

Summary

1. Notes

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR. [🔗](#)

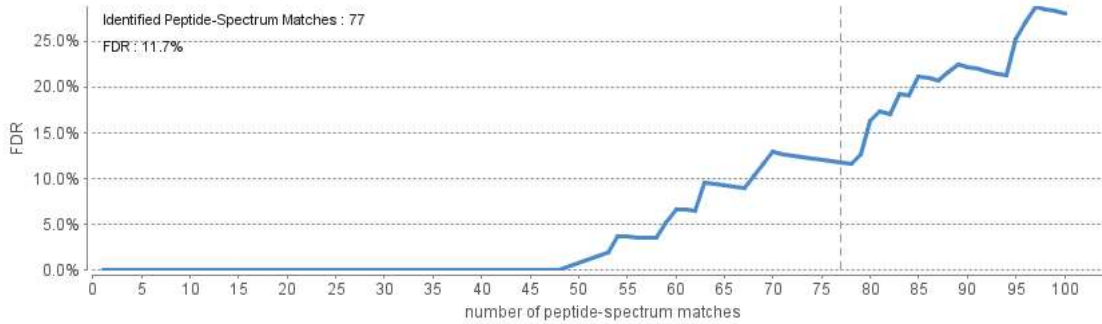


Figure 2. PSM score distribution. (a) Distribution of PEAKS peptide score; (b) Scatterplot of PEAKS peptide score versus precursor mass error. [🔗](#)

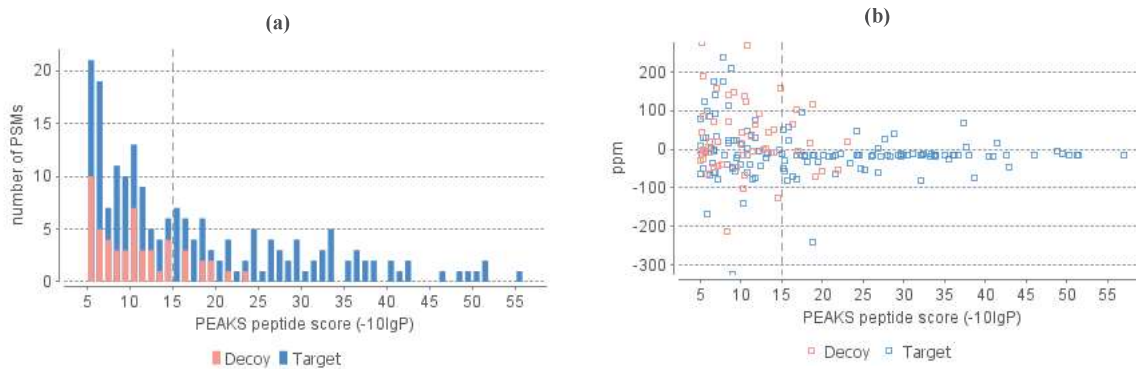


Figure 3. De novo result validation. Distribution of residue local confidence: (a) Residues in de novo sequences validated by confident database peptide assignment; (b) Residues in "de novo only" sequences. [🔗](#)

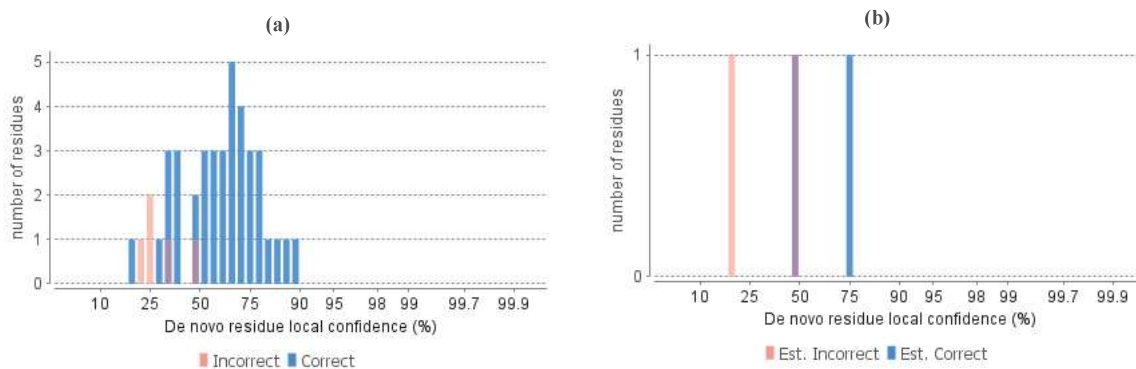


Table 1. Statistics of data.

