

MATRIX SCIENCE MASCOT Search Results

Protein View: A0A3Q1MU98

Complement component C9 OS=Bos taurus OX=9913 GN=C9 PE=1 SV=1

Database: Uniprot_bovine
Score: 131
Expect: 1.1e-008
Nominal mass (M_r): 58618
Calculated pI: 5.74

Sequence similarity is available as [an NCBI BLAST search of A0A3Q1MU98 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: 16%

Matched peptides shown in **bold red**.

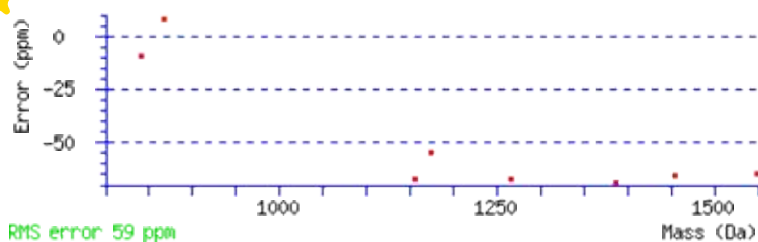
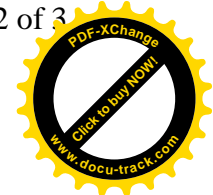
1 MSAGQRFafa ICILEISLLR AGPTPSYDPA ER**QGTPLPID** CRMSSWSEWS
51 KCDPCLKQMF RSR**SIEIFGQ** FNGRKCVDAV GDRQQCVPT E ACEDPEEGCG
101 NDFQCGTGRC IKNRLLCNED NDCGDYSD E NCEQDPRPPC RNRVVEESEL
151 ARTAGFGINI LGMDPLSTPF DNQYYNGLCD **RVWDGNTLT**Y **YRRPWNVASL**
201 **FYDTK**ADKNF RTENHEESIQ ILRTIIEKK LNFNAGLSVK YTPVEAIEKN
251 KCVLDLEHSDK GSTSSPSKLA AEAKFRFTYS KDDIYR**LLSS** **YSAKQEKMF**L
301 **HVK**GKVHLGR FVMRSRDVML QTTFLDSINT LPTTYEKGEY FAFLETYGT H
351 YSSSGSLGGL YELIYVLDK SMEQKETNPE ADLFDDVITF IRGGTRKYAT
401 ELKEKLLRGA RMINVTDFVN WAASLNHAPV LISQKLVP IY DLIPVK**MKDA**
451 **HLKKQ**NLERA **IEDYINEFSV** RKCQPCQNGG TVVLLDGECV CSCPKEFKGV
501 ACEIKK

Unformatted sequence string: [506 residues](#) (for pasting into other applications).

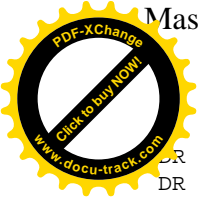
Sort peptides by ☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Show predicted peptides also

Query	Start - End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Peptide
36	33 - 42	1156.5005	1155.4932	1155.5706	-67.0	0		R.QGTPLPIDCR.M
43	64 - 74	1267.5582	1266.5509	1266.6357	-66.9	0		R.SIEIFGQFNGR.K
44	64 - 74	1267.5582	1266.5510	1266.6357	-66.9	0	29	R.SIEIFGQFNGR.K
52	182 - 192	1387.5682	1386.5609	1386.6568	-69.2	0		R.VWDGNTLTYYR.R
53	182 - 192	1387.5682	1386.5610	1386.6568	-69.1	0	18	R.VWDGNTLTYYR.R
65	193 - 205	1550.6960	1549.6887	1549.7889	-64.6	0		R.RPWNVASLTYDTK.A
66	193 - 205	1550.6960	1549.6888	1549.7889	-64.6	0		R.RPWNVASLTYDTK.A
9	287 - 294	868.4844	867.4771	867.4702	8.03	0		R.LLSSYSAK.Q
39	295 - 303	1175.5602	1174.5529	1174.6169	-54.4	1		K.QEKMF LHVK.G + Oxidation (M)
2	447 - 453	842.4471	841.4398	841.4480	-9.70	1		K.MKDAHLK.K
57	460 - 471	1455.6167	1454.6094	1454.7041	-65.1	0		R.AIEDYINEFSVR.K
58	460 - 471	1455.6167	1454.6094	1454.7041	-65.1	0	57	R.AIEDYINEFSVR.K



