Protein Report
nawa-method-mouse_2021-01-05 11:33:47

Project Info

Name:	Nawa	**Date:**	May 16, 2019

Sample Info & Protocols

Name:	kotani
Date:	Jan 5, 2021

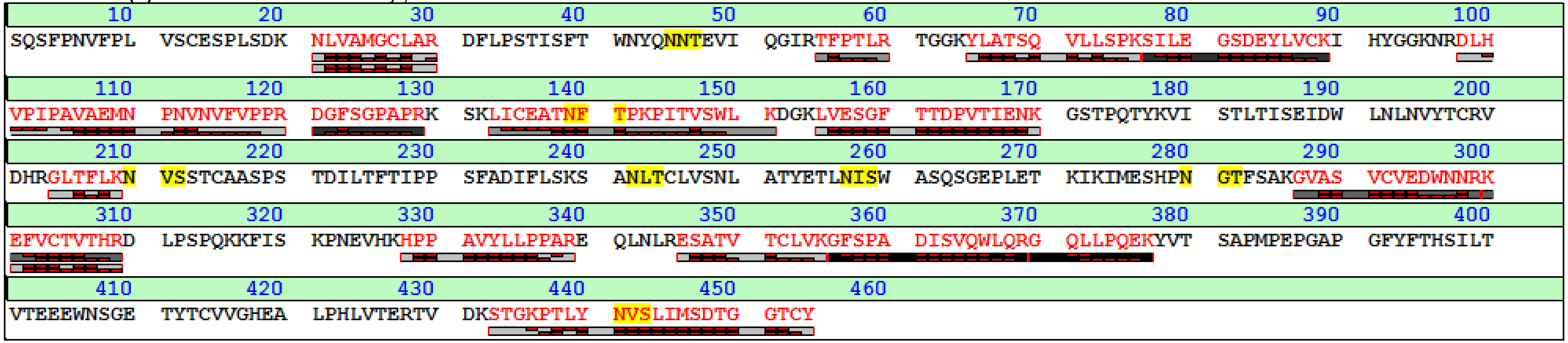
Search Result Info

Search Result:	nawa-method-mouse_2021-01-05 11:33:47		
Location:	/Nawa/kotani/0302-kotani-D_Tray01-E3_01_6616.mgf		
Search Method:	nawa-method-mouse	**Version:**	1.0
Search Engine(s):	Mascot, 2.4.1	**Ident. Compound(s):**	74/1489 (FDR:0.99%)
Database(s):	SwissProt, SwissProt_2020_06.fasta		
Note:			

Results

Protein 1: Immunoglobulin heavy constant mu OS=Mus musculus OX=10090 GN=Ighm PE=1 SV=2

Accession:	IGHM_MOUSE	**Score:**	1217.7
Database:	SwissProt	**Seq. Coverage [%]:**	44.7
MW [kDa] / pI:	49.9 / 6.6	**No. of Peptides:**	18
Modification(s):	Carbamidomethyl, Oxidation		



10	20	30	40	50	60	70	80	90	100
SQSFPNVFPL	VSCESPLSDK	NLVAMGCLAR	DFLPSTISFT	WNYQNNTEVI	QGIRTFPTLR	TGGKYLATSQ	VLLSPKSILE	GSDEYLVCKI	HYGGKNRDLH
110	**120**	**130**	**140**	**150**	**160**	**170**	**180**	**190**	**200**
VPIPAVAEMN	PNVNVFVPPR	DGFSGPAPRK	SKLICEATNF	TPKPITVSWL	KDGKLVESGF	TTDPVTIENK	GSTPQTYKVI	STLTISEIDW	LNLNVYTCRV
210	**220**	**230**	**240**	**250**	**260**	**270**	**280**	**290**	**300**
DHRGLTFLKN	VSSTCAASPS	TDILTFTIPP	SFADIFLSKS	ANLTCLVSNL	ATYETLNISW	ASQSGEPLET	KIKIMESHPN	GTFSAKGVAS	VCVEDWNNRK
310	**320**	**330**	**340**	**350**	**360**	**370**	**380**	**390**	**400**
EFVCTVTHRD	LPSPQKKFIS	KPNEVHKHPP	AVYLLPPARE	QLNLRESATV	TCLVKGFSPA	DISVQWLQRG	QLLPQEKYVT	SAPMPEPGAP	GFYFTHSILT
410	**420**	**430**	**440**	**450**	**460**				
VTEEEWNSGE	TYTCVVGHEA	LPHLVTERTV	DKSTGKPTLY	NVSLIMSDTG	GTCY				

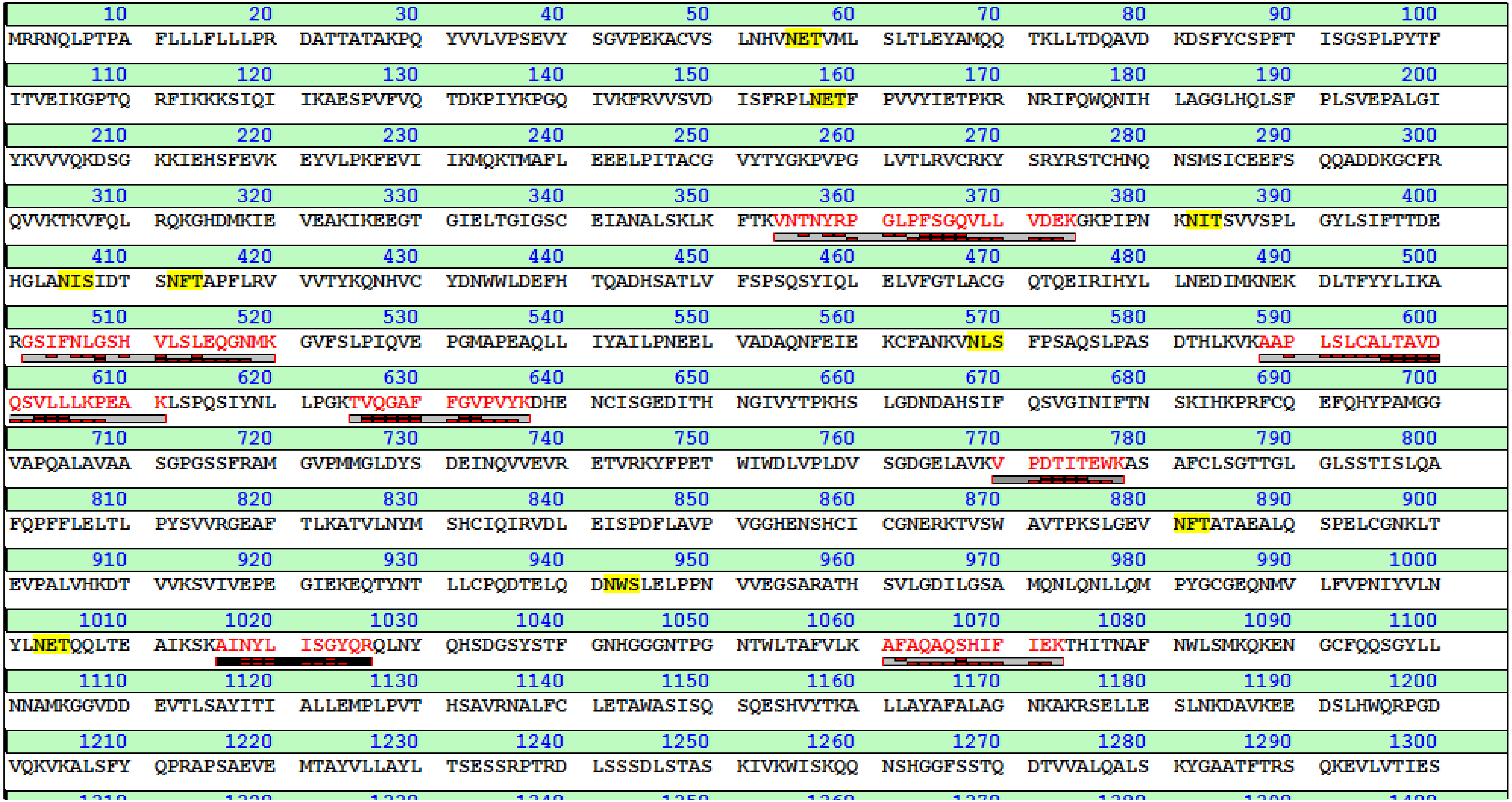
MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
690	552.7835	2	-5.00	-0.0028	38.03	45.2	2	0.0	0	K.NLVAMGCLAR.D	Carbamidomethyl: 7	21-30
359	560.7804	2	-5.92	-0.0033	27.96	38.6	1	0.0	0	K.NLVAMGCLAR.D	Carbamidomethyl: 7; Oxidation: 5	21-30
483	367.7126	2	-2.21	-0.0008	31.77	28.8	1	0.0	0	R.TFPTLR.T		55-60
729	660.3771	2	-7.58	-0.0050	39.24	67.9	2	0.0	0	K.YLATSQVLLSPK.S		65-76
801	756.8631	2	-4.04	-0.0031	41.44	81.4	2	0.0	0	K.SILEGSDEYLVCK.I	Carbamidomethyl: 12	77-89
1304	842.4405	3	-10.44	-0.0088	58.28	107.5	1	0.0	0	R.DLHVPIPAVAEMNPNVNVFVPPR.D		98-120

