



Protein Identification

By in-gel trypsin digestion, LC-MS/MS peptide analysis and database searching

Order 12345

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Principal Investigator: Alphalyse



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Appendices

- Sample1_IDs.xlsx

SAMPLE



Samples received

The following sample was received at AlphaLyse for protein analysis.

Sample 1

Objective

Identification of proteins in gel piece. The protein gel piece is digested with trypsin and the resulting peptides analyzed by LC-MS/MS.

The MS data are searched against the SwissProt database containing all known public amino acid sequences to identify the protein.

The analysis provides the name of the identified protein in the database, the database accession number, the theoretical amino acid sequence and a list of observed peptides.

SAMPLE



Analytical Procedure

Introduction

Unknown proteins in electrophoresis gels can be identified by mass spectrometric peptide analysis and database searching. The proteins are cleaved into peptides by specific proteolytic cleavage and the peptide masses and peptide fragment masses determined at high sensitivity by nanoflow HPLC coupled to electrospray mass spectrometry (nanoLC-MS/MS). The database search can find the matching proteins if the amino acid sequences are present in the database. The observed peptides partially verify the database protein sequences in the protein sequence coverage maps.

Experimental

DIGESTION

The proteins in the gel piece were reduced and alkylated with iodoacetamide, i.e. carbamidomethylated, and subsequently digested with trypsin that cleaves after lysine and arginine residues. The resulting peptides were concentrated by Speed Vac lyophilization.

nanoLC-MASS SPECTROMETRY

The peptides were dissolved and injected on an Evosep One-LC system for MS/MS analysis on a Bruker Maxis Impact QTOF mass spectrometer.

DATABASE SEARCH

The public protein databases are downloaded from SwissProt. The Mascot software finds matching proteins in the database by their peptide masses and peptide fragment masses. The database search considers fixed modification of cysteines by carbamidomethylation, variable oxidation of methionine residues that may be a result of the sample preparation procedure, as well as N-terminal methionine truncation. The database search does not consider other known protein features recorded in the database, such as signal sequences, sequence variants and other post translational modifications. The protein identification is based on a probability-scoring algorithm and the significant best matching protein is shown in the Results. Homologous proteins with a lower score are not shown in the report. If the protein from the correct organism is not present in the database, then a significant matching homologous protein from another organism is reported. If several different proteins are identified with a significant score, then several protein identifications are reported for the sample.

The identified database protein sequences are shown together with the obtained sequence coverage maps. The peptides used for the identification are highlighted in the sequence and the matching peptides are listed for comparison of the determined and calculated peptide masses. The same peptide mass can appear in multiple identifications. It is considered a positive identification when at least 2 matching peptides have an Ions Score above 20, or if a protein under 20 kDa has 1 peptide with an Ions Score above 50. The sequence coverage % is not considered for the identification. The total Mascot score provided for each identification is a total sum of all the individual peptide scores.

PROTEIN STRUCTURE AND FUNCTION

The identified protein can be looked up at the UniProt and NCBI websites (National Center for Biotechnology Information) by selecting the UniProt/NCBI Entry hyperlink. UniProt and NCBI contain collected information about the protein function and structure, and links to bioinformatics tools such as Conserved functional domains and Blast homology searches.

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SUMMARY TABLE OF IDENTIFIED PROTEINS

The table shows the customer Sample name, the name of the protein identified in the database, the database entry name (accession number), the calculated molecular weight (MW) of the database sequence including eventual signal sequences and fixed modifications used in the database search, the identification Score calculated by the Mascot database search software, and the Sequence Coverage % calculated as the number of amino acids in observed peptides/total number of amino acids in database sequence."






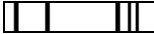

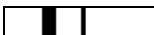

SAMPLE



Results

The Mascot protein identifications along with the peptide identifications and search settings are documented in the Sample1_IDs.xlsx file associated with each sample

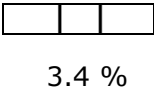
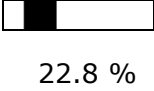
MS analysis 1: Sample 1

