

Supplemental data S2. Proteins identified as sources of endogenous peptides detected in VOO, with $-10\log P$ score above 30. Protein coverage, supporting peptides and best peptide-spectrum matches (PSM) are shown. Protein $-10\log P$ score, sum of the $-10\log P$ scores of the protein's supporting peptides; Coverage (%), percentage of the protein sequence that is covered by the supporting peptides; Area Sample, protein relative abundance; #Peptides, number of high-confidence supporting peptides; #Unique, number of high confidence supporting peptides that are mapped to only one protein group; PTM, posttranslational modifications. Description, as seen in the FASTA data base.

Protein List

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) Sample 1	Area Sample 1	#Peptides	#Unique	#Spec Sample 1	PTM	Avg. Mass	Description
1	1	OE9A032471P1	155.75	9	9	2.8186E6	6	6	8	N	51572	OE9A032471P1
1	2	OE9A042009P1	155.75	9	9	2.8186E6	6	6	8	N	51725	OE9A042009P1
165	11	OE9A085162P3	93.56	4	4	1.0776E6	1	1	1	N	40777	OE9A085162P3
165	12	OE9A085162P1	93.56	4	4	1.0776E6	1	1	1	N	44093	OE9A085162P1
165	13	OE9A085162P2	93.56	3	3	1.0776E6	1	1	1	N	55757	OE9A085162P2
3	3	OE9A001718P2	75.15	7	7	4.5393E5	2	2	3	N	47253	OE9A001718P2
3	4	OE9A001718P1	75.15	7	7	4.5393E5	2	2	3	N	49955	OE9A001718P1
9	245	OE9A057915P1	43.19	7	7	4.0106E6	1	1	1	N	21805	OE9A057915P1
2	82	OE9A117792P1	43.16	2	2	6.1091E6	1	1	1	Y	38475	OE9A117792P1
166	177	OE9A087501P1	39.01	4	4	3.4884E7	1	1	1	N	27647	OE9A087501P1
40	222	OE9A013295P1	32.74	1	1	9.6294E5	1	1	2	N	72709	OE9A013295P1
40	223	OE9A042038P1	32.74	1	1	9.6294E5	1	1	2	N	75341	OE9A042038P1
40	224	OE9A062197P1	32.74	1	1	9.6294E5	1	1	2	N	75780	OE9A062197P1
41	244	OE9A106456P1	31.66	1	1	7.3958E4	1	1	1	N	86941	OE9A106456P1
93	239	OE9A058866P1	31.36	1	1	4.1833E6	1	1	1	N	108486	OE9A058866P1
167	249	OE9A054657P1	30.94	3	3	0	1	1	1	N	30439	OE9A054657P1
167	250	OE9A104108P1	30.94	2	2	0	1	1	1	N	41131	OE9A104108P1
42	289	OE9A026632P1	30.30	4	4	4.3063E5	1	1	1	N	30682	OE9A026632P1
168	293	OE9A100476P1	30.09	2	2	2.2457E5	1	1	1	N	38275	OE9A100476P1
106	101	OE9A087887P1	29.54	3	3	0	1	1	1	N	28540	OE9A087887P1
total 20 proteins												

OE9A032471P1

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Protein Coverage:

1

MAKICLLSLS LVLLFSLSFA QQQLKGQCQI QKINALQPQY KIQSEGGVTE SYDYNDDQFQ CAGAAFLRHT IYRRSLLLP

81

YTSSPLLAYA VKSGILGIM ISGCPETFES SQESQQESHG QGQRFDRHQ KIGNFRQGDI IAVPAGAAHW IYNSGNEELV

161

LVLQDTSNN VNQLDDIPRR FFLA

GNPRSG QEQEQQPWQ PEKQYSRFDN VFKGFAVQVL AEA FNVDLET AKKLQENDQ

241

RGHVMVIEQG LQVISPPFTG EEQQYGEQNR RANGLEETIC TARVRQNIDN PSRADIYNPR AGRFTTANSL TLPILSFLQL

321

SAARGVLHRK AIMSPHWYMN CHTIVYATKG NARMQIVDNR GQAVFDDTIQ EGQVVVPHN FAVVKQAGDQ GFEWVEFNTN

401

ENAMINTISG R

TSFSRGLPV DVIVNAYQVS RKVAEQLKFN RQETL

IFSGG ESSGQPRVSS V

Supporting Peptides:

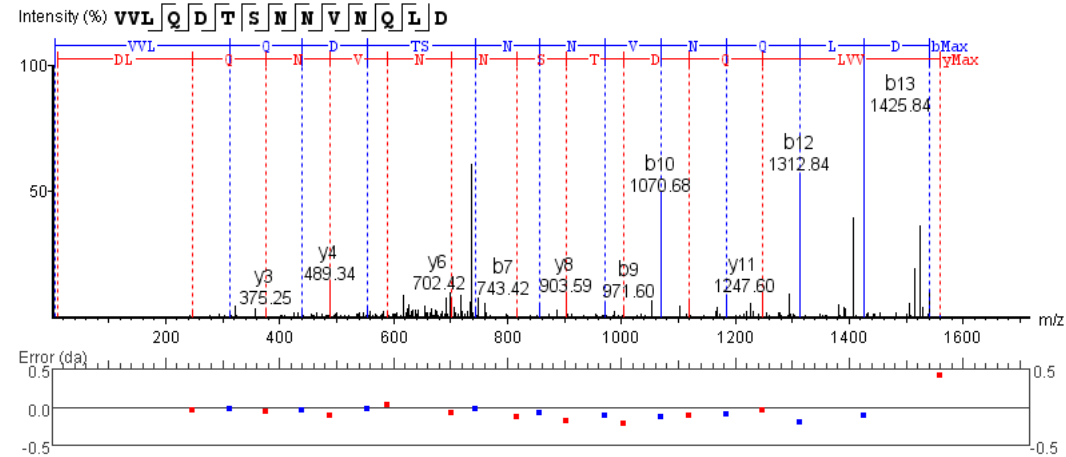
Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
L.VVLQDTSNNVNQLD.D	Y	77.73	1557.7634	14	5.9	779.8878	2	24.96	1	4137	P2860-Aislado informe 2.raw	3.4433E5	1	1	162	175			PEAI DE
L.VVLQDTSNNVNQLDDIPRRFFLA.G	Y	63.26	2673.3875	23	5.2	892.1344	3	48.98	1	10542	P2860-Aislado informe 2.raw	0	0	0	162	184			PEAI DE
L.IFSGGESSGQPR.V	Y	57.53	1220.5785	12	6.8	611.2961	2	22.47	1	3436	P2860-Aislado informe 2.raw	1.2435E5	1	1	446	457			PEAI DE

total 6 peptides

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
Q.DTSNNVNQLDDIPRR.F	Y	46.89	1755.8500	15	5.1	586.2892	3	26.25	1	4526	P2860-Aislado informe 2.raw	1.5401E5	1	1	166	180			PEA/DE
L.QDTSNNVNQLDDIPRR.F	Y	33.36	1883.9086	16	8.0	628.9771	3	26.36	1	4524	P2860-Aislado informe 2.raw	2.0584E6	1	1	165	180			PEA/DE
M.INTISGR.T	Y	31.90	759.4239	7	8.6	380.7197	2	20.53	1	2900	P2860-Aislado informe 2.raw	1.3753E5	1	1	405	411			PEA/DE

total 6 peptides

Best Unique PSM (Scan 4137, m/z=779.8878, z=2, RT=24.96, ppm=5.9):



OE9A042009P1

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Protein Coverage:

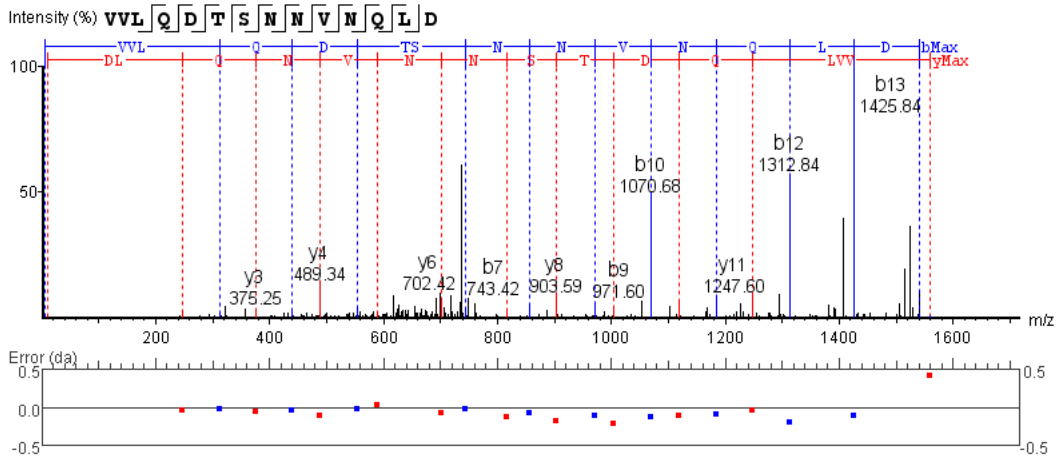
1 MAKIICLLSL SLVLLFSLSF AQQQLKGQCQ IQKINALQPQ YKIQSEGGVT ESYDYNDDQF RCAGAAFLRH TIYRRSLLLP
81 SYTSSPLLAY AVKGSIGLGI MISGCPETFE SSQESQQESQ GQGQRFDRH QKIGNFLQGD IIAFPAGAAH WIYNSGNEEL
161 VL**VVLQDTSN NVNQLDDIPR RFFLA**GNPRS GQEQQQQQLW QPEKQYSRFD NVFKGFAVQV LAEAFNVDL TAKKLQEND
241 QRGHVMNIEQ GLQVISPPFT GEEQQYGEQN RRANGLEETI CTARVRQNI NPSRADIYNP RAGRFTTANS LTLPILSFLQ
321 LSAARGVLHR KAIMSPHWYM NCHTIVYATK GNARMQIVDN RGQAVFDDTI QEGQVVVVPH NFAVVKQAGD QGFWEVFNT
401 NENAM**INTIS** GRTSSFRGLP VDVIVNAYQV SRKVAEQLKF NRQETL**IFSG GESSGQPRVS** SV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
L.VVLQDTSNNVNQLD.D	Y	77.73	1557.7634	14	5.9	779.8878	2	24.96	1	4137	P2860-Aislado informe 2.raw	3.4433E5	1	1	163	176			PEA/DE
L.VVLQDTSNNVNQLDDIPRRFFLA.G	Y	63.26	2673.3875	23	5.2	892.1344	3	48.98	1	10542	P2860-Aislado informe 2.raw	0	0	0	163	185			PEA/DE
L.IFSGGESSGQPR.V	Y	57.53	1220.5785	12	6.8	611.2961	2	22.47	1	3436	P2860-Aislado informe 2.raw	1.2435E5	1	1	447	458			PEA/DE
Q.DTSNNVNQLDDIPRR.F	Y	46.89	1755.8500	15	5.1	586.2892	3	26.25	1	4526	P2860-Aislado informe 2.raw	1.5401E5	1	1	167	181			PEA/DE
L.QDTSNNVNQLDDIPRR.F	Y	33.36	1883.9086	16	8.0	628.9771	3	26.36	1	4524	P2860-Aislado informe 2.raw	2.0584E6	1	1	166	181			PEA/DE
M.INTISGR.T	Y	31.90	759.4239	7	8.6	380.7197	2	20.53	1	2900	P2860-Aislado informe 2.raw	1.3753E5	1	1	406	412			PEA/DE

total 6 peptides

Best Unique PSM (Scan 4137, m/z=779.8878, z=2, RT=24.96, ppm=5.9):



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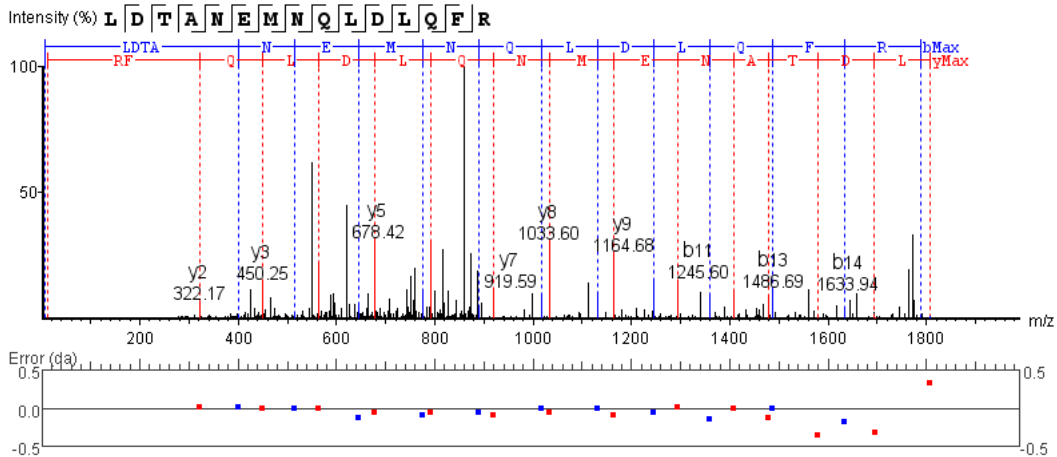
Protein Coverage:

1 MRQQEQGSES QKQFFDRHQK VRQFRQGDVL ALPAGITLWL YNNGQEPLVT VSLLDTANEM NQLDLQFRNF FLAGNRNPQQ
81 SQGQQQQEESQ SEGESPINNI FYGFDPKVLA DVYNVEPETI RKLKGEQDQR GRIVKAERFN VVLPREGQEE EQEGQQQGQG
161 RNGLEETLCT LRLRENLGRP SRADVYNPRA GRLATLNSQT LPILNYLQLS AVKGVLYRNA IMAPHWNVNA HSVIYITRGS
241 SRLQVVGHSQ NLVFDGEVKE NQLIIIPQSF VVIKKAGDQG CEWIAFKTND NAMISPLAGR LSAFRSMPVD VLANAYRVSK
321 QEAQVLKFSR DESTLFSSSS SSMSLEKPKA MEYARDVIET VI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
L.LDTANEMNQLDLQFR.N	Y	93.56	1806.8571	15	8.3	904.4365	2	34.18	1	6794	P2860-Aislado informe 2.raw	1.0776E6	1	1	54	68			PEAKS DB
total 1 peptides																			

Best Unique PSM (Scan 6794, m/z=904.4365, z=2, RT=34.18, ppm=8.3):



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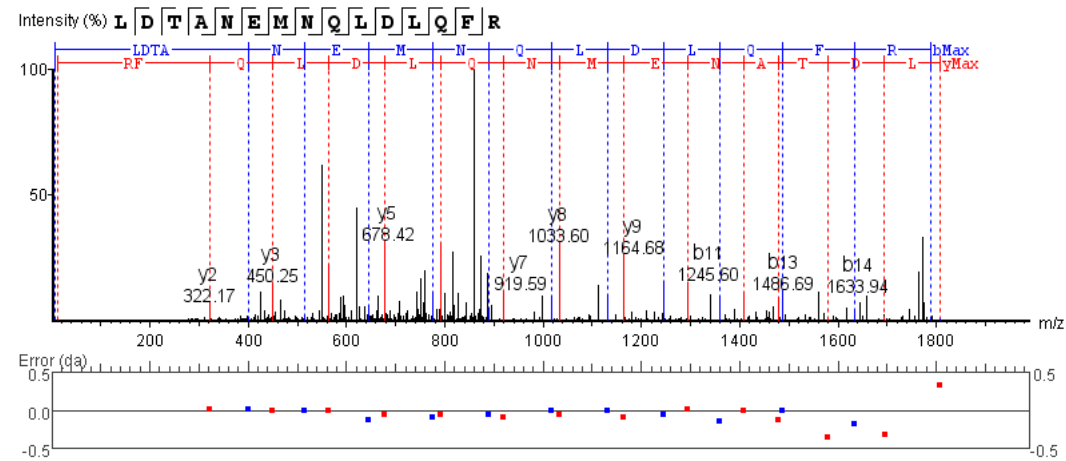
Protein Coverage:

1 MRQQEQGSES QKQFFDRHQK VRQFRQGDVL ALPAGITLWL YNNGQEPLVT VSLLDTANEM NQLDLQFRVR ISEISWLVSN
81 IIRDFIEIFT IFFFQNFFLA GNRNPQQSQG QQQEEESQSEG ESPINNIFYG FPDKVLADVY NVEPETIRKL KGEQDQGRRI
161 VKAERFNVVL PREGQEEEQE GQQGQGGRNG LEETLCTLRL RENLGRPSRA DVYNPRAGRL ATLNSQTLPI LNYLQLSAVK
241 GVLRYNAIMA PHWNVNAHSV IYITRGSSRL QVVGHSGNLV FDGEVKENQL IIIPQSFVVI KKAGDQGC EW IAFKTDNAM
321 ISPLAGRLSA FRSMFPVDVLA NAYRVSKQEA QVLKFSRDES TLFSSSSSSM SLEPKAMEY ARDVIETVI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
L.LDTANEMNQDLQFR.V	Y	93.56	1806.8571	15	8.3	904.4365	2	34.18	1	6794	P2860-Aislado informe 2.raw	1.0776E6	1	1	54	68			PEAKS DB
total 1 peptides																			