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
179	452.2163	2	-7.28	-0.0033	22.08	50.7	2	0.0	0	R.DGFSGPAPR.K		121-129
1142	740.0627	3	-9.23	-0.0068	52.79	98.8	2	0.0	0	K.LICEATNFTPKPITVSWLK.D	Carbamidomethyl: 3	133-151
761	875.4442	2	-5.37	-0.0047	40.24	127.3	2	0.0	0	K.LVESGFTTDPVTIENK.G		155-170
675	339.7111	2	-5.25	-0.0018	37.58	21.1	2	0.0	0	R.GLTFLK.N		204-209
643	753.3401	2	-4.80	-0.0036	36.66	82.8	2	0.0	0	K.GVASVCVEDWNNR.K	Carbamidomethyl: 6	287-299
119	426.2193	3	-2.60	-0.0011	19.42	25.1	2	0.0	1	R.KEFVCTVTHR.D	Carbamidomethyl: 5	300-309
202	574.7762	2	-5.73	-0.0033	22.94	58.6	2	0.0	0	K.EFVCTVTHR.D	Carbamidomethyl: 4	301-309
663	665.8803	2	-7.28	-0.0048	37.20	69.4	2	0.0	0	K.HPPAVYLLPPAR.E		328-339
389	554.2881	2	-2.27	-0.0013	28.86	54.0	1	0.0	0	R.ESATVTCLVK.G	Carbamidomethyl: 7	346-355
1250	802.4093	2	-7.10	-0.0057	56.52	85.3	2	0.0	0	K.GFSPADISVQWLQR.G		356-369
248	456.7596	2	-3.27	-0.0015	24.64	41.8	2	0.0	0	R.GQLLPQEK.Y		370-377
1178	1183.0427	2	-11.37	-0.0135	53.97	133.5	2	0.0	0	K.STGKPTLYNVSLIMSDTGGTCY.-	Carbamidomethyl: 21	433-454

Protein 2: Pregnancy zone protein OS=Mus musculus OX=10090 GN=Pzp PE=1 SV=3

Accession:	PZP_MOUSE	**Score:**	550.8
Database:	SwissProt	**Seq. Coverage [%]:**	9.8
MW [kDa] / pI:	165.7 / 6.2	**No. of Peptides:**	10
Modification(s):	Carbamidomethyl		



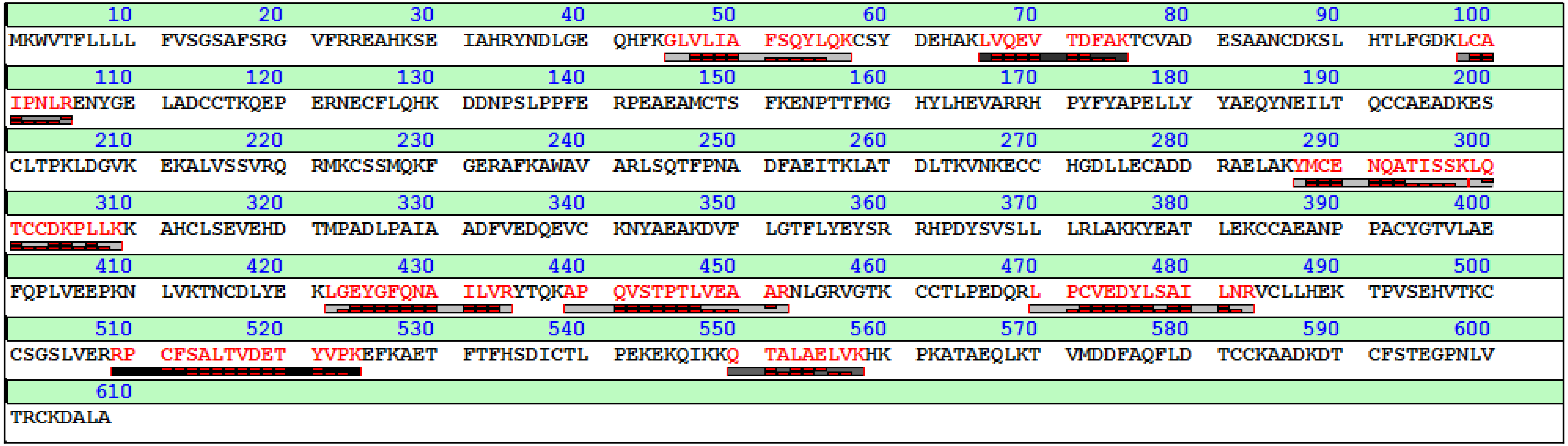
10	20	30	40	50	60	70	80	90	100
MRRNQLPTPA	FLLLFLLLPR	DATTATAKPQ	YVVLVPSEVY	SGVPEKACVS	LNHVNETVML	SLTLEYAMQQ	TKLLTDQAVD	KDSFYCSPFT	ISGSPLPYTF
110	120	130	140	150	160	170	180	190	200
ITVEIKGPTQ	RFIKKKSIQI	IKAESPVFVQ	TDKPIYKPGQ	IVKFRVVSVD	ISFRPLNETF	PVVYIETPKR	NRIFQWQNIH	LAGGLHQLSF	PLSVEPALGI
210	220	230	240	250	260	270	280	290	300
YKVVVQKDSG	KKIEHSFEVK	EYVLPKFEVI	IKMQKTMAFL	EEELPITACG	VYTYGKPVPG	LVTLRVCRKY	SRYRSTCHNQ	NSMSICEEFS	QQADDKGCFR
310	320	330	340	350	360	370	380	390	400
QVVKTKVFQL	RQKGHDMKIE	VEAKIKEEGT	GIELTGIGSC	EIANALSKLK	FTKVNTNYRP	GLPFSGQVLL	VDEKGKPIPN	KNITSVVSPL	GYLSIFTTDE
410	420	430	440	450	460	470	480	490	500
HGLANISIDT	SNFTAPFLRV	VVTYKQNHVC	YDNWWLDEFH	TQADHSATLV	FSPSQSYIQL	ELVFGTLACG	QTQEIRIHYL	LNEDIMKNEK	DLTFYYLIKA
510	520	530	540	550	560	570	580	590	600
RGSIFNLGSH	VLSLEQGNMK	GVFSLPIQVE	PGMAPEAQLL	IYAILPNEEL	VADAQNFEIE	KCFANKVNLS	FPSAQSLPAS	DTHLKVKAAP	LSLCALTAVD
610	620	630	640	650	660	670	680	690	700
QSVLLLKPEA	KLSPQSIYNL	LPGKTVQGAF	FGVPVYKDHE	NCISGEDITH	NGIVYTPKHS	LGDNDAHSIF	QSVGINIFTN	SKIHKPRFCQ	EFQHYPAMGG
710	720	730	740	750	760	770	780	790	800
VAPQALAVAA	SGPGSSFRAM	GVPMMGLDYS	DEINQVVEVR	ETVRKYFPET	WIWDLVPLDV	SGDGELAVKV	PDTITEWKAS	AFCLSGTTGL	GLSSTISLQA
810	820	830	840	850	860	870	880	890	900
FQPFFLELTL	PYSVVRGEAF	TLKATVLNYM	SHCIQIRVDL	EISPDFLAVP	VGGHENSHCI	CGNERKTVSW	AVTPKSLGEV	NFTATAEALQ	SPELCGNKLT
910	920	930	940	950	960	970	980	990	1000
EVPALVHKDT	VVKSVIVEPE	GIEKEQTYNT	LLCPQDTELQ	DNWSLELPPN	VVEGSARATH	SVLGDILGSA	MQNLQNLLQM	PYGCGEQNMV	LFVPNIYVLN
1010	1020	1030	1040	1050	1060	1070	1080	1090	1100
YLNETQQLTE	AIKSKAINYL	ISGYQRQLNY	QHSDGSYSTF	GNHGGGNTPG	NTWLTAFVLK	AFAQAQSHIF	IEKTHITNAF	NWLSMKQKEN	GCFQQSGYLL
1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
NNAMKGGVDD	EVTLSAYITI	ALLEMPLPVT	HSAVRNALFC	LETAWASISQ	SQESHVYTKA	LLAYAFALAG	NKAKRSELLE	SLNKDAVKEE	DSLHWQRPGD
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
VQKVKALSFY	QPRAPSAEVE	MTAYVLLAYL	TSESSRPTRD	LSSSDLSTAS	KIVKWISKQQ	NSHGGFSSTQ	DTVVALQALS	KYGAATFTRS	QKEVLVTIES