# of MS Scans	0
# of MS/MS Scans	344

Table 2. Result filtration parameters.

Peptide -10lgP	≥15
Protein -10lgP	≥20
Proteins unique peptides	≥0
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	77
Peptide Sequences	74

Table 4. PTM profile.

Name	ΔMass	#PSM	Position
Carbamidomethyl	57.02	6	N-term
Deamidation	.98	2	NQ
Acetylation	42.01	1	N-term
Methyl ester	14.02	1	E
Carbamidomethyl	57.02	1	C
Pyro-glu from Q	-17.03	1	N-term

Protein Groups	5
Proteins	7
Proteins (#Unique Peptides)	1 (>2); 0 (=2); 6 (=1);
FDR (Peptide-Spectrum Matches)	11.7%
FDR (Peptide Sequences)	12.2%
FDR (Protein)	42.9%
De Novo Only Spectra	1

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. (a) Distribution of precursor mass error in ppm; (b) Scatterplot of precursor m/z versus precursor mass error in ppm.

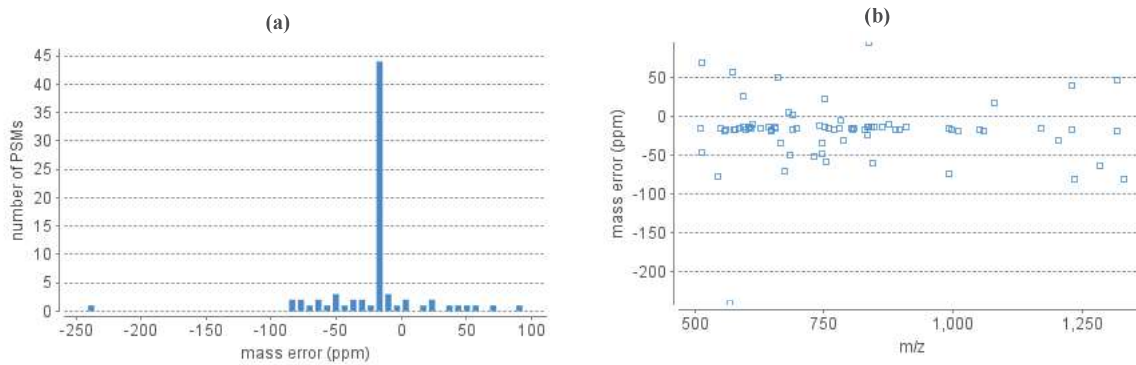


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Sample 1	67	7	0	0	0

4. Other Information

Table 6. Search parameters.

Query Type: Homology Match
 Fixed Modifications:
 Carbamidomethylation: 57.02
 Variable Modifications:
 Oxidation (M): 15.99
 Fragment ion tolerance: 0.1
 L equals I: true
 Q equals K: true
 Report number: 1
 Maximum # of PTMs: 3
 De novo score (ALC%) threshold: 15
 Peptide hit threshold (-10logP): 30.0
 Peaks run ID: 12
 Merge Options: 0.1 min. 0.1 Da
 Precursor Options: corrected
 Charge Options: no correction
 Filter Options: no filter
 Process: true

Table 7. Instrument parameters.

Fractions: CLAUDIA_33.mgf
 Ion Source: ESI(nano-spray)
 Fragmentation Mode: CID, CAD(y and b ions)
 MS Scan Mode: 3D Ion Trap
 MS/MS Scan Mode: Time of Flight (TOF)

