

MASCOT Search Results

Protein View: Q693V9

Complement component 3d (Fragment) OS=Bos taurus OX=9913 PE=2 SV=1

Database: Uniprot_bovine
Score: 251
Expect: 1.1e-020
Nominal mass (M_r): 34593
Calculated pI: 6.68

Sequence similarity is available as [an NCBI BLAST search of Q693V9 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: 48%

Matched peptides shown in **bold red**.

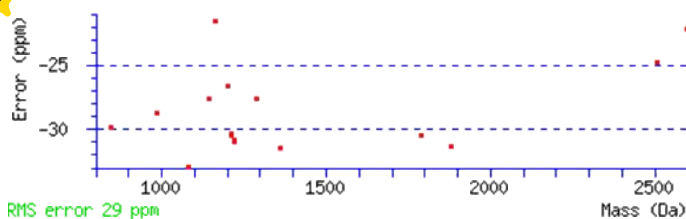
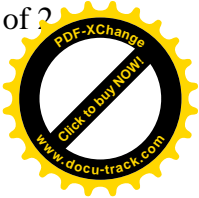
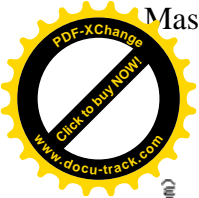
1 HLIQTPSGCG EQNMIGMTPT VIAVHYLDST DQWEKFGLEK **RQESLELIRK**
51 **GYTQQLAFRQ** KSSAYAAFQY RPPSTWLTAY VVKVFALAAN LIAIDSKDLC
101 ETVKWLILEK **QKPDGIFQED** GPVIHQEMIG GFRDTREKDV SLTAFVLIAL
151 HEAK**DICEAQ** VNSLGRSIK **AGDFLENHYR** ELRRPYTVAI **AAYALALLGK**
201 LEGDRLTKFL NTAKEN**NRWE** **EPNQKLYNVE** **ATSYALLALL** **ARKDYDTTPP**
251 **VVRWLNEQR**Y YGGGYGSTQA TFMVFQALAQ YQKDVDPHKE LNLDVSIQLP
301 SRN

Unformatted sequence string: [303 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
31	41 - 49	1143.6165	1142.6092	1142.6407	-27.6	1		K.RQESLELIR.K
14	42 - 49	987.5186	986.5113	986.5396	-28.7	0		R.QESLELIR.K
38	50 - 59	1211.6163	1210.6090	1210.6458	-30.4	1		R.KGYTQQLAFR.Q
39	50 - 59	1211.6163	1210.6091	1210.6458	-30.4	1		R.KGYTQQLAFR.Q
24	51 - 59	1083.5225	1082.5152	1082.5509	-33.0	0	14	K.GYTQQLAFR.Q
25	51 - 59	1083.5225	1082.5152	1082.5509	-32.9	0		K.GYTQQLAFR.Q
75	62 - 83	2506.2144	2505.2071	2505.2692	-24.8	0		K.SSAYAAFQYRPPSTWLTAYVVK.V
76	62 - 83	2506.2144	2505.2071	2505.2692	-24.8	0		K.SSAYAAFQYRPPSTWLTAYVVK.V
77	111 - 133	2598.2195	2597.2122	2597.2697	-22.1	0		K.QKPDGIFQEDGPVIHQEMIGGFR.D
48	155 - 166	1361.6049	1360.5976	1360.6405	-31.5	0		K.DICEAQVNSLGR.S
40	171 - 180	1221.5270	1220.5197	1220.5574	-30.9	0	40	K.AGDFLENHYR.E
41	171 - 180	1221.5270	1220.5197	1220.5574	-30.9	0		K.AGDFLENHYR.E
59	184 - 200	1790.9982	1789.9909	1790.0454	-30.4	0		R.RPYTVAI AAYALALLGK.L
60	184 - 200	1790.9982	1789.9909	1790.0454	-30.4	0		R.RPYTVAI AAYALALLGK.L
37	217 - 225	1200.5436	1199.5363	1199.5683	-26.7	1		K.NRWEENQK.L
63	226 - 242	1880.9891	1879.9818	1880.0407	-31.3	0		K.LYNVEATSYALLALLAR.K
64	226 - 242	1880.9891	1879.9819	1880.0407	-31.3	0	80	K.LYNVEATSYALLALLAR.K
44	243 - 253	1290.6333	1289.6260	1289.6616	-27.6	1		R.KDYDTTPPVVR.W
33	244 - 253	1162.5488	1161.5415	1161.5666	-21.6	0		K.DYDTTPPVVR.W
2	254 - 259	845.4012	844.3939	844.4191	-29.8	0		R.WLNEQR.Y