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
1079	782.7462	3	-9.02	-0.0071	50.63	85.5	1	0.0	0	K.VNTNYRPGLPFSGQVLLVDEK.G		354-374
1193	677.6756	3	-10.10	-0.0068	54.43	23.3	1	0.0	0	R.GSIFNLGSHVLSLEQGNMK.G		502-520
1420	836.7986	3	-11.68	-0.0098	62.44	131.8	1	0.0	0	K.AAPLSLCALTAVDQSVLLLKPEAK.L	Carbamidomethyl: 7	588-611
1063	706.875	2	-10.28	-0.0073	50.10	64.1	1	0.0	0	K.TVQGAFFGVPVYK.D		625-637
636	544.7796	2	-9.48	-0.0052	36.42	52.2	1	0.0	0	K.VPDTITEWK.A		770-778
787	649.3414	2	-11.08	-0.0072	40.96	39.6	1	0.0	0	K.AINYLISGYQR.Q		1016-1026
565	497.2616	3	-6.40	-0.0032	34.26	22.4	1	0.0	0	K.AFAQAQSHIFIEK.T		1061-1073
711	608.8265	2	-9.44	-0.0057	38.64	56.0	2	0.0	0	R.LPDLPGNYVTK.G		1323-1333
705	545.2951	2	-10.05	-0.0055	38.40	22.5	1	0.0	0	K.YNILPVADGK.A		1348-1357
1301	894.4775	2	-11.92	-0.0107	58.16	53.4	1	0.0	0	K.APFALQVNTLPLNFDK.A		1358-1373

Protein 3: Albumin OS=Mus musculus OX=10090 GN=Alb PE=1 SV=3

Accession:	ALBU_MOUSE	**Score:**	534.2
Database:	SwissProt	**Seq. Coverage [%]:**	19.7
MW [kDa] / pI:	68.6 / 5.7	**No. of Peptides:**	10
Modification(s):	Carbamidomethyl		



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        10         20         30         40         50         60         70         80         90        100
MKWVTFLLLL FVSGSAFSRG VFRREAHKSE IAHRYNDLGE QHFKGLVLIA FSQYLQKCSY DEHAKLVQEV TDFAKTCVAD ESAANCDKSL HTLFGDKLCA
       110        120        130        140        150        160        170        180        190        200
IPNLRENYGE LADCCTKQEP ERNECFLQHK DDNPSLPPFE RPEAEAMCTS FKENPTTFMG HYLHEVARRH PYFYAPELLY YAEQYNEILT QCCAEADKES
       210        220        230        240        250        260        270        280        290        300
CLTPKLDGVK EKALVSSVRQ RMKCSSMQKF GERAFKAWAV ARLSQTFPNA DFAEITKLAT DLTKVNKECC HGDLLECADD RAELAKYMCE NQATISSKLQ
       310        320        330        340        350        360        370        380        390        400
TCCDKPLLKK AHCLSEVEHD TMPADLPAIA ADFVEDQEVC KNYAEAKDVF LGTFLYEYSR RHPDYSVSLL LRLAKKYEAT LEKCCAEANP PACYGTVLAE
       410        420        430        440        450        460        470        480        490        500
FQPLVEEPKN LVKTNCDLYE KLGEYGFQNA ILVRYTQKAP QVSTPTLVEA ARNLGRVGTK CCTLPEDQRL PCVEDYLSAI LNRVCLLHEK TPVSEHVTKC
       510        520        530        540        550        560        570        580        590        600
CSGSLVERRP CFSALTVDET YVPKEFKAET FTFHSDICTL PEKEKQIKKQ TALAELVKHK PKATAEQLKT VMDDFAQFLD TCCKAADKDT CFSTEGPNLV
       610
TRCKDALA
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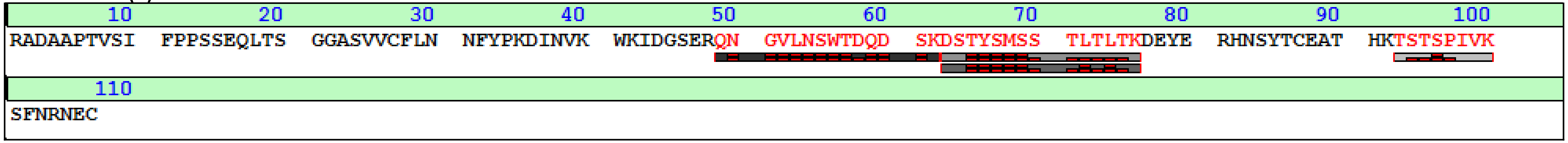
MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
1396	740.4231	2	-12.19	-0.0090	61.57	38.2	1	0.0	0	K.GLVLIAFSQYLQK.C		45-57
596	575.3072	2	-6.86	-0.0039	35.21	58.8	2	0.0	0	K.LVQEVTDFAK.T		66-75
635	478.7671	2	-8.02	-0.0038	36.41	21.8	2	0.0	0	K.LCAIPNLR.E	Carbamidomethyl: 2	98-105
191	716.3119	2	-5.41	-0.0039	22.54	69.2	2	0.0	0	K.YMCENQATISSK.L	Carbamidomethyl: 3	287-298
231	459.238	3	-5.64	-0.0026	24.11	41.2	2	0.0	0	K.LQTCCDKPLLK.K	Carbamidomethyl: 4, 5	299-309
1026	740.3949	2	-8.72	-0.0065	48.89	89.5	2	0.0	0	K.LGEYGFQNAILVR.Y		422-434
593	720.3906	2	-7.87	-0.0057	35.10	78.1	2	0.0	0	K.APQVSTPTLVEAAR.N		439-452
1480	831.9193	2	-12.41	-0.0103	64.62	81.0	1	0.0	0	R.LPCVEDYLSAILNR.V	Carbamidomethyl: 3	470-483
841	628.3111	3	-9.56	-0.0060	42.74	32.3	2	0.0	0	R.RPCFSALTVDETYVPK.E	Carbamidomethyl: 3	509-524
689	486.7852	2	-9.55	-0.0046	37.94	24.2	1	0.0	0	K.QTALAELVK.H		550-558

Protein 4: Immunoglobulin kappa constant OS=Mus musculus OX=10090 GN=Igkc PE=1 SV=2

Accession:	IGKC_MOUSE	**Score:**	305.8
Database:	SwissProt	**Seq. Coverage [%]:**	33.6
MW [kDa] / pI:	11.9 / 5.6	**No. of Peptides:**	4
Modification(s):	Oxidation		



10 20 30 40 50 60 70 80 90 100

RADAAPTVSI FPPSSEQLTS GGASVVCFLN NFYPKDINVK WKIDGSERQN GVLNSWTDQD SKDSTYSMSS TLTLTKDEYE RHNSYTCEAT HKTSTSPIVK

110

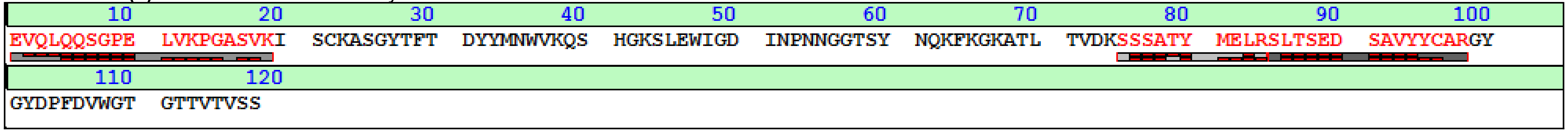
SFNRNEC

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
609	796.366	2	-6.26	-0.0050	35.59	102.7	4	0.0	0	R.QNGVLNSWTDQDSK.D		49-62
480	775.8602	2	-7.93	-0.0062	31.66	95.2	2	0.0	0	K.DSTYSMSSTLTLTK.D	Oxidation: 6	63-76
773	767.8647	2	-5.47	-0.0042	40.54	95.7	1	0.0	0	K.DSTYSMSSTLTLTK.D		63-76
94	416.7409	2	-3.52	-0.0015	18.53	12.2	1	0.0	0	K.TSTSPIVK.S		93-100

Protein 5: Ig heavy chain V region AC38 205.12 OS=Mus musculus OX=10090 PE=1 SV=1

Accession:	HVM51_MOUSE	**Score:**	249.6
Database:	SwissProt	**Seq. Coverage [%]:**	36.4
MW [kDa] / pI:	12.9 / 6.8	**No. of Peptides:**	3
Modification(s):	Carbamidomethyl		



10 20 30 40 50 60 70 80 90 100

EVQLQQSGPE LVKPGASVKI SCKASGYTFT DYYMNWVKQS HGKSLEWIGD INPNNGGTSY NQKFKGKATL TVDKSSSATY MELRSLTSED SAVYYCARGY

110 120

GYDPFDVWGT GTTVTVSS

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
516	665.3641	3	-6.98	-0.0046	32.74	106.4	2	0.0	0	-.EVQLQQSGPELVKPGASVK.I		1-19
463	572.7642	2	-8.01	-0.0046	31.06	44.6	2	0.0	0	K.SSSATYMELR.S		75-84
533	811.3549	2	-8.47	-0.0069	33.22	98.6	2	0.0	0	R.SLTSEDSAVYYCAR.G	Carbamidomethyl: 12	85-98

Protein 6: Fibronectin OS=Mus musculus OX=10090 GN=Fn1 PE=1 SV=4

Accession:	FINC_MOUSE	**Score:**	212.3
Database:	SwissProt	**Seq. Coverage [%]:**	2.3
MW [kDa] / pI:	272.4 / 5.4	**No. of Peptides:**	4
Modification(s):	Carbamidomethyl		