Best Unique PSM (Scan 6794, m/z=904.4365, z=2, RT=34.18, ppm=8.3):



OE9A085162P2

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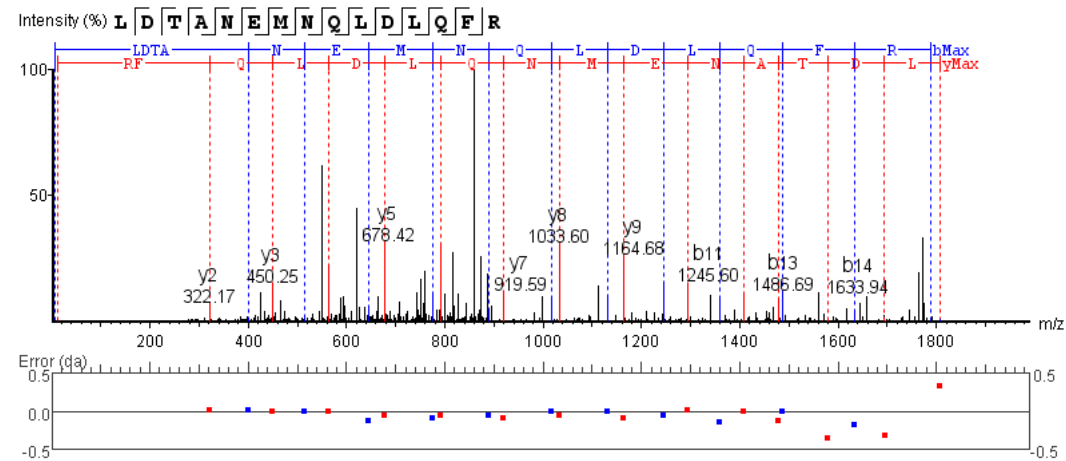
Protein Coverage:

1	MAKLSLHFLS	FTLLFLFGGC	LAQLGSQQQF	LWQKLQQQQQ	HRLRAKTDCH	IERLTAQEPT	RRYDSEAGYA	EYWDPNNKQF
81	ECAGVAAVRT	SIQKNGLFLP	HYNNVAQLIY	VVQKGKLLGA	VIPGCAETFE	TEMRQQEQGS	ESQKQFFDRH	QKVRQFRQGD
161	VLALPAGITL	WLYNNGQEPL	VTVSL	LDTAN EMNQLDLQFR	NFFLAGNRNP	QQSQGQQQEE	SQSEGESPIN	NIFYGFDPKV
241	LADVYNVEPE	TIRKLKGEQD	QRGRIVKAER	FNVVLPREGQ	EEEQEGQQGQ	GGRNGLEETL	CTLRLRENLG	RPSRADVYNP
321	RAGRLATLNS	QTLPIILNYLQ	LSAVKGVLYR	NAIMAPHWNV	NAHSVIYIYR	GSSRLQVVGH	SGNLVFDGEV	KENQLIIIPQ
401	SFVVIKKAGD	QGCEWIAFKT	NDNAMISPLA	GRLSAFRSMP	VDVLANAYRV	SKQEAQVLKF	SRDESTLFSS	SSSSMSLEKP
481	KAMEYARDVI	ETVI						

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
L.LDTANEMNQLDLQFR.N	Y	93.56	1806.8571	15	8.3	904.4365	2	34.18	1	6794	P2860-Aislado informe 2.raw	1.0776E6	1	1	186	200			PEAKS DB
total 1 peptides																			

Best Unique PSM (Scan 6794, m/z=904.4365, z=2, RT=34.18, ppm=8.3):



OE9A001718P2

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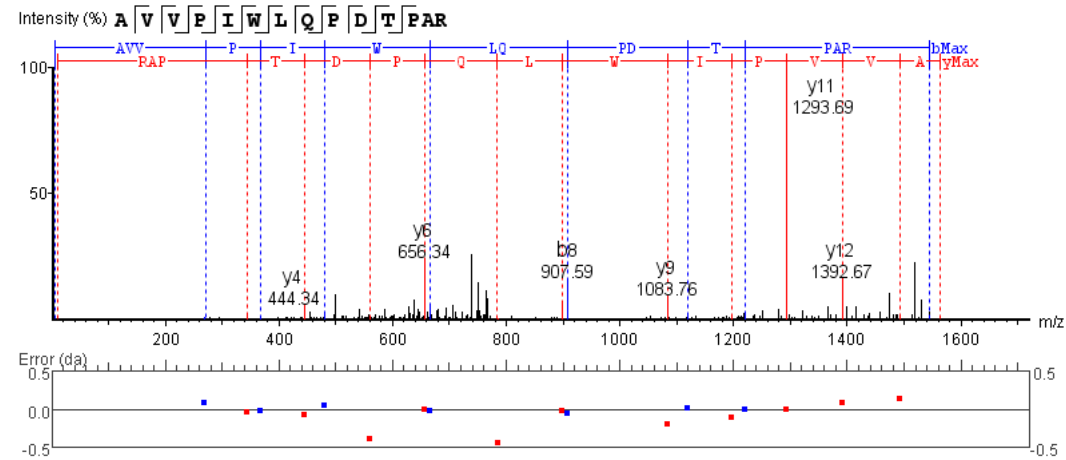
Protein Coverage:

1	MKQAAGHGLL	FMVLFFLLPI	GSLSDDHHRH	KSSFRRVLIG	HDSDKYAVIF	DAGSTGSR	VH VFRFDQNQDL LPIGN	EELELY	
81	VSTKPGLSSY	AADPQAAASS	LRPLLEEAE	A VVPIWLQPD	PAR	LGATAGL	RLVEGDAAEK	ILDAVRNLFK	NESHLKYKHD
161	WVSILDGVQE	GYMWVTINY	LLNTLGRSYA	ETVATIDLGG	ASVQMAYAIS	DENAAKAPHV	AANETYLLQK	NLKGNTYNLY	
241	VHSYLKYGSK	AARAEIFKAS	RNSTNPCILE	GYEGTYTYGG	VVYRVSA PRK	GANMKRCQIL	TRKALKINAP	CKYDSCTFNG	
321	IWNGGGGDGE	KNLYLSSSFY	WTALDSGILK	QNATGGRILV	NAYKDTAKTA	CSTKFMDVKS	KFPDVQEENI	PYLCMDLVYI	
401	YTLLVDGLGE	LKFLLILPEE	IINYNTNTA						

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
E.AVVPIWLQPDTPAR.L	Y	57.79	1561.8616	14	9.6	781.9397	2	38.09	1	7972	P2860-Aislado informe 2.raw	4.3861E5	1	1	110	123			PEAKS DB
R.VHVFRFDQNQDLLPIGN.E	Y	34.71	2011.0275	17	8.8	671.3506	3	48.03	1	10402	P2860-Aislado informe 2.raw	1.5322E4	1	1	59	75			PEAKS DB
total 2 peptides																			

Best Unique PSM (Scan 7972, m/z=781.9397, z=2, RT=38.09, ppm=9.6):



OE9A001718P1

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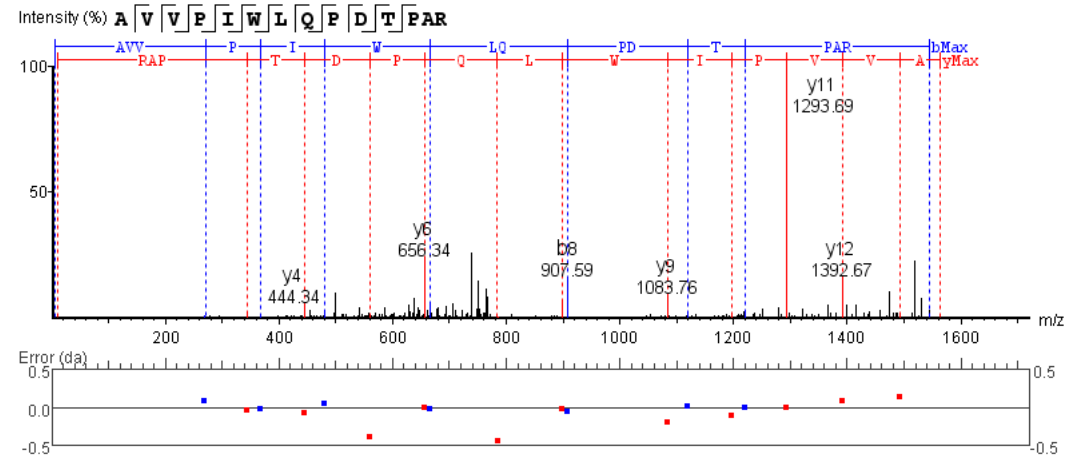
Protein Coverage:

1	MKQAAHGHL	FMVLFFLLPI	GSLSSDHRH	KSSFRRVLIG	HDSDKYAVIF	DAGSTGSR	VH VFRFDQNQDL LPIGN	EELELY
81	VSTKPLSSY	AADPQAAASS	LRPLLEEAE	A VVPIWLQPD	PARLGATAGL	RLVEGDAAEK	ILDAVRNLFK	NESHLKYKH
161	WVSILDGVQE	GYMWVTINY	LLNTLGRSYA	ETVATIDLGG	ASVQMAYAIS	DENAAKAPHV	AANETYLLQK	NLKGNTYNLY
241	VHSYLKYGSK	AARAEIFKAS	RNSTNPCILE	GYEGTYTYGG	VVYRVSAPRK	GANMKRCQIL	TRKALKINAP	CKYDSCTFNG
321	IWNGGGGDGE	KNLYLSSSFY	WTALDSGILK	QNATGGRILV	NAYKDTAKTA	CSTKFMDVKS	KFPDVQEENI	PYLCMDLVYI
401	YTLLVDGLDL	NASQKVEVVK	DVKYKNSEVE	ASWPLGCAID	VTSSLTSKGL	IEKI		

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
E.AVVPIWLQPDTPAR.L	Y	57.79	1561.8616	14	9.6	781.9397	2	38.09	1	7972	P2860-Aislado informe 2.raw	4.3861E5	1	1	110	123			PEAKS DB
R.VHVFRFDQNQDLLPIGN.E	Y	34.71	2011.0275	17	8.8	671.3506	3	48.03	1	10402	P2860-Aislado informe 2.raw	1.5322E4	1	1	59	75			PEAKS DB
total 2 peptides																			

Best Unique PSM (Scan 7972, m/z=781.9397, z=2, RT=38.09, ppm=9.6):



OE9A057915P1

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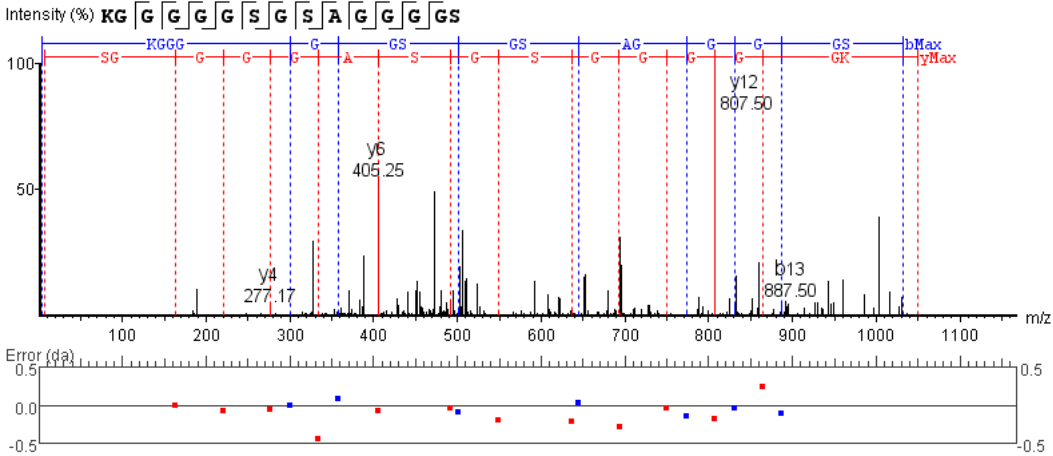
Protein Coverage:

1 ERVPVVKDET VVQDNDFEKR TSASVASTLQ SPPNKAEGTD NSNANAQNGT CSARSLKSA SISASKCIGV KGTNNTEES
81 IAEHSEETQI YHSVVPYIDF ESISGRSFRK LDYPKNSVMP PSISPFTLV L GCHAGGKAGG KGGEGGKGGV GGVGAGKGGG
161 GGSGSAGGGG SAKGSDGIGA SSGMMKAPGG GGATISRNLK AILKDILLKP GLPAGEKAGK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
G.KGGGGSGSAGGGGS.A	Y	31.14	1048.4534	15	-4.9	525.2275	2	35.95	1	7525	P2860-Aislado informe 2.raw	4.0106E6	1	1	157	171			PEAKS DB
total 1 peptides																			

Best Unique PSM (Scan 7525, m/z=525.2275, z=2, RT=35.95, ppm=-4.9):



OE9A117792P1

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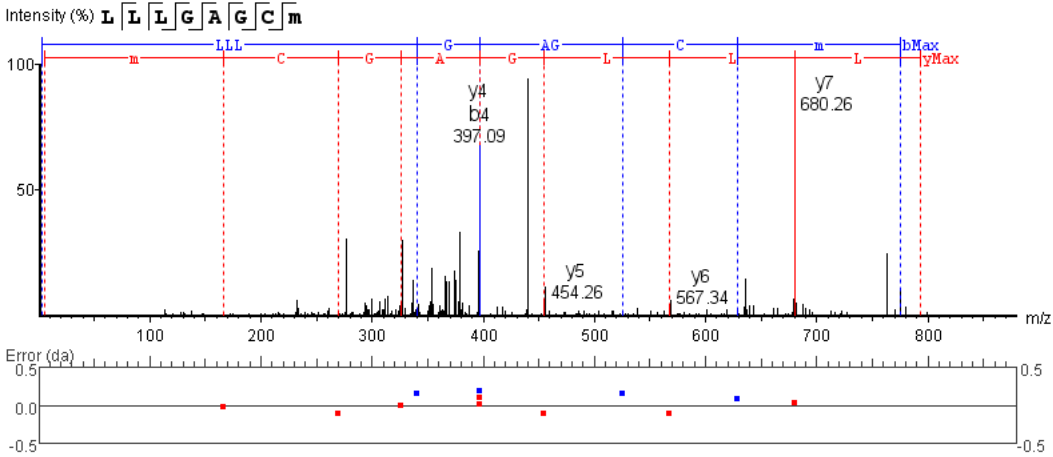
Protein Coverage:

1 MVSPSPASAV AVAWRQVRHE AIQVEVADWS VRALRGKESK ELVVDGGSAL CESWAAACRR VRDESRIQW LHLLQSSLRV
81 QLGFVFLFWV RQYQLLSPKR SFFFIINAF A AGVILLIGFI HVLPAFESL TSPHLSSVAM VSAIGTLMVD AYATSHYNKK
161 SSSMAQIASG DEGGVVPVHT HPTHGHAHGS ASVETDSGET QVLRHRVISQ VLEIIHVSVI IGIALGASES PKTIKPLIAA
241 LTFHQFFEGI GLGGCITQAK FKSRAVVIMA IFFSLTTPIG IVIGIGISNI YSETSPTALI IEGIFNSASA GILIYMALVD
321 LLSADFISPK MQGNGKLQSG ANVSLLL GAG CMSLLAKWA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
S.LLLGAGCM(+15.99).S	Y	34.51	792.3874	8	1.4	397.1985	2	33.76	1	7091	P2860-Aislado informe 2.raw	6.1091E6	1	1	345	352	Oxidation (M)	M8:Oxidation (M):10 00.00	PEAKS DB
total 1 peptides																			

Best Unique PSM (Scan 7091, m/z=397.1985, z=2, RT=33.76, ppm=1.4):



OE9A087501P1

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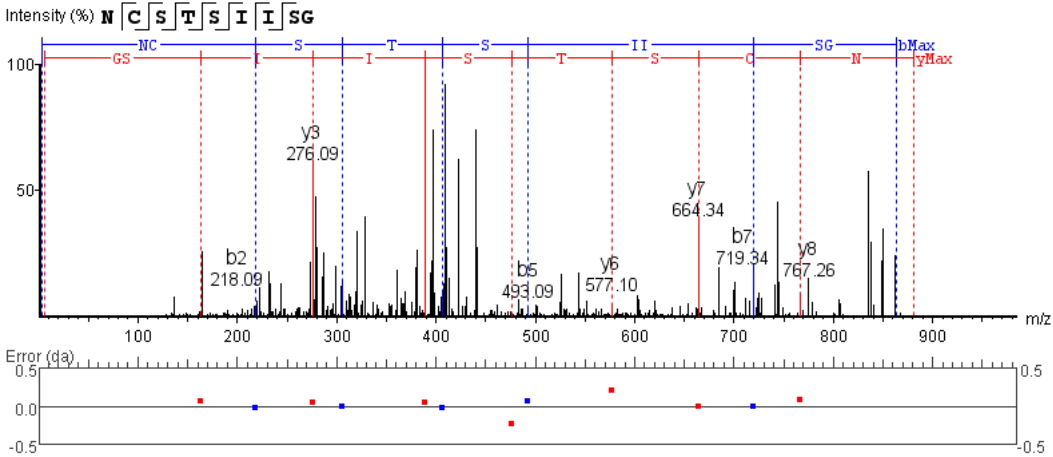
Protein Coverage:

