

MASCOT Search Results

Protein View: A0A3Q1M3L6

Uncharacterized protein OS=Bos taurus OX=9913 PE=1 SV=1

Database: Uniprot_bovine
Score: 82
Expect: 0.00079
Nominal mass (M_r): 41077
Calculated pI: 5.16

Sequence similarity is available as [an NCBI BLAST search of A0A3Q1M3L6 against nr.](#)

Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: [Carbamidomethyl \(C\)](#)
Variable modifications: [Oxidation \(M\)](#)

Protein sequence coverage: 26%

Matched peptides shown in **bold red**.

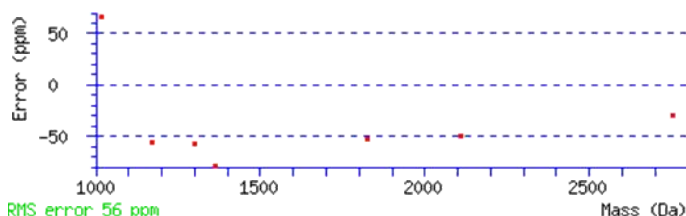
1 MPEPVTVTWN SGALKSGVHT FPAVLQSSGL YSLSSMVTVP ASSSGQTFTC
51 NVAHPASSTK VDKAVDPTCK PSPCDCCPPP ELPGGPSVFI FPPKPKDTLT
101 ISGTPEVTCV VVDVGHDDPE **VKFSWFVDDV EVNTATTKPR** EEQFNSTYRV
151 VSALR**IQHQD WTGGKEFKCK VHNEGLPAPI VRTISRTKGP AREPQVYVLA**
201 **PPQEELSKST VSLTCMVTSF YPDYIAVEWQ** RRGQPESEDK YGTTTPQLDA
251 DSSYFLYSKL RVDNRNSWQEG DTYTCVVMHE ALHNHYTQKS TSKSADLLE
301 EEICADAQDG ELDGLWTTIS IFITLFLLSV CYSATVTLFK **VKWIFSSVVE**
351 **LKRTIVPDYR** NMIGQGA

Unformatted sequence string: [367 residues](#) (for pasting into other applications).

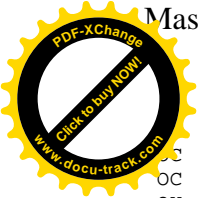
Sort peptides by Residue Number Increasing Mass Decreasing Mass

Show predicted peptides also

| Query | Start - End | Observed | Mr(expt) | Mr(calc) | ppm | M | Score | Peptide |
|--------------------|-------------|-----------|-----------|-----------|-------|---|-------|------------------------------------|
| 65 | 123 - 140 | 2111.9341 | 2110.9268 | 2111.0324 | -50.0 | 0 | 46 | K.FSWFVDDVEVNTATTKPR.E |
| 66 | 123 - 140 | 2111.9341 | 2110.9268 | 2111.0324 | -50.0 | 0 | | K.FSWFVDDVEVNTATTKPR.E |
| 32 | 156 - 165 | 1169.5049 | 1168.4976 | 1168.5625 | -55.5 | 0 | | R.IQHQDWTGGK.E |
| 35 | 171 - 182 | 1301.6583 | 1300.6510 | 1300.7252 | -57.0 | 0 | | K.VHNEGLPAPIVR.T |
| 36 | 171 - 182 | 1301.6583 | 1300.6511 | 1300.7252 | -57.0 | 0 | | K.VHNEGLPAPIVR.T |
| 55 | 193 - 208 | 1826.8557 | 1825.8484 | 1825.9462 | -53.5 | 0 | | R.EPQVYVLAPPQEELSK.S |
| 75 | 209 - 231 | 2753.2139 | 2752.2066 | 2752.2877 | -29.5 | 0 | | K.STVSLTCMVTSFYPDYIAVEWQR.N |
| 39 | 343 - 353 | 1363.6659 | 1362.6586 | 1362.7660 | -78.8 | 1 | | K.WIFSSVELKR.T |
| 22 | 353 - 360 | 1019.6312 | 1018.6239 | 1018.5560 | 66.7 | 1 | | K.RTIVPDYR.N |



