



MASCOT Search Results

Protein View: A0A4W2D411

Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4
SV=1

Database: Uniprot_bovine
Score: 86
Expect: 0.00032
Nominal mass (M_r): 190190
Calculated pI: 8.36

Sequence similarity is available as [an NCBI BLAST search of A0A4W2D411 against nr.](#)

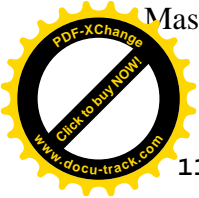
Search parameters

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

Protein sequence coverage: 9%

Matched peptides shown in **bold red**.

1	MGCEAPPLPP	PPPPRPQLSA	GLRIPCETRD	WGRALTLGKG	WQPGLPGMTA
51	PRPMLPSGRY	SMITPNILRL	ESEETVVLEA	HGGQGTIQVS	VTVHDFPAKK
101	QVLSNENTQL	NSNNGYLSTV	TIKIPASKEL	KSDKGHKFVT	VVATFGNVQV
151	EKVVLISLQS	GYLFIQTDKT	IYTPGSTVLY	RVFTVDHKLL	PVGQTVFITI
201	ETPDGIPVKR	DSKSSQNQFG	ILTLSWNIPE	LVNMGVWKIK	AYYEDSPQQV
251	FSAEFEVKEY	VLPSFEVQLE	PEEKFYIIDD	PDGLKVNIIA	RFLYGEQVDG
301	TAFVIFGVQD	GDRRISLTHS	LTRVPINDGN	GEAILKRQVL	LNGVQPSRAD
351	ALVGKSIYVS	ATVILQSGSD	MVEAERTGIP	IVTSPYQIHF	TKTPKFFKPA
401	MPFDLMVYVT	NPDGSPARHI	PVVTQGSNVQ	SLTQDDGVAK	LSINTQNKRD
451	PLTITVTRTK	DNIPEGRQAT	RTMQALPYNT	QGNSNNYLHL	SVPRVELKPG
501	ETLNVNFHLR	TDPGEQAKIR	YYTYMIMNKG	KLLKVGRQYR	EPGQDLVVLP
551	LTITSDFIPS	FRLVAYYTLI	NAKGQREVVA	DSVWVDVKDS	CMGTLVVKNG
601	GKEEKHHRPG	QQITLKIAD	QGARVGLVAV	DKGVFVLNKK	NKLTQRKIWD
651	VVEKADIGCT	PGSGR NYAGV	FTDAGLTLKT	SQGLETTQRA	DPQCPQPATR
701	RRR SVQLMEK	RMDK AGQYSS	DLR KCCEDGM	RDNPMKFPCQ	RR AQFILQGD
751	ACVK AFLDCC	EYITQLRQQH	SRDGALELAR	SDLDDDIPE	EDIISR SQFP
801	ESWLWTVIED	LK QADKNGIS	TKLMNVFLKD	SITTWEILAV	SLSDKK GICV
851	ADPYEVTVMQ	DF FIDLRLPY	SVVRNEQVEI	RAILYNYREA	ENLK VRVELL
901	YNPAFCSLAT	AKKR HQQTIT	IPARSSVAVP	YVIVPLKIGL	HEVEVK AAVY
951	NHFISDGVKK	TLKVVPPEGVR	VNKTVAVRTL	NPEHLGQGGV	QREEVPAADL
1001	SDQVPDTESE	TKILLQGTPV	AQMTEDAIDG	ERLKHLIQTP	SGCGEQNMIG
1051	MTPTVIAVHY	LDSTDQWEKF	GLEKRQESLE	LIRKGYTQQ	AFRQKSSAYA
1101	AFQYRPPSTW	LTAYVVKVFA	LAANLIAIDS	KDLCETVKWL	ILEKQKPDGI



