60	0.52
				VETGVLKPGMVVTFAPVNVTTEVK	53	1.20	0.47			
				YYVTIIDAPGHR	51	0.24	0.00			
33	IPI00382470	101024	Heat shock protein HSP 90-alpha 2	ADLINNLGTIAK	49	0.28	0.00	156	0.25	0.05
				TLTIVDTGIGMTK	68	0.21	0.00			
34	IPI00301936	36773	ELAV-like protein 1	DANLYISGLPR	66	0.28	0.00	135	0.25	0.04
				SLFSSIGEVESAK	69	0.22	0.22			
35	IPI00418471	54190	Vimentin	ILLAELEQLK	53	1.74	0.33	118	1.74	0.00
				NLQEAEEWYK	65	1.69	0.00			
36	IPI00479186	59535	pyruvate kinase 3 isoform 1	GDLGIEIPAEK	43	0.15	0.00	172	0.33	0.22
				IYVDDGLISLQVK	42	0.57	0.00			
				NTGIICTIGPASR	50	0.26	0.16			
37	IPI00030910	73720	GPI-anchored membrane protein 1	SFMALSQDIQK	46	2.85	0.00	100	2.90	0.00
				YQEVTNNLEFAK	54	2.97	0.00			
38	IPI00221092	16895	40S ribosomal protein S16	GPLQSVQVFGR	61	2.73	0.86	104	1.73	1.42

				LLEPVLLLGK	43	0.72	0.38			
39	IPI00011913	31525	Heterogeneous nuclear ribonucleopro	GDVAEGDLIEHFSQFGTVEK	33	0.62	0.00	87	0.60	0.03
				LFIGGLNVQTSESGLR	54	0.58	0.00			
40	IPI00175098	25646	similar to ribosomal protein L10	FNADEFEDMVAEK	76	11.26	4.70	100	7.66	5.09
				VHIGQVIMSIR	34	4.05	0.00			
41	IPI00031691	22468	60S ribosomal protein L9	FLDGIYVSEK	30	1.98	0.00	81	1.87	0.17
				TICSHVQNMIK	51	1.75	0.85			
42	IPI00012074	72446	Heterogeneous nuclear ribonucleopro	AGPIWDLR	34	1.02	0.63	133	1.10	0.71
				LMMDPLSGQNR	34	0.87	0.00			
				NLATTVTEEILEK	38	2.10	1.63			
				SAFLCGVMK	37	0.43	0.00			
43	IPI00011274	47393	heterogeneous nuclear ribonucleopro	DLTEYLSR	42	0.52	0.00	89	0.33	0.28
				GFGFVLFK	47	0.13	0.06			
44	IPI00018140	71105	Isoform 1 of Heterogeneous nuclear r	GYAFVTFCTK	41	0.53	0.00	102	0.66	0.32
				SAFLCGVMK	37	0.43	0.00			
45	IPI00013070	97287	Isoform 1 of Heterogeneous nuclear r	AIVICPTDEDLK	36	1.03	0.31	60	1.26	0.33
				WMGIAFR	34	1.49	0.00			

Supplemental Table S3 (I)

Rat Testicle tissue_Binding specificity ratio_C8_C8-OCH$_3$

	Accession	MW	Protein Name	Peptide Sequence	Peptide Score	Peptide C8-OCH3/C8 ratio	StDev	Peptide C8/C8-OCH3 ratio	Protein Score	Protein C8/C8-OCH3 ratio	StDev
1	IPI00196684	45797	PKA RIIα	AATIVATSDGSLWGLDR	130	0.108	0.04	9.29	1444	10.6	2.92
				AATIVATSDGSLWGLDRVTFR	48	0.112	0.00	8.90			
				CLVMDVQAFER	73	0.234	0.00	4.27			
				GQYFGELALVTNKPR	85	0.071	0.00	14.05			
				GSFGELALMYNTPR	122	0.104	0.01	9.65			