Protein List

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
1	195	Q8FDW4 SAT_ECOL6	202.60	42	52	51	Y	140042	Serine protease sat autotransporter OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) OX=199310 GN=sat PE=1 SV=2
3	378	A7FCR5 LIGB_YERP3	27.63	1	1	1	N	63624	DNA ligase B OS=Yersinia pseudotuberculosis serotype O:1b (strain IP 31758) OX=349747 GN=ligB PE=3 SV=1
4	463	Q76N89 HECW1_HUMAN	26.79	0	1	1	Y	179553	E3 ubiquitin-protein ligase HECW1 OS=Homo sapiens OX=9606 GN=HECW1 PE=1 SV=3
2	373	B5Z6D1 CH60_HELPG	23.45	1	1	1	Y	58228	60 kDa chaperonin OS=Helicobacter pylori (strain G27) OX=563041 GN=groL PE=3 SV=1
2	374	B6JPA7 CH60_HELP2	23.45	1	1	1	Y	58300	60 kDa chaperonin OS=Helicobacter pylori (strain P12) OX=570508 GN=groL PE=3 SV=1
2	372	Q7U317 CH60_HELHP	23.45	1	1	1	Y	57651	60 kDa chaperonin OS=Helicobacter hepaticus (strain ATCC 51449 / 3B1) OX=235279 GN=groL PE=3 SV=1
6	207	Q82WTS CYS_A_NITEU	21.49	2	1	1	N	40893	Sulfate/thiosulfate import ATP-binding protein CysA OS=Nitrosomonas europaea (strain ATCC 19718 / CIP 103999 / KCTC 2705 / NBRC 14298) OX=228410 GN=cysA PE=3 SV=1
total 7 proteins									

[Q8FDW4|SAT_ECOL6](#)

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[| Protein Coverage](#) | [Supporting Peptides](#) |

Protein Coverage:

1 MNKIYSLKYS AATGGIAVS ELAKRVSGKT NRKLVATMLS LAVAGTVNAA NIDISNVWAR **DYLDLAQNKG IFQPGATDVT** Carba
 81 **ITLKN**GDKFS FHNLSIPDFS GAAASGAATA IGGYSVTVVA HNKKNPQAAE TQVYAQSSYR VVDRRNSNDF EIQRNLK**FVV** Carba
 161 **ETVGATPAET NPTTYSDALE RYGI**VTS DGS **KKIIGFRAGS GGTSFINGES KISTNSAYSH DLLSASLFEV TQW**DSYGM**MI** Carba
 241 **YKNDKTFRNL EIFGDSGSGA YLYDNKLEK**W VLVGTTHGIA SVNGDQLTWI TKYND**KLVSE LKDTYSHKIN LNGNNVTIKN** Carba
 321 **TDITLHQNNA DTTGTQEK**IT **KDKDIVFTNG GDVLFKDNLD FGSGGIIFDE GHEY**NINGQG FTFKGAGIDI **GKESIVN**WNA Carba
 401 **LYSSDDVLHK IGPGLTNVQK** **KOGANIK**IGE GNVILNEEGT FNNIYLASGN **GKVILNKDNS LGNDQYAGIF FTK**RGGTLDDL Carba
 481 NGHNQTFTRI **AATDDGTTIT NSD**TTKEAVL AINNEDSYIY HGNINGNIK**L THNINSQDKK** TNAKLILDGS **VNTKNDVEVS** Carba
 561 **NASLTMQGH**A **TEHAIFR**SSA NHCSL**VFLCG TDWVTVLKET** ESSYNKKFNS **DYKSNNQQTS FDQP**DWKTGV **FKFDTLHLNN** Carba
 641 **ADFSISR**NAN **VEGNISANKS AITIGDKNVY** IDNLAGKNIT **NGGFDFKQTI STNLSIGETK** FTGGITAHNS QIAIGDQAVV Carba
 721 TLNGATF**LDN TPISIDK**GAK **VIAQNSM**FTT **KGIDISGELT MMGIPEQNSK TVTPGLHYAA DGFRLSGGNA NFIARNMASV** Carba
 801 TGNİYADDA TITLGQPETE TPTISSAYQA WAETLLY**GF**D **TAYRGAITAP KATVSMNNAI WHLNSQSSIN RLET**K**DSMVR** Carba
 881 FTGDNGKFTT LTVNNLTIDD SAFVLRANLA QADQLVVNKS LSGK**NNLLLV DFIEKNGNSN GLNIDLV**SAP **KGTA**VDV**FKA** Carba
 961 TTR**SIGFSDV TPVIEQK**NDT DKATWTLIGY KSVANADAAK KATLLMSGGY **KAF**LAEVNNL NKRMGDLRDI NGESGAWARI Carba
 1041 ISGTGSAGGG FSDNYTHVQV GADNKHELDG LDLFTGVTMT YTD SHAGSDA FSGETKSVGA GLYASAMFES GAYIDLIGKY Carba
 1121 VHHDNEYTAT FAGLGRDYS SHSWYAGAEV GYRYHVTDSA WIEPQAEVY GAVSGKQFSW KDQGMNLTMK DKDFNPLIGR Carba
 1201 TGVDVGKSFS GKDWKVTARA GLGYQFDLFA NGETVLRDAS GEKRIKGEKD GRMLMNVGLN AEIRDNLRFQ LEFEKSAFGK Carba
 1281 YNVDNAINAN FRYSF Mutat