Id#	Id	Protein name	Coverage	MW	Score
1.1	HS71A_HUMAN	Heat shock 70 kDa protein 1A OS=Homo sapiens OX=9606 GN=HSPA1A PE=1 SV=1	 70.2 %	70294	2902
1.2	GRP75_BOVIN	Stress-70 protein, mitochondrial OS=Bos taurus OX=9913 GN=HSPA9 PE=2 SV=1	 47.6 %	73981	2502
1.3	Q9CDI9_LACLA	Cell shape-determining protein MreC OS= L. Lactis GN=mreC PE=1 SV=1	 40.2 %	31383	1168
1.4	MTA_HUMAN	Metastasis-associated protein OS=Homo sapiens OX=9606 GN=MTA2 PE=1 SV=1	 44.9 %	75717	1370
1.5	HSP6C_BOVIN	Heat shock cognate 71 kDa protein OS=Bos taurus OX=9913 GN=HSPA8 PE=1 SV=2	 22.1 %	71424	850
1.6	P66A_HUMAN	Transcriptional repressor p66-alpha OS=Homo sapiens OX=9606 GN=GATAD2A PE=1 SV=1	 13.7 %	68363	451
1.7	NUCL_HUMAN	Nucleolin OS=Homo sapiens OX=9606 GN=NCL PE=1 SV=3	 8.0 %	76625	220
1.8	IGH2M_MOUSE	Ig gamma-2 chain C region, membrane-bound form OS=Mus musculus OX=10090 GN=Ighg1 PE=1 SV=2	 12.0 %	44043	157
1.9	IF2B1_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens OX=9606	 4.0 %	63783	96

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		GN=IGF2BP1 PE=1 SV=2		
1.10	DDX5_HUMAN	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens OX=9606 GN=DDX5 PE=1 SV=1		69618 94
1.11	UBIQ_CAMDR	Ubiquitin OS=Camelus dromedarius OX=9838 PE=3 SV=2		8560 61

See Sample1_IDs.xlsx for details.

Protein details

1.1 Protein identification information

Heat shock 70 kDa protein 1A OS=Homo sapiens OX=9606 GN=HSPA1A PE=1 SV=1

Protein ID: HS71A_HUMAN	MW: 70294	pI: 5.48
Mascot score: 2902	Seq. Coverage: 70.2 %	Unique peptides: 37
Uniprot link	Conserved Domain link	Blast link

Peptide map:

1 MAK**AAAIGID** LGTTYSCVGV FQHGKVEIIA NDQGNRTTPS YVAFTDTERL IGDAAKNQVA
61 LNPQNTVFDA KRLIGRKFGD PVVQSDMKHW PFQVINDGDK PKVQVSYKGE TKAFYPPEEIS
121 SMVLTKMKEI AEAYLGYPVT NAVITVPAYF NDSQRQATKD AGVIAGLNVL RIINEPTAAA
181 IAYGLDR**TGK** GER**NVLIFDL** GGGTFDVSIL TIDDGIFEVK ATAGDTHLGG EDFDNRLVNH
241 FVEEFKR**KHK** KDISQNKRAV RRLRTACERA KRTLSSSTQA SLEIDSLFEG IDFYTSITRA
301 RFEELCSDLF RSTLEPVEKA LRDAKLDKAQ IHDLVLVGGG TRIPKVQKLL QDFFNGRDLN
361 KSINPDEAVA YGAAVQAAIL MGDKSENVQD LLLLDVAPLS LGLETAGGVM TALIKRNSTI
421 PTK**QTQIFTT** YSDNQPGVLI QVYEGERAMT KDNLLGRFE LSGIPPAPRG VPQIEVTFDI
481 DANGILNVTA TDKSTGKANK ITITNDK**GRL** SKEEIERMVQ EAEKYKAEDE VQRETVSAKN
541 ALESYAFNMK SAVEDEGLKG KISEADKKKV LDKCQEVISW LDANTLAEKD EFEHKRKELE
601 QVCNPIISGL YQGAGGPGPG GFGAQGPKGG SGSGPTIEEV D

1.2 Protein identification information

Stress-70 protein, mitochondrial OS=Bos taurus OX=9913 GN=HSPA9 PE=2 SV=1

Protein ID: GRP75_BOVIN	MW: 73981	pI: 5.97
Mascot score: 2502	Seq. Coverage: 47.6 %	Unique peptides: 30
Uniprot link	Conserved Domain link	Blast link



Peptide map:

1 MISASRAAVS RFGVTAASRG PTAARHQDGW NGLSHEAFRI VSRRDYASEA IKGAVVGIDL
 61 GTTNSCVAVM EGKQAKVLEN AEGARTTPSV VAFTADGERL VGMPAKRQAV TNPNTTFYAT
 121 KRLLIGR^{RYDD} PEVQKDIK^{NV} PFKIVRASNG DAWVEAHGKL YSPSQIGAFV LMKMKETAEN
 181 YLGHTAKNAV ITVPAYFNDS QRQATKDAGQ ISGLNVL^{RVI} NEPTAAALAY GLDKSEDKII
 241 AVYDLGGGTF DISILEIQKG VFEVKSTNGD TFLGGEDFDQ ALLRHIVKEF KRETGV^{DLTK}
 301 DN^{MAL}QRVRE AAEKAKCELS SSVQTDINLP YLTMDASGPK HLNMKLTRAQ FEGIV^{TDLIR}
 361 RTIAPCQK^{AM} QDAEVSKSDI GEVILVGGMT RMPKVQQT^{VQ} DLFGRAPSKA VNPDEAVAIG
 421 AAIQGGVLAG DVTDVLLLDV TPLSLGIETL GGVFTKLINR NTTIPTKKSQ VFSTAADG^{QT}
 481 QVEIKVCQGE REMAGDNKLL GQFTLIGIPP APRGVPQIEV TFDIDANGIV HVS^{AK}DKGTG
 541 REQQI^{VIQSS} GGLSKDDIEN MVKNAEKYAE ED^{RR}KKERVE AVNMAEGIIH DTETKMEEFK
 601 DQLPADECNK LKEEISKMRE LLARKDSETG ENIRQAASSL QOASL^{KLFEM} AYKKMASERE
 661 GSGSSGTGEQ KDNQKEEKQ

1.3 Protein identification information

Cell shape-determining protein MreC OS= L. Lactis GN=mreC PE=1 SV=1

Protein ID:	MW: 31383	pI: 8.96
Mascot score: 1168	Seq. Coverage: 40.2 %	Unique peptides: 19
Uniprot link	Conserved Domain link	Blast link

Peptide map:

1 MKLSLVAAML LLLSARAEE EDKKEDVGTV VGIDLGTTYS CVGVFKNGRV EIIANDQGNR
 61 ITPSYVA^{FTP} EGERLIGDAA KNQLTSNPEN TVF^{DAKRLIG} RTW^{NDPSVQO} DIKFLPFKVV
 121 EKKTKPYIQV DIGGGQTKTF APEEISAMVL TKMKETA^{EAY} LGKKV^{THAVV} TVPAYFNDAQ
 181 RQATKDAGTI AGLNVMRIIN EPTAAAIAYG LDKREGEKNI LVFDLGGGTF DVSL^{LLTIDNG}
 241 VFEVVATNGD THLGGEDFDQ RVMEHF^{IKLY} Q

1.4 Protein identification information

Metastasis-associated protein MTA2 OS=Homo sapiens OX=9606 GN=MTA2 PE=1 SV=1

Protein ID: MTA2_HUMAN	MW: 75717	pI: 9.7
Mascot score: 1370	Seq. Coverage: 44.9 %	Unique peptides: 22
Uniprot link	Conserved Domain link	Blast link

Peptide map:

1 MAANMYRVGD YVYFENSSN PYLVRRIEEL NKTANGNVEA KVVCLFRRD ISSSLNSLAD
 61 SNAREFEEES KQPGVSEQQR HQLKHRELFL SRQFESLPAT HIRGKCSVTL LNETDILSQY
 121 LEKEDCFYYS LVFDPVQKTL LADQGEIRVG CKYQAEIPDR LVEGESDNRN QQKMEMKVWD
 181 PDNPLTDRQI DQFLVVARAV GTFARALDCS SSIRQPSLHM SAAAA^{SRDIT} LFHAMDTLQR

