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

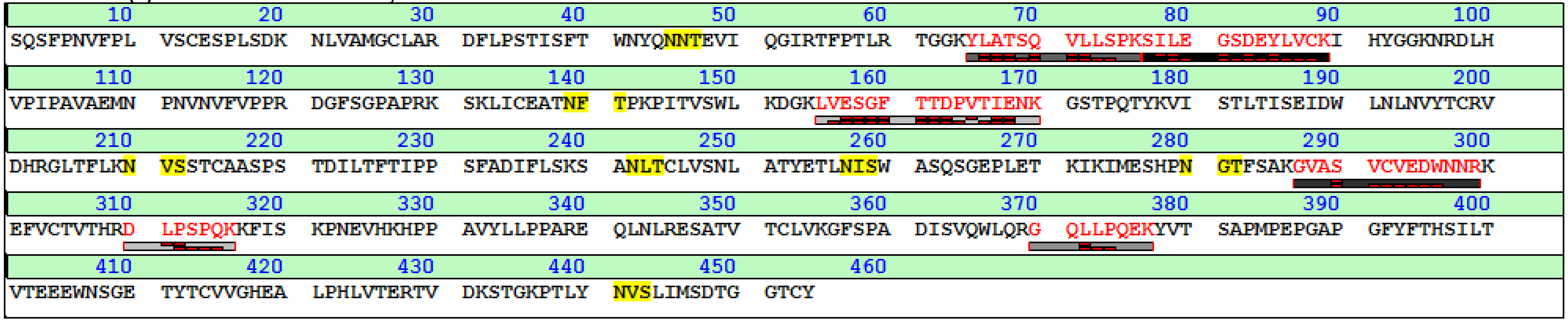
Search Result Info

Search Result:	nawa-method-mouse_2021-01-05 11:33:47		
Location:	/Nawa/kotani/0206-3_Tray01-F2_01_6388.mgf		
Search Method:	nawa-method-mouse	**Version:**	1.0
Search Engine(s):	Mascot, 2.4.1	**Ident. Compound(s):**	11/858
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:**	261.5
Database:	SwissProt	**Seq. Coverage [%]:**	15.2
MW [kDa] / pI:	49.9 / 6.6	**No. of Peptides:**	6
Modification(s):	Carbamidomethyl		



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        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
299	660.3746	2	-11.36	-0.0075	40.93	56.4	2	0.0	0	K.YLATSQVLLSPK.S		65-76
328	756.8582	2	-10.51	-0.0080	42.60	61.8	1	0.0	0	K.SILEGSDEYLVCK.I	Carbamidomethyl: 12	77-89
301	875.4386	2	-11.76	-0.0103	41.18	80.5	2	0.0	0	K.LVESGFTTDPVTIENK.G		155-170
275	753.3324	2	-15.02	-0.0113	37.92	23.5	1	0.0	0	K.GVASVCVEDWNNR.K	Carbamidomethyl: 6	287-299
643	392.7074	2	-15.82	-0.0062	58.07	25.8	4	0.0	0	R.DLPSPQK.K		310-316
170	456.7564	2	-10.27	-0.0047	25.54	13.4	1	0.0	0	R.GQLLPQEK.Y		370-377

Protein 2: Keratin, type I cytoskeletal 14 OS=Mus musculus OX=10090 GN=Krt14 PE=1 SV=2

Accession:	K1C14_MOUSE	**Score:**	103.9
Database:	SwissProt	**Seq. Coverage [%]:**	4.5
MW [kDa] / pI:	52.8 / 5.1	**No. of Peptides:**	2
Modification(s):	Oxidation		

10	20	30	40	50	60	70	80	90	100
MATCSRQFTS	SSSMKGSCGI	GGGSSRMSSI	LAGGSCRAPS	TYGGMSVTSS	RFSSGGACGI	GGGYGGSFSS	SSFGGGLGSG	FGGRFDGFGG	GFGGGLGGGF
110	120	130	140	150	160	170	180	190	200
GGGLGGGLGG	GIGDGLLVGS	EKVTMQNLND	RLATYLDKVR	ALEEANTELE	VKIRDWYQRQ	RPTEIKDYSP	YFKTIEDLKS	KILAATVDNA	NVLLQIDNAR
210	220	230	240	250	260	270	280	290	300
LAADDFRTKF	ETEQSLRMSV	EADINGLRRV	LDELTLARAD	LEMQIESLKE	ELAYLKKNHE	EEMASMRGQV	GGDVNVEMDA	APGVDLSRIL	NEMRDQYEKM
310	320	330	340	350	360	370	380	390	400
AEKNRKDAEE	WFFSKTEELN	REVATNSELV	QSGKSEISEL	RRTMQNLEIE	LQSQLSMKAS	LENNLEETKG	RYCMQLAQIQ	EMIGSVEEQL	AQLRCEMEQQ
410	420	430	440	450	460	470	480	490	
NQEYKILLDV	KTRLEQEIAT	YRRLLEGEDA	HLSSSQFSSS	SQFSSGSQSS	RDVTSTNRQI	RTKVMDVHDG	KVVSTHEQVL	RTKN	

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
660	553.7586	2	-14.41	-0.0080	58.66	50.4	8	0.0	0	K.VTMQNLNDR.L	Oxidation: 3	123-131
724	681.3405	2	-12.46	-0.0085	61.02	53.5	4	0.0	0	R.EVATNSELVQSGK.S		322-334

Protein 3: Immunoglobulin kappa constant OS=Mus musculus OX=10090 GN=Igkc PE=1 SV=2

Accession:	IGKC_MOUSE	**Score:**	81.3
Database:	SwissProt	**Seq. Coverage [%]:**	13.1
MW [kDa] / pI:	11.9 / 5.6	**No. of Peptides:**	1
Modification(s):	Oxidation		

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        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
796	775.8557	2	-13.73	-0.0107	63.66	81.2	6	0.0	0	K.DSTYSMSSTLTLTK.D	Oxidation: 6	63-76

Protein 4: Band 3 anion transport protein OS=Mus musculus OX=10090 GN=Slc4a1 PE=1 SV=1

Accession:	B3AT_MOUSE	**Score:**	44.7
Database:	SwissProt	**Seq. Coverage [%]:**	1.5
MW [kDa] / pI:	103.1 / 5.3	**No. of Peptides:**	1