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NGNSN(+.98)GLNIDLVSAPK.G	Y	56.93	1612.8057	-15.5	807.3976	2	0.41	850	1	936	951	Deamidation (NQ)
K.QTISTNLSIGETK.F	Y	51.40	1390.7303	-15.6	696.3616	2	0.34	802	1	688	700	
R.SIGFSDVTPVIEQK.N	Y	51.27	1518.7930	-15.8	760.3918	2	0.42	828	1	964	977	
K.TVTPGLHYAADGFR.L	Y	50.18	1503.7469	-14.7	752.8697	2	0.35	824	1	771	784	
K.FDTLHLNNAFDSISR.N	Y	49.46	1748.8481	-11.3	875.4215	2	0.43	887	1	633	647	
K.GIFQ(+.98)PGATDVTITLK.N	Y	48.73	1560.8398	-5.7	781.4227	2	0.45	840	1	70	84	Deamidation (NQ)
K.DNSLGNQYAGIFFTK.R	Y	46.00	1788.8318	-16.9	895.4080	2	0.46	896	1	458	473	
K.IGPGLTNVQK.K	Y	42.90	1025.5869	-46.1	513.7771	2	0.27	698	1	411	420	
K.NDVEVSNASLTMQGHATEHAIFR.S	Y	42.55	2526.1921	-14.8	843.0589	3	0.50	865	1	555	577	
R.DYLDLAQNK.G	Y	41.37	1078.5294	16.3	1079.5543	1	0.35	962	1	61	69	
L.VFLC(+57.02)GTDWVTVLK.E	Y	40.92	1536.8010	-17.6	769.3943	2	0.51	835	1	586	598	Carbamidomethylation
R.LSGGANFIAR.N	Y	40.35	1118.5833	-17.4	560.2892	2	0.30	718	1	785	795	
K.DNLDFGSGGIIFDEGHEY.N	Y	38.69	1983.8486	-75.1	992.8571	2	0.50	923	2	357	374	
R.IAATDDGTTITNSDITK.E	Y	38.02	1723.8112	-14.2	862.9006	2	0.27	883	1	490	506	
W.NALYSSDDVLHK.I	Y	37.66	1360.6622	5.4	681.3420	2	0.43	787	1	399	410	
R.YGN(sub I)VTSDGSK.K	Y	37.36	1026.4618	69.4	514.2738	2	0.27	700	1	182	191	Mutation
G.F(+57.02)DTAYR.G	Y	36.70	828.3766	-17.0	829.3698	1	0.26	856	1	839	844	Carbamidomethylation (DHKE, X@N-term)
R.AGSGGTSFINGESK.I	Y	36.03	1310.6102	-13.9	656.3033	2	0.26	768	1	198	211	
K.DKDIVFTL(sub N)GGDVLFK.D	Y	35.54	1665.8977	-25.0	833.9353	2	0.43	858	1	342	356	Mutation
K.INLNGNNVTIK.N	Y	35.08	1198.6670	-16.8	600.3307	2	0.33	736	1	309	319	
K.GIDISGELTMMGIPEQNSK.T	Y	33.82	2018.9652	-18.3	1010.4714	2	0.51	926	1	752	770	
K.DKDIVFTNGGDVLFK.D	Y	33.78	1666.8566	-14.8	834.4232	2	0.44	859	1	342	356	
K.NGNSNGLNIDLVSAPK.G	Y	33.69	1611.8217	-17.1	806.9043	2	0.39	849	1	936	951	
K.V(+57.02)ILNK.D	Y	33.35	642.4064	-13.7	643.4049	1	0.23	758	1	453	457	Carbamidomethylation (DHKE, X@N-term)
K.LILDGVSNTK.N	Y	33.18	1058.5972	-18.8	1059.5846	1	0.33	948	1	545	554	
G.M(+57.02)MIYK.N	Y	32.32	741.3553	-11.6	742.3540	1	0.29	812	1	238	242	Carbamidomethylation (DHKE, X@N-term)
K.T(+57.02)GVFK.F	Y	32.20	607.3329	-16.5	608.3302	1	0.22	744	1	628	632	Carbamidomethylation (DHKE, X@N-term)
R.NLEIFGDSGSGAY.L	Y	32.05	1328.5884	-81.6	1329.4873	1	0.45	1016	1	249	261	
K.SAITIGDK.N	Y	31.99	803.4388	-15.2	804.4339	1	0.25	847	1	660	667	
K.Q(-17.03)GANIK.I	Y	31.08	612.3231	-11.4	613.3234	1	0.15	747	1	422	427	Pyro-glu from Q
R.GAITAPK.A	Y	30.38	656.3857	-15.6	657.3827	1	0.20	772	1	845	851	