				IVKTDEHVIDQGDDGDNFYVIER	91	0.088	0.00	11.42			
				LLGPCMDIMK	59	0.082	0.00	12.16			
				MFGSNLDLLDPGQ	47	0.070	0.24	14.31			
				NLDQEQLSQVLDAMFEK	132	0.083	0.00	12.11			
				QQPPDLVDFAVEYFTR	59	0.098	0.04	10.16			
2	IPI00231770	43296	PKA RIα	RGAISAEVYTEEDAASYVR	87	1.315	0.90	0.76	512	0.7	0.22
				RNIQQYNSFVSLSV	39	1.826	0.00	0.55			
				SLRECELYVQKHNIQALLK	49	1.100	0.00	0.91			
				VLGPCSDILK	43	2.461	0.90	0.41			
3	IPI00764045	44984	PKA RIIβ	AATITATSPGALWGLDRVTFR	40	0.132	0.04	7.55	749	9.6	8.34
				AATITATSPGALWGLDRVTFRR	31	0.217	0.08	4.61			
				CLAMDVQAFER	64	0.038	0.00	26.08			
				EGEHVIDQGDDGDNFYVIDR	87	0.206	0.00	4.86			
				HQPADLLEFALQHFTR	56	0.216	0.00	4.63			
				NLDPEQMSQVLDAMFEK	108	0.099	0.00	10.05			
4	IPI00766097	76929	PKG Iα / PKGIβ	CQSVLPVPSTHIGPR	43	NaN	0.00	NaN	312	NaN	NaN
				GIDMIEFPK	40	NaN	0.00	NaN			
				LSDFNIIDTLGVGGFGR	102	NaN	0.00	NaN			
				LVDFGFAK	28	NaN	0.00	NaN			
				SVPTFQSLPDEILSK	65	NaN	0.00	NaN			
				VNVTREDSPSEDPVFLR	34	0.225	0.00	NaN			
11	IPI00213479	92660	AKAP1	DLSFPYEAVEGCKQESALGR	60	1.130	0.00	0.88	247	1.1	0.31
				TYVSCLSSPLSGPTK	76	1.111	0.00	0.90			
				VVLSLMGDEAK	61	0.702	0.03	1.42			
10	IPI00364858	96338	AKAP2	NLMQTLMEDYETHK	58	0.700	0.00	1.43	437	1.3	0.33
				STASLLATQESDVMVGPFK	37	1.054	0.00	0.95			
				SVNVSLTQEELDSGLDELSVR	161	0.585	0.50	1.71			
				TLSMIEEEIRAAQEREEELK	30	0.864	0.00	1.16			
8	IPI00201274	96002	AKAP3	SVGEVLQSVLRYEK	30	0.260	0.09	3.85	661	2.7	1.04
				EVVSDLIDSFMK	53	0.527	0.09	1.90			
				FCEDEEATGGALSGLTK	61	0.440	0.00	2.27			
5	IPI00212365	94916	AKAP4	GAPGPSTCAKENQLESQKMDMSNM	33	0.192	0.00	5.20	1823	3.0	2.22
				NLHNITGVLMTDSDFVSAVK	87	1.865	0.00	0.54			
				RPEDQSQDSTEMDFISGMK	53	1.125	0.00	0.89			
				SVATPDGECSMDDLSYYVNR	72	0.171	0.00	5.84			
				TFLYSELSNK	38	0.236	0.97	4.24			
				YALGFQHALSPSASSCK	123	0.286	0.05	3.49			
				YSNNGAALAELEEQAALASNGPR	123	1.142	0.50	0.88			
12	IPI00421609	39621	AKAP7	HLTLPFHGIGTFQGQVGFVK	47	0.327	0.91	3.06	142	3.5	0.41
				LADGDHVSALLEIAETAK	37	0.217	1.79	4.62			
				LADGDHVSALLEIAETAKR	58	0.363	1.19	2.75			
14	IPI00471827	74284	AKAP10	SIEQDAVNTFTK	59	1.183	0.12	1.18	59	1.2	0.00
7	IPI00779281	209546	AKAP11	LSPLINEACRYCDLK	30	0.151	0.190	6.61	859	8.2	2.03
				SCQPLQNHGLCQNTSSLSGYSCGE	90	0.158	0.01	6.33			