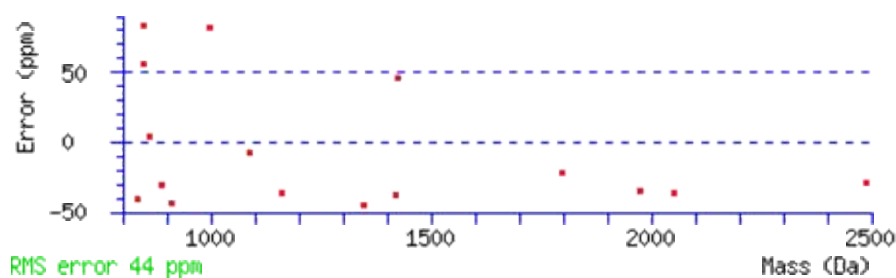
1151 FQEDGPVIHQ EMIGGFRDTR EKDVSLTAFV LIALHEAKDI CEAQVNSLGR
1201 SIAKAGDFLE NHYRELRRPY TVAIAAYALA LLGKLEGDRL TKFLNTAKEK
1251 NRWEEPQKL YNVEATSYAL LALLARKDYD TTPPVVRWLN EQRYGGGYG
1301 STQATFMVFQ ALAQYQKDVP DHKELNLDVS IQLPSRNSAV RHRILWESAS
1351 LLRSEETKEN ERFTVKAEGK GQGTLNVVTV YHAKLKGKVS CKKFDLRVSI
1401 RPAPETVKKP QDAKGSMILD ICTKYLGDQD ATMSILDISM MTGFSPDVED
1451 LK**TLSTGVDR** YISKYEMNRD SNKNTLIIYL DKVSHTVEDC LSKFVHQYFN
1501 VGLIQPGAVK VYSYNNLDET CIRFYHPDKE DGMLSKLCHK DTCRCAEENC
1551 FMHHTKEKVT LEDRLDKACE PGVDYVYKTR LIQKKLEDDF DEYIMVIENI
1601 IKSGSATSSG RTPGWSCGPR LKNVKMRRTS NSARTWPTSQ RTWSSLAAPT
1651 DPTIHPLIH TVHAIKLHFC STCLLKSGGL

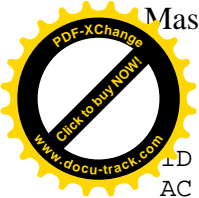
Unformatted sequence string: 1680 residues (for pasting into other applications).

Sort peptides by Residue Number Increasing Mass Decreasing Mass

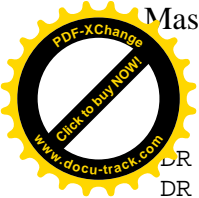
Show predicted peptides also

Query	Start - End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Peptide
<input checked="" type="checkbox"/> <u>54</u>	521 - 531	1427.7352	1426.7279	1426.6625	45.9	1		R.YYTY + Oxidat: (M)
<input checked="" type="checkbox"/> <u>32</u>	655 - 665	1090.4866	1089.4793	1089.4873	-7.34	0		K.ADIG
<input checked="" type="checkbox"/> <u>5</u>	704 - 710	850.5049	849.4976	849.4266	83.6	0		R.SVQI + Oxidat: (M)
<input checked="" type="checkbox"/> <u>23</u>	715 - 723	996.5558	995.5485	995.4672	81.7	0		K.AGQY
<input checked="" type="checkbox"/> <u>49</u>	743 - 754	1349.6270	1348.6197	1348.6809	-45.4	0		R.AQFI
<input checked="" type="checkbox"/> <u>71</u>	797 - 812	1977.9272	1976.9199	1976.9884	-34.6	0		R.SQFE
<input checked="" type="checkbox"/> <u>8</u>	823 - 829	864.5046	863.4973	863.4939	3.99	0		K.LMNV
<input checked="" type="checkbox"/> <u>77</u>	847 - 867	2488.1152	2487.1079	2487.1814	-29.6	0		K.GICV
<input checked="" type="checkbox"/> <u>1</u>	868 - 874	833.4543	832.4470	832.4807	-40.4	0		R.LPYS
<input checked="" type="checkbox"/> <u>2</u>	868 - 874	833.4543	832.4471	832.4807	-40.4	0	29	R.LPYS
<input checked="" type="checkbox"/> <u>16</u>	875 - 881	887.4306	886.4233	886.4508	-31.0	0		R.NEQV
<input checked="" type="checkbox"/> <u>18</u>	882 - 888	912.4536	911.4463	911.4865	-44.0	0		R.AILY
<input checked="" type="checkbox"/> <u>19</u>	882 - 888	912.4536	911.4463	911.4865	-44.0	0	28	R.AILY
<input checked="" type="checkbox"/> <u>73</u>	895 - 912	2052.0193	2051.0120	2051.0874	-36.7	1		K.VRVE
<input checked="" type="checkbox"/> <u>68</u>	897 - 912	1796.8849	1795.8776	1795.9178	-22.4	0		R.VELI
<input checked="" type="checkbox"/> <u>36</u>	915 - 924	1164.6057	1163.5984	1163.6411	-36.7	0		R.HQQT
<input checked="" type="checkbox"/> <u>53</u>	947 - 959	1420.6680	1419.6607	1419.7147	-38.0	0		K.AAVY
<input checked="" type="checkbox"/> <u>4</u>	1453 - 1460	848.4947	847.4874	847.4400	56.0	0		K.TLST