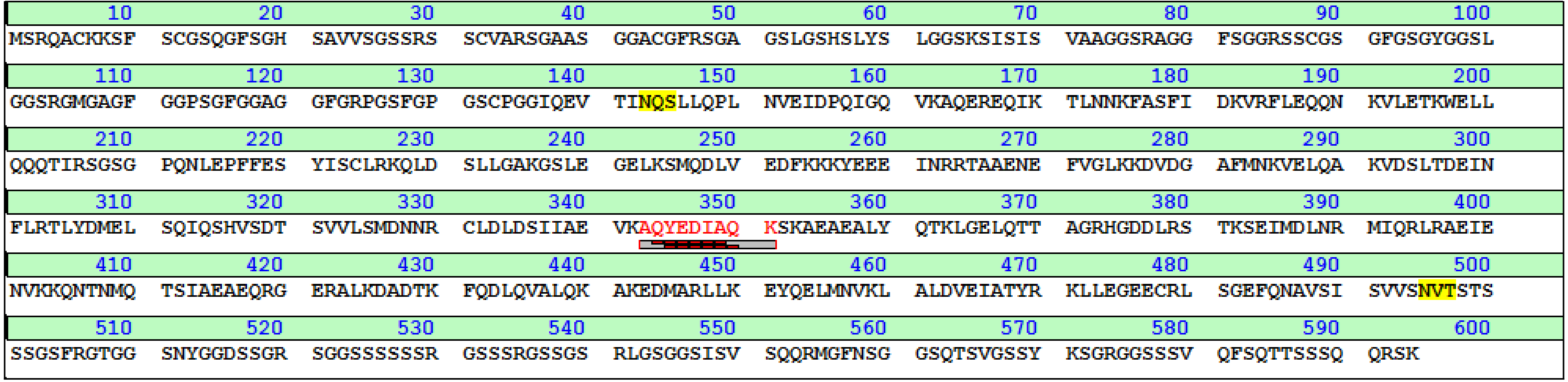
10	20	30	40	50	60	70	80	90	100
MGDMRDHEEV	LEIPDRDSEE	ELENIIGQIA	YRDLTIPVTE	MQDPEALPTE	QTATDYVPSS	TSTPHPSSGQ	VYVELQELMM	DQRNQELQWV	EAAHWIGLEE
110	120	130	140	150	160	170	180	190	200
NLREDGVWGR	PHLSYLTFWS	LLELQKVFSK	GTFLLGLAET	SLAGVANHLL	DCFIYEDQIR	PQDREELLRA	LLLKRSHAED	LGNLEGVKPA	VLTRSGGASE
210	220	230	240	250	260	270	280	290	300
PLLPHQPSLE	TQLYCGQAEG	GSEGPSTSGT	LKIPPDSETT	LVLVGRANFL	EKPVLGFVRL	KEAVPLEDLV	LPEPVGFLLV	LLGPEAPHVD	YTQLGRAAAT
310	320	330	340	350	360	370	380	390	400
LMTERVFRIT	ASMAHNREEL	LRSLESFLDC	SLVLPPTDAP	SEKALLNLVP	VQKELLRRRY	LPSPAKPDPN	LYNTLDLNGG	KGGPGDEDDP	LRRTGRIFGG
410	420	430	440	450	460	470	480	490	500
LIRDIRRRYP	YYLSDITDAL	SPQVLAAVIF	IYFAALSPAV	TFGGLLGEKT	RNLMGVSELL	ISTAVQGILF	ALLGAQPLLV	LGFSGPLLVF	EEAFFSFCES
510	520	530	540	550	560	570	580	590	600
NNLEYIVGRA	WIGFWLILLV	MLVVAFEGSF	LVQYISRYTQ	EIFSFLISLI	FIYETFSKLI	KIFQDYPLQQ	TYAPVVMKPK	PQGPVPNTAL	FSLVLMAGTF
610	620	630	640	650	660	670	680	690	700
LLAMTLRKFK	NSTYFPGKLR	RVIGDFGVPI	SILIMVLVDS	FIKGTYTQKL	SVPDGLKVSN	SSARGWVIHP	LGLYRLFPTW	MMFASVLPAL	LVFILIFLES
710	720	730	740	750	760	770	780	790	800
QITTLIVSKP	ERKMIKGSGF	HLDLLLVVGM	GGVAALFGMP	WLSATTVRSV	THANALTVMG	KASGPGAAAQ	IQEVKEQRIS	GLLVSVLVGL	SILMEPILSR
810	820	830	840	850	860	870	880	890	900
IPLAVLFGIF	LYMGVTSLSG	IQLFDRILLL	FKPPKYHPDV	PFVKRVKTWR	MHLFTGIQII	CLAVLWVVKS	TPASLALPFV	LILTVPLRRL	ILPLIFRELE
910	920	930							
LQCLDGDDAK	VTFDEENGLD	EYDEVPMPV							

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
761	663.8443	2	-14.97	-0.0099	62.34	44.7	3	0.0	0	K.ASGPGAAAQIQEVK.E		762-775

Protein 5: Keratin, type II cytoskeletal 2 oral OS=Mus musculus OX=10090 GN=Krt76 PE=1 SV=1

Accession:	K22O_MOUSE	**Score:**	41.2
Database:	SwissProt	**Seq. Coverage [%]:**	1.5
MW [kDa] / pI:	62.8 / 8.7	**No. of Peptides:**	1



10	20	30	40	50	60	70	80	90	100
MSRQACKKSF	SCGSQGFSGH	SAVVSGSSRS	SCVARSGAAS	GGACGFRSGA	GSLGSHSLYS	LGGSKSISIS	VAAGGSRAGG	FSGGRSSCGS	GFGSGYGGSL
110	120	130	140	150	160	170	180	190	200
GGSRGMGAGF	GGPSGFGGAG	GFGRPGSFGP	GSCPGGIQEV	TINQSLLQPL	NVEIDPQIGQ	VKAQEREQIK	TLNNKFASFI	DKVRFLEQQN	KVLETKWELL
210	220	230	240	250	260	270	280	290	300
QQQTIRSGSG	PQNLEPFFES	YISCLRKQLD	SLLGAKGSLE	GELKSMQDLV	EDFKKKYEEE	INRRTAAENE	FVGLKKDVDG	AFMNKVELQA	KVDSLTDEIN
310	320	330	340	350	360	370	380	390	400
FLRTLYDMEL	SQIQSHVSDT	SVVLSMDNNR	CLDLDSIIAE	VKAQYEDIAQ	KSKAEAEALY	QTKLGELQTT	AGRHGDDLRS	TKSEIMDLNR	MIQRLRAEIE
410	420	430	440	450	460	470	480	490	500
NVKKQNTNMQ	TSIAEAEQRG	ERALKDADTK	FQDLQVALQK	AKEDMARLLK	EYQELMNVKL	ALDVEIATYR	KLLEGEECRL	SGEFQNAVSI	SVVSNVTSTS
510	520	530	540	550	560	570	580	590	600
SSGSFRGTGG	SNYGGDSSGR	SGGSSSSSSR	GSSSRGSSGS	RLGSGGSISV	SQQRMGFNSG	GSQTSVGSSY	KSGRGGSSSV	QFSQTTSSSQ	QRSK

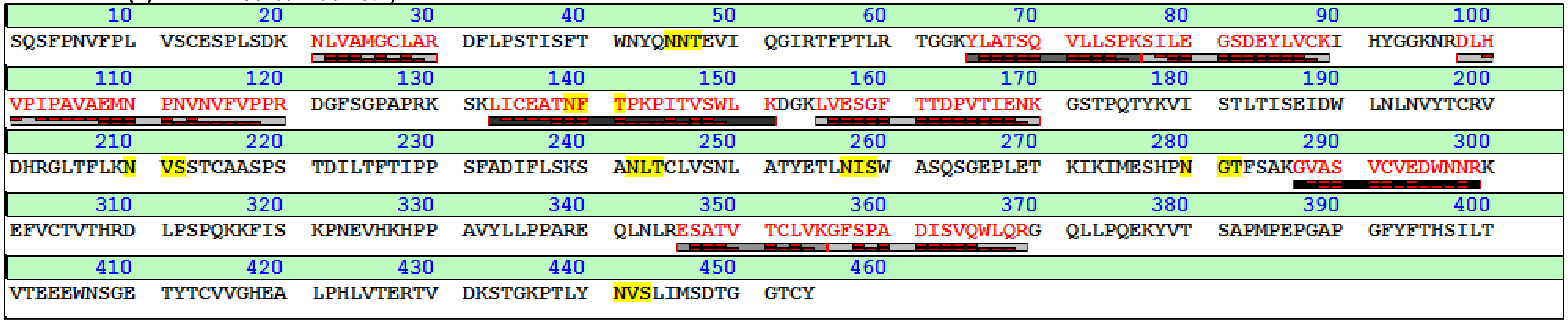
MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
826	533.2575	2	-12.56	-0.0067	64.80	41.2	6	0.0	0	K.AQYEDIAQK.S		343-351