ID A0A3Q1M3L6_BOVIN Unreviewed; 367 AA.
AC A0A3Q1M3L6;
DT 10-APR-2019, integrated into UniProtKB/TrEMBL.
DT 10-APR-2019, sequence version 1.
DT 11-DEC-2019, entry version 5.
DE SubName: Full=Uncharacterized protein {ECO:0000313|Ensembl:ENSBTAP00000064749};
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;



OC Eutheria; Laurasiatheria; Artiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913 {ECO:0000313|Ensembl:ENSBTAP00000064749, ECO:0000313|Proteomes:UP000009136};
 RN [1] {ECO:0000313|Ensembl:ENSBTAP00000064749, ECO:0000313|Proteomes:UP000009136}
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Hereford {ECO:0000313|Ensembl:ENSBTAP00000064749,
 RC ECO:0000313|Proteomes:UP000009136};
 RA Rosen B.D., Bickhart D.M., Koren S., Schnabel R.D., Hall R., Zimin A.,
 RA Dreischoer C., Schultheiss S., Schroeder S.G., Elsik C.G., Couldrey C.,
 RA Liu G.E., Van Tassell C.P., Phillippy A.M., Smith T.P.L., Medrano J.F.;
 RT "ARS-UCD1.2.";
 RL Submitted (MAR-2018) to the EMBL/GenBank/DDBJ databases.
 RN [2] {ECO:0000313|Ensembl:ENSBTAP00000064749}
 RP IDENTIFICATION.
 RC STRAIN=Hereford {ECO:0000313|Ensembl:ENSBTAP00000064749};
 RG Ensembl;
 RL Submitted (JAN-2019) to UniProtKB.
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 CC -----
 DR Ensembl; ENSBTAT00000083559; ENSBTAP00000064749; ENSBTAG00000055240.
 DR GeneTree; ENSGT00940000162793; -.
 DR Proteomes; UP000009136; Chromosome 20.
 DR GO; GO:0016021; C:integral component of membrane; IEA:UniProtKB-KW.
 DR Gene3D; 2.60.40.10; -; 3.
 DR InterPro; IPR007110; Ig-like_dom.
 DR InterPro; IPR036179; Ig-like_dom_sf.
 DR InterPro; IPR013783; Ig-like_fold.
 DR InterPro; IPR003006; Ig/MHC_CS.
 DR InterPro; IPR003597; Ig_C1-set.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00407; IGc1; 3.
 DR SUPFAM; SSF48726; SSF48726; 3.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 PE 1: Evidence at protein level;
 KW Immunoglobulin domain {ECO:0000256|SAAS:SAAS00653601};
 KW Membrane {ECO:0000256|SAM:Phobius};
 KW Proteomics identification {ECO:0000213|PeptideAtlas:A0A3Q1M3L6};
 KW Reference proteome {ECO:0000313|Proteomes:UP000009136};
 KW Transmembrane {ECO:0000256|SAM:Phobius};
 KW Transmembrane helix {ECO:0000256|SAM:Phobius}.
 FT TRANSMEM 314..339
 FT /note="Helical"
 FT /evidence="ECO:0000256|SAM:Phobius"
 FT DOMAIN 1..66
 FT /note="Ig-like"
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 FT DOMAIN 86..185
 FT /note="Ig-like"
 FT /evidence="ECO:0000259|PROSITE:PS50835"
 FT DOMAIN 194..292
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 SQ SEQUENCE 367 AA; 40476 MW; AF804286143DA888 CRC64;
 MPEPVTVTWN SGALKSGVHT FPAVLQSSGL YSLSSMVTVP ASSSGQTFTC NVAHPASSTK
 VDKAVDPTCK BSPDCDCPPP ELPGGPSVFI FPPKPKDILT ISGTPEVTCV VVDVGHDDPE
 VKFSWFVDDV EVNTATTKPR EEQFNSTYRV VSALRIQHOD WTGGKEFKCK VHNEGLPAPI
 VRTISRKGP AREPQVYVLA PPQEELSKST VSLTCMVSF YPDYIAVEWQ RNGQPESSEK
 YGTTTPQLDA DSSYFLYSLK RVDNRNSWQEG DTYTCVVMHE ALHNHYTQKS TSKSADLLE
 EEICADAQDG ELDGLWTTIS IFITLFLLSV CYSATVTLEK VKWIFSSVVE LKRTIVPDYR
 NMIGQGA
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