ID A0A3Q1MU98_BOVIN Unreviewed; 506 AA.
AC A0A3Q1MU98;
DT 10-APR-2019, integrated into UniProtKB/TrEMBL.
DT 10-APR-2019, sequence version 1.
DT 07-OCT-2020, entry version 9.
DE RecName: Full=Complement component C9 {ECO:0000256|ARBA:ARBA00018261};
GN Name=C9 {ECO:0000313|Ensembl:ENSBTAP00000074107,
GN ECO:0000313|VGNC:VGNC:26647};
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:ENSBTAP00000074107, ECO:0000313|Proteomes:UP000009:
RN [1] {ECO:0000313|Ensembl:ENSBTAP00000074107, ECO:0000313|Proteomes:UP000009136}
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Hereford {ECO:0000313|Ensembl:ENSBTAP00000074107,
RC ECO:0000313|Proteomes:UP000009136};
RA Rosen B.D., Bickhart D.M., Koren S., Schnabel R.D., Hall R., Zimin A.,
RA Dreischer C., Schultheiss S., Schroeder S.G., Elvik 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:ENSBTAP00000074107}
RP IDENTIFICATION.
RC STRAIN=Hereford {ECO:0000313|Ensembl:ENSBTAP00000074107};
RG Ensembl;
RL Submitted (JAN-2019) to UniProtKB.
CC -!- SUBCELLULAR LOCATION: Cell membrane {ECO:0000256|ARBA:ARBA00004651};
CC Multi-pass membrane protein {ECO:0000256|ARBA:ARBA00004651}. Membrane
CC {ECO:0000256|ARBA:ARBA00004141}; Multi-pass membrane protein
CC {ECO:0000256|ARBA:ARBA00004141}. Secreted
CC {ECO:0000256|ARBA:ARBA00004613}. Target cell membrane
CC {ECO:0000256|ARBA:ARBA00004276}; Multi-pass membrane protein
CC {ECO:0000256|ARBA:ARBA00004276}.
CC -!- SIMILARITY: Belongs to the complement C6/C7/C8/C9 family.
CC {ECO:0000256|ARBA:ARBA00009214}.
CC -!- CAUTION: Lacks conserved residue(s) required for the propagation of
CC feature annotation. {ECO:0000256|PROSITE-ProRule:PRU00124}.
CC -----
CC Copyrighted by the UniProt Consortium, see <https://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution (CC BY 4.0) License
CC -----
DR Ensembl; ENSBTAT00000083951; ENSBTAP00000074107; ENSBTAG00000016149.
DR VGNC; VGNC:26647; C9.
DR GeneTree; ENSGT00940000159777; -.
DR Proteomes; UP000009136; Chromosome 20.
DR ExpressionAtlas; A0A3Q1MU98; baseline.
DR GO; GO:0005576; C:extracellular region; IEA:UniProtKB-SubCell.
DR GO; GO:0005579; C:membrane attack complex; IEA:UniProtKB-KW.
DR GO; GO:0044218; C:other organism cell membrane; IEA:UniProtKB-SubCell.
DR GO; GO:0006957; P:complement activation, alternative pathway; IEA:UniProtKB-KW.
DR GO; GO:0006958; P:complement activation, classical pathway; IEA:UniProtKB-KW.
DR GO; GO:0019835; P:cytolysis; IEA:UniProtKB-KW.
DR CDD; cd00112; LDLa; 1.
DR Gene3D; 2.20.100.10; -; 1.
DR Gene3D; 4.10.400.10; -; 1.
DR InterPro; IPR037567; Complement_C9.
DR InterPro; IPR000742; EGF-like_dom.
DR InterPro; IPR009030; Growth_fac_rcpt_cys_sf.
DR InterPro; IPR036055; LDL_receptor-like_sf.
DR InterPro; IPR023415; LDLR_class-A_CS.
DR InterPro; IPR002172; LDrepeatLR_classA_rpt.
DR InterPro; IPR001862; MAC_perforin.