Results

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

Accession:	IGHM_MOUSE	**Score:**	643.3
Database:	SwissProt	**Seq. Coverage [%]:**	28.6
MW [kDa] / pI:	49.9 / 6.6	**No. of Peptides:**	9
Modification(s):	Carbamidomethyl		



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				

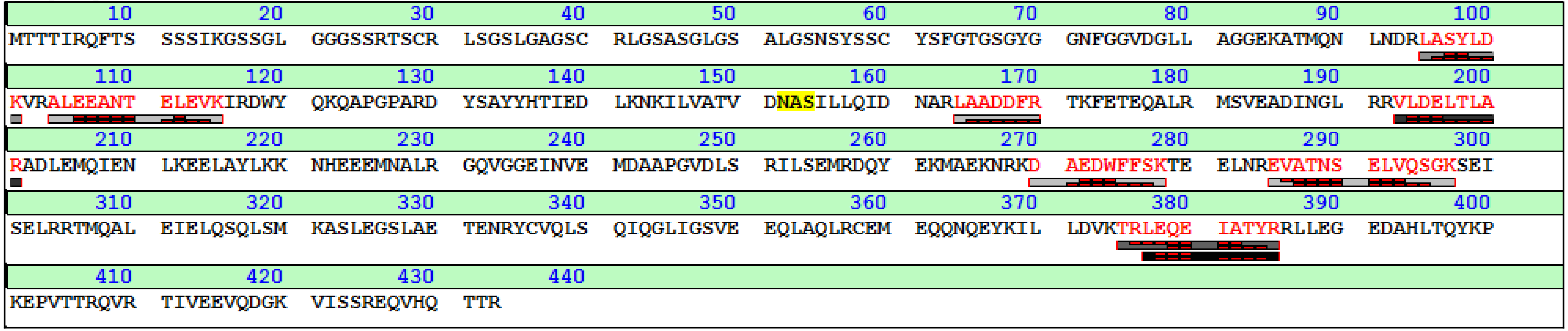
MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
700	552.7776	2	-15.67	-0.0087	37.93	43.3	2	0.0	0	K.NLVAMGCLAR.D	Carbamidomethyl: 7	21-30
744	660.3715	2	-16.06	-0.0106	39.24	81.6	2	0.0	0	K.YLATSQVLLSPK.S		65-76
806	756.8532	2	-17.12	-0.0130	41.28	73.7	2	0.0	0	K.SILEGSDEYLVCK.I	Carbamidomethyl: 12	77-89
1322	842.4299	3	-23.02	-0.0194	58.42	42.6	1	0.0	0	R.DLHVPIPAVAEMNPNVNVFVPPR.D		98-120
1159	740.0537	3	-21.39	-0.0158	52.79	82.2	1	0.0	0	K.LICEATNFTPKPITVSWLK.D	Carbamidomethyl: 3	133-151
773	875.4346	2	-16.33	-0.0143	40.20	115.2	2	0.0	0	K.LVESGFTTDPVTIENK.G		155-170
659	753.3327	2	-14.62	-0.0110	36.57	69.4	2	0.0	0	K.GVASVCVEDWNNR.K	Carbamidomethyl: 6	287-299
396	554.2826	2	-12.19	-0.0068	28.72	47.5	2	0.0	0	R.ESATVTCLVK.G	Carbamidomethyl: 7	346-355

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
1271	802.3947	2	-25.30	-0.0203	56.65	87.9	2	0.0	0	K.GFSPADISVQWLQR.G		356-369

Protein 2: Keratin, type I cytoskeletal 17 OS=Mus musculus OX=10090 GN=Krt17 PE=1 SV=3

Accession:	K1C17_MOUSE	**Score:**	313.5
Database:	SwissProt	**Seq. Coverage [%]:**	15.7
MW [kDa] / pI:	48.1 / 5.0	**No. of Peptides:**	8



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        10         20         30         40         50         60         70         80         90        100
MTTTIRQFTS SSSIKGSSGL GGGSSRTSCR LSGSLGAGSC RLGSASGLGS ALGSNSYSSC YSFGTGSGYG GNFGGVDGLL AGGEKATMQN LNDRLASYLD
       110        120        130        140        150        160        170        180        190        200
KVRALEEANT ELEVKIRDWY QKQAPGPARD YSAYYHTIED LKNKILVATV DNASILLQID NARLAADDFR TKFETEQALR MSVEADINGL RRVLDELTLA
       210        220        230        240        250        260        270        280        290        300
RADLEMQIEN LKEELAYLKK NHEEEMNALR GQVGGEINVE MDAAPGVDLS RILSEMRDQY EKMAEKNRKD AEDWFFSKTE ELNREVATNS ELVQSGKSEI
       310        320        330        340        350        360        370        380        390        400
SELRRTMQAL EIELQSQLSM KASLEGSLAE TENRYCVQLS QIQGLIGSVE EQLAQLRCEM EQQNQEYKIL LDVKTRLEQE IATYRRLLEG EDAHLTQYKP
       410        420        430        440
KEPVTTRQVR TIVEEVQDGK VISSREQVHQ TTR
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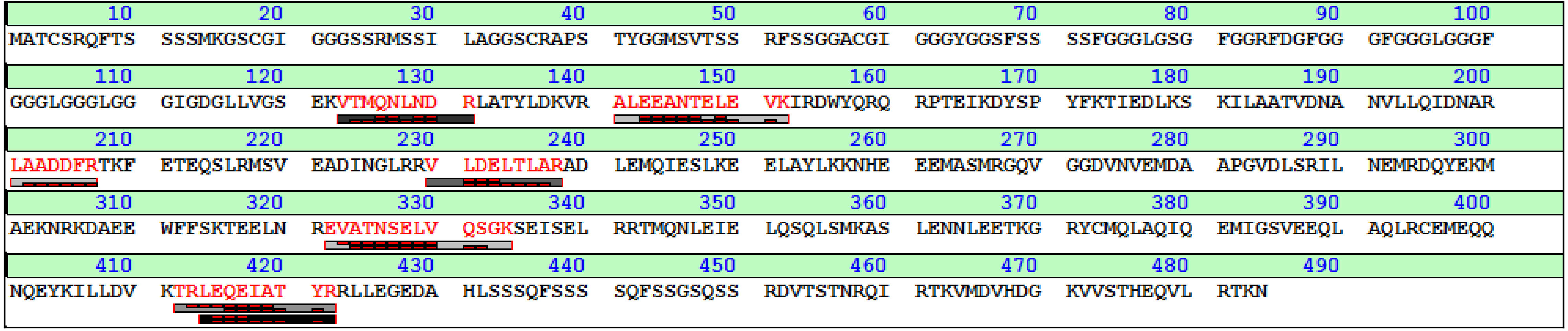
MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
260	405.2194	2	-10.89	-0.0044	24.84	28.6	1	0.0	0	R.LASYLDK.V		95-101
471	673.3362	2	-14.43	-0.0097	30.90	40.1	1	0.0	0	R.ALEEANTELEVK.I		104-115
305	404.1987	2	-11.65	-0.0047	26.09	16.3	2	0.0	0	R.LAADDFR.T		164-170
740	515.2911	2	-18.40	-0.0095	39.13	44.2	2	0.0	0	R.VLDELTLAR.A		193-201
1125	572.7363	2	-25.53	-0.0146	51.66	25.3	1	0.0	0	K.DAEDWFFSK.T		270-278
184	681.3416	2	-10.84	-0.0074	22.23	86.7	1	0.0	0	R.EVATNSELVQSGK.S		285-297

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
537	460.5746	3	-13.39	-0.0062	32.88	19.9	2	0.0	1	K.TRLEQEIATYR.R		375-385
337	561.7863	2	-12.14	-0.0068	27.01	52.3	2	0.0	0	R.LEQEIATYR.R		377-385