total 57 peptides

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.GIFQPGATDVITTLK.N	Y	29.93	1559.8558	-16.0	780.9227	2	0.46	838	1	70	84	
K.GTAVDVFKA	Y	29.67	835.4440	-13.7	836.4398	1	0.32	861	1	952	959	
T.VGATPAETNPPTYSDALER.Y	Y	29.62	1991.9436	-17.7	996.9614	2	0.35	925	1	163	181	
K.TGVFK.F	Y	29.25	550.3115	-15.6	551.3102	1	0.20	714	1	628	632	
R.NANVEGNISANK.S	Y	28.73	1229.6000	40.1	1230.6566	1	0.22	989	2	648	659	
K.NTDITLHQNNADTTGTQEK.I	Y	28.22	2099.9719	-17.5	1050.9749	2	0.26	946	1	320	338	
K.LVSELK.D	Y	27.89	687.4167	-17.0	688.4123	1	0.24	794	1	297	302	
K.TVTPGLHY.A	Y	27.08	886.4548	-17.4	887.4467	1	0.30	890	1	771	778	
T.E(+57.02)(+14.02)HAIFR.S	Y	26.77	842.4399	-61.3	843.3955	1	0.46	869	1	572	577	Carbamidomethylation (DHKE, X@N-term); Methyl ester
K.SNNQQTSTFDQPDWK.T	Y	26.14	1693.7332	-14.0	847.8620	2	0.32	872	1	614	627	
F.LN(sub D)NTPISIDK.G	Y	26.07	1113.6030	-18.4	557.7985	2	0.30	716	1	728	737	Mutation
K.GAGIDIGK.E	Y	25.11	729.4021	-52.0	730.3715	1	0.31	811	1	385	392	
K.L(+57.02)VSELK.D	Y	24.72	744.4381	-49.0	745.4089	1	0.33	815	1	297	302	Carbamidomethylation (DHKE, X@N-term)
Y.LYDNKLEK.W	Y	24.51	1021.5444	-16.0	511.7713	2	0.23	695	1	262	269	
W.HLNSQSSINR.L	Y	24.37	1154.5792	-16.8	578.2872	2	0.19	728	1	862	871	
K.NNLLLVDFIEK.N	Y	24.19	1316.7340	45.6	1317.8013	1	0.52	1012	2	925	935	
K.VILNK.D	Y	24.11	585.3850	-15.7	586.3831	1	0.20	731	1	453	457	
K.VIAQNSMF.T	Y	22.16	908.4426	-13.4	909.4377	1	0.36	899	1	741	748	
K.FVVETVGATPAETNPPTYSDALER.Y	Y	21.62	2567.2390	-63.7	1284.5450	2	0.43	999	1	158	181	
K.LTHNINSQDKK.T	Y	20.69	1296.6786	-18.9	649.3343	2	0.20	761	1	530	540	
K.NITNNGFDFK.Q	Y	20.12	1168.5513	-16.3	1169.5396	1	0.35	982	1	678	687	
K.DSMVR.F	Y	18.97	606.2795	-14.4	607.2781	1	0.08	743	1	876	880	
K.FVET.V	Y	17.84	593.3060	-14.5	594.3047	1	0.31	734	1	158	162	
K.AFLAEV.N	Y	17.32	648.3483	-16.7	649.3447	1	0.39	762	1	1012	1017	
K.IIGFR.A	N	16.73	604.3696	-15.8	605.3674	1	0.31	741	1	193	197	
K.ISTNSAYSHDLLSASLFEVTQW.D	Y	15.60	2468.1860	-81.3	1235.0000	2	0.59	991	1	212	233	
total 57 peptides												