DR InterPro; IPR020864; MACPF.
DR InterPro; IPR020863; MACPF_CS.
DR InterPro; IPR000884; TSP1_rpt.
DR InterPro; IPR036383; TSP1_rpt_sf.
DR PANTHER; PTHR45742:SF3; PTHR45742:SF3; 2.
DR Pfam; PF00057; Ldl_recept_a; 1.
DR Pfam; PF01823; MACPF; 1.
DR PRINTS; PR00764; COMPLEMENTC9.
DR SMART; SM00192; LDLa; 1.
DR SMART; SM00457; MACPF; 1.
DR SMART; SM00209; TSP1; 1.
DR SUPFAM; SSF57184; SSF57184; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS50068; LDLRA_2; 1.
DR PROSITE; PS00279; MACPF_1; 1.
DR PROSITE; PS51412; MACPF_2; 1.
DR PROSITE; PS50092; TSP1; 1.
PE 1: Evidence at protein level;
KW Coiled coil {ECO:0000256|SAM:Coils};
KW Complement alternate pathway {ECO:0000256|ARBA:ARBA00023162};
KW Complement pathway {ECO:0000256|ARBA:ARBA00023058};
KW Cytolysis {ECO:0000256|ARBA:ARBA00023058};
KW Disulfide bond {ECO:0000256|ARBA:ARBA00023157, ECO:0000256|PROSITE-
KW ProRule:PRU00124}; Glycoprotein {ECO:0000256|ARBA:ARBA00023180};
KW Immunity {ECO:0000256|ARBA:ARBA00023058, ECO:0000256|ARBA:ARBA00023162};
KW Innate immunity {ECO:0000256|ARBA:ARBA00023058,
KW ECO:0000256|ARBA:ARBA00023162};
KW Membrane {ECO:0000256|ARBA:ARBA00022452, ECO:0000256|ARBA:ARBA00022537};
KW Membrane attack complex {ECO:0000256|ARBA:ARBA00023058};
KW Proteomics identification {ECO:0000213|PeptideAtlas:A0A3Q1MU98};
KW Reference proteome {ECO:0000313|Proteomes:UP000009136};
KW Secreted {ECO:0000256|ARBA:ARBA00022525}; Signal {ECO:0000256|SAM:SignalP};
KW Target cell membrane {ECO:0000256|ARBA:ARBA00022537};
KW Target membrane {ECO:0000256|ARBA:ARBA00022537};
KW Transmembrane {ECO:0000256|ARBA:ARBA00022452};
KW Transmembrane beta strand {ECO:0000256|ARBA:ARBA00022452}.
FT SIGNAL 1..21
FT /evidence="ECO:0000256|SAM:SignalP"
FT CHAIN 22..506
FT /note="Complement component C9"
FT /evidence="ECO:0000256|SAM:SignalP"
FT /id="PRO_5018711762"
FT DOMAIN 136..472
FT /note="MACPF"
FT /evidence="ECO:0000259|PROSITE:PS51412"
FT COILED 447..467
FT /evidence="ECO:0000256|SAM:Coils"
FT DISULFID 105..123
FT /evidence="ECO:0000256|PROSITE-ProRule:PRU00124"
FT DISULFID 117..132
FT /evidence="ECO:0000256|PROSITE-ProRule:PRU00124"
SQ SEQUENCE 506 AA; 57400 MW; 96AF4A8F30D3EB39 CRC64;
MSAGQRFafa ICILEISLLR AGPTPSYDPA ERQGTPLPID CRMSSWSEWS KCDPCLKQMF
RSRSIEIFGQ FNGRKCVDAV GDRQQCVPT E ACEDPEEGCG NDFQCGTGRC IKNRLLCNED
NDCGDYSDDED NCEQDPRPPC RNRVVEESEL ARTAGFGINI LGMDPLSTPF DNQYYNGLCD
RVWDGNTLT YRRPWNVASL TYDTKADKNF RTENHEESIQ ILRTIIEKK LNFNAGLSVK
YTPVEAIEKN KCVDLHSDK GSTSSPSKLA AEAKFRFTYS KDDIYRLLS YSAQEKMF
HVKGKVHLGR FVMRSRDVML QTTFLD SINT LPTTYEKGEY FAFLETYGT YSSSGSLGGL
YELIYVLDKK SMEQKETNPE ADLFDDVITF IRGGTRKYAT ELKEKLLRGA RMINVTDFVN
WAASLNHAPV LISQKLVPIY DLIPVKMKDA HLKKQNLERA IEDYINEFSV RKCQPCQNGG
TVVLLDGECV CSCPKEFKGV ACEIKK

//

Mascot: <http://www.matrixscience.com/>