Protein 3: Keratin, type I cytoskeletal 14 OS=Mus musculus OX=10090 GN=Krt14 PE=1 SV=2

Accession:	K1C14_MOUSE	**Score:**	312.6
Database:	SwissProt	**Seq. Coverage [%]:**	12.6
MW [kDa] / pI:	52.8 / 5.1	**No. of Peptides:**	7



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        10         20         30         40         50         60         70         80         90        100
MATCSRQFTS SSSMKGSCGI GGGSSRMSSI LAGGSCRAPS TYGGMSVTSS RFSSGGACGI GGGYGGSFSS SSFGGGLGSG FGGRFDGFGG GFGGGLGGGF
       110        120        130        140        150        160        170        180        190        200
GGGLGGGLGG GIGDGLLVGS EKVTMQNLND RLATYLDKVR ALEEANTELE VKIRDWYQRQ RPTEIKDYSP YFKTIEDLKS KILAATVDNA NVLLQIDNAR
       210        220        230        240        250        260        270        280        290        300
LAADDFRTKF ETEQSLRMSV EADINGLRRV LDELTLARAD LEMQIESLKE ELAYLKKNHE EEMASMRGQV GGDVNVEMDA APGVDLSRIL NEMRDQYEKM
       310        320        330        340        350        360        370        380        390        400
AEKNRKDAEE WFFSKTEELN REVATNSELV QSGKSEISEL RRTMQNLEIE LQSQLSMKAS LENNLEETKG RYCMQLAQIQ EMIGSVEEQL AQLRCEMEQQ
       410        420        430        440        450        460        470        480        490
NQEYKILLDV KTRLEQEIAT YRRLLEGEDA HLSSSQFSSS SQFSSGSQSS RDVTSTNRQI RTKVMDVHDG KVVSTHEQVL RTKN
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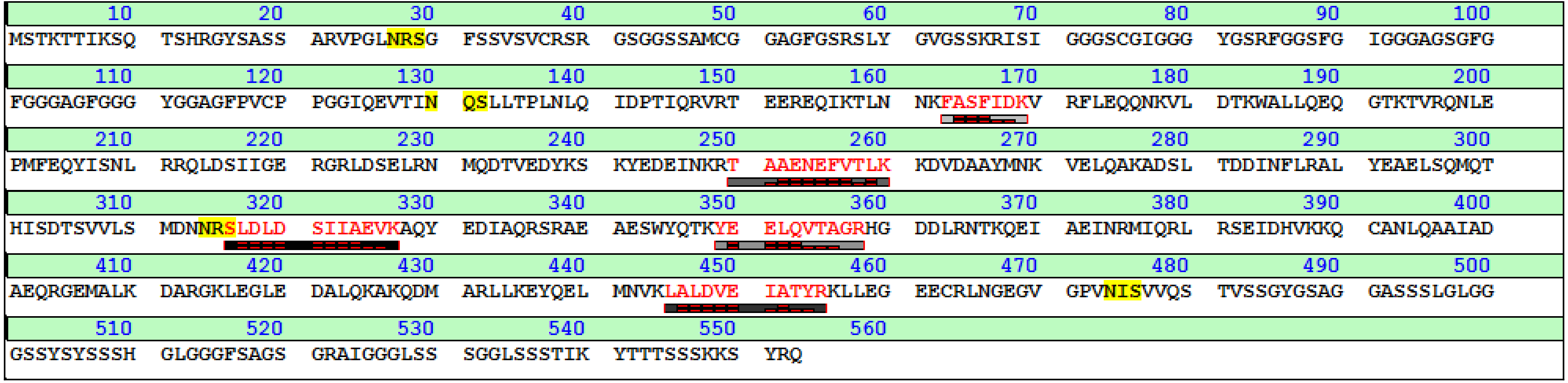
MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
223	545.7634	2	-10.49	-0.0057	23.83	53.0	1	0.0	0	K.VTMQNLNDR.L		123-131
471	673.3362	2	-14.43	-0.0097	30.90	40.1	1	0.0	0	R.ALEEANTELEVK.I		141-152
305	404.1987	2	-11.65	-0.0047	26.09	16.3	2	0.0	0	R.LAADDFR.T		201-207
740	515.2911	2	-18.40	-0.0095	39.13	44.2	2	0.0	0	R.VLDELTLAR.A		230-238
184	681.3416	2	-10.84	-0.0074	22.23	86.7	1	0.0	0	R.EVATNSELVQSGK.S		322-334

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
537	460.5746	3	-13.39	-0.0062	32.88	19.9	2	0.0	1	K.TRLEQEIATYR.R		412-422
337	561.7863	2	-12.14	-0.0068	27.01	52.3	2	0.0	0	R.LEQEIATYR.R		414-422

Protein 4: Keratin, type II cytoskeletal 6A OS=Mus musculus OX=10090 GN=Krt6a PE=1 SV=3

Accession:	K2C6A_MOUSE	**Score:**	300.7
Database:	SwissProt	**Seq. Coverage [%]:**	9.2
MW [kDa] / pI:	59.3 / 8.0	**No. of Peptides:**	5



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				

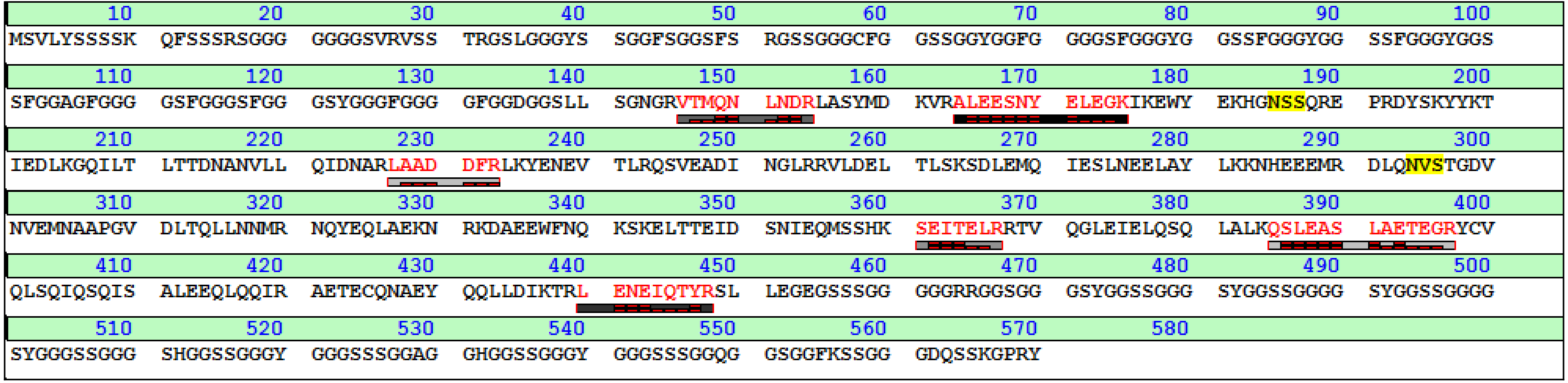
MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
590	414.2129	2	-13.59	-0.0056	34.47	31.9	2	0.0	0	K.FASFIDK.V		163-169
634	611.8098	2	-15.59	-0.0095	35.82	74.7	1	0.0	0	R.TAAENEFVTLK.K		250-260
1332	651.8469	2	-21.94	-0.0143	58.76	82.0	2	0.0	0	R.SLDLDSIIAEVK.A		316-327

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
385	583.2886	2	-12.73	-0.0074	28.41	30.6	1	0.0	0	K.YEELQVTAGR.H		349-358
987	632.3375	2	-21.04	-0.0133	47.12	81.4	2	0.0	0	K.LALDVEIATYR.K		445-455