A7FCR5|LIGB_YERP3[back to list](#)[| Protein Coverage | Supporting Peptides |](#)**Protein Coverage:**

1 MNILNLKIIM FLLISNIIIV GGAWATSTCP DWPATRIAVE INALEQQLNK WSAAYHQQGH SPVTDDIYDQ LQDKLRVWQS
81 CRGLPDKTES QPIPGKGQFL HPVAHTGLKK LKDETALTRW MAGRKNLWVQ PKVDGVAVTL VYHGGKLVQL LSRGNGVKGQ
161 NWTEKAPFIS AIPQYIANAP ALLTLQGELE LLMDGHQQAQ SGGVNARSTV AGALMRKSPS PLLAQVGVFI WAWPDGPTTM
241 KEKVALLQVM GFPFTAKYSE PVMSHLDDVVQ WRQFWFQAPL PFVTDGVVVR QEEEPAGRYW QATPGQWSMA WKYPPLQHIA
321 EVKDIH**FTLG R**RTGKGTVVLE VLPKIDDKW IRRVNIGSVT RWKQWDIAPG DHITLALAGH GIPRLDNVVW RVHQRNTITA
401 PNWDKFKHQLS CFQRLPHGCE PQFLSRLIWL SGPGLDIGG IGGGFQWELI HHELINDLVG WLLLTPEQIA SIPGIGNARA
481 EKIQQQFQRA KQPPFSRWLL ALGFPQVVSV DAQWQVLLRR SLSEWATMAG IGQMRKQIK HFLDHPDVQA LADFLSTQKV
561 VGFELTE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.FTLGR.T	Y	27.63	592.3333	25.7	593.3558	1	0.25	733	1	327	331	
total 1 peptides												

Q76N89|HECW1_HUMAN[back to list](#)[| Protein Coverage | Supporting Peptides |](#)**Protein Coverage:**