ID A0A4W2D411_BOBOX Unreviewed; 1680 AA.
AC A0A4W2D411;
DT 18-SEP-2019, integrated into UniProtKB/TrEMBL.
DT 18-SEP-2019, sequence version 1.
DT 26-FEB-2020, entry version 5.
DE SubName: Full=Complement C3 {ECO:0000313|Ensembl:ENSBIXP000000018941};
GN Name=C3 {ECO:0000313|Ensembl:ENSBIXP000000018941};
OS Bos indicus x Bos taurus (Hybrid cattle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Laurasiatheria; Artiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=30522 {ECO:0000313|Ensembl:ENSBIXP000000018941, ECO:0000313|Prote
RN [1] {ECO:0000313|Ensembl:ENSBIXP000000018941, ECO:0000313|Proteomes:UP000314
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Low W.Y., Tearle R., Bickhart D.M., Rosen B.D., Koren S., Rhie A.,
RA Hiendler S., Phillippy A.M., Smith T.P.L., Williams J.L.;
RT "Haplotype-resolved cattle genomes."
RL Submitted (NOV-2018) to the EMBL/GenBank/DDBJ databases.
RN [2] {ECO:0000313|Ensembl:ENSBIXP000000018941}
RP IDENTIFICATION.
RG Ensembl;
RL Submitted (JUL-2019) to UniProtKB.
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; ENSBIXT00000032285; ENSBIXP000000018941; ENSBIXG000000022699.
DR Proteomes; UP000314981; Chromosome 7.
DR GO; GO:0005615; C:extracellular space; IEA:InterPro.
DR GO; GO:0004866; F:endopeptidase inhibitor activity; IEA:InterPro.
DR GO; GO:0006956; P:complement activation; IEA:InterPro.
DR GO; GO:0006954; P:inflammatory response; IEA:InterPro.
DR CDD; cd00017; ANATO; 1.
DR Gene3D; 2.40.50.120; -; 1.
DR Gene3D; 2.60.40.10; -; 2.
DR Gene3D; 2.60.40.690; -; 1.
DR InterPro; IPR009048; A-macroglobulin_rcpt-bd.
DR InterPro; IPR036595; A-macroglobulin_rcpt-bd_sf.
DR InterPro; IPR011625; A2M_N_BRD.
DR InterPro; IPR011626; Alpha-macroglobulin_TED.
DR InterPro; IPR000020; Anaphylatoxin/fibulin.
DR InterPro; IPR018081; Anaphylatoxin_comp_syst.
DR InterPro; IPR001840; Anaphylatoxin_comp_syst_dom.
DR InterPro; IPR041425; C3/4/5_MG1.
DR InterPro; IPR035711; Complement_C3-like.
DR InterPro; IPR013783; Ig-like_fold.
DR InterPro; IPR001599; Macroglobln_a2.
DR InterPro; IPR019742; MacrogloblnA2_CS.
DR InterPro; IPR002890; MG2.
DR InterPro; IPR041555; MG3.
DR InterPro; IPR040839; MG4.
DR InterPro; IPR018933; Netrin_module_non-TIMP.
DR InterPro; IPR008930; Terpenoid_cyclase/PrenylTrfase.
DR InterPro; IPR008993; TIMP-like_OB-fold.
DR PANTHER; PTHR11412:SF81; PTHR11412:SF81; 1.
DR Pfam; PF00207; A2M; 1.
DR Pfam; PF07703; A2M_BRD; 1.
DR Pfam; PF07677; A2M_recep; 1.
DR Pfam; PF01821; ANATO; 1.
DR Pfam; PF17790; MG1; 1.
DR Pfam; PF01835; MG2; 1.
DR Pfam; PF17791; MG3; 1.
DR Pfam; PF17789; MG4; 1.
DR Pfam; PF01759; NTR; 1.
DR Pfam; PF07678; TED_complement; 1.