Protein 5: Keratin, type I cytoskeletal 10 OS=Mus musculus OX=10090 GN=Krt10 PE=1 SV=3

Accession: K1C10_MOUSE
Database: SwissProt
MW [kDa] / pI: 57.7 / 5.0
Score: 286.4
Seq. Coverage [%]: 10.0
No. of Peptides: 6



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        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
```

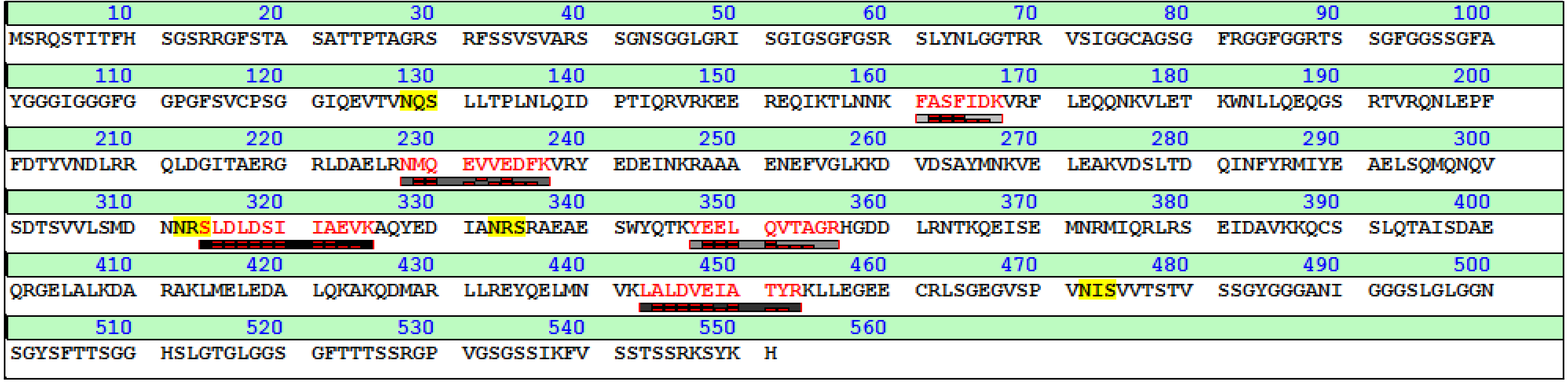
MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
223	545.7634	2	-10.49	-0.0057	23.83	53.0	1	0.0	0	R.VTMQNLNDR.L		146-154
401	691.319	2	-12.62	-0.0087	28.85	74.8	2	0.0	0	R.ALEESNYELEGK.I		164-175
305	404.1987	2	-11.65	-0.0047	26.09	16.3	2	0.0	0	R.LAADDFR.L		227-233

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
277	424.2246	2	-11.85	-0.0050	25.41	32.1	2	0.0	0	K.SEITELR.R		361-367
638	695.8345	2	-13.75	-0.0096	35.93	75.8	2	0.0	0	K.QSLEASLAETEGR.Y		385-397
312	583.289	2	-12.05	-0.0070	26.28	34.4	2	0.0	0	R.LENEIQTYR.S		440-448

Protein 6: Keratin, type II cytoskeletal 75 OS=Mus musculus OX=10090 GN=Krt75 PE=1 SV=1

Accession:	K2C75_MOUSE	**Score:**	277.0
Database:	SwissProt	**Seq. Coverage [%]:**	9.1
MW [kDa] / pI:	59.7 / 8.5	**No. of Peptides:**	5



10	20	30	40	50	60	70	80	90	100
MSRQSTITFH	SGSRRGFSTA	SATTPTAGRS	RFSSVSVARS	SGNSGGLGRI	SGIGSGFGSR	SLYNLGGTRR	VSIGGCAGSG	FRGGFGGRTS	SGFGGSSGFA
110	120	130	140	150	160	170	180	190	200
YGGGIGGGFG	GPGFSVCPSG	GIQEVTVNQS	LLTPLNLQID	PTIQRVRKEE	REQIKTLNNK	FASFIDKVRF	LEQQNKVLET	KWNLLQEQGS	RTVRQNLEPF
210	220	230	240	250	260	270	280	290	300
FDTYVNDLRR	QLDGITAERG	RLDAELRNMQ	EVVEDFKVRY	EDEINKRAAA	ENEFVGLKKD	VDSAYMNKVE	LEAKVDSLTD	QINFYRMIYE	AELSQMQNQV
310	320	330	340	350	360	370	380	390	400
SDTSVVLSMD	NNRSLDLDSI	IAEVKAQYED	IANRSRAEAE	SWYQTKYEEL	QVTAGRHGDD	LRNTKQEISE	MNRMIQRLRS	EIDAVKKQCS	SLQTAISDAE
410	420	430	440	450	460	470	480	490	500
QRGELALKDA	RAKLMELEDA	LQKAKQDMAR	LLREYQELMN	VKLALDVEIA	TYRKLLEGEE	CRLSGEGVSP	VNISVVTSTV	SSGYGGGANI	GGGSLGLGGN
510	520	530	540	550	560				
SGYSFTTSGG	HSLGTGLGGS	GFTTTSSRGP	VGSGSSIKFV	SSTSSRKSYK	H				

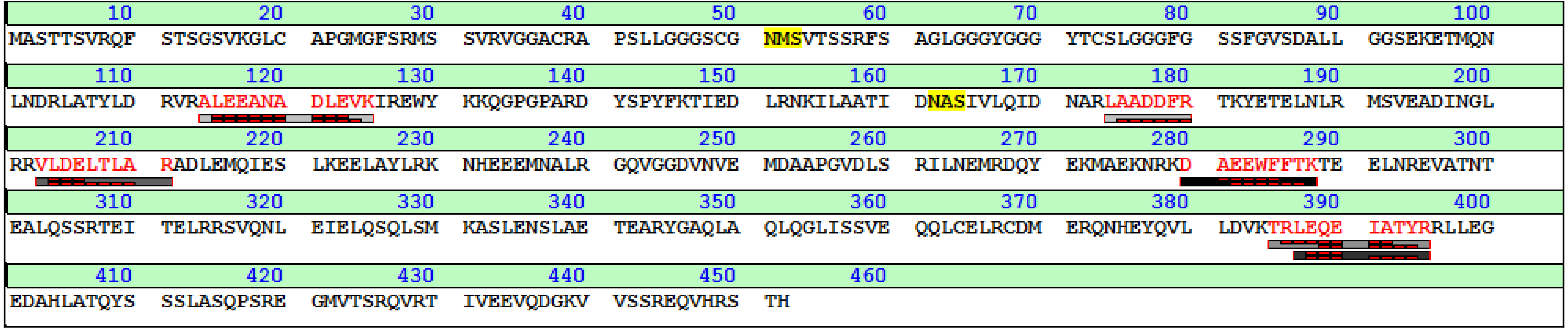
MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
590	414.2129	2	-13.59	-0.0056	34.47	31.9	2	0.0	0	K.FASFIDK.V		161-167
1018	619.777	2	-20.52	-0.0127	48.12	51.0	2	0.0	0	R.NMQEVVEDFK.V		228-237

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
1332	651.8469	2	-21.94	-0.0143	58.76	82.0	2	0.0	0	R.SLDLDSIIAEVK.A		314-325
385	583.2886	2	-12.73	-0.0074	28.41	30.6	1	0.0	0	K.YEELQVTAGR.H		347-356
987	632.3375	2	-21.04	-0.0133	47.12	81.4	2	0.0	0	K.LALDVEIATYR.K		443-453

Protein 7: Keratin, type I cytoskeletal 42 OS=Mus musculus OX=10090 GN=Krt42 PE=1 SV=1

Accession:	K1C42_MOUSE	**Score:**	260.2
Database:	SwissProt	**Seq. Coverage [%]:**	10.6
MW [kDa] / pI:	50.1 / 5.1	**No. of Peptides:**	6



10	20	30	40	50	60	70	80	90	100
MASTTSVRQF	STSGSVKGLC	APGMGFSRMS	SVRVGGACRA	PSLLGGGSCG	NMSVTSSRFS	AGLGGGYGGG	YTCSLGGGFG	SSFGVSDALL	GGSEKETMQN
110	**120**	**130**	**140**	**150**	**160**	**170**	**180**	**190**	**200**
LNDRLATYLD	RVRALEEANA	DLEVKIREWY	KKQGPGPARD	YSPYFKTIED	LRNKILAATI	DNASIVLQID	NARLAADDFR	TKYETELNLR	MSVEADINGL
210	**220**	**230**	**240**	**250**	**260**	**270**	**280**	**290**	**300**
RRVLDELTLA	RADLEMQIES	LKEELAYLRK	NHEEEMNALR	GQVGGDVNVE	MDAAPGVDLS	RILNEMRDQY	EKMAEKNRKD	AEEWFFTKTE	ELNREVATNT
310	**320**	**330**	**340**	**350**	**360**	**370**	**380**	**390**	**400**
EALQSSRTEI	TELRRSVQNL	EIELQSQLSM	KASLENSLAE	TEARYGAQLA	QLQGLISSVE	QQLCELRCDM	ERQNHEYQVL	LDVKTRLEQE	IATYRRLLEG