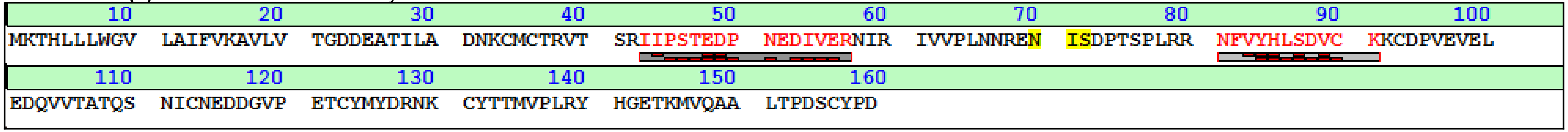
10	20	30	40	50	60	70	80	90	100
MLRGPGPGRL	LLLAVLCLGT	SVRCTEAGKS	KRQAQQIVQP	QSPVAVSQSK	PGCFDNGKHY	QINQQWERTY	LGNALVCTCY	GGSRGFNCES	KPEPEETCFD
110	120	130	140	150	160	170	180	190	200
KYTGNTYKVG	DTYERPKDSM	IWDCTCIGAG	RGRISCTIAN	RCHEGGQSYK	IGDKWRRPHE	TGGYMLECLC	LGNGKGEWTC	KPIAEKCFDH	AAGTSYVVGE
210	220	230	240	250	260	270	280	290	300
TWEKPYQGWM	MVDCTCLGEG	NGRITCTSRN	RCNDQDTRTS	YRIGDTWSKK	DNRGNLLQCV	CTGNGRGEWK	CERHALQSAS	AGSGSFTDVR	TAIYQPQTHP
310	320	330	340	350	360	370	380	390	400
QPAPYGHCVT	DSGVVYSVGM	QWLKSQGNKQ	MLCTCLGNGV	SCQETAVTQT	YGGNSNGEPC	VLPFTYNGRT	FYSCTTEGRQ	DGHLWCSTTS	NYEQDQKYSF
410	420	430	440	450	460	470	480	490	500
CTDHAVLVQT	RGGNSNGALC	HFPFLYNNRN	YTDCTSEGRR	DNMKWCGTTQ	NYDADQKFGF	CPMAAHEEIC	TTNEGVMYRI	GDQWDKQHDL	GHMMRCTCVG
510	520	530	540	550	560	570	580	590	600
NGRGEWACIP	YSQLRDQCIV	DDITYNVNDT	FHKRHEEGHM	LNCTCFGQGR	GRWKCDPIDQ	CQDSETRTFY	QIGDSWEKFV	HGVRYQCYCY	GRGIGEWHCQ
610	620	630	640	650	660	670	680	690	700
PLQTYPGTTG	PVQVIITETP	SQPNSHPIQW	NAPEPSHITK	YILRWRPKTS	TGRWKEATIP	GHLNSYTIKG	LTPGVIYEGQ	LISIQQYGHR	EVTRFDFTTS
710	720	730	740	750	760	770	780	790	800
ASTPVTSNTV	TGETAPYSPV	VATSESVTEI	TASSFVVSWV	SASDTVSGFR	VEYELSEEGD	EPQYLDLPST	ATSVNIPDLL	PGRKYIVNVY	QISEEGKQSL
810	820	830	840	850	860	870	880	890	900
ILSTSQTTAP	DAPPDPTVDQ	VDDTSIVVRW	SRPQAPITGY	RIVYSPSVEG	SSTELNLPET	ANSVTLSDLQ	PGVQYNITIY	AVEENQESTP	VFIQQETTGT
910	920	930	940	950	960	970	980	990	1000
PRSDNVPPPT	DLQFVELTDV	KVTIMWTPPD	SVVSGYRVEV	LPVSLPGEHG	QRLPVNRNTF	AEITGLSPGV	TYLFKVFAVH	QGRESNPLTA	QQTTKLDAPT
1010	1020	1030	1040	1050	1060	1070	1080	1090	1100
NLQFVNETDR	TVLVTWTPPR	ARIAGYRLTA	GLTRGGQPKQ	YNVGPLASKY	PLRNLQPGSE	YTVTLVAVKG	NQQSPKATGV	FTTLQPLRSI	PPYNTEVTET
1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
TIVITWTPAP	RIGFKLGVRP	SQGGEAPREV	TSDSGSIVVS	GLTPGVEYTY	TIQVLRDGQE	RDAPIVNRVV	TPLSPPTNLH	LEANPDTGVL	TVSWERSTTP
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
DITGYRITTT	PTNGQQGTSL	EEVVHADQSS	CTFENLNPGL	EYNVSVYTVK	DDKESAPISD	TVVPEVPQLT	DLSFVDITDS	SIGLRWTPLN	SSTIIGYRIT

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
240	611.2577	2	-10.09	-0.0062	24.39	28.6	1	0.0	0	R.TFYSCTTEGR.Q	Carbamidomethyl: 5	370-379
1401	979.5056	2	-11.76	-0.0115	61.74	83.4	1	0.0	0	R.NTFAEITGLSPGVTYLFK.V		958-975
931	652.366	2	-9.30	-0.0061	45.63	70.9	1	0.0	0	K.ATGVFTTLQPLR.S		1077-1088
1433	953.5292	2	-14.96	-0.0143	62.88	29.5	1	0.0	0	R.VTWAPPPSIELTNLLVR.Y		1375-1391

Protein 7: Immunoglobulin J chain OS=Mus musculus OX=10090 GN=Jchain PE=1 SV=4

Accession:	IGJ_MOUSE	**Score:**	152.9
Database:	SwissProt	**Seq. Coverage [%]:**	16.4
MW [kDa] / pI:	18.0 / 4.7	**No. of Peptides:**	2
Modification(s):	Carbamidomethyl		



10	20	30	40	50	60	70	80	90	100
MKTHLLLWGV	LAIFVKAVLV	TGDDEATILA	DNKCMCTRVT	SRIIPSTEDP	NEDIVERNIR	IVVPLNNREN	ISDPTSPLRR	NFVYHLSDVC	KKCDPVEVEL

110	120	130	140	150	160
EDQVVTATQS	NICNEDDGVP	ETCYMYDRNK	CYTTMVPLRY	HGETKMVQAA	LTPDSCYPD

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
540	863.9219	2	-7.44	-0.0064	33.48	89.4	2	0.0	0	R.IIPSTEDPNEDIVER.N		43-57
600	461.2207	3	-6.76	-0.0031	35.34	63.5	2	0.0	0	R.NFVYHLSDVCK.K	Carbamidomethyl: 10	81-91

Protein 8: Hemoglobin subunit beta-1 OS=Mus musculus OX=10090 GN=Hbb-b1 PE=1 SV=2

Accession:	HBB1_MOUSE	**Score:**	150.6
Database:	SwissProt	**Seq. Coverage [%]:**	25.9
MW [kDa] / pI:	15.8 / 7.1	**No. of Peptides:**	3

10	20	30	40	50	60	70	80	90	100
MVHLTDAEKA	AVSCLWGKVN	SDEVGGEALG	RLLVVYPWTQ	RYFDSFGDLS	SASAIMGNAK	VKAHGKKVIT	AFNDGLNHLD	SLKGTFASLS	ELHCDKLHVD
110	120	130	140	150					
PENFRLLGNM	IVIVLGHHLG	KDFTPAAQAA	FQKVVAGVAT	ALAHKYH					

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
1100	637.8595	2	-10.85	-0.0069	51.31	51.7	2	0.0	0	R.LLVVYPWTQR.Y		32-41
959	586.3069	3	-9.48	-0.0056	46.65	73.1	1	0.0	0	K.VITAFNDGLNHLDSLK.G		68-83
582	647.8194	2	-8.57	-0.0056	34.73	25.8	1	0.0	0	K.DFTPAAQAAFQK.V		122-133

Protein 9: C4b-binding protein OS=Mus musculus OX=10090 GN=C4bpa PE=1 SV=3

Accession:	C4BPA_MOUSE	**Score:**	127.2
Database:	SwissProt	**Seq. Coverage [%]:**	6.0
MW [kDa] / pI:	51.5 / 6.8	**No. of Peptides:**	2
Modification(s):	Carbamidomethyl		

10	20	30	40	50	60	70	80	90	100
MCAKQQQTLL	PTRAAHGRLH	RNRDAVAWPF	STLCRVSGPT	LFQMTFTAAL	WVAVFGKCGP	PPAIPNALPA	SDVNRTDFES	HTTLKYECLP	GYGRGISRMM
110	120	130	140	150	160	170	180	190	200
VYCKPSGEWE	ISVSCAKKHC	RNPGYLDNGY	VNGETITFGS	QIEFSCQEGF	ILVGSSTSSC	EVRGKGVAWS	NPFPECVIVK	CGPPPDISNG	KHSGTEDFYP
210	220	230	240	250	260	270	280	290	300
YNHGISYTCD	PGFRLVGSPF	IGCTVVNKTV	PVWSSSPPTC	EKIICSQPNI	LHGVIVSGYK	ATYTHRDSVR	LACLNGTVLR	GRHVIECQGN	GNWSSLPTCE
310	320	330	340	350	360	370	380	390	400
FDCDLPPAIV	NGYYTSMVYS	KITLVTYECD	KGYRLVGKAI	ISCSFSKWKG	TAPQCKALCQ	KPEVGNGTLS	DEKDQYVESE	NVTIQCDSGF	AMLGSQSISC
410	420	430	440	450	460	470			
SESGTWYPEV	PRCEQEASED	LKPALTGNKT	MQYVPNSHDV	KMALEIYKLT	LEVELLQLQI	QKEKHTEAH			