				SSDVSSSPLNQSHHSGMLCVMR	44	0.130	0.458	7.67			
				FSASLASSITR	60	0.104	0.020	9.59			
				TSVTTSISEPWTQR	74	0.090	0.198	11.06			
6	IPI00198250	181514	AKAP12	ALGSLGGSPSLPDQDK	93	0.705	0.08	1.42	774	1.7	0.75
				HPEGIVSEVEMLSSQER	75	0.390	0.02	2.56			
				IVLNVIQTAVDQFAR	126	0.710	0.12	1.41			
				AADVTYDSEVMGVAGCQEK	103	1.235		0.81			
				TLVHTVSVAVIDGTR	85	0.410	0.00	2.44			
13	IPI00213019	55722	AKAP14	EKKVQLIDPKEK	24	0.730	0.68	9.75	41	9.0	0.00
				HILLESIPFKVV	25	0.510	0.71	6.35			
				MNNKKKPPNQKAK	22	0.671	0.00	10.13			
				RTVTFVTDVKDK	28	0.540	0.01	9.35			
				VVLFTPEIK	48	0.200	0.00	9.39			
9	IPI00231052	49327	MAP2	APHWTSASLTEAAAHPHSPEMK	60	0.146	0.00	6.85	417	6.2	1.95
				ENGINGELTSADRETAEEVSAR	61	0.130	0.00	7.71			
				RGVSGDREENSFSLNSSISSAR	36	0.251	0.00	3.99			
15	IPI00213904	97084	PDE10A11	FNREVDLYTGYTTR	51	0.000	0.00	0.02	92	0.0	0.00
				GSVIGVVQMVNK	72	0.146	0.08	0.00			
				LTANDIYAEFWAEGDEMKK	35	0.130	0.11	0.00			
				NILCMPIVSR	38	0.251	0.02	0.00			
				TGEVLNIPDAYADPR	51	0.100	0.00	0.00			
				TLLVEDILGDERFPR	57	0.100	0.00	0.00			
				VIRGEETAMWISGPATSK	35	0.100	0.00	0.00			
16	IPI00779862	40233	A-kinase anchoring protein-as	AIVDLDPSEDKMEWIK	63	0.000	0.00	6.04	255	6.6	0.78
				FLALGCSSLGGTLNTAMK	104	0.000	0.00	7.14			

17	IPI00189795	50788	Tuba1 Tubulin alpha-1 chain	IHFPLATYAPVISAEK	52	0.166	0.00	6.04	637	13.1	11.36
				NLDIERPTYTNLNR	39	0.140	0.00	7.14			
				TIGGGDDSFNTFFSETGAGK	115	0.038	0.01	26.24			
18	IPI00207355	69771	Hspa2 Heat shock-related 70	ARFEELNADLFR	55	0.166	0.00	6.03	69642	24.6	26.28
				NQVAMNPTNTIFDAKR	90	0.223	0.00	4.49			
				TTPSYVAFTDTERLIGDAAK	48	0.037	0.00	27.04			
				VQSAVITVPAYFNDSQR	67	0.016	0.00	60.89			
19	IPI00400573	50225	Tubb2c Tubulin beta-2C cha	AVLVDLEPGTMDSVR	26	0.217	0.00	4.60	49801	7.9	3.46
				GHYTEGAELVDSVLDVVRK	26	0.087	0.00	11.49			
				NSSYFVEWIPNNVK	60	0.132	0.11	7.56			
20	IPI00197711	36712	Ldha L-lactate dehydrogenase	DLADELALVDVIEDK	97	0.305	0.03	3.28	36451	1.0	0.98
				DLADELALVDVIEDKLK	74	0.558	0.00	1.79			
				QVVDSAYEVIKLK	72	0.699	0.00	1.43			
21	IPI00201032	38339	Hnrpd Isoform 1 of Heterogen	FGDVVDCTLKLDPITGR	70	0.131	0.02	7.64	38192	20.5	0.02
				MFIGGLSWDTTKK	66	0.030	0.00	33.33			
22	IPI00362587	52870	Fus Fusion, derived from t(12;	AAIDWFDGKEFSGNPIK	88	0.040	0.00	25.00	52673	24.1	0.00