1 MPSCFPITGK TTLAQNVIFD PSPSRSMENPN RVLIVMNGLK DVSIELLEWV LKNFTFHDG TITIFGVSPW LNIPLSAKTW
81 SDIWSMDLED LSIVKERIEW KNDPKYQKVL RLVDLCQKYG VVPEIRTEMG HPLRLLVVEQ ISSLNATLVV FDKYHDRKNI
161 EYYAEKVPCN MVVVNDNGEV ELIKKRSCMD SDVENTPTTI AESSDAAAMA **NCSTSIISGQ** LKKRLKSKSR GKRDKEMKYP
241 DTD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
A.NCSTSIISG.Q	Y	39.01	880.3961	9	9.5	441.2062	2	35.88	1	7180	P2860-Aislado informe 2.raw	3.4884E7	1	1	211	219			PEAKS DB
total 1 peptides																			

Best Unique PSM (Scan 7180, m/z=441.2062, z=2, RT=35.88, ppm=9.5):



OE9A013295P1

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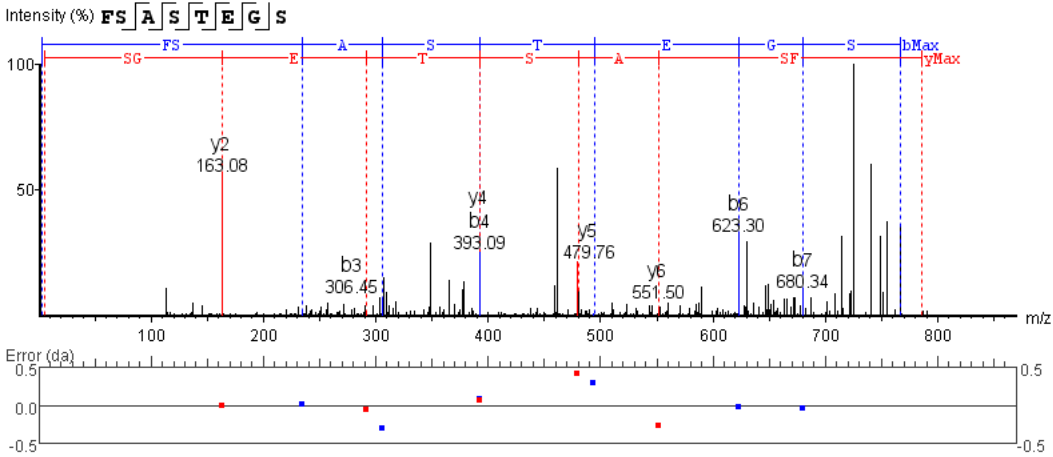
Protein Coverage:

1 MHPRKLLVLL IFISLSFHPD YVLPENVNLD FPFFTLRNIT LLGDSYIRNG VVGLTRELEV PSSSSGSVIY NYPVAFFDPE
81 TNITASFSTR FSFSIDNVNP SSFGDGLTFF LSPNNQTLGS PGGYLGVLNS SQLTKERFIA IEFDRQDLL FNDPDENHVG
161 LDINSLNSIK TANSMIQGVN LKGGNLITAW IDYENEKKKL EIFLSYSSFK PEEPLLRGVG DLSDYLKEFM YVG**FSASTEG**
241 **S**TELFHIQNW NFRTLGRPI RPKIHPYNVS ESSVPLRPPI TVSDSGNRHH KRIGLGLGIG FPAFFCTVLV GFGWISIKKW
321 KGIKSERTIK AEMVTGPRQF SYKELKSATR GFHSSRILGH GAFGTVFKA FMDLGTISAV KRSKHTHEGK TEFLSELSII
401 ASLRHKNLVQ LQGWCVEKGE LLLVYDFMPS GSLDKVLYQE SENGPNLKWY YRYNSAVGLA SVLTYLHQEC EQQVIHRDIK
481 TSNVMDGNY NARLGDFGLA RLMDHGTSPV STLTAGTMGY LAPEYLQYGA ATEKTDVFSY GVVILELACG RRPRIEDES
561 QKPVNLVDWV WRKYSEGKLL EAADQRMNGE FKKEEMKRL LIGLSCANPN SSERPSMRRV FQILNNEADP VVVPKVKPSL
641 ISRTACH

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
G.FSASTEGS.T	Y	32.74	784.3239	8	0.5	393.1665	2	25.27	1	4197	P2860-Aislado informe 2.raw	9.6294E5	2	2	234	241			PEAKS DB
total 1 peptides																			

Best Unique PSM (Scan 4197, m/z=393.1665, z=2, RT=25.27, ppm=0.5):



OE9A042038P1

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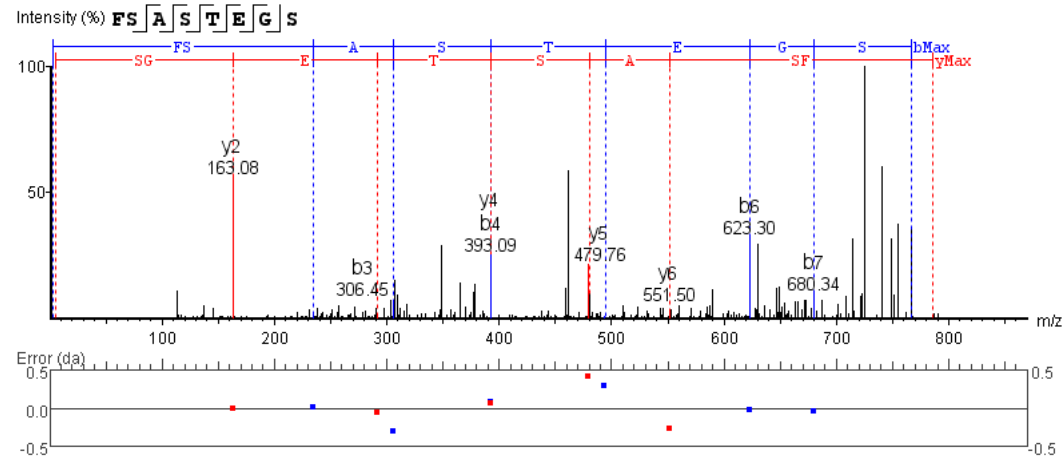
Protein Coverage:

1	MSPRKLLVFL	ILINLSVHPD	YVSSANVNLD	FFFTFRNIT	LLGDSYLRNG	VIGLTRELGV	PSSSSGTVIY	NHPVAFFDPE
81	TNITASFSTR	FSFSIDNVNP	SSFGDGLAFF	LSPNNQTLGS	PGGYLGLVNS	SEFSKNRFIA	IEFDTKQDLH	FNDPDENHVG
161	LDINSLISIK	TANSMIRGVN	LKSGNLITAW	IDYENEKKKF	EIFLSYSSFK	PEEPLLRVSI	DLSDYLKEFM	YVG FSASTEG
241	S TELHCIENTW	SFRTMGFRPI	RPKVQPHSVS	ESSVPLKPPI	TVSGSGNRHH	KRIGLGLGIG	FPAFFGAVLV	IFGWISVKKW
321	KGTKSERIIK	AELVTGPRQF	SYKELKSATR	GFHSSRILGH	GAFGTVYKAF	FMDLGTISAV	KRSKHTHEGK	TEFLSELSII
401	ASLRHKNLVQ	LQGWCVEKGE	LLLVDYDFMPN	GSLDKVLYQE	SENNNPLKWT	YRYIIAVGLA	SVLTYLHQEC	EQQVIHRDIK
481	TSNVMLDGNV	NARLGDFGLA	RLMDHGTSPV	STLTAGTMGY	LVPEYLQYGT	ATEKTDVYSY	GVVVLELACG	RRPIEREDES
561	QKQVNLVDWV	WRKYSEGKLI	EAADQRMNGE	FKEEEMRRL	LIGLSCANPD	SSERPSMRRV	LQILNNEADP	VIVPKVKPSL
641	IFNSNLPLSI	DEIVSDCEEC	SSPGSELEIK	VY				

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
G.FSASTEGS.T	Y	32.74	784.3239	8	0.5	393.1665	2	25.27	1	4197	P2860-Aislado informe 2.raw	9.6294E5	2	2	234	241			PEAKS DB
total 1 peptides																			

Best Unique PSM (Scan 4197, m/z=393.1665, z=2, RT=25.27, ppm=0.5):