410	**420**	**430**	**440**	**450**	**460**				
EDAHLATQYS	SSLASQPSRE	GMVTSRQVRT	IVEEVQDGKV	VSSREQVHRS	TH				

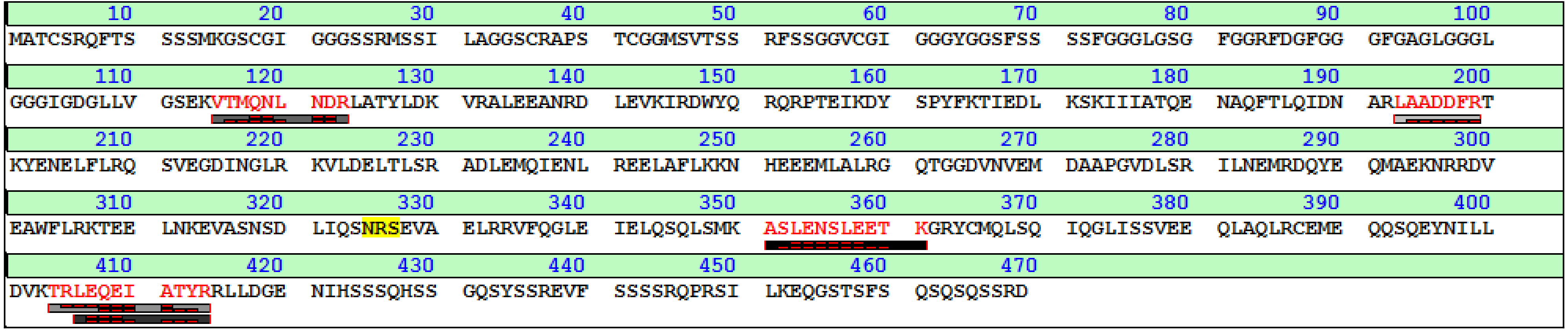
MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
457	651.3248	2	-12.29	-0.0080	30.40	81.4	2	0.0	0	R.ALEEANADLEVK.I		114-125
305	404.1987	2	-11.65	-0.0047	26.09	16.3	2	0.0	0	R.LAADDFR.T		174-180
740	515.2911	2	-18.40	-0.0095	39.13	44.2	2	0.0	0	R.VLDELTLAR.A		203-211
1093	586.7527	2	-23.64	-0.0139	50.59	45.9	1	0.0	0	K.DAEEWFFTK.T		280-288

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range
537	460.5746	3	-13.39	-0.0062	32.88	19.9	2	0.0	1	K.TRLEQEIATYR.R		385-395
337	561.7863	2	-12.14	-0.0068	27.01	52.3	2	0.0	0	R.LEQEIATYR.R		387-395

Protein 8: Keratin, type I cytoskeletal 16 OS=Mus musculus OX=10090 GN=Krt16 PE=1 SV=3

Accession:	K1C16_MOUSE	**Score:**	206.8
Database:	SwissProt	**Seq. Coverage [%]:**	8.1
MW [kDa] / pI:	51.6 / 5.1	**No. of Peptides:**	5



10	20	30	40	50	60	70	80	90	100
MATCSRQFTS	SSSMKGSCGI	GGGSSRMSSI	LAGGSCRAPS	TCGGMSVTSS	RFSSGGVCGI	GGGYGGSFSS	SSFGGGLGSG	FGGRFDGFGG	GFGAGLGGGL
110	**120**	**130**	**140**	**150**	**160**	**170**	**180**	**190**	**200**
GGGIGDGLLV	GSEKVTMQNL	NDRLATYLDK	VRALEEANRD	LEVKIRDWYQ	RQRPTEIKDY	SPYFKTIEDL	KSKIIIATQE	NAQFTLQIDN	ARLAADDFRT
210	**220**	**230**	**240**	**250**	**260**	**270**	**280**	**290**	**300**
KYENELFLRQ	SVEGDINGLR	KVLDELTLSR	ADLEMQIENL	REELAFLKKN	HEEEMLALRG	QTGGDVNVEM	DAAPGVDLSR	ILNEMRDQYE	QMAEKNRRDV
310	**320**	**330**	**340**	**350**	**360**	**370**	**380**	**390**	**400**
EAWFLRKTEE	LNKEVASNSD	LIQSNRSEVA	ELRRVFQGLE	IELQSQLSMK	ASLENSLEET	KGRYCMQLSQ	IQGLISSVEE	QLAQLRCEME	QQSQEYNILL
410	**420**	**430**	**440**	**450**	**460**	**470**			
DVKTRLEQEI	ATYRRLLDGE	NIHSSSQHSS	GQSYSSREVF	SSSSRQPRSI	LKEQGSTSFS	QSQSQSSRD			

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
223	545.7634	2	-10.49	-0.0057	23.83	53.0	1	0.0	0	K.VTMQNLNDR.L		115-123
305	404.1987	2	-11.65	-0.0047	26.09	16.3	2	0.0	0	R.LAADDFR.T		193-199
425	610.7968	2	-11.60	-0.0071	29.53	65.2	2	0.0	0	K.ASLENSLEETK.G		351-361
537	460.5746	3	-13.39	-0.0062	32.88	19.9	2	0.0	1	K.TRLEQEIATYR.R		404-414
337	561.7863	2	-12.14	-0.0068	27.01	52.3	2	0.0	0	R.LEQEIATYR.R		406-414

Protein 9: Keratin, type II cytoskeletal 1 OS=Mus musculus OX=10090 GN=Krt1 PE=1 SV=4

Accession:	K2C1_MOUSE	**Score:**	178.7
Database:	SwissProt	**Seq. Coverage [%]:**	4.7
MW [kDa] / pI:	65.6 / 8.4	**No. of Peptides:**	3

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
590	414.2129	2	-13.59	-0.0056	34.47	31.9	2	0.0	0	K.FASFIDK.V		199-205
494	738.387	2	-12.56	-0.0093	31.63	85.2	2	0.0	0	R.FLEQQNQVLQTK.W		208-219
589	633.3134	2	-13.96	-0.0088	34.46	61.6	2	0.0	0	R.TNAENEFVTIK.K		286-296

Protein 10: Keratin, type II cytoskeletal 73 OS=Mus musculus OX=10090 GN=Krt73 PE=1 SV=1

Accession:	K2C73_MOUSE	**Score:**	169.8
Database:	SwissProt	**Seq. Coverage [%]:**	5.6
MW [kDa] / pI:	58.9 / 8.4	**No. of Peptides:**	3

10	20	30	40	50	60	70	80	90	100
MNRQFTCKPG	VANRGFSGCS	AVLSGGSSSS	YRAAGKGLSG	GFSSRSLYSL	RSPRSISFNV	ASSSGRTGGY	GFGRNRASGF	AGSMFGSGAL	GPSNPSLCLP
110	**120**	**130**	**140**	**150**	**160**	**170**	**180**	**190**	**200**
GGIHQVTVNK	SLLAPLNVEL	DPEIQKVRAQ	EREQIKALNN	KFASFIDKVR	FLEQQNQVLQ	TKWELLQQLD	LSNCRRNLEP	VYEAHISSLQ	KQLDSLSGDR
210	**220**	**230**	**240**	**250**	**260**	**270**	**280**	**290**	**300**
