

MASCOT Search Results

Protein View: R9QSM8

Alpha-2-macroglobulin OS=Bos taurus OX=9913 GN=A2M PE=2 SV=1

Database: Uniprot_bovine
Score: 90
Expect: 0.00014
Nominal mass (M_r): 134613
Calculated pI: 5.75

Sequence similarity is available as [an NCBI BLAST search of R9QSM8 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: 19%

Matched peptides shown in *bold red*.

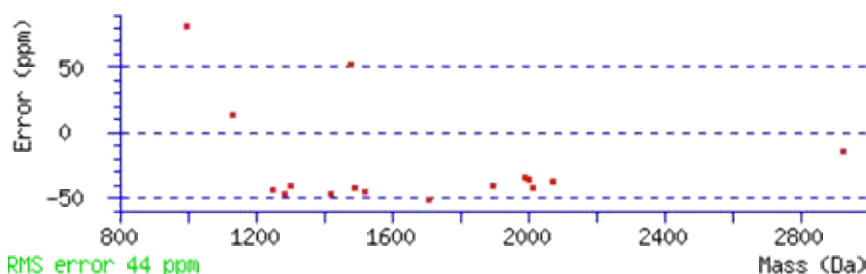
1	MGKNKLLYPS	LTL L L L L L L L P	TDASVSGKPQ	YMLVLP S L L H	TETPEKGCLL
51	LSHLNETVTV	SASLESVREN	RS L F T D V V A E	KDLFHCVSFT	LPRSPTSQEV
101	MFLTIQVKG P	TQEFKKRTTV	LVKNEESLVF	VQTDKPIYKP	EQTVKFRIVL
151	LDES F H P L N E	LVPLVYVEDP	KGNRIAQWQN	LEV ENGLQQL	TFPLSSEPFQ
201	GSYKVVVQK G	SGGTA EHPFT	VEEFVL PKFE	VQVRMPKIIT	ILEEEVQVSV
251	CGLYTYGKPV	PGRVTMNMCR	KYRNP S N C Y G	EESNAVCEKF	SGELNNEGCF
301	SQQVNTKIFQ	LKRQEFEMKI	EVEAKIQEEG	TEVELTGKGA	TEITTTITK L
351	SFVTVD S N L R	RGIPFTGKVL	LVDGKGVPMP	NKVIFITANE	ANHNSNTTTD
401	EHGLAQFSIT	TTKIKGTSL S	IRVKYKD H S P	CYGYQWLSEE	HQDAYHSANL
451	VFSR SNSFVY	LEPLPRELPC	GKTQTVQAHY	VLKGQVLKDL	KELVFYYLIM
501	AKGGIVRS GT	HTLPVEQGDM	QGHFSMSVPV	ESDIAPVAR L	LIYAILPDGE
551	VVGDSAR Y E I	EHCLANK VGL	NFSPGQS FPA	SQAHLRVTAS	PQSLCALRAV
601	DQSVLLMRPE	AELSAATVYN	LLPVKDLSSF	PSSVNQQEED	NEDCISHDNV
651	YINGIMYFPV	SNTNEK DMYS	FLQDMGLKAF	TNSKIHKPKI	CPQPEEHRIQ
701	HHTLLASPVR	AEMGRNR DFV	HFDDTSEPPT	ETVRKYFPET	WIWDLVVVSS
751	SGVHEVEVTV	PDTIT EWKAG	ALCLSR DTGL	GLSPTASLRV	FQPF FVELTM
801	PYSVIR GEAF	TLKATVLN Y L	PKCIRVSVQL	EASPAFLAVP	EKEQETYCIC
851	GNGRQTVSWA	VTPKSLGNVN	FTVSAEAVES	QELCGSEVPV	VPEHGRKDTI
901	IKPLLVEPEG	LEKEVIFNSL	LCPSVDFVFL	GAEDGGQVLR	HFPPAAATDT
951	AADAHDPARP	GAKVSESLSL	KLPPNVVEES	AR ASFSVLGD	ILGSAMRNTQ
1001	NLLQMPYGC G	EQNMARFAPN	IYVLDYLN ET	QQLTAE L K S K	A I L Y L N T G Y Q
1051	RQLLYKHFDG	SYSTFGEHRG	NSEGNTWLTA	FVLKSFAQAR	GYIFIDEAHI
1101	TEALTWLAQK	QKSNGCFRST	GTLLNNAIKG	GVDDEVTL SA	YITIALLEMP
1151	LPVTHPVVRN	ALFCLDSAWK	CLKTMSMKTA	LLDSL F H R L R	SPWK K D N F

Unformatted sequence string: 1198 residues (for pasting into other applications).