OE9A062197P1

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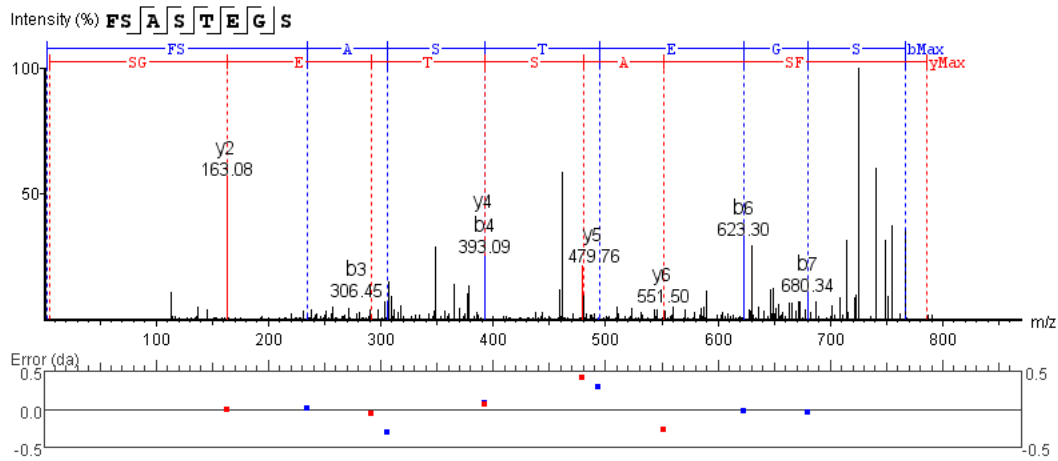
Protein Coverage:

1	MNSRKLLVVS	TLLFLFNFWQ	HPLLVSSENV	NLDFFVFSFR	NFTILGDSYL	RNGVFGLTRE	LEVPTSSSGC	VIYNHPIEFF
81	DRETNITASF	STRFSFSIGN	VNPSSFGDGL	TFFISPNNQT	VGNAGGYLGL	VNSSQLTKNR	FTAIEFDTRQ	DLHFNDPDDN
161	HVGLDINSLI	SIKTANPTLQ	SVNLKSGNLI	TAWIDYMNEK	KKLDVFLSYS	SFKPEKPLL	VNVDLSGYLN	EFMYVG FSAS
241	TEGS TELHYI	ENWSFQTMGF	HPVRPRIHPH	NVSDSSVPHT	PPTPVSDSGN	KNHKRIRLGL	GVGFPAFFCS	VLVVFGWISF
321	KKWRESRTEK	CLKAELVTGP	RQYSYKEIKS	ATRGFHSSRI	VGHGAFGTVY	KAFFTDLGTI	SAVKRSKHAH	EGKTEFLAEL
401	SIIACLRHKN	LVPLQGWCV	KGELLLVYEF	MPHGSLDSSL	YSDSEHGNNL	QWSYRYNIAV	GLASVLTYLH	QECEQQVIHR
481	DVKTSNIMLD	ANYNARLGDF	GLARIMDHGK	SPVSTLTAGT	MGYLAPEYLQ	YGKATEKTDV	FSYGVVILEL	ASGRRPIERE
561	TGSQKMVNLV	DWAWMLHSEG	KIIEAADKNM	NGEYDEKEMK	KLLLIGLSCA	NPDSMERPSM	RAVLQILNNE	AEPMVVPKAK
641	PTLTFSNSLP	LSIDDIVLDC	EDIVIPESQF	EIRPE				

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
G.FSASTEGS.T	Y	32.74	784.3239	8	0.5	393.1665	2	25.27	1	4197	P2860-Aislado informe 2.raw	9.6294E5	2	2	237	244			PEAKS DB
total 1 peptides																			

Best Unique PSM (Scan 4197, m/z=393.1665, z=2, RT=25.27, ppm=0.5):



OE9A106456P1

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| [Protein Coverage](#) | [Supporting Peptides](#) | [Best Unique PSM](#) |

Protein Coverage:

1 MEIEDDSGGQ DLKSGTALPS RSGKSTMVGL DKELIEILNW **LDGNSSAR** DTLSIVGMPGIG KTTFAGKIYD HQRVQEIFHV

81 RAWVTVSQNY DERKILLDLL ESMKKLSGEM HNLETSCLKD KLHKNLKGRR YLIVIDDIWD TKVWNDVNRL FPVDQKRSRI

161 ILTTRLESVA VHVNSSRFAF RRMFLNGVE SWNLFCVKVF GDCCPGELYQ TGTEIAKKCG GLPLAIVLIG GLLSKSNQTQ

241 SYWDHVAKNL SSVIASHDDQ SSKILHLSYN NLPHHLRECF LYMGIFPEDY EILASKLVKL WTAEGFIETE TSKSLEDVAK

321 EYLKNLVERS LILVSKRSSD GEIKTCKIHD LLREFCVREA KESFFHVTDT SLRDLPTNIS TSHITDPSLR SLPDKIISLR

401 RVSIHPNTQT SHPHADRLPT STVRSVLNFD PTLSSLVEFL NSSLIRVLDV VNGNSSDFPT EIVKLLNLRY LSCLNGVREL

481 PSPIHELRLNL QTLILSCMES SFRLPLEIWR MTQLRHVHLD LVSLPDPIIE RVEENPLVV LHDQLSLSTV MNFKFVENIL

561 RRIPNLKKLG ILFDEIGEDW SDYCLNNLAL LQNLALCKL FNWPYKPLQ KIIFPPSLKK LTLRGCFPLW EDMTIIGSLE

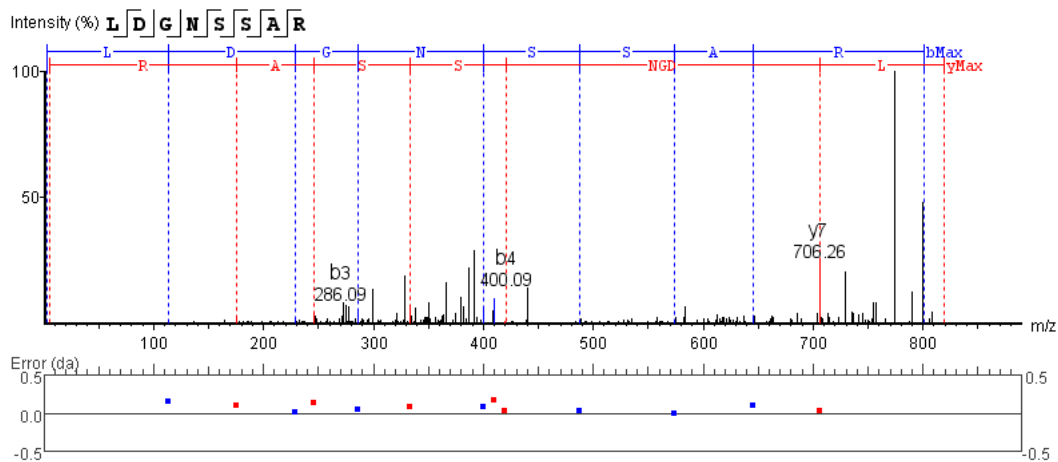
641 KLQVLKLRK AFSGTVWEPK EGEFLELEFL LLENNLEDW NAERTHFPKL EHLILDNCQR LKEVPCGIGE IPTLQKIELY

721 YCSDSLVTS KDIYEEQQES GNEDFQVRIV EMTAEAYET

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
W.LDGNSSAR.D	Y	31.66	818.3882	8	-4.9	410.1964	2	18.63	1	2491	P2860-Aislado informe 2.raw	7.3958E4	1	1	41	48			PEAKS DB
total 1 peptides																			

Best Unique PSM (Scan 2491, m/z=410.1964, z=2, RT=18.63, ppm=-4.9):



OE9A058866P1

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Protein Coverage:

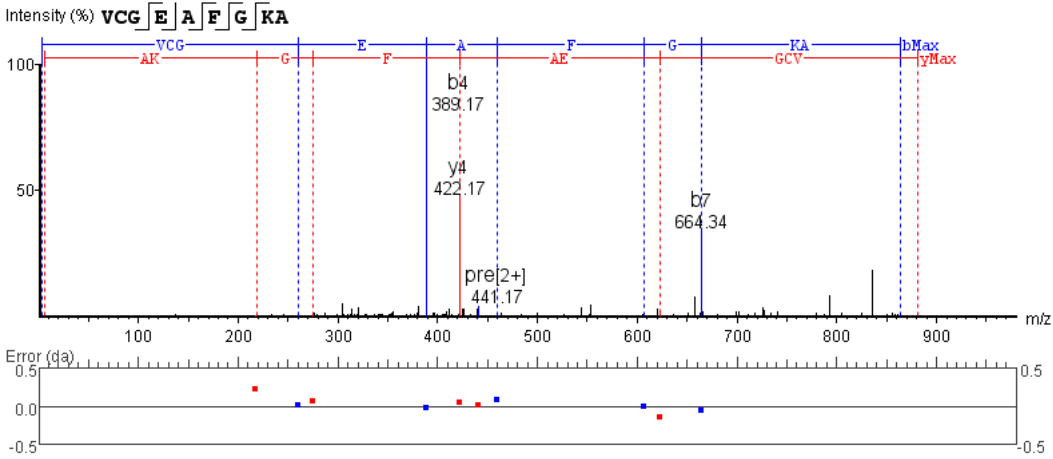
1 MASLASPVNL GSVSMISSCQ FEGSVCLVRR VAFRGNGNNF RRFLGGKRWR YVGICKYSVT TNYITEQGTSTSTDSTCRGS
81 KDNDDTDFLK AAPKPVLPKG SKVEPVLDMF WDEVKLKEDS SNEKTSESEE ERSKVIESLG EVLEMAEKLE KSKEPNVSVN
161 KPSGNKNAGL KNGKPVNSMA DSNSKSKTSK SVWRKGNPVA AAPKVVKKEPP KQDSRIDNRG KDASHAVTTP RPPQPPQNVN
241 PQLQAKPSVA PPVSIKKPVI LKDVNAATKS SVADETNSTT AKKERKPILI DKFASKKPVV DPLIAQAVLA PPKPGKSPPP
321 GKFKDEFRRK GGPSGGSRRR MFDDDIPDED ASELDVSIPG AATARKGRKW TKASRKAARL QAAKDAAPVK VEIMEVDEDG
401 MLTEELAYNL AISEGEILGY LYSKGIKPDG VQKLSKDMVK MICREYEVEI IDTAPVRVEE MAKKKEMFDN DDLKLEDRP
481 PVLTIMGHVD HGKTTLLDYI RSKVAASEA GGITQIGIGAY KVQVPIDGKP QICVFLDTPG HEAFGAMRAR GARVTDIAVI
561 VVAADDGIQP QTNEAIAHAK SAVVPIIVAI NKIDKDGANP DRVMQDLSSI GLMPEEWGGD IPVVKISALK GENVDDLLET
641 IMLVAELQDL KANPHRNAKG TVIEAGLDKS KGPVATFIVQ NGTLNRGDVV **VCGEAFGKA** ALFDDKGKRI DEAGPSMPVQ

721 VIGLNNVPLA GDEFEVVGSL DVAHEKAELQ ANYLRNERIT AKAGDGKVTL SSLASAVSAG KLTGLDLHLQ NIILKVDLQG
801 SIEAIRQALQ VLPQNTVTLK FLLQATGDVS TSDVDLAVAS KAIIFGFNVK APGSIKSYAD NKGVEIRLYR VIYELIDNVR
881 KAMEGLLETV EEQVPIGSAE VRAVFSSGSS RVAGCMVTDG KIVKDSGIRV LRGKKEVHVG VLSSLRRVKE LVKEVNAGLE
961 CGIGVEEFDD WEEGDRIEAF NTVQKKRTLE EASASMTAAL EGVGIEL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
V.VCGEAFGKA.R	Y	31.36	880.4113	9	-8.2	441.2060	2	33.38	1	6569	P2860-Aislado informe 2.raw	4.1833E6	1	1	691	699			PEAKS DB
total 1 peptides																			

Best Unique PSM (Scan 6569, m/z=441.2060, z=2, RT=33.38, ppm=-8.2):



OE9A054657P1

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| [Protein Coverage](#) | [Supporting Peptides](#) | [Best Unique PSM](#) |

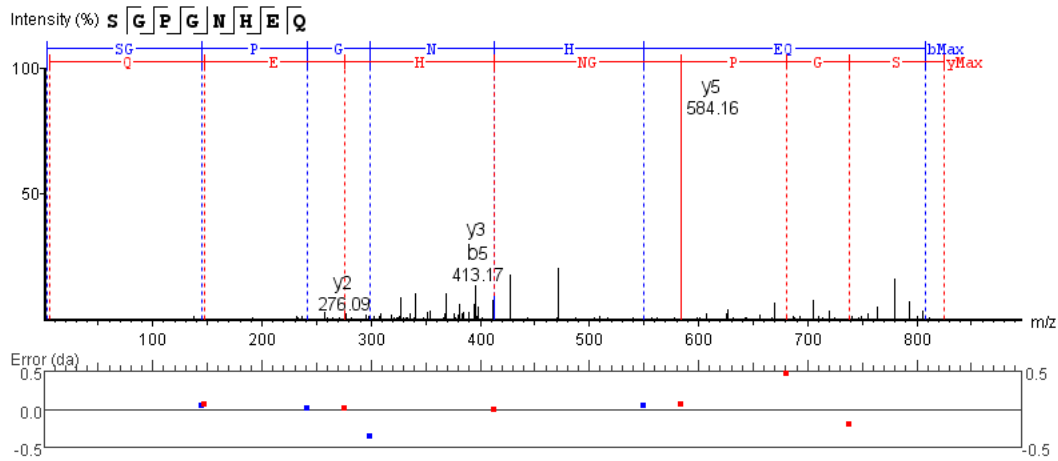
Protein Coverage:

1 MPLLKEEPAD LEGSLAVTPS PPPQTGALVA APSKRSSRDR HTKVEGRGR IRMPAACAAR IFQLTRELGH KSNDETIRWL
81 LERAEPAAIE ATGTVPPSPS PSTRQKRAQS SEFYDVTNSS NLAPVAPIAP QGLVPVFPSPG TFFMIPPTAG AATIAAAGLS
161 NQPQFWAIPA TATPVFSISG RPISNFVSAM QAGVNMSFST STTTTTTTIN PTAVGGGAAA SSGNTESGEN SGGKISISTT
241 MAPSSSSVTS KTTVATGTQT LRDFSLEIYD KKELQIMSGS **S GPGNHEQ**TPS SKP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
G.SGPGNHEQ.T	Y	30.94	824.3413	8	-6.5	413.1722	2	30.38	1	5739	P2860-Aislado informe 2.raw	0	0	0	280	287			PEAKS DB
total 1 peptides																			

Best Unique PSM (Scan 5739, m/z=413.1722, z=2, RT=30.38, ppm=-6.5):



OE9A104108P1

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| [Protein Coverage](#) | [Supporting Peptides](#) | [Best Unique PSM](#) |

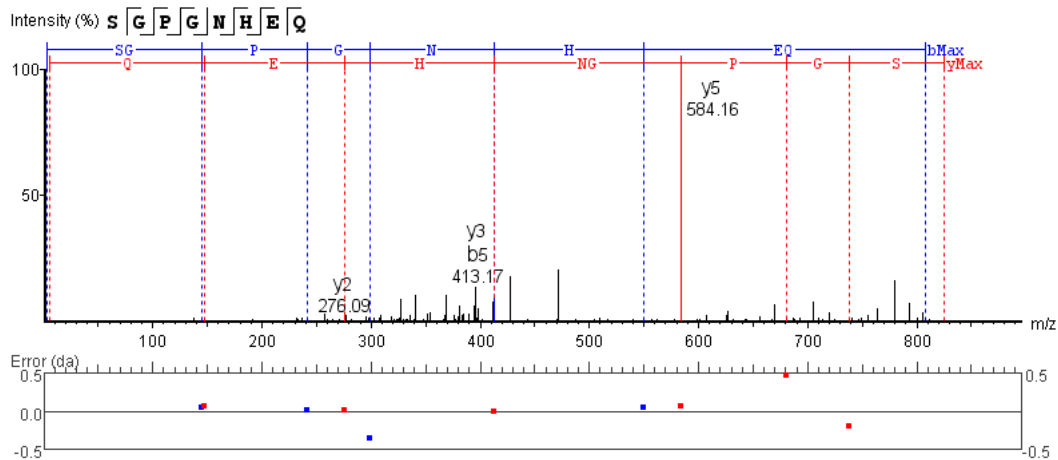
Protein Coverage:

1 MASIHRNHHS QPQHSHHHS PPHIERQEH D EVITLPSDPL LGESHEYITIT AFGPPPDAAE TNPSPPPLPP PSSDIMPLLK
81 EEPADLEGSL AVTPSPPPQT GALVAAPPKR SSRDRHTKVE GRGRRIRMPA ACAARIFQLT RELGHKSDGE TIRWLLERAE
161 PAIEEATGTG TVPAIAVSVN GTLKIPTTPS TASTSPETAG DGARKRRKRA QSSEFYDVAN SSNLAPVAPI APQGLVPLFP
241 SGTFMFIPPT AGAATIAAAG PSNQPFQWAI PATATPVFSI SGRPMSNFVS AMQAGVNMSF STSSTTTTIN PTAVGGGAAA
321 SSGNTESGEN SGGKISISTT MAPSSSVTS KTTVATGTQT LRDFSLEIYD KKELQFMSG S **GPGNHEQ**TPS SKP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
G.SGPGNHEQ.T	Y	30.94	824.3413	8	-6.5	413.1722	2	30.38	1	5739	P2860-Aislado informe 2.raw	0	0	0	380	387			PEAKS DB
total 1 peptides																			