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ID      Q693V9_BOVIN                      Unreviewed;          303 AA.
AC      Q693V9;
DT      13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT      13-SEP-2004, sequence version 1.
DT      26-FEB-2020, entry version 71.
DE      SubName: Full=Complement component 3d {ECO:0000313|EMBL:ACG50173.1};
DE      SubName: Full=Complement component C3d {ECO:0000313|EMBL:AAT76518.1};
DE      Flags: Fragment;
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|EMBL:AAT76518.1};
RN      [1] {ECO:0000313|EMBL:AAT76518.1}
RP      NUCLEOTIDE SEQUENCE.
RA      Collada C., Casado R., Gomez L., Allona I., Aragoncillo C.;
RL      Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
RN      [2] {ECO:0000313|EMBL:AAT76518.1}
RP      NUCLEOTIDE SEQUENCE.
RX      PubMed=16904753; DOI=10.1016/j.vetimm.2006.07.005;
RA      Firth M.A., Moore D.P., Pei Y., Shewen P.E., Lo R.Y.C., Yoo D.,
RA      Hodgins D.C.;
RT      "Cloning of a gene fragment encoding bovine complement component C3d with
RT      expression and characterization of derived fusion proteins.";
RL      Vet. Immunol. Immunopathol. 114:61-71(2006).
RN      [3] {ECO:0000313|EMBL:ACG50173.1}
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Liver {ECO:0000313|EMBL:ACG50173.1};
RA      Liu D., Niu Z.X.;
RT      "Cloning and structural analysis of simmental cattle complement component
RT      3d gene.";
RL      Submitted (JUL-2008) to the EMBL/GenBank/DDBJ databases.
CC      -----
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DR      EMBL; AY630404; AAT76518.1; -; mRNA.
DR      EMBL; EU868825; ACG50173.1; -; mRNA.
DR      SMR; Q693V9; -.
DR      eggNOG; KOG1366; Eukaryota.
DR      eggNOG; ENOG410XRED; LUCA.
DR      HOGENOM; CLU_001634_4_0_1; -.
DR      GO; GO:0005615; C:extracellular space; IEA:InterPro.
DR      GO; GO:0006956; P:complement activation; IEA:InterPro.
DR      InterPro; IPR011626; Alpha-macroglobulin_TED.
DR      InterPro; IPR035711; Complement_C3-like.
DR      InterPro; IPR019742; MacrogloblnA2_CS.
DR      InterPro; IPR008930; Terpenoid_cyclase/PrenylTrfase.
DR      PANTHER; PTHR11412:SF81; PTHR11412:SF81; 1.
DR      Pfam; PF07678; TED_complement; 1.
DR      SUPFAM; SSF48239; SSF48239; 1.
DR      PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
PE      2: Evidence at transcript level;
FT      DOMAIN                2..281
FT                               /note="TED_complement"
FT                               /evidence="ECO:0000259|Pfam:PF07678"
FT      NON_TER                1
FT                               /evidence="ECO:0000313|EMBL:AAT76518.1"
FT      NON_TER                303
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SQ      SEQUENCE   303 AA;  34443 MW;  2F3A15020CEA3797 CRC64;
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      KSSAYAAFQY RPPSTWLTAY VVKVFALAAN LIAIDSKDLC ETVKWLILEK QKPDGIFQED
      GPVIHQEMIG GFRDRTREKDV SLTAFVLIAL HEAKDICEAQ VNSLGRSIAK AGDFLENHYR
      ELRRPYTVAI AAYALALLGK LEGDRLTKFL NTAKEKNRWE EPNQKLYNVE ATSYALLALL
      ARKDYDTTPP VVRWLNEQRY YGGYGSTQA TFMVFQALAQ YQKDVDPHKE LNLDSVSIQLP
      SRN

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