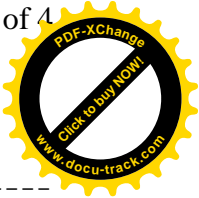
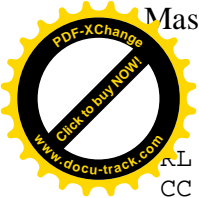
Sort peptides by ☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Show predicted peptides also

Query	Start - End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Peptide
48	82 - 93	1491.6775	1490.6702	1490.7340	-42.8	0		K.DLFF
56	94 - 108	1707.8094	1706.8021	1706.8913	-52.3	0		R.SPTS
61	210 - 228	2001.9189	2000.9116	2000.9844	-36.4	0		K.GSGG
33	350 - 360	1250.6191	1249.6118	1249.6667	-43.9	0		K.LSFV
34	350 - 360	1250.6191	1249.6119	1249.6667	-43.8	0		K.LSFV
42	455 - 466	1421.6768	1420.6695	1420.7350	-46.1	0	14	R.SNSF
43	455 - 466	1421.6768	1420.6695	1420.7350	-46.1	0		R.SNSF
58	540 - 557	1900.9595	1899.9522	1900.0306	-41.2	0	13	R.LLIY
59	540 - 557	1900.9595	1899.9522	1900.0306	-41.2	0		R.LLIY
62	568 - 586	2012.9465	2011.9392	2012.0228	-41.5	0		K.VGLN
63	568 - 586	2012.9465	2011.9393	2012.0228	-41.5	0		K.VGLN
37	587 - 598	1302.6307	1301.6234	1301.6762	-40.5	0		R.VTAS
75	599 - 625	2927.5508	2926.5435	2926.5837	-13.7	0		R.AVDQ
47	667 - 678	1479.7271	1478.7198	1478.6422	52.5	0		K.DMY
								+ 2
								Oxidat:
								(M)
60	718 - 734	1991.8297	1990.8224	1990.8909	-34.4	0		R.DEVE
35	777 - 789	1287.6302	1286.6229	1286.6830	-46.7	0		R.DTGI
66	790 - 806	2073.0088	2072.0015	2072.0805	-38.1	0		R.VFQE
50	983 - 997	1523.7185	1522.7112	1522.7814	-46.1	0		R.ASFS
19	1111 - 1118	996.5488	995.5415	995.4607	81.2	1		K.QKSN
27	1119 - 1129	1131.6523	1130.6450	1130.6295	13.7	0		R.STGI



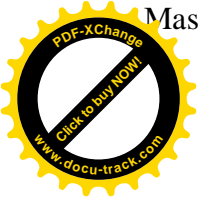
ID R9QSM8_BOVIN Unreviewed; 1198 AA.
 AC R9QSM8;
 DT 18-SEP-2013, integrated into UniProtKB/TrEMBL.
 DT 18-SEP-2013, sequence version 1.
 DT 11-DEC-2019, entry version 23.
 DE SubName: Full=Alpha-2-macroglobulin {ECO:0000313|EMBL:AGC26508.1};
 GN Name=A2M {ECO:0000313|EMBL:AGC26508.1};
 OS Bos taurus (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:AGC26508.1};
 RN [1] {ECO:0000313|EMBL:AGC26508.1}
 RP NUCLEOTIDE SEQUENCE.
 RA Wang X.;
 RT "Identification and characterization of novel splice variants and
 RT expression analysis of the A2M gene in healthy and mastitis-infected
 RT mammary tissues of Chinese Holstein dairy cow.";



Submitted (APR-2012) to the EMBL/GenBank/DDBJ databases.

Copyrighted by the UniProt Consortium, see <https://www.uniprot.org/terms>
Distributed under the Creative Commons Attribution (CC BY 4.0) License