Best Unique PSM (Scan 5739, m/z=413.1722, z=2, RT=30.38, ppm=-6.5):



OE9A026632P1

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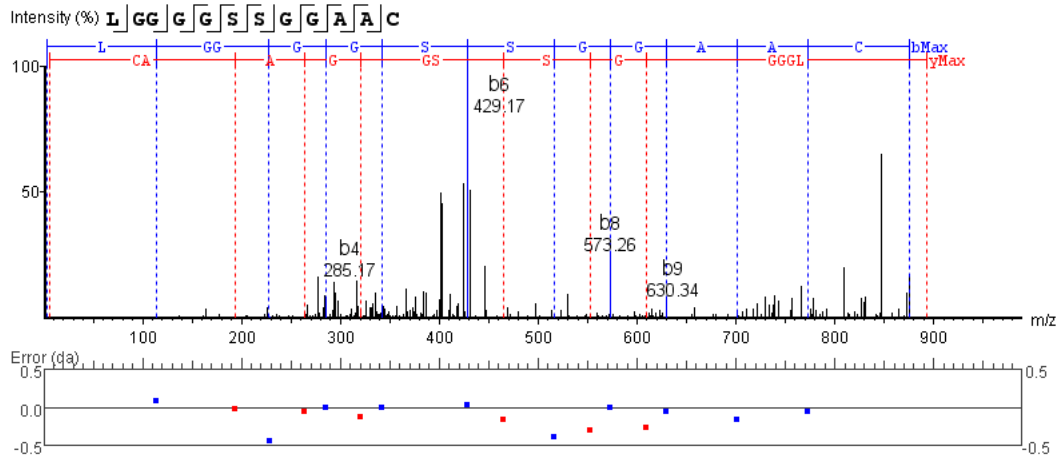
Protein Coverage:

1 MKNTSSGDAE GSSPNSTNPP QQLDQSSPTS SPLRRPPMAP SVMGNLGHSG FRPYRPQGRQ QFDQSSPQRG SNSNISSPMQ
81 RPPVAPPPPP PPPLPLPVIG HTGQSAFMAH WPQGPQPQRQ **FLGGGGSSGG AAC**ASGNASS NGLFGAQAIP VGRSGGYRFG
161 GVGIGNPVIR KRVKEGNQGG QAEGGNPFQC RVC GKQFQSA KALFGHMRQL PDRGWKGTFP PPSFRAEEEF AEVPGHLNPG
241 RAAAAGDAAA AQAGEEATEV HEGREEAGDG LVGPQNYKLP DLNYKPPHDD HDAAA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
F.LGGGGSSGGAAC.A	Y	30.30	892.3708	12	-3.4	447.1878	2	20.67	1	2916	P2860-Aislado informe 2.raw	4.3063E5	1	1	122	133			PEAKS DB
total 1 peptides																			

Best Unique PSM (Scan 2916, m/z=447.1878, z=2, RT=20.67, ppm=-3.4):



OE9A100476P1

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[Protein Coverage](#) | [Supporting Peptides](#) | [Best Unique PSM](#) |

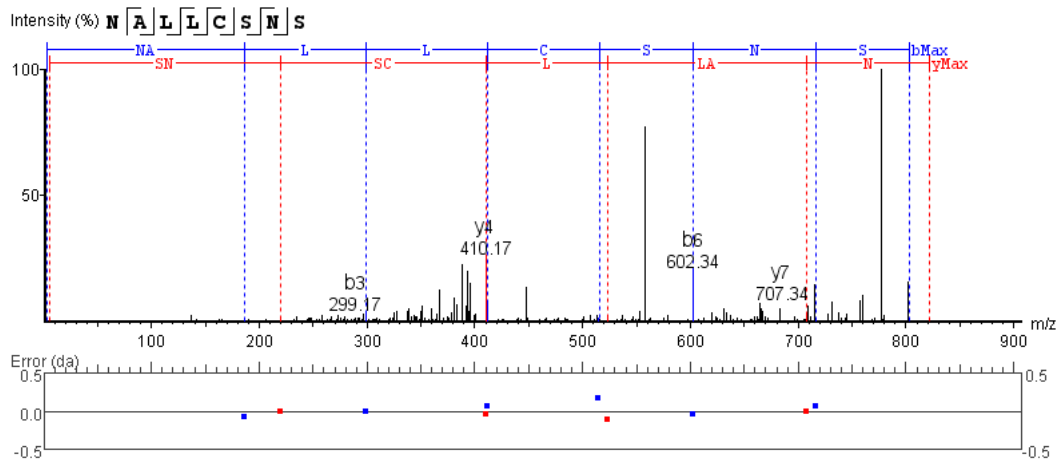
Protein Coverage:

1 MVTAKESCQQ LSAWNLPLND TLLQLRHNNLS LSCFPNSSSY AANVGFPGHS ICNLPGLKTG QLNRS DGFFQ NLPPCWESSS
 81 PIINPYLKDS QFGLSHGIGM SMNPAGSSST SQKKFLIFDQ SGNNTLFFS PSFFPSQNQI IASTAAAGDH GTLDEVAVQT
 161 EQEQQLVKP VVQEKWDENH LTVGSEVRED TEEINALLCS NSTDEYDEV T SMGHTPTTIE ERYDKDIQIG ELVEEVASSN
 241 GSTKRQKLLD GGYKKSSLVD MGDPLEMASP QNYEDGEESS CAGENN FYDD IDS IKKVKV K KIRESLKILE SIIPGLKNKD
 321 PLLIIDRAII YLNSLKLEAE TLGISYL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
I.NALLCSNS.T	Y	30.09	820.3749	8	8.1	411.1950	2	27.63	1	4927	P2860-Aislado informe 2.raw	2.2457E5	1	1	195	202			PEAKS DB
total 1 peptides																			

Best Unique PSM (Scan 4927, m/z=411.1950, z=2, RT=27.63, ppm=8.1):



OE9A087887P1

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[Protein Coverage](#) | [Supporting Peptides](#) | [Best Unique PSM](#) |

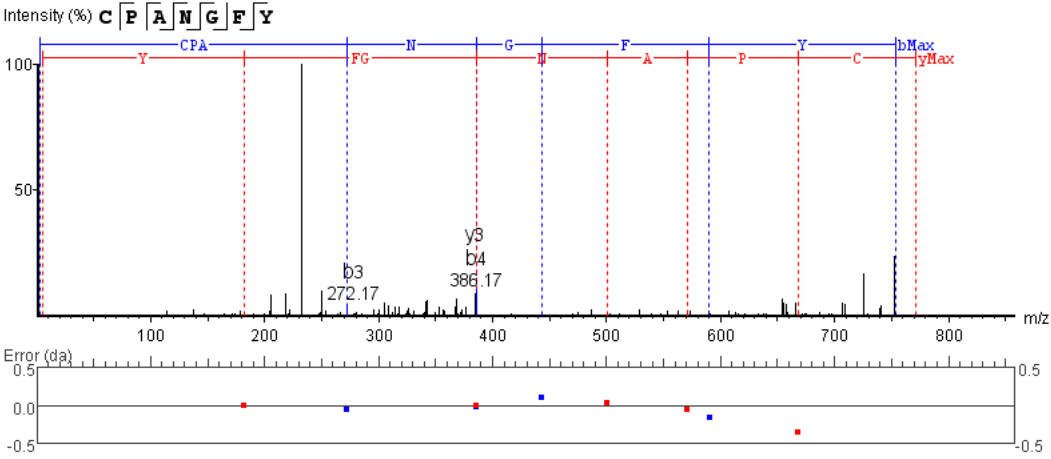
Protein Coverage:

1 MKTFVLVLLC LSSLMGALAQ GGVGSIISKS IFDQMLKHRN DANCPANGFY TYEAFIAAAN SFGAFGTTGD TDTRKREVA
 81 FLAQTSHETT GGWASAPDGP YAWGYCHKQE EGNPPDYCVA NQWPCAPGK KYFGRGPIQI SYN NYGPAG RAIGSDLLNN
 161 PDAVANDPTI SFKTALWFWM TPQTPKPSCH DAISGRWRPS AADSTAGRLP GYGVTNTIIN GGIECGKGSN PQVEDRIGFY
 241 KRYCDLLGVG YGPNLDCYNQ RPFA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area Sample 1	#Feature	#Feature Sample 1	Start	End	PTM	AScore	Found By
N.CPANGFY.T	Y	29.54	770.3057	7	6.7	386.1598	2	26.19	1	4510	P2860-Aislado informe 2.raw	0	0	0	44	50			PEAKS DB
total 1 peptides																			

Best Unique PSM (Scan 4510, m/z=386.1598, z=2, RT=26.19, ppm=6.7):



Peptide List

Prepared with PEAKS™ (bioinform.com)