LR PRINTS; PR00004; ANAPHYLATOXN.
DR SMART; SM01360; A2M; 1.
DR SMART; SM01359; A2M_N_2; 1.
DR SMART; SM01361; A2M_recep; 1.
DR SMART; SM00104; ANATO; 1.
DR SUPFAM; SSF47686; SSF47686; 1.
DR SUPFAM; SSF48239; SSF48239; 1.
DR SUPFAM; SSF49410; SSF49410; 1.
DR SUPFAM; SSF50242; SSF50242; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
PE 4: Predicted;
KW Reference proteome {ECO:0000313|Proteomes:UP000314981}.
FT DOMAIN 725..760
FT /note="Anaphylatoxin-like"
FT /evidence="ECO:0000259|PROSITE:PS01178"
FT REGION 1..21
FT /note="Disordered"
FT /evidence="ECO:0000256|SAM:MobiDB-lite"
FT COMPIAS 1..19
FT /note="Pro-rich"
FT /evidence="ECO:0000256|SAM:MobiDB-lite"
SQ SEQUENCE 1680 AA; 188712 MW; 8BF7AA0F008ADC2B CRC64;
MGCEAPPLPP PPPRPQLSA GLRIPCETRD WGRALTLGKG WQPLPGMTA PRPMLPSGRY
SMITPNILRL ESEETVVLEA HGGQGTIQVS VTVHDFPAKK QVLSNENTQL NSNNGYLSTV
TIKIPASKEL KSDKGHKFVT VVATFGNVQV EKVVLSLQSG YLFIQTDKT IYTPGSTVLVY
RVFTVDHKKLL PVGQTVFITI ETPDGIPVKR DSKSSQNQFG ILTSLWNIPE LVNMGVWIKI
AYYEDSPQQV FSAEFEVKEY VLPSFEVQLE PEEKFYIDD PDGLKVNIIA RFLYGEQVDG
TAFVIFGVQD GDRRISLTHS LTRVPINDGN GEAILKRQVL LNGVQPSRAD ALVGKSIYVS
ATVILQSGSD MVEAERTGIP IVTSPYQIHF TKTPKFFKPA MPFDLMVYVT NPDGSPARHI
PVVTQGSNVQ SLTQDDGVAK LSINTQNKRD PLTITVTRTK DNIPEGRQAT RTMQALPYNT
QGNSNNYLHL SVPRVELKPG ETLNVNFHLR TDPGEQAKIR YYTYMIMNKG KLLKVGRQYR
EPGQDLVVLPL LTITSDFIPS FRLVAYYTLI NAKGQREVVA DSVWVDVKDS CMGTLVVKNG
GKEEKHHRPG QQITLKIAD QGARVGLVAV DKGVFVLNKK NKLTQRKIWD VVEKADIGCT
PGSGRNYAGV FTDAGLTLKT SQGLETTQRA DPQCPQPATR RRRSVQLMEK RMDKAGQYSS
DLRKCCEDGM RDNPMKFPCQ RRAQFILQGD ACVKAFLDCC EYITQLRQQH SRDGALELAR
SDLDDDIPE EDIISRSQFP ESWLWTVIED LKQADKNGIS TKLMNVFLKD SITTWEILAV
SLSDKKGICV ADPYEVTVMQ DFFIDLRLPY SVVRNEQVEI RAILYNYREA ENLKVRVELL
YNPAFCSLAT AKKRHQQTIT IPARSSVAVP YVIVPLKIGL HEVEVKAAYV NHFISDGVKK
TLKVVPGEVR VNKTAVAVRTL NPEHLGQGGV QREEVPAADL SDQVPDTESE TKILLQGTPV
AQMTEDAIDG ERLKHLIQTP SGCGEQNMIG MTPTVIAVHY LDSTDQWEKF GLEKRQESLE
LIRKGYTQQL AFRQKSSAYA AFQYRPPSTW LTAYVVKVFA LAANLIAIDS KDLCTVVKWL
ILEKQKPDGI FQEDGPVIHQ EMIGGFRDTR EKDVSLTAFV LIALHEAKDI CEAQVNSLGR
SIKAGDFLE NHYRELRRPY TVAIAAYALA LLGKLEGDRL TKFLNTAKEK NRWEEPQKL
YNVEATSYAL LALLARKDYD TTPPVVRWLN EQRYGGGGYG STQATFMVFQ ALAQYQKDVP
DHKELNLDVS IQLPSRNSAV RHRILWESAS LLRSEETKEN ERFTVKAEGK GQGTLSVVTV
YHAKLKGVKS CKKFDLRVSI RPAPETVKKP QDAKGSMLD ICTKYLGDQD ATMSILDISM
MTGFSPDVED LKTLSTGVDR YISKYEMNRD SNKNTLIIYL DKVSHTVEDC LSKVHQYFN
VGLIQPGAVK VYSYNNLDET CIRFYHPDKE DGMLSKLCHK DTCRCAEENC FMHTEKEVT
LEDRLDKACE PGVDYVYKTR LIQKKLEDDF DEYIMVIENI IKSGSATSSG RTPGWSCGPR
LKNVKMRTR NSARTWPTSQ RTWSSLAAPT DPTHIHPLIH TVHAIKLHFC STCLLKSGGL

//

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