DR EMBL; JQ918150; AGC26508.1; -; mRNA.
DR eggNOG; ENOG410KCRI; Eukaryota.
DR eggNOG; ENOG410XQIV; LUCA.
DR OrthoDB; 354230at2759; -.
DR GO; GO:0005615; C:extracellular space; IEA:InterPro.
DR GO; GO:0004866; F:endopeptidase inhibitor activity; IEA:InterPro.
DR Gene3D; 2.60.40.10; -; 2.
DR InterPro; IPR011625; A2M_N_BRD.
DR InterPro; IPR011626; Alpha-macroglobulin_TED.
DR InterPro; IPR013783; Ig-like_fold.
DR InterPro; IPR014756; Ig_E-set.
DR InterPro; IPR001599; Macroglobln_a2.
DR InterPro; IPR019742; MacrogloblnA2_CS.
DR InterPro; IPR002890; MG2.
DR InterPro; IPR041555; MG3.
DR InterPro; IPR040839; MG4.
DR InterPro; IPR008930; Terpenoid_cyclase/PrenylTrfase.
DR InterPro; IPR010916; TonB_box_CS.
DR Pfam; PF00207; A2M; 1.
DR Pfam; PF07703; A2M_BRD; 1.
DR Pfam; PF01835; MG2; 1.
DR Pfam; PF17791; MG3; 1.
DR Pfam; PF17789; MG4; 1.
DR Pfam; PF07678; TED_complement; 1.
DR SMART; SM01360; A2M; 1.
DR SMART; SM01359; A2M_N_2; 1.
DR SUPFAM; SSF48239; SSF48239; 1.
DR SUPFAM; SSF81296; SSF81296; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
PE 2: Evidence at transcript level;
KW Signal {ECO:0000256|SAM:SignalP}.
FT SIGNAL 1..23
FT /evidence="ECO:0000256|SAM:SignalP"
FT CHAIN 24..1198
FT /evidence="ECO:0000256|SAM:SignalP"
FT /id="PRO_5004488606"
FT DOMAIN 459..607
FT /note="A2M_N_2"
FT /evidence="ECO:0000259|SMART:SM01359"
FT DOMAIN 740..830
FT /note="A2M"
FT /evidence="ECO:0000259|SMART:SM01360"
SQ SEQUENCE 1198 AA; 133386 MW; 9871AD7632A2EDBE CRC64;
MGKNKLLYPS LTL L L L L L L L L L P TDASVSGKPQ YMLVPSLLH TETPEKGCLL LSHLNETVTV
SASLESVREN RSLFTDVVAE KDLFHCVSFT LPRSPTSQEV MFLTIQVKGP TQEFKKRTTV
LVKNEESLVF VQTDKPIYKP EQTVKFRIVL LDESFHPLNE LVPLVYVEDP KGNRIAQWQN
LEVENGLQQL TFPLSSEPFQ GSYKVVVQKG SGGTAEHPFT VEEFVLPKFE VQVRMPKIIT
ILEEEVQVSV CGLYTYGKPV PGRVTMNMCR KYRNP SNCYG EESNAVCEKF SGELNNEGCF
SQQVNTKIFQ LKRQEFEMKI EVEAKIQEEG TEVELTGKGA TEITTTITKL SFVTVDNLRL
RGIPFTGKVL LVDGKGVPMP NKVIFITANE ANHNSNTTDD EHGLAQFSIT TTKIKGTSLS
IRVKYKDHS CYGYQWLSEE HQDAYHSANL VFSRSNSFVY LEPLPRELPC GKTQTVQAHY
VLKGQVLKDL KELVFYYLIM AKGGIVRSGT HTLPVEQGDM QGHFSMSVPV ESDIAPVARL
LIYAILPDGE VVGDSARYEI EHCLANKVGL NFSPGQSFPQ SQAHLRVTAS PQSLCALRAV
DQSVLLMRPE AELSAATVYN LLPVKDLSSF PSSVNQQEED NEDCISHDNV YINGIMYFPV
SNTNEKDMYS FLQDMGLKAF TNSKIHKPKI CPQPEEHRIQ HHTLLASVPR AEMGRNPDFV
HFDDTSEPPT ETVRKYFPET WIWDLVVVSS SGVHEVEVTV PDTITEWKAG ALCLSRDTGL
GLSPTASLRV FQPFVVELTM PYSVIRGEAF TLKATVLNLYL PKCIRVSVQL EASPAFLAVP
EKEQETYCIC GNGRQTVSWA VTPKSLGNVN FTVSAEAVES QELCGSEVPV VPEHGRKDTI
IKPLLVEPEG LEKEVIFNSL LCPSVDFVFL GAEDGGQVLR HFPPAAATDT ADAHDPARP



GAKVSESLSL KLPPNVVEES ARASFSVLGD ILGSAMRNTQ NLLQMPYGCG EQNMARFAPN
IYVLDYLNET QQLTAEKSK AILYLNTGYQ RQLLYKHFDG SYSTFGEHRG NSEGNTWLTA
FVLKSFAQAR GYIFIDEAHI TEALTWLAQK QKSNGCFRST GTLLNNAIKG GVDDEVTLTA
YITIALLEMP LPVTHPVVRN ALFCLDSAWK CLKTMSMKTA LLDSLFRHLR SPWKKDNF

//

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