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
899	666.6943	3	-7.87	-0.0052	44.59	63.7	1	0.0	0	K.IICSQPNILHGVIVSGYK.A	Carbamidomethyl: 3	243-260
581	621.3025	2	-8.44	-0.0052	34.72	63.5	2	0.0	0	K.ITLVTYECDK.G	Carbamidomethyl: 8	322-331

Protein 10: Keratin, type II cytoskeletal 1 OS=Mus musculus OX=10090 GN=Krt1 PE=1 SV=4

Accession: K2C1_MOUSE
Database: SwissProt
MW [kDa] / pI: 65.6 / 8.4
Score: 119.0
Seq. Coverage [%]: 3.6
No. of Peptides: 2

10	20	30	40	50	60	70	80	90	100
MSLQCSSRSL	CRGGGGSRNF	SSGSAGLVSF	QRRSTSSSMR	RSGGGGGGRF	SGGGFCGSSG	SGFGSKSLMN	LGGGRSISKS	VAGGGGSFCG	GFGGGSYGGG
110	120	130	140	150	160	170	180	190	200
GFGGGSYGGG	GFGGGSFGGG	GFGGSGFGGG	LGGGGGFGSG	GGFGGGRFGS	MGPVCPPGGI	QEVTINQSLL	QPLNVEVDPQ	IQKVKSQERE	QIKSLNDKFA
210	220	230	240	250	260	270	280	290	300
SFIDKVRFLE	QQNQVLQTKW	ELLQQVDTTT	RTQNLDPFFE	NYISILRRKV	DSLKSDQSRM	DSELKNMQDL	VEEYRTKYED	EINKRTNAEN	EFVTIKKDVD
310	320	330	340	350	360	370	380	390	400
SAYMTKVELQ	AKADALQQDI	DFFSALYQME	MSQMQTQISE	TNVVLSMDNN	RSLDLDGIIS	EVKAQYDSIC	QRSKAEAETF	YQSKYEELQI	TAGKHGDSVR
410	420	430	440	450	460	470	480	490	500
NTKMEISELN	RMIQRLRSEI	DGCKKQISQI	QQNINDAEQR	GEKALKDAQN	KLNEIEDALS	QCKEDLARLL	RDFQELMNTK	LALDMEIATY	KKLLEGEEIR
510	520	530	540	550	560	570	580	590	600
MSGECTPNVS	VSVSTSHTSM	SGSSSRGGGS	GGGRYGGGGS	YGGGSGGGSY	GGSSGGGGSG	GSYGGGSGGG	SYGGGSGGGS	SGSHRGGSGG	GGGSSGGSYG
610	620	630	640						
GSSGGGRGGS	SSGGGGVKSS	GSSTVKFVST	SYSRGTK						

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
492	738.3906	2	-7.68	-0.0057	32.05	62.7	2	0.0	0	R.FLEQQNQVLQTK.W		208-219

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
580	633.317	2	-8.28	-0.0052	34.70	56.3	1	0.0	0	R.TNAENEFVTIK.K		286-296

Protein 11: Hemoglobin subunit alpha OS=Mus musculus OX=10090 GN=Hba PE=1 SV=2

Accession:	HBA_MOUSE	**Score:**	113.5
Database:	SwissProt	**Seq. Coverage [%]:**	19.0
MW [kDa] / pI:	15.1 / 8.0	**No. of Peptides:**	2

```
        10         20         30         40         50         60         70         80         90        100
MVLSGEDKSN IKAAWGKIGG HGAEYGAEAL ERMFASFPTT KTYFPHFDVS HGSAQVKGHG KKVADALASA AGHLDDLPGA LSALSDLHAH KLRVDPVNFK
       110        120        130        140        150
LLSHCLLVTL ASHHPADFTP AVHASLDKFL ASVSTVLTSK YR
```

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
348	510.5784	3	-8.91	-0.0045	27.61	41.5	2	0.0	0	K.IGGHGAEYGAEALER.M		18-32
902	627.3573	2	791.72	0.4963	44.69	72.0	2	0.0	0	K.FLASVSTVLTSK.Y		129-140

Protein 12: Ig kappa chain V-II region 26-10 OS=Mus musculus OX=10090 PE=1 SV=1

Accession:	KV2A7_MOUSE	**Score:**	96.3
Database:	SwissProt	**Seq. Coverage [%]:**	11.5
MW [kDa] / pI:	12.3 / 9.0	**No. of Peptides:**	1

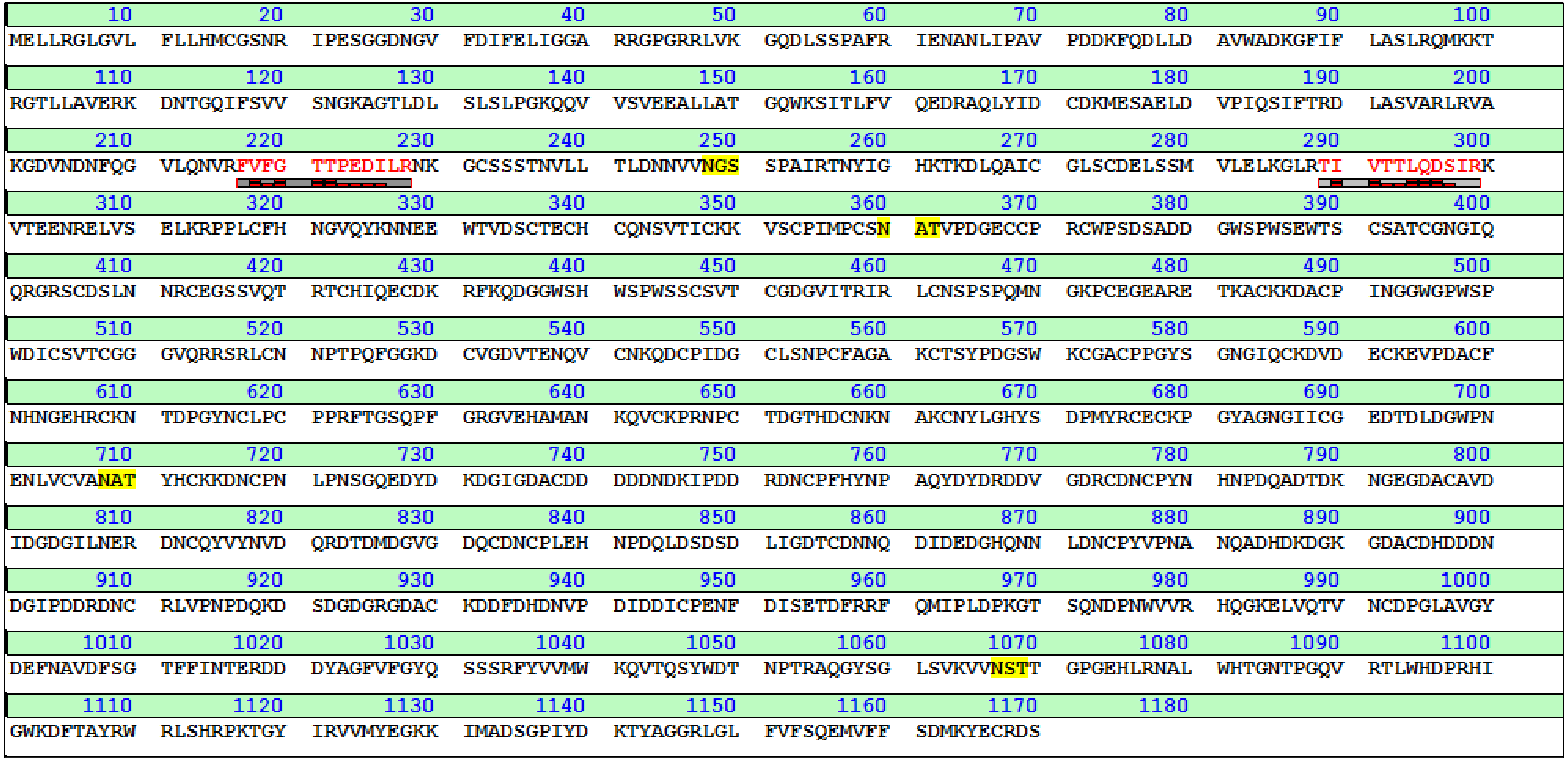
```
        10         20         30         40         50         60         70         80         90        100
DVVMTQTPLS LPVSLGDQAS ISCRSSQSLV HSNGNTYLNW YLQKAGQSPK LLIYKVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDLGI YFCSQTTHVP
       110        120
PTFGGGTKLE IKR
```

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
564	652.3075	2	-6.71	-0.0044	34.24	96.3	1	0.0	0	R.FSGSGSGTDFTLK.I		67-79