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241 NGYDLAKAMS TLVPQGGPVL CRDEMEEWSA SEAMLFEEAL EKYGKDFNDI RQDFLPWKSL
301 ASIVQFYMW KTTDRYIQQK RLKAAEADSK **LKQVYIPTYT KPNPNQIISV GSKPGMNGAG**
361 **FQKGLTCE**SC **HTTQSAQWYA** **WGPPNMQCRL** **CASCWIYWKK** **YGGLKTPTQL** **EGATRGTTEP**
421 **HSRGHLSRPE** **AQSLSPYTT**S **ANRAKLLAKN** **RQTFLLQ**TK LTRLARRMCR DLLQPRRAAR
481 **RPYAPINANA** IKAEC SIRLP KAAKTPLKIH PLVRLPLATI VKDLVAQAPL KPKT PRGTKT
541 PINRNQLSQN RGLGGIMVKR AYETMAGAGV PFSANGRPLA SGIRSSSQPA **AKRQKLN**PAD
601 **APNPVVFV**AT **KD**TRALRKAL THLEMRAAR **RPNLPLKVKP** **TLIAVRPPVP** **LPAPSH**PAST
661 **NEPIV**LED

1.5 Protein identification information

Heat shock cognate 71 kDa protein OS=Bos taurus OX=9913 GN=HSPA8 PE=1 SV=2

Protein ID: HSP7C_BOVIN	MW: 71424	pI: 5.37
Mascot score: 850	Seq. Coverage: 22.1 %	Unique peptides: 13
Uniprot link	Conserved Domain link	Blast link

Peptide map:

1 MSKGPVAVGID LGTTYSCVGV FQHGK**VEIIA** **NDQGNRTTPS** **YVAFTDTERL** **IGDAAKNQVA**
61 **MNPNTV**FDA **KRL**IGRRFDD AVVQSDMKHW PFMVVNDAGR PKVQVEYKGE TK**SFY**PEEVS
121 **SMVLT**KMKEI AEAYLGK**TVT** **NAVVTVPAYF** **NDSQRQATKD** **AGTIAGLNVL** **RIINEPTAAA**
181 **IAYGLD**KKVG AERNVLIFDL GGGTFDVSIL TIEDGIFEVK STAGDTHLGG EDFDNRMVNH
241 FIAEFKRKHK KDISENKRAV RRLRTACERA KRTLSSSTQA SIEIDSLYEG IDFYTSITRA
301 RFEELNADLF RGTLDPVEKA LRD**AKLDSQ** **IHDIVLVGGS** **TRIPKIQKLL** **QDF**FNGKELN
361 KSINPDEAVA YGAAVQAAIL SGDKSENVQD LLLLDVTPLS LGIETAGGVM TVLIKRNTTI
421 PTKQTQTFIT YSDNQPGVLI QVYEGERAMT KDNLLGKFE LTGIPPAPRG VPQIEVTFDI
481 DANGILNVSA VDKSTGKENK **ITITNDK**GRL SKEDIERMVQ EAEKYKAEDE KQRDKVSSKN
541 **SLESYAF**NMK ATVEDEKLQG KINDEDKQKI LDKCNEIINW LDKNQTAEKE EFEHQQKELE
601 KVCNPIITKL YQSAGMPGG MPGGMPGGFP GGGAPPSGGA SSGPTIEEVD

1.6 Protein identification information

Transcriptional repressor p66-alpha OS=Homo sapiens OX=9606 GN=GATAD2A PE=1 SV=1

Protein ID: P66A_HUMAN	MW: 68363	pI: 9.95
Mascot score: 451	Seq. Coverage: 13.7 %	Unique peptides: 6
Uniprot link	Conserved Domain link	Blast link

Peptide map:

1 MTEEACRTRS QKRALERDPT EDDVESKIK MERGLLASDL NTDGDMR**VTP** **EPGAGPTQGL**
61 **LR**A TEATAMA MGRGEGLVGD GPVDMRTSHS DMKSERRPPS PDVIVLSDNE QPSSPRVNGL
121 TTVALKETST EALMKSSPEE RERMIKQLKE ELRLEEAKLV LLKKLRQSQI **QK**EATA**QKPT**
181 **GSVGS**T**V**TTP **PPLVR**GTQNI PAGKPSLQTS SARMPGSVIP PPLVRGGQQA SSKLGPQASS
241 QVVMPLVRG AQQIHSIRQH SSTGPPLLL APRASVPSVQ IQGQRIIQG LIRVANVPNT