1	MLLHLCSVKN	LYQNRFLGLA	AMASPSR	NSQ	SRRRCKEPLR	YSYNPDQFHN	MDLRGGPHDG	VTIPRSTSDT	DLVTSDSRST	
81	LMVSSSYYSI	GHSQDLVIHW	DIKEEVDAGD	WIGMYLIDEV	LSENFLDYKN	RGVNGSHRQ	IIWKIDASSY	FVEPETKICF		
161	KYYHGVSGAL	RATTPSVTVK	NSAAPIFKSI	GADETVOGQG	SRRLISFSL	DFQAMGLKKG	MFFNPDYLYK	ISIQPGKHSI		
241	FPALPHHGQE	RRSKIIGNTV	NPIWQAEQFS	FVSLPTDVLE	IEVKDKFAKS	RPIIKRFLGK	LSMPVQRLL	RHAIGDRVVS		
321	YTLGRRLPTD	HVSGQLQFRF	EITSSIHDD	EEISLSTEPE	SAQIQDSPMN	NLMESGSGEP	RSEAPESSES	WKPEQLGEGS		
401	VPDGPNGQSI	ELSRPAEEAA	VITEAGDQGM	VSVGPEGAGE	LLAQVQKDIQ	PAPSAEELAE	QLDLGEEASA	LLLEDGEAPA		
481	STKEEPLLEE	ATTQSRAGRE	EEKEQEVEEG	DVSTLEQEGE	RLQLRASVGR	KSRPCSLPVS	ELETVIASAC	GDPETPRTHY		
561	IRIHTLLHSM	PSAQGGSAAE	EEDGAEVEEST	LKDSSEKDG	SEVDTVAADP	SALEEDREEP	EGATPGTAHP	GHSGGHFPPL		
641	ANGAAQDGD	HPSTGSESDS	SPRQGGDHSC	EGCDASCCSP	SCYSSSCYST	SCYSSSCYSA	SCYSPSCYNG	NRFASHTRFS		
721	SVDSAKISES	TVFSSQDDEE	EENSASFESVP	DSMQSPELDP	ESTNGAGPWQ	DELAAPSGHV	ERSPEGLESP	VAGPSNRREG		
801	ECPILHNSQP	VSQPLSLRPE	HHHYPTIDEF	LPPNWEARID	SHGRVIFYVDH	VNRTTTWQRP	TAAATPDGMR	RSGSIQQMEQ		
881	LNRRYQNIQR	TIATERSEED	SGSQSCEQAP	AGGGGGGGSD	SEAESSQSSL	DLRREGSLSP	VNSQKITLLL	QSPAVKFITN		
961	PEFFTVLHAN	YSAYRVFTSS	TCLKHMILKV	RRDARNFERY	QHNRDLVNF	NMFADTRLEL	PRGWEIKTDQ	QGKSFFVDHN		
1041	SRATTFIDPR	IPLQNGRLPN	HLTHRQHLQR	LRSYSAGEAS	EVSRNRGASL	LARPGHSLVA	AIRSQHQHE	LPLAYNDKIV		
1121	AFLRQPNIFE	MLQERQPSLA	RNHTLREKIH	YIRTEGNHGL	EKLSCDADLV	ILLSLFEEEI	MSYVPLQAAF	HPGYSFSPRC		
1201	SPCSPQNSP	GLQRASARAP	SPYRRDFEAK	LRNFYRKLEA	KGFGQGP	GKI	KLIIRRDHLL	EGTFNQVMAY	SRKELQRNKL	
1281	YVTFVGEGL	DYSGPSREFF	FLLSQELFNP	YYGLFEYSAN	DTYTVQISPM	SAFVENHLEW	FRFSGRILGL	ALIHQYLLDA		
1361	FFTRPFYKAL	LRLPCDLSDL	EYLDEEFHQ	LQWMKDNNT	DILDLTFTVN	EEVFGQVTER	ELKSGGANTQ	VTEKNKKEYI		
1441	ERMVKRVER	GVVQTEALV	RGFYEVVDSR	LVSVFDAREL	ELVIAGTAEI	DLNDWRNTE	YRGYHDGHL	VIRWFVAAVE		
1521	RFNNEQRLRL	LQFVTGTSSV	PYEGFAALRG	SNGLRRFCIE	KWGKITSLPR	AHTCFNRLDL	PPYPSYMLY	EKLLTAVEET		
1601	STFGL									

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.MASPE(sub S)R,N	Y	26.79	689.3167	2.0	690.3253	1	0.14	799	1	22	27	Mutation
total 1 peptides												

B5Z6D1|CH60_HELPG

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Protein Coverage:

1	MAKEIKFSDS	ARNLLFEGVR	QLHDAVKVTM	GPRGRNVLIQ	KSYGAPSITK	DGVSVAKEIE	LSCPVANMGA	QLVKEVASKT	
81	ADAAGDGT	ATVLAYSIFK	EGLRNITAGA	NPIEVKRGMD	KAAEAIINEL	KKASKKVGK	EEITQVATIS	ANSDHNIGKL	
161	IADAMEKVGK	DGVITVEEAK	GIEDELVDVE	GMQFDRGYLS	PYFVTNAEK	TAQLDNAYIL	LTDKKISSMK	DILPPLEKTM	
241	KEGKPLLI	EDIEGEALTT	LVVNKLGRVL	NIAAVKAPGF	GDRRKEMLKD	IAVLTGGQVI	SEELGLSLEN	AEVEFLGKAG	
321	RIVIDKDN	TT IVDGK	GHSDD	VKDRVAQIKT	QIASTTSYD	KEKLQERLAK	LSGGVAVIKV	GAASEVEMKE	KKDRVDDALS
401	ATKAAVEEGI	VIGGGAALIR	AAQKVHLNLH	DDEKVGYEII	MRAIKAPLAQ	IAINAGYDGG	VVVNEVEKHE	GHFGFNASNG	
481	KYVDMFKEGI	IDPLKVERIA	LQNAVSVSSL	LLTTEATVHE	IKEEKAAPAM	PDMGGMGGM	GMGMM		

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.D(sub T)TIVDGK,G	Y	23.45	746.3810	-35.4	747.3618	1	0.40	817	1	329	335	Mutation
total 1 peptides												

B6JPA7|CH60_HELP2

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Protein Coverage:

1	MAKEIKFSDS	ARNLLFEGVR	QLHDAVKVTM	GPRGRNVLIQ	KSYGAPSITK	DGVSVAKEIE	LSCPVANMGA	QLVKEVASKT	
81	ADAAGDGT	ATVLAYSIFK	EGLRNITAGA	NPIEVKRGMD	KAAEAIINEL	KKASKKVGK	EEITQVATIS	ANSDHNIGKL	
161	IADAMEKVGK	DGVITVEEAK	GIEDELVDVE	GMQFDRGYLS	PYFVTNAEK	TAQLDNAYIL	LTDKKISSMK	DILPPLEKTM	
241	KEGKPLLI	EDIEGEALTT	LVVNKLGRVL	NIAAVKAPGF	GDRRKEMLKD	IAILTGGQVI	SEELGLSLEN	AEVEFLGKAG	
321	RIVIDKDN	TT IVDGK	GHSDD	VKDRVQIKT	QIASTTSYD	KEKLQERLAK	LSGGVAVIKV	GAASEVEMKE	KKDRVDDALS
401	ATKAAVEEGI	VIGGGAALIR	AAQKVHLNLH	DDEKVGYEII	MRAIKAPLAQ	IAINAGYDGG	VVVNEVEKHE	GHFGFNASNG	
481	KYVDMFKEGI	IDPLKVERIA	LQNAVSVSSL	LLTTEATVHE	IKEEKATPAM	PDMGGMGGM	GMGMM		

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.D(sub T)TIVDGK,G	Y	23.45	746.3810	-35.4	747.3618	1	0.40	817	1	329	335	Mutation
total 1 peptides												

Q7U317|CH60_HELHP

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Protein Coverage:

1 MASKEINFSD SARNKLYEGI KQLSDAVKVT MGPKGRNVL I QKSYGAPTIT KDGVSVAKEI ELADPIANMG AQLVKEVASK
 81 TADAAGDGT TATVLAYSIIY KEGLRNITAG ANPIEVKRG M DKASAAIIIE LKKSSKKIGG KSDIAQVATI SANSDENIGA
 161 LIAEAMEKVG KDGVITVEEA KGINDELSV EGMQFDRGYL SAYFVTNTDK MTAQLENAYV LLTDKKISNM KEILP LLEAT
 241 MQSGKPLLI AEDIEGEALT TLVVNKL RGV LNVSAVKAPG FGDRRKAMLQ DIAILTGGQV ISEELGKTLE AATLADLGSA
 321 ARIVIDKDN **TIVDGK** GKTK DVKDRIAQIK TEIENTTSDY DREKLQERLA KLSGGVAVIK VGAASEVEMK EKKDRVDDAL
 401 SATKAAVDEG IVIGGGSALI RASQKVKLKL EGDEAIGYDI IKRAIKAPLA QIATNAGYDA GVVVNEVEKN SKDGF GFNAT
 481 TGEYVDMFKE GIIDPLKVTR VALQNAVSVS SLLLTTEATI NEIKEDKPAP AMPDMGGMGG MGGMM

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.D(sub T)TIVDGK.G	Y	23.45	746.3810	-35.4	747.3618	1	0.40	817	1	330	336	Mutation
total 1 peptides												

Q82WT5|CYSA_NITEU[back to list](#)| [Protein Coverage](#) | [Supporting Peptides](#) |**Protein Coverage:**

1 MTIEIHDL SK QFGSFTALND INLK**VNPGEL** LALLGPGSG KTTLLRVIAG LETADSGQVL FNEEDSTD KH IRDRHVG FVF
 81 QHYALFRNMT IFENVAFLR VRPRKQRPNA PEINHRVTEL LQLVQLDWLA DRYPHQLSGG QRQRIALARA LAVEPSVLLL
 161 DEFFGALDAK VRKELRAWLR KLHDDMHITS VVTHDQEEA LEVADRIVVM NRGRIEQIGT PDEVYK PAN PFVYEF LGHV
 241 NLFHGRVHQG HAWIGDLEVD APEYSEAEDL SAIAYVRPHD IEVDRTLNGE PALAAHIVHI LAIGPVVRLE LAGKDNQSTN
 321 SIYAEISKER FRELQLARGD QVFIKPRKLD LFPNHAQNGS IH

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VNPGEL.L	Y	21.49	627.3228	-16.5	628.3197	1	0.28	752	1	25	30	
total 1 peptides												