Protein 13: Thrombospondin-1 OS=Mus musculus OX=10090 GN=Thbs1 PE=1 SV=1

Accession:	TSP1_MOUSE	**Score:**	92.0
Database:	SwissProt	**Seq. Coverage [%]:**	2.0
MW [kDa] / pI:	129.6 / 4.7	**No. of Peptides:**	2



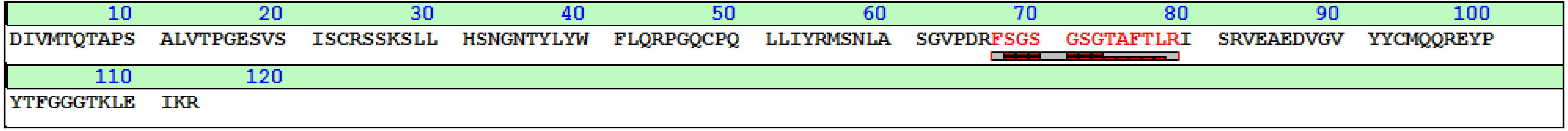
10	20	30	40	50	60	70	80	90	100
MELLRGLGVL	FLLHMCGSNR	IPESGGDNGV	FDIFELIGGA	RRGPGRRLVK	GQDLSSPAFR	IENANLIPAV	PDDKFQDLLD	AVWADKGFIF	LASLRQMKKT
110	120	130	140	150	160	170	180	190	200
RGTLLAVERK	DNTGQIFSVV	SNGKAGTLDL	SLSLPGKQQV	VSVEEALLAT	GQWKSITLFV	QEDRAQLYID	CDKMESAELD	VPIQSIFTRD	LASVARLRVA
210	220	230	240	250	260	270	280	290	300
KGDVNDNFQG	VLQNVRFVFG	TTPEDILRNK	GCSSSTNVLL	TLDNNVVNGS	SPAIRTNYIG	HKTKDLQAIC	GLSCDELSSM	VLELKGLRTI	VTTLQDSIRK
310	320	330	340	350	360	370	380	390	400
VTEENRELVS	ELKRPPLCFH	NGVQYKNNEE	WTVDSCTECH	CQNSVTICKK	VSCPIMPCSN	ATVPDGECCP	RCWPSDSADD	GWSPWSEWTS	CSATCGNGIQ
410	420	430	440	450	460	470	480	490	500
QRGRSCDSLN	NRCEGSSVQT	RTCHIQECDK	RFKQDGGWSH	WSPWSSCSVT	CGDGVITRIR	LCNSPSPQMN	GKPCEGEARE	TKACKKDACP	INGGWGPWSP
510	520	530	540	550	560	570	580	590	600
WDICSVTCGG	GVQRRSRLCN	NPTPQFGGKD	CVGDVTENQV	CNKQDCPIDG	CLSNPCFAGA	KCTSYPDGSW	KCGACPPGYS	GNGIQCKDVD	ECKEVPDACF
610	620	630	640	650	660	670	680	690	700
NHNGEHRCKN	TDPGYNCLPC	PPRFTGSQPF	GRGVEHAMAN	KQVCKPRNPC	TDGTHDCNKN	AKCNYLGHYS	DPMYRCECKP	GYAGNGIICG	EDTDLDGWPN
710	720	730	740	750	760	770	780	790	800
ENLVCVANAT	YHCKKDNCPN	LPNSGQEDYD	KDGIGDACDD	DDDNDKIPDD	RDNCPFHYNP	AQYDYDRDDV	GDRCDNCPYN	HNPDQADTDK	NGEGDACAVD
810	820	830	840	850	860	870	880	890	900
IDGDGILNER	DNCQYVYNVD	QRDTDMDGVG	DQCDNCPLEH	NPDQLDSDSD	LIGDTCDNNQ	DIDEDGHQNN	LDNCPYVPNA	NQADHDKDGK	GDACDHDDDN
910	920	930	940	950	960	970	980	990	1000
DGIPDDRDNC	RLVPNPDQKD	SDGDGRGDAC	KDDFDHDNVP	DIDDICPENF	DISETDFRRF	QMIPLDPKGT	SQNDPNWVVR	HQGKELVQTV	NCDPGLAVGY
1010	1020	1030	1040	1050	1060	1070	1080	1090	1100
DEFNAVDFSG	TFFINTERDD	DYAGFVFGYQ	SSSRFYVVMW	KQVTQSYWDT	NPTRAQGYSG	LSVKVVNSTT	GPGEHLRNAL	WHTGNTPGQV	RTLWHDPRHI
1110	1120	1130	1140	1150	1160	1170	1180		
GWKDFTAYRW	RLSHRPKTGY	IRVVMYEGKK	IMADSGPIYD	KTYAGGRLGL	FVFSQEMVFF	SDMKYECRDS			

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
1181	697.862	2	-10.55	-0.0074	54.02	37.4	1	0.0	0	R.FVFGTTPEDILR.N		217-228
912	623.8471	2	-10.60	-0.0066	45.04	54.6	2	0.0	0	R.TIVTTLQDSIR.K		289-299

Protein 14: Ig kappa chain V-II region 7S34.1 OS=Mus musculus OX=10090 PE=1 SV=1

Accession:	KV2A6_MOUSE	**Score:**	86.8
Database:	SwissProt	**Seq. Coverage [%]:**	11.5
MW [kDa] / pI:	12.5 / 8.9	**No. of Peptides:**	1



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        10         20         30         40         50         60         70         80         90        100
DIVMTQTAPS ALVTPGESVS ISCRSSKSLL HSNGNTYLYW FLQRPGQCPQ LLIYRMSNLA SGVPDRFSGS GSGTAFTLRI SRVEAEDVGV YYCMQQREYP