VRLDSELRGM	RDAVEDCKKR	YEEEINKRTT	AENEFVVLKK	DVDAAYMSKV	ELQAKVDALD	GEIKFLKCLY	EGEITQMQSH	ISDTSVVLSM	DNNRNLDLDS
310	**320**	**330**	**340**	**350**	**360**	**370**	**380**	**390**	**400**
IIAEVRAQYE	DIALKSKAEA	EMVYQTKFQE	LQLAAGRHGD	DLKHTRNEIS	ELTRLIQRLR	SEIESVKKQC	SNLETAIADA	EQRGDCALKD	ARAKLDELER
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**	**490**	**500**
ALHQAKEELA	RMLREHQELM	SMKLALDIEI	ATYRKLLEGE	ECRMSGEHTS	AVSISVISSS	APGTVGAGTS	FGFSSAGTYG	YRQSSVAGGY	GILSGGCVTG
510	**520**	**530**	**540**						
SGNCSPRGDT	KNRLGSASEF	KEVSGKTLAL	GSPSKKTMR						

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
590	414.2129	2	-13.59	-0.0056	34.47	31.9	2	0.0	0	K.FASFIDK.V		142-148
494	738.387	2	-12.56	-0.0093	31.63	85.2	2	0.0	0	R.FLEQQNQVLQTK.W		151-162
1114	639.3431	2	-24.29	-0.0155	51.27	52.6	2	0.0	0	K.LALDIEIATYR.K		424-434

Protein 11: Actin, cytoplasmic 1 OS=Mus musculus OX=10090 GN=Actb PE=1 SV=1

Accession:	ACTB_MOUSE	**Score:**	166.2
Database:	SwissProt	**Seq. Coverage [%]:**	9.1
MW [kDa] / pI:	41.7 / 5.3	**No. of Peptides:**	2

10	20	30	40	50	60	70	80	90	100
MDDDIAALVV	DNGSGMCKAG	FAGDDAPRAV	FPSIVGRPRH	QGVMVGMGQK	DSYVGDEAQS	KRGILTLKYP	IEHGIVTNWD	DMEKIWHHTF	YNELRVAPEE
110	**120**	**130**	**140**	**150**	**160**	**170**	**180**	**190**	**200**
HPVLLTEAPL	NPKANREKMT	QIMFETFNTP	AMYVAIQAVL	SLYASGRTTG	IVMDSGDGVT	HTVPIYEGYA	LPHAILRLDL	AGRDLTDYLM	KILTERGYSF
210	**220**	**230**	**240**	**250**	**260**	**270**	**280**	**290**	**300**
TTTAEREIVR	DIKEKLCYVA	LDFEQEMATA	ASSSSLEKSY	ELPDGQVITI	GNERFRCPEA	LFQPSFLGME	SCGIHETTFN	SIMKCDVDIR	KDLYANTVLS
310	**320**	**330**	**340**	**350**	**360**	**370**	**380**		
GGTTMYPGIA	DRMQKEITAL	APSTMKIKII	APPERKYSVW	IGGSILASLS	TFQQMWISKQ	EYDESGPSIV	HRKCF		

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
763	652.0147	3	-17.82	-0.0116	39.83	75.1	2	0.0	0	R.VAPEEHPVLLTEAPLNPK.A		96-113
1015	895.9289	2	-23.10	-0.0207	48.00	91.2	1	0.0	0	K.SYELPDGQVITIGNER.F		239-254

Protein 12: Pregnancy zone protein OS=Mus musculus OX=10090 GN=Pzp PE=1 SV=3

Accession:	PZP_MOUSE	**Score:**	98.3
Database:	SwissProt	**Seq. Coverage [%]:**	2.1
MW [kDa] / pI:	165.7 / 6.2	**No. of Peptides:**	2
Modification(s):	Carbamidomethyl		

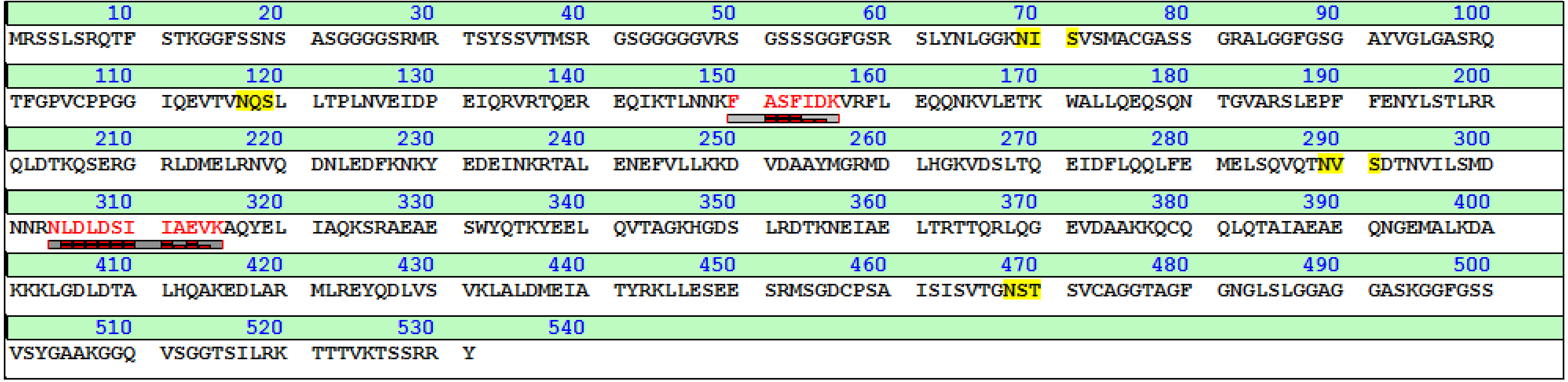
10	20	30	40	50	60	70	80	90	100
MRRNQLPTPA	FLLLFLLLPR	DATTATAKPQ	YVVLVPSEVY	SGVPEKACVS	LNHVNETVML	SLTLEYAMQQ	TKLLTDQAVD	KDSFYCSPFT	ISGSPLPYTF
110	120	130	140	150	160	170	180	190	200
ITVEIKGPTQ	RFIKKKSIQI	IKAESPVFVQ	TDKPIYKPGQ	IVKFRVVSVD	ISFRPLNETF	PVVYIETPKR	NRIFQWQNIH	LAGGLHQLSF	PLSVEPALGI
210	220	230	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
1433	836.7841	3	-29.01	-0.0243	62.28	67.3	1	0.0	0	K.AAPLSLCALTAVDQSVLLLKPEAK.L	Carbamidomethyl: 7	588-611
603	435.767	2	-16.07	-0.0070	34.83	31.0	1	0.0	0	R.LLLQEVR.L		1316-1322

Protein 13: Keratin, type II cytoskeletal 79 OS=Mus musculus OX=10090 GN=Krt79 PE=1 SV=2

Accession:	K2C79_MOUSE	**Score:**	80.4
Database:	SwissProt	**Seq. Coverage [%]:**	3.6
MW [kDa] / pI:	57.5 / 7.6	**No. of Peptides:**	2



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
590	414.2129	2	-13.59	-0.0056	34.47	31.9	2	0.0	0	K.FASFIDK.V		150-156
1324	665.3489	2	-26.68	-0.0177	58.53	48.5	2	0.0	0	R.NLDLDSIIAEVK.A		304-315

Protein 14: Immunoglobulin kappa constant OS=Mus musculus OX=10090 GN=Igkc PE=1 SV=2

Accession:	IGKC_MOUSE	**Score:**	67.6
Database:	SwissProt	**Seq. Coverage [%]:**	13.1
MW [kDa] / pI:	11.9 / 5.6	**No. of Peptides:**	1