				LKGEATVSFDDPPSAK	46	0.035	0.00	28.57			
				TGQPMINLYTDRETGK	63	0.054	0.04	18.65			
23	IPI00197579	50095	Tubb5 Isoform 1 of Tubulin be	AILVDLEPGTMDSVR	27	0.023	0.01	44.28	49671	18.4	0.00
				ALTVPELTQQVFDAK	68	0.169	0.01	5.92			
				ISVYYNEATGGKYVPR	77	0.200	0.01	5.00			
24	IPI00200047	69622	Rbm14 similar to RNA-binding	ASYVAPLTAQPATYR	71	0.100	0.00	10.00	69494	31.2	0.02
				IFVGNVSAACTSQELR	110	0.030	0.02	33.51			
25	IPI00191692	37623	Tfg 38 kDa protein	NVMSAFGLTDDQVSGPPSAPTEDR	104	0.020	0.00	50.00	37589	37.4	0.00
				QSTQVMAASMSAFDPLK	87	0.030	0.00	33.33			
				QSTQVMAASMSAFDPLKNQDEINK	77	0.035	0.02	28.73			
26	IPI00206780	93214	Plg Plasminogen precursor	ILGSDVQQIAVTK	73	0.055	0.01	18.28	90536	35.3	0.09
				NYCRNPDGDVNGPWCYTMNPR	77	0.020	0.00	50.00			
				VVGGCVANPHSWPWQISLR	75	0.027	0.01	37.51			
27	IPI00363176	40735	Zadh2_predicted similar to zi	DCPVPLPGDGDLLVR	40	0.020	0.00	50.00	40476	74.8	0.04
				FVGINASDINYSAGR	70	0.006	0.00	167.17			
				LIVIGFISGYQSPTGLSPVK	66	0.137	0.00	7.29			
				LSPNFHEAVTLRR	36	0.166	0.07	6.03			
				LVVELPHPVSSKL	41	0.060	0.00	16.61			
28	IPI00554039	36045	GAPDH	IVSNASCTTNCLAPLAK	91	0.026	0.01	38.13	35783	19.0	0.00
				LISWYDNEYGYSNR	74	0.122	0.00	8.20			
29	IPI00326948	81551	Hsd17b4 Hsd17b4 protein	AAVAVPSRPPDAVLR	26	0.094	0.02	10.60	81089	18.5	0.24
				AAVAVPSRPPDAVLRDTTSLNQAAL	26	0.040	0.00	25.04			
				GALVVVNDLGGDFK	65	0.050	0.00	20.00			
30	IPI00464815	47440	Eno1 Alpha-enolase	AAVPSGASTGIYEALELRDNDK	57	0.079	0.04	12.72	47128	9.1	5.37
				LAMQEFMILPVGASSFR	93	0.087	0.00	11.50			
				LAQSNGWGVMVSHR	47	0.337	0.23	2.97			
				VNQIGSVTESLQACK	47	0.744	0.35	1.34			
31	IPI00382376	39856	Hnrpa3 Isoform 1 of Heteroge	IFVGGIKEDTEEYNLRDYFEK	41	0.354	0.00	2.83	39652	2.5	0.23
				YGKIETIEVMEDR	51	0.222	0.00	4.50			
32	IPI00365665	96513	Hnrpul1_predicted similar to E	EALGGQALYPHVLVK	87	17.287	25.40	0.06	96002	50.6	0.00
				KYNILGTNAIMDK	37	0.007	0.00	149.10			
				NYILDQTNVYGSAQR	44	0.384	0.00	2.60			
33	IPI00421395	33918	RGD1304704 LRRGT00192	HILGFDTGDAVLNEAAQILR	95	0.059	0.00	16.85	33825	6.0	0.00
				LLHIEELRELQTK	57	1.520	0.00	0.66			
34	IPI00364132	74882	Taf15_predicted similar to TA	AAIDWFDGKEFHGNIIK	86	1.638	1.26	0.61	74643	3.3	0.00