       110        120
YTFGGGTKLE IKR
```

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
613	644.3149	2	-7.97	-0.0051	35.71	86.8	1	0.0	0	R.FSGSGSGTAFTLR.I		67-79

Protein 15: CD5 antigen-like OS=Mus musculus OX=10090 GN=Cd5l PE=1 SV=3

Accession:	CD5L_MOUSE	**Score:**	84.8
Database:	SwissProt	**Seq. Coverage [%]:**	8.8
MW [kDa] / pI:	38.8 / 5.0	**No. of Peptides:**	3
Modification(s):	Carbamidomethyl		

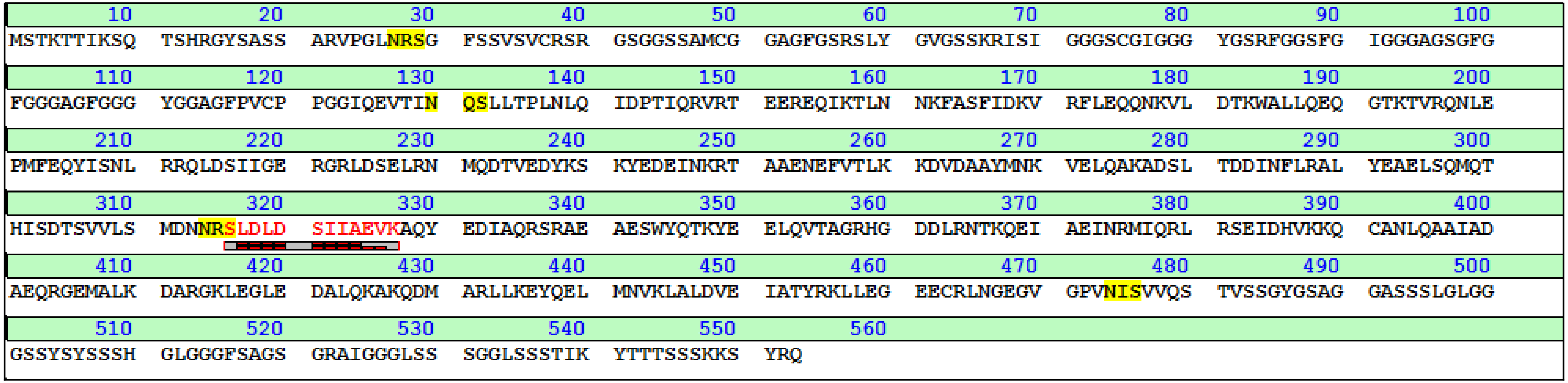
10	20	30	40	50	60	70	80	90	100
MAPLFNLMLA	ILSIFVGSCF	SESPTKVQLV	GGAHRCEGRV	EVEHNGQWGT	VCDDGWDRRD	VAVVCRELNC	GAVIQTPRGA	SYQPPASEQR	VLIQGVDCNG
110	**120**	**130**	**140**	**150**	**160**	**170**	**180**	**190**	**200**
TEDTLAQCEL	NYDVFDCSHE	EDAGAQCENP	DSDLLFIPED	VRLVDGPGHC	QGRVEVLHQS	QWSTVCKAGW	NLQVSKVVCR	QLGCGRALLT	YGSCNKNTQG
210	**220**	**230**	**240**	**250**	**260**	**270**	**280**	**290**	**300**
KGPIWMGKMS	CSGQEANLRS	CLLSRLENNC	THGEDTWMEC	EDPFELKLVG	GDTPCSGRLE	VLHKGSWGSV	CDDNWGEKED	QVVCKQLGCG	KSLHPSPKTR
310	**320**	**330**	**340**	**350**	**360**				
KIYGPGAGRI	WLDDVNCSGK	EQSLEFCRHR	LWGYHDCTHK	EDVEVICTDF	DV				

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
594	501.7679	2	-8.15	-0.0041	35.12	10.6	1	0.0	0	K.AGWNLQVSK.V		168-176
115	626.7707	2	-5.39	-0.0034	19.29	10.8	1	0.0	0	K.MSCSGQEANLR.S	Carbamidomethyl: 3	209-219
722	653.8034	2	-7.72	-0.0050	38.98	63.4	1	0.0	0	R.IWLDDVNCSGK.E	Carbamidomethyl: 8	310-320

Protein 16: Keratin, type II cytoskeletal 6A OS=Mus musculus OX=10090 GN=Krt6a PE=1 SV=3

Accession:	K2C6A_MOUSE	**Score:**	67.5
Database:	SwissProt	**Seq. Coverage [%]:**	2.2
MW [kDa] / pI:	59.3 / 8.0	**No. of Peptides:**	1



10	20	30	40	50	60	70	80	90	100
MSTKTTIKSQ	TSHRGYSASS	ARVPGLNRSG	FSSVSVCRSR	GSGGSSAMCG	GAGFGSRSLY	GVGSSKRISI	GGGSCGIGGG	YGSRFGGSFG	IGGGAGSGFG
110	120	130	140	150	160	170	180	190	200
FGGGAGFGGG	YGGAGFPVCP	PGGIQEVTIN	QSLLTPLNLQ	IDPTIQRVRT	EEREQIKTLN	NKFASFIDKV	RFLEQQNKVL	DTKWALLQEQ	GTKTVRQNLE
210	220	230	240	250	260	270	280	290	300
PMFEQYISNL	RRQLDSIIGE	RGRLDSELRN	MQDTVEDYKS	KYEDEINKRT	AAENEFVTLK	KDVDAAYMNK	VELQAKADSL	TDDINFLRAL	YEAELSQMQT
310	320	330	340	350	360	370	380	390	400
HISDTSVVLS	MDNNRSLDLD	SIIAEVKAQY	EDIAQRSRAE	AESWYQTKYE	ELQVTAGRHG	DDLRNTKQEI	AEINRMIQRL	RSEIDHVKKQ	CANLQAAIAD
410	420	430	440	450	460	470	480	490	500
AEQRGEMALK	DARGKLEGLE	DALQKAKQDM	ARLLKEYQEL	MNVKLALDVE	IATYRKLLEG	EECRLNGEGV	GPVNISVVQS	TVSSGYGSAG	GASSSLGLGG
510	520	530	540	550	560				
GSSYSYSSSH	GLGGGFSAGS	GRAIGGGLSS	SGGLSSSTIK	YTTTSSSKKS	YRQ				

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
1318	651.8546	2	-10.13	-0.0066	58.81	67.5	2	0.0	0	R.SLDLDSIIAEVK.A		316-327

Protein 17: Keratin, type II cytoskeletal 79 OS=Mus musculus OX=10090 GN=Krt79 PE=1 SV=2

Accession:	K2C79_MOUSE	**Score:**	58.0
Database:	SwissProt	**Seq. Coverage [%]:**	2.3
MW [kDa] / pI:	57.5 / 7.6	**No. of Peptides:**	1

10	20	30	40	50	60	70	80	90	100
MRSSLSRQTF	STKGGFSSNS	ASGGGGSRMR	TSYSSVTMSR	GSGGGGGVRS	GSSSGGFGSR	SLYNLGGKNI	SVSMACGASS	GRALGGFGSG	AYVGLGASRQ
110	120	130	140	150	160	170	180	190	200
TFGPVCPPGG	IQEVTVNQSL	LTPLNVEIDP	EIQRVRTQER	EQIKTLNNKF	ASFIDKVRFL	EQQNKVLETK	WALLQEQSQN	TGVARSLEPF	FENYLSTLRR
210	220	230	240	250	260	270	280	290	300
QLDTKQSERG	RLDMELRNVQ	DNLEDFKNKY	EDEINKRTAL	ENEFVLLKKD	VDAAYMGRMD	LHGKVDSLTQ	EIDFLQQLFE	MELSQVQTNV	SDTNVILSMD
310	320	330	340	350	360	370	380	390	400
NNRNLDLDSI	IAEVKAQYEL	IAQKSRAEAE	SWYQTKYEEL	QVTAGKHGDS	LRDTKNEIAE	LTRTTQRLQG	EVDAAKKQCQ	QLQTAIAEAE	QNGEMALKDA
410	420	430	440	450	460	470	480	490	500
KKKLGDLDTA	LHQAKEDLAR	MLREYQDLVS	VKLALDMEIA	TYRKLLESEE	SRMSGDCPSA	ISISVTGNST	SVCAGGTAGF	GNGLSLGGAG	GASKGGFGSS
510	520	530	540						
VSYGAAKGGQ	VSGGTSILRK	TTTVKTSSRR	Y						

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
1319	665.3596	2	-10.60	-0.0070	58.83	58.0	2	0.0	0	R.NLDLDSIIAEVK.A		304-315

Protein 18: Ig heavy chain V-III region J606 OS=Mus musculus OX=10090 PE=1 SV=1

Accession:	HVM32_MOUSE	**Score:**	47.9
Database:	SwissProt	**Seq. Coverage [%]:**	19.1
MW [kDa] / pI:	12.8 / 6.9	**No. of Peptides:**	2

10	20	30	40	50	60	70	80	90	100
EVKLEESGGG	LVQPGGSMKL	SCVASGFTFS	NYWMNWVRQS	PEKGLEWVAE	IRLKSNNYAT	HYAESVKGRF	TISRDDSKSS	VYLQMNNLRA	EDTGIYYCTT
110	120								
GFAYWGQGTL	VTVSA								

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
1027	536.7877	2	-9.73	-0.0052	48.90	37.2	1	0.0	0	K.GLEWVAEIR.L		44-52
281	495.5563	3	655.01	0.3244	25.64	10.6	2	0.0	0	K.SNNYATHYAESVK.G		55-67