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301 SLLVNIPQPT PASLKGTTAT SAQANSTPTS VASVV TSAES PASRQAAAKL ALRKQLEKTL
361 LEIPPPKPPA PEMNFLPSAA NNEFIYLVGL EEVQNLLET QGRMSAATVL SREPYMCAQC
421 KTDFTCRWRE EKSGAIMCEN CMTTNQKKAL KVEHTSRLKA AFVKALQEEQ EIEQRLLQQG
481 TAPAQAKAEP TAAPHPVLKQ VIKPRRKLAF RSGEARDWSN GAVLQASSQL SRGSATTPRG
541 VLHTFSPSPK LQNSASATAL VSRTGRHSER TVSAGKGSAT SNWKKTPLST GGTlafvSps
601 LAVHKSSSAV DRQREYLLDM IPPRSIPQSA TWK
    
```

1.7 Protein identification information

Nucleolin OS=Homo sapiens OX=9606 GN=NCL PE=1 SV=3

Protein ID: NUCL_HUMAN	MW: 76625	pI: 4.6
Mascot score: 220	Seq. Coverage: 8.0 %	Unique peptides: 3
Uniprot link	Conserved Domain link	Blast link

Peptide map:

```

1 MVKLAKAGKN QGDPKKMAPP PKEVEEDED EEMSEDEED SSGEEVVIQ KKGKAAATS
61 AKKVVVSPK KAVATPAK AAVTPGKAA ATPAKKTVP AKAVTTPGK GATPGKALVA
121 TPGKGAaip AKGAKNGNA KKEDSDEED DDSEDEED EDEDEDEDEI EPAAMKAAA
181 APASEDEDDE DDEDEDDEDD DEEDDSEEEA METTPAKGK AAKVVPVAK NVAEDEDEEE
241 DDEDEDDEDD EDEDEDDED DEEEEEEEEE EPVKEAPGK KKEMAKQAA PEAKKQVEG
301 TEPTTAFNLF VGNLNFKSA PELKTGISDV FAKNDLAVD VRIGMTRKFG YVDFESAEDL
361 EKALELTGLK VFGNEIKLEK PKGKDSKER DARTLLAKNL PYKVTQDELK EVFEDAAEIR
421 LVSKDGKSKG IAYIEFKTEA DAEKTFEEKQ GTEIDGRSIS LYTGEGKQON QDYRGGKNST
481 WSGESKTLVL SNLSYSATEE TLQEVFEKAT FIKVPQNQNG KSKGYAFIEF ASFEDAKEAL
541 NSCNKREIEG RAIRLELQGP RGSPNARSQP SKTLFVKGLS EDTTEETLKE SFDGsvrari
601 VTDRETGSSK GFGFVDFNSE EDAKAAKEAM EDGEIDGNKV TLDWAKPKGE GGFGGRGGGR
661 GGFGGRGGGR GRRGGFGRG RGGFGRRGGF RGGRRGGGDH KPQgkktkfe
    
```

1.8 Protein identification information

Ig gamma-1 chain C region, membrane-bound form OS=Mus musculus OX=10090 GN=Ighg1 PE=1 SV=2

Protein ID: IGH1M_MOUSE	MW: 44043	pI: 6.02
Mascot score: 157	Seq. Coverage: 12.0 %	Unique peptides: 3
Uniprot link	Conserved Domain link	Blast link

Peptide map:

```

1 AKTTPPSVYP LAPGSAAQTN SMVTLGCLVK GYFPEPVTVT WNSGSLSSGV HTFPAVLQSD
61 LYTLSSSVTV PSSRPSETV TCNVAHPASS TKVDKKIVPR DCGCKPCICT VPEVSSVFI F
121 PPKPKDVLTI TLTPKVTQCV VDISKDDPEV QFSWFVDDVE VHTAQTPRE EQFNSTFRSV
181 SELPIMHQDW LNGKEFKCRV NSAAFPAPIE KTISKTKGRP KAPQVYTIPP PKEQMAKDKV
241 SLTCMITDFP PEDITVEWQW NGQPAENYKN TQPIMNNGS YFVYSKLNQV KSNWEAGNTF
301 TCSVLHEGLH NHHTEKLSLH SPGLQLDETC AEAQDGELDG LWTTITIFIS LFLLSVCYSA
    
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361 AVTLFKVKWI FSSVVELKQT LVPEYKNMIG QAP

1.9 Protein identification information

Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens OX=9606 GN=IGF2BP1 PE=1 SV=2