				NGDWVCPNPSCGNMNFAR	66	1.200	0.00	0.83			
35	IPI00208098	29969	Gpx4 Phospholipid hydropero	ICVNGDDAHPLWK	61	0.117	0.00	8.53	29304	8.9	0.18
				QEPGSNQEIKEFAAGYNVR	78	0.110	0.00	9.09			
				TDVNYTQLVDLHAR	80	0.110	0.00	9.09			
36	IPI00213546	70904	Hspa1l_mapped;Hspa1l Heat	LVSHFVEEFK	24	0.156	0.06	6.40	70549	4.1	0.00
				NQVAMNPQNTVFDAK	45	0.320	0.00	3.13			
37	IPI00208659	144814	Cfh Complement inhibitory fac	CIKTDCDNLPTFEIAKPTEK	33	0.378	0.00	2.64	140344	5.4	0.00
				CTITGWIPAPR	49	0.122	0.00	8.20			
38	IPI00231783	36874	Ldhb L-lactate dehydrogenase	MVVDSAYEVIK	35	1.000	0.00	1.00	36612	4.9	0.00
				MVVDSAYEVIKLK	49	0.094	0.00	10.67		5.4	
39	IPI00464822	36089	Ldhc Lactate dehydrogenase	SCDILWNIQK	45	0.330	0.00	3.03	35713	3.6	0.33
				VNMNTEEEALFKK	47	0.410	0.00	2.44		3.5	
40	IPI00337168	58576	Cct4 T-complex protein 1 sub	VIDPATATSVDLR	47	0.183	0.00	5.47	58099	3.1	0.00
				GIHPTIISESFQK	49	0.400	0.00	2.50		3.9	
				VVSQYSSLLSPMSVNAVMK	32	0.804	0.63	1.24		5.7	
41	IPI00325713	61130	Cyp11a1 Cytochrome P450 1	DHAAAWDVIFSK	35	0.128	0.06	7.81	60941	8.4	0.00
				NFVPLLEGVAQDFIK	62	0.122	0.00	8.20		8.5	
42	IPI00210090	88492	Hnrpu SP120	GYFEYIEENK	41	0.110	0.00	9.09	87748	6.8	0.16
				SSGPTSLFAVTVAPPGAR	56	0.120	0.00	8.33		4.7	
43	IPI00554081	55549	RGD1305486 Protein FAM9	GNISIAHLLAAR	70	0.320	0.00	3.13	55070	2.7	0.00
				LCAWLVSELR	55	0.385	0.00	2.60		3.6	
44	IPI00231134	35853	Gnb2l1 Guanine nucleotide-bi	LWNTLGVCK	34	0.404	0.00	2.48	35419	3.6	0.00
				YTVQDESHSEWVSCVR	72	0.173	0.00	5.79		3.5	
45	IPI00194567	90667	Trim28 similar to Transcriptio	ADVQSIIGLQR	66	0.410	0.00	2.44	88956	2.8	0.15
				IVAERPGTNSTGPGPMAPPRAPGPL	29	0.441	0.00	2.27		3.0	
				LTEDKADVQSIIGLQR	41	0.260	0.00	3.84		3.1	
46	IPI00200121	117152	Man2c1 Alpha-mannosidase	FVSPIYFTDCNLR	62	0.340	0.00	2.94	115971	3.0	0.00
				LTFSPFQVR	28	0.394	0.00	2.53		3.8	
47	IPI00763620	45554	RGD1564209_predicted simil	AAQLGFGGIYVR	34	0.285	0.00	3.51	44784	4.9	0.00
				SQYLQFQLADMATK	47	0.183	0.00	5.46		5.4	

48	IPI00734566	135981	Mtmr3 Myotubularin related pr	SHLDDDGMPVYTDTIQQR	51	0.172	0.00	5.81	133500	4.0	0.00
				SRLESQYLTSSLR	35	0.200	0.00	5.00		2.4	
49	IPI00365961	43287	Dazap1 DAZ associated prote	IFVGGIPHNCGETELREYFK	32	0.930	0.00	1.08	43086	1.1	0.00
				LFVGGLDWSTTQETLR	37	0.904	0.00	1.11		1.1	