Protein 19: Keratin, type I cytoskeletal 10 OS=Mus musculus OX=10090 GN=Krt10 PE=1 SV=3

Accession:	K1C10_MOUSE	**Score:**	41.0
Database:	SwissProt	**Seq. Coverage [%]:**	2.1
MW [kDa] / pI:	57.7 / 5.0	**No. of Peptides:**	1

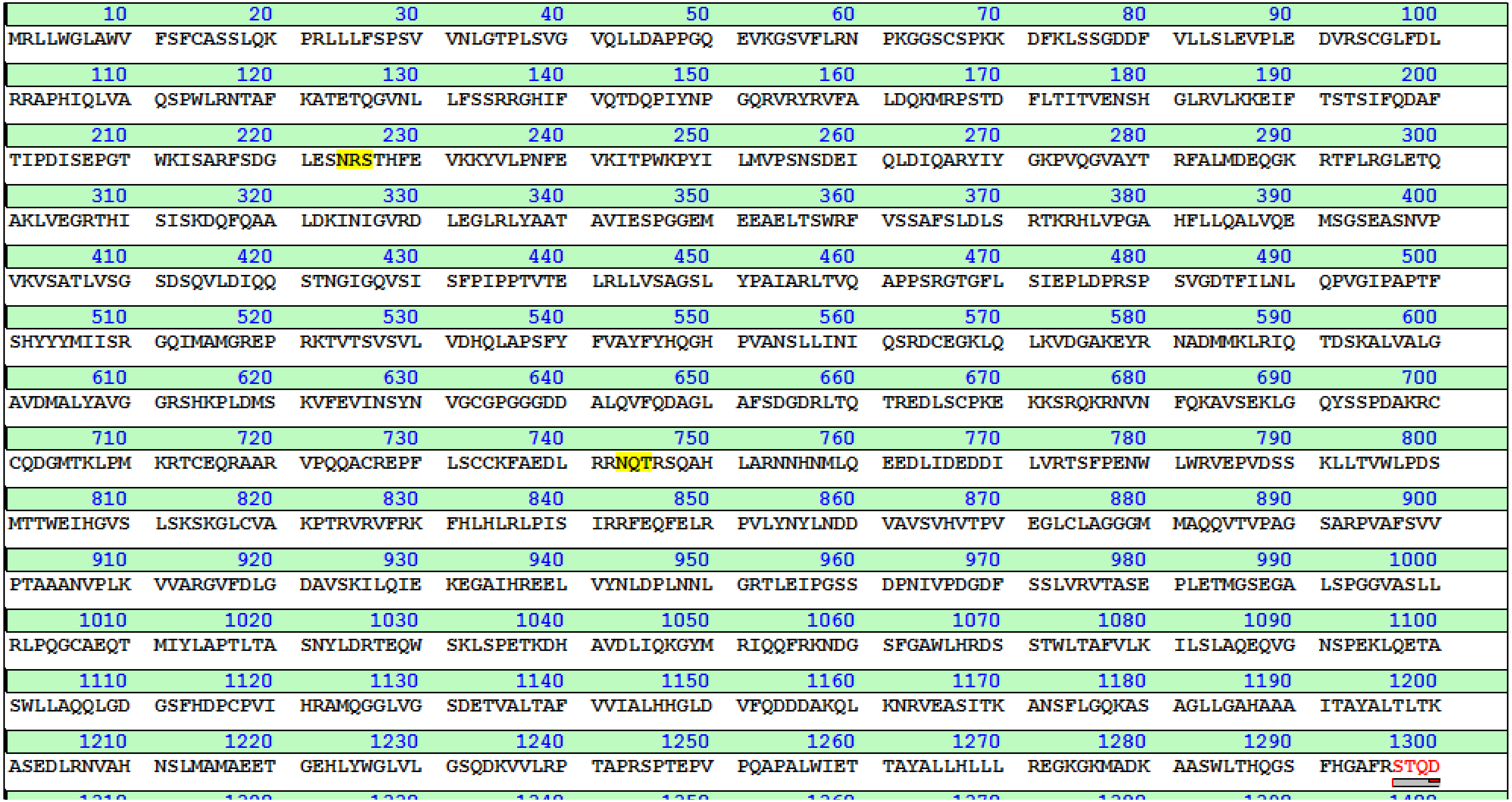
10	20	30	40	50	60	70	80	90	100
MSVLYSSSSK	QFSSSRSGGG	GGGGSVRVSS	TRGSLGGGYS	SGGFSGGSFS	RGSSGGGCFG	GSSGGYGGFG	GGGSFGGGYG	GSSFGGGYGG	SSFGGGYGGS
110	120	130	140	150	160	170	180	190	200
SFGGAGFGGG	GSFGGGSFGG	GSYGGGFGGG	GFGGDGGSLL	SGNGRVTMQN	LNDRLASYMD	KVRALEESNY	ELEGKIKEWY	EKHGNSSQRE	PRDYSKYYKT
210	220	230	240	250	260	270	280	290	300
IEDLKGQILT	LTTDNANVLL	QIDNARLAAD	DFRLKYENEV	TLRQSVEADI	NGLRRVLDEL	TLSKSDLEMQ	IESLNEELAY	LKKNHEEEMR	DLQNVSTGDV
310	320	330	340	350	360	370	380	390	400
NVEMNAAPGV	DLTQLLNNMR	NQYEQLAEKN	RKDAEEWFNQ	KSKELTTEID	SNIEQMSSHK	SEITELRRTV	QGLEIELQSQ	LALKQSLEAS	LAETEGRYCV
410	420	430	440	450	460	470	480	490	500
QLSQIQSQIS	ALEEQLQQIR	AETECQNAEY	QQLLDIKTRL	ENEIQTYRSL	LEGEGSSSGG	GGGRRGGSGG	GSYGGSSGGG	SYGGSSGGGG	SYGGSSGGGG
510	520	530	540	550	560	570	580		
SYGGGSSGGG	SHGGSSGGGY	GGGSSSGGAG	GHGGSSGGGY	GGGSSSGGQG	GSGGFKSSGG	GDQSSKGPRY			

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
402	691.3228	2	-7.12	-0.0049	29.19	41.0	1	0.0	0	R.ALEESNYELEGK.I		164-175

Protein 20: Complement C4-B OS=Mus musculus OX=10090 GN=C4b PE=1 SV=3

Accession:	CO4B_MOUSE	**Score:**	40.1
Database:	SwissProt	**Seq. Coverage [%]:**	1.4
MW [kDa] / pI:	192.8 / 7.4	**No. of Peptides:**	1



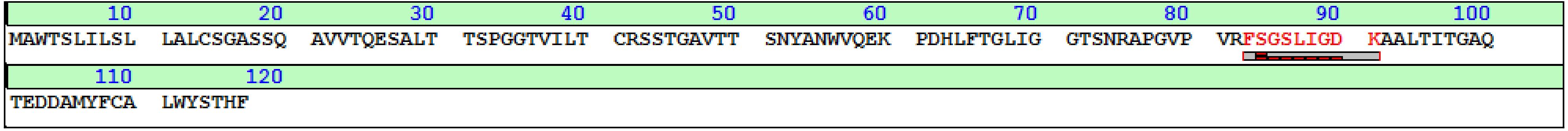
10	20	30	40	50	60	70	80	90	100
MRLLWGLAWV	FSFCASSLQK	PRLLLFSPSV	VNLGTPLSVG	VQLLDAPPGQ	EVKGSVFLRN	PKGGSCSPKK	DFKLSSGDDF	VLLSLEVPLE	DVRSCGLFDL
110	120	130	140	150	160	170	180	190	200
RRAPHIQLVA	QSPWLRNTAF	KATETQGVNL	LFSSRRGHIF	VQTDQPIYNP	GQRVRYRVFA	LDQKMRPSTD	FLTITVENSH	GLRVLKKEIF	TSTSIFQDAF
210	220	230	240	250	260	270	280	290	300
TIPDISEPGT	WKISARFSDG	LESNRSTHFE	VKKYVLPNFE	VKITPWKPYI	LMVPSNSDEI	QLDIQARYIY	GKPVQGVAYT	RFALMDEQGK	RTFLRGLETQ
310	320	330	340	350	360	370	380	390	400
AKLVEGRTHI	SISKDQFQAA	LDKINIGVRD	LEGLRLYAAT	AVIESPGGEM	EEAELTSWRF	VSSAFSLDLS	RTKRHLVPGA	HFLLQALVQE	MSGSEASNVP
410	420	430	440	450	460	470	480	490	500
VKVSATLVSG	SDSQVLDIQQ	STNGIGQVSI	SFPIPPTVTE	LRLLVSAGSL	YPAIARLTVQ	APPSRGTGFL	SIEPLDPRSP	SVGDTFILNL	QPVGIPAPTF
510	520	530	540	550	560	570	580	590	600
SHYYYMIISR	GQIMAMGREP	RKTVTSVSVL	VDHQLAPSFY	FVAYFYHQGH	PVANSLLINI	QSRDCEGKLQ	LKVDGAKEYR	NADMMKLRIQ	TDSKALVALG
610	620	630	640	650	660	670	680	690	700
AVDMALYAVG	GRSHKPLDMS	KVFEVINSYN	VGCGPGGGDD	ALQVFQDAGL	AFSDGDRLTQ	TREDLSCPKE	KKSRQKRNVN	FQKAVSEKLG	QYSSPDAKRC
710	720	730	740	750	760	770	780	790	800
CQDGMTKLPM	KRTCEQRAAR	VPQQACREPF	LSCCKFAEDL	RRNQTRSQAH	LARNNHNMLQ	EEDLIDEDDI	LVRTSFPENW	LWRVEPVDSS	KLLTVWLPDS
810	820	830	840	850	860	870	880	890	900
MTTWEIHGVS	LSKSKGLCVA	KPTRVRVFRK	FHLHLRLPIS	IRRFEQFELR	PVLYNYLNDD	VAVSVHVTPV	EGLCLAGGGM	MAQQVTVPAG	SARPVAFSVV
910	920	930	940	950	960	970	980	990	1000
PTAAANVPLK	VVARGVFDLG	DAVSKILQIE	KEGAIHREEL	VYNLDPLNNL	GRTLEIPGSS	DPNIVPDGDF	SSLVRVTASE	PLETMGSEGA	LSPGGVASLL
1010	1020	1030	1040	1050	1060	1070	1080	1090	1100
RLPQGCAEQT	MIYLAPTLTA	SNYLDRTEQW	SKLSPETKDH	AVDLIQKGYM	RIQQFRKNDG	SFGAWLHRDS	STWLTAFVLK	ILSLAQEQVG	NSPEKLQETA
1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
SWLLAQQLGD	GSFHDPCPVI	HRAMQGGLVG	SDETVALTAF	VVIALHHGLD	VFQDDDAKQL	KNRVEASITK	ANSFLGQKAS	AGLLGAHAAA	ITAYALTLTK
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
ASEDLRNVAH	NSLMAMAEET	GEHLYWGLVL	GSQDKVVLRP	TAPRSPTEPV	PQAPALWIET	TAYALLHLLL	REGKGKMADK	AASWLTHQGS	FHGAFRSTQD

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
1398	922.7743	3	-13.91	-0.0128	61.61	40.1	1	0.0	0	R.STQDTVVTLDALSAYWIASHTTEEK.A		1297-1321

Protein 21: Ig lambda-2 chain V region OS=Mus musculus OX=10090 PE=3 SV=1

Accession:	LV2A_MOUSE	**Score:**	38.6
Database:	SwissProt	**Seq. Coverage [%]:**	7.7
MW [kDa] / pI:	12.2 / 5.4	**No. of Peptides:**	1



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        10         20         30         40         50         60         70         80         90        100
MAWTSLILSL LALCSGASSQ AVVTQESALT TSPGGTVILT CRSSTGAVTT SNYANWVQEK PDHLFTGLIG GTSNRAPGVP VRFSGSLIGD KAALTITGAQ
       110        120
TEDDAMYFCA LWYSTHF
```

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
445	462.2419	2	-7.30	-0.0034	30.50	38.6	1	0.0	0	R.FSGSLIGDK.A		83-91