Protein ID: IGF2BP1_HUMAN	MW: 63783	pI: 9.26
Mascot score: 96	Seq. Coverage: 4.0 %	Unique peptides: 2
<i>Uniprot link</i>	<i>Conserved Domain link</i>	<i>Blast link</i>

Peptide map:

1 MNKLYIGNLN ESVTPADLEK VFAEHKISYS GQFLVKSGYA FVDCPDEHWA MKAIETFSGK
 61 VELQGRLEI EHSVPPKQRS RKIQIRNIPP QLRWEVLDSL LAQYGTVENC EQVNTSESETA
 121 VVNVTYSNRE QTRQAIMKLN GHQLENHALK VSYIPDEQIA QGPENGRGG FGSRGQPRQG
 181 SPVAAGAPAK **QQQVDIPLRL LVPTQYVGAI IGKEGATIRN** ITKQTQSKID VHRKENAGAA
 241 EKAVISVHSTP EGCSSACKMI LEIMHKEAKD TKTADDEVPLK ILAHNNFVGR LIGKEGRNLK
 301 KVEQDTETKI TISSLQDLTL YNPERTITVK GAIENCCRAE QEIMKKVREA YENDVAAMSL
 361 QSHLIPGLNL AAVGLFPASS SAVPPPPSSV TGAAPYSSFM QAPEQEMVQV FIPAQAVGAI
 421 IGKKGQHIKQ LSRFASASIK IAPPETPDSK VRMVIITGPP EAQFKAQGRI YGKLKEENFF
 481 GPKEEVKLET HIRVPASAAG RVIGKGGKTV NELQNLTAEE VVVRDQTPD ENDQVIVKII
 541 GHFYASQMAQ RKIRDILAQV KQQHQKQSN QAQARRK

1.10 Protein identification information

Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens OX=9606 GN=DDX5 PE=1 SV=1

Protein ID: DDX5_HUMAN	MW: 69618	pI: 9.06
Mascot score: 94	Seq. Coverage: 3.4 %	Unique peptides: 2
<i>Uniprot link</i>	<i>Conserved Domain link</i>	<i>Blast link</i>

Peptide map:

1 MSGYSSDRDR GRDRGFGAPR FGGSRAGPLS GKKFGNPGEK LVKKKWNLDE LPKFEKNFYQ
 61 EHPDLARRTA QEVETYRRSK EITVRGHNCP KPVLNIFYEAN FPANVMDVIA RQNFTEPTAI
 121 QAQGWPVALS GLDMVGVAQT GSGKTLISYLL PAIVHINHQP FLERGDGPIC LVLAPTRELA
 181 QVQVQAAEY CRACRLKSTC IYGGAPKGPQ IRDLERGVEI CIATPGR**LID FLECGK**TNLR
 241 RTTYLVLDEA DRMLDMGFEP QIRKIVDQIR PDRQTLMWSA TWPKEVRQLA EDFLKDYYIHI
 301 NIGALELSAN HNILQIVDVC HDVEKDEKLI RLMEEIMSEK ENKTIVFVET KRRCDLTK
 361 MRRDGPWAMG IHGDKSQER DWVLNEFKHG **KAPILIATDV ASRGLDVEDV** KVVINYDYPN
 421 SSEDYIHRIG RTARSTKTGT AYTFFTPNNI KQVSDLISVL REANQAINPK LLQLVEDRGS
 481 GRSRGRGGMK DRRRDYRSAG KRGGFNTFRD RENYDRGYSS LLKRDFGAKT QNGVYSAANY
 541 TNGSFGSNFV SAGIQTSFRF GNPTGTQYQNG YDSTQQYGSN VPMHNGMNQ QAYAYPATAA
 601 APMIGYPMPT GYSQ

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1.11 Protein identification information

Ubiquitin OS=Camelus dromedarius OX=9838 PE=3 SV=2

Protein ID: UBIQ_CAMDR	MW: 8560	pI: 6.56
Mascot score: 61	Seq. Coverage: 22.8 %	Unique peptides: 1
<i>Uniprot link</i>	<i>Conserved Domain link</i>	<i>Blast link</i>

Peptide map:

1 MQIFVKTLTG K**TITLEVEPS DTIENVK**AKI QDKEGIPPDQ QRLIFAGKQL EDGRTLSDYN
61 IQKESTLHLV LRLRGG

SAMPLE