```
        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
779	767.8552	2	-17.84	-0.0137	40.37	67.6	2	0.0	0	K.DSTYSMSSTLTLTK.D		63-76

Protein 15: Tubulin alpha-1C chain OS=Mus musculus OX=10090 GN=Tuba1c PE=1 SV=1

Accession:	TBA1C_MOUSE	**Score:**	65.2
Database:	SwissProt	**Seq. Coverage [%]:**	3.1
MW [kDa] / pI:	49.9 / 5.0	**No. of Peptides:**	1

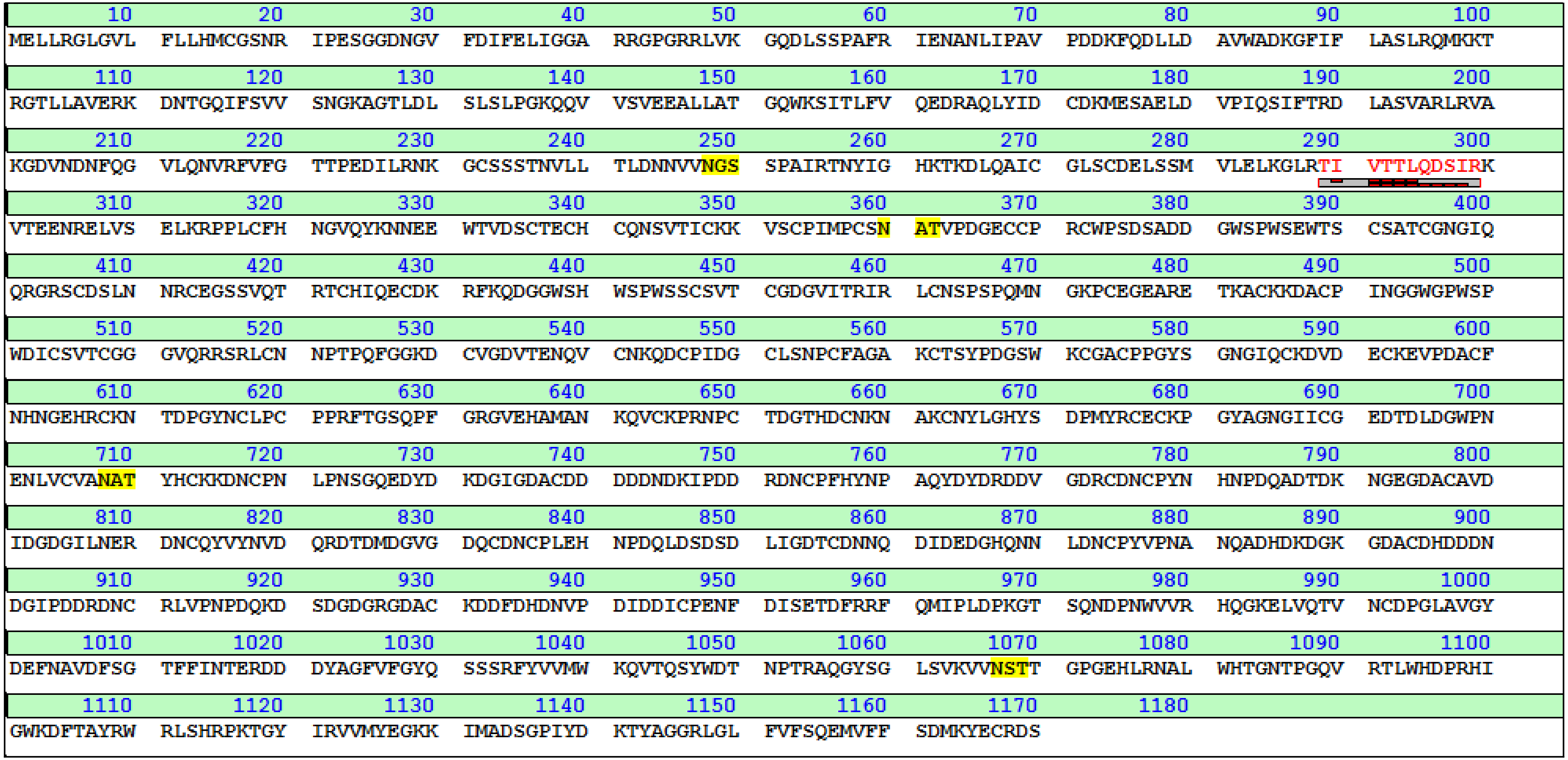
10	20	30	40	50	60	70	80	90	100
MRECISIHVG	QAGVQIGNAC	WELYCLEHGI	QPDGQMPSDK	TIGGGDDSFN	TFFSETGAGK	HVPRAVFVDL	EPTVIDEVRT	GTYRQLFHPE	QLITGKEDAA
110	120	130	140	150	160	170	180	190	200
NNYARGHYTI	GKEIIDLVLD	RIRKLADQCT	GLQGFLVFHS	FGGGTGSGFT	SLLMERLSVD	YGKKSKLEFS	IYPAPQVSTA	VVEPYNSILT	THTTLEHSDC
210	220	230	240	250	260	270	280	290	300
AFMVDNEAIY	DICRRNLDIE	RPTYTNLNRL	ISQIVSSITA	SLRFDGALNV	DLTEFQTNLV	PYPRIHFPLA	TYAPVISAEK	AYHEQLTVAE	ITNACFEPAN
310	320	330	340	350	360	370	380	390	400
QMVKCDPRHG	KYMACCLLYR	GDVVPKDVNA	AIATIKTKRT	IQFVDWCPTG	FKVGINYQPP	TVVPGGDLAK	VQRAVCMLSN	TTAIAEAWAR	LDHKFDLMYA
410	420	430	440	450					
KRAFVHWYVG	EGMEEGEFSE	AREDMAALEK	DYEEVGADSA	EGDDEGEEY					

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
1454	744.4232	2	-26.90	-0.0200	63.01	65.2	2	0.0	0	R.LISQIVSSITASLR.F		230-243

Protein 16: Thrombospondin-1 OS=Mus musculus OX=10090 GN=Thbs1 PE=1 SV=1

Accession:	TSP1_MOUSE	**Score:**	39.9
Database:	SwissProt	**Seq. Coverage [%]:**	0.9
MW [kDa] / pI:	129.6 / 4.7	**No. of Peptides:**	1



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
918	623.8416	2	-19.41	-0.0121	44.90	39.9	1	0.0	0	R.TIVTTLQDSIR.K		289-299