

MASCOT Search Results

Protein View: Q2KJF1

Alpha-1B-glycoprotein OS=Bos taurus OX=9913 GN=A1BG PE=1 SV=1

Database: Uniprot_bovine
Score: 98
Expect: 2.4e-005
Nominal mass (Mr): 54091
Calculated pI: 5.29

Sequence similarity is available as [an NCBI BLAST search of Q2KJF1 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: 23%

Matched peptides shown in **bold red**.

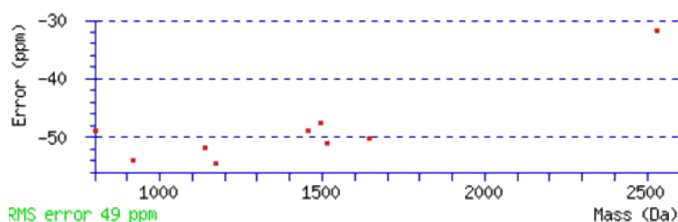
1 MSAWAALLLL WGLSLSPVTE QATFFDPRPS LWAEAGSPLA PWADVTLTCQ
51 SPLPTQEFQL LKDGVGQEPV HLESPAHEHR **FPLGPTSTT** RGLYRCSYKG
101 NNDWISPSNL VEVGTAEPLP APSISTSPVS WITPGLNTTL LCLSGLR**GVT**
151 **FLRL**LEGEDQ FLEVAEAPEA TQATFPVHRA GNYSCSYRTH AAGTPSEPSA
201 TVTIEELDPP PAPTTLVDRE SAK**VLRPGSS** **ASLTCVAPLS** **GVDFQLR**GA
251 EEQLVPRAST SPDRVFFR**LS** **ALAAGDGS**GY TCRYLRL**SEL** **AAWSR**SAPA
301 ELVLSDGTLP APELSAEPAL LSPTPGALVQ LRCRAPRAGV RFALVRKDAG
351 GRQVQR**VLSP** **AGPEAQFELR** GVSVDGSGNY SCVYVDTSPF FAGSKPSATL
401 ELRVDGDLPR PQLRALWTGA **LTPGR**DAVLR **CEAEVPDVSF** **LLLR**AGEEEP
451 LAVAWSTHGP ADLVLTSVGP QHAGTYSCRY RTGGPR**SLLS** **ELSDPVELR**V
501 AGS

Unformatted sequence string: [503 residues](#) (for pasting into other applications).

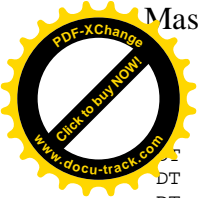
Sort peptides by Residue Number Increasing Mass Decreasing Mass

Show predicted peptides also

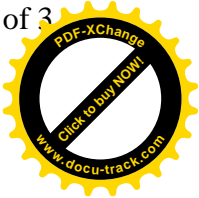
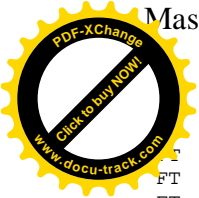
Query	Start - End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Peptide
37	81 - 91	1175.5778	1174.5705	1174.6346	-54.6	0		R.FPLGPTSTTR.G
1	148 - 154	805.4537	804.4464	804.4858	-48.9	0		R.GVTFLLR.L
77	224 - 247	2530.2642	2529.2569	2529.3374	-31.8	0		K.VLRPGSSASLTCVAPLSGVDFQLR.R
53	269 - 283	1498.6241	1497.6168	1497.6882	-47.6	0		R.LSALAAGDGSYTCR.Y
15	288 - 295	919.4136	918.4063	918.4559	-54.0	0		R.SELAASR.D
54	357 - 370	1513.7238	1512.7165	1512.7936	-51.0	0	27	R.VLSPAGPEAQFELR.G
55	357 - 370	1513.7238	1512.7165	1512.7936	-51.0	0		R.VLSPAGPEAQFELR.G
31	415 - 425	1142.5725	1141.5652	1141.6244	-51.8	0		R.ALWTGALTPGR.D
32	415 - 425	1142.5725	1141.5652	1141.6244	-51.8	0		R.ALWTGALTPGR.D
65	431 - 444	1647.7585	1646.7512	1646.8338	-50.1	0		R.CEAEVPDVSFLLLR.A
66	431 - 444	1647.7585	1646.7512	1646.8338	-50.1	0	27	R.CEAEVPDVSFLLLR.A
49	487 - 499	1457.7133	1456.7060	1456.7773	-48.9	0		R.SLLSELSDPVELR.V



ID A1BG_BOVIN Reviewed; 503 AA.
AC Q2KJF1;



DT 02-SEP-2008, integrated into UniProtKB/Swiss-Prot.
 DT 07-MAR-2006, sequence version 1.
 DT 12-AUG-2020, entry version 92.
 DE RecName: Full=Alpha-1B-glycoprotein {ECO:0000250|UniProtKB:P04217};
 DE AltName: Full=Alpha-1-B glycoprotein {ECO:0000250|UniProtKB:P04217, ECO:0000312|EMBL:AAI05375.1};
 DE Flags: Precursor;
 GN Name=A1BG {ECO:0000312|EMBL:AAI05375.1};
 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;
 RN [1] {ECO:0000312|EMBL:AAI05375.1}
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=Hereford {ECO:0000312|EMBL:AAI05375.1};
 RC TISSUE=Testis {ECO:0000312|EMBL:AAI05375.1};
 RG NIH - Mammalian Gene Collection (MGC) project;
 RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
 RN [2] {ECO:0000305}
 RP PROTEIN SEQUENCE OF 22-36, INTERACTION WITH CRISP3, AND GLYCOSYLATION.
 RC TISSUE=Serum {ECO:0000269|PubMed:20116414};
 RX PubMed=20116414; DOI=10.1016/j.bbagen.2010.01.011;
 RA Udby L., Johnsen A.H., Borregaard N.;
 RT "Human CRISP-3 binds serum alpha1B-glycoprotein across species.";
 RL Biochim. Biophys. Acta 1800:481-485(2010).
 CC -!- SUBUNIT: Interacts with CRISP3. {ECO:0000269|PubMed:20116414}.
 CC -!- SUBCELLULAR LOCATION: Secreted {ECO:0000305}.
 CC -!- TISSUE SPECIFICITY: Plasma. {ECO:0000305}.
 CC -----
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 CC -----
 DR EMBL; BC105374; AAI05375.1; -; mRNA.
 DR RefSeq; NP_001039708.1; NM_001046243.2.
 DR STRING; 9913.ENSBTAP00000012837; -.
 DR MEROPS; I43.950; -.
 DR PaxDb; Q2KJF1; -.
 DR PeptideAtlas; Q2KJF1; -.
 DR PRIDE; Q2KJF1; -.
 DR Ensembl; ENSBTAT00000012837; ENSBTAP00000012837; ENSBTAG00000009735.
 DR GeneID; 518955; -.
 DR KEGG; bta:518955; -.
 DR CTD; 1; -.
 DR VGNC; VGNC:25433; A1BG.
 DR eggNOG; ENOG502RYEX; Eukaryota.
 DR GeneTree; ENSGT00980000198504; -.
 DR HOGENOM; CLU_042929_1_0_1; -.
 DR InParanoid; Q2KJF1; -.
 DR OMA; IKHQFLL; -.
 DR OrthoDB; 1327293at2759; -.
 DR TreeFam; TF336644; -.
 DR Reactome; R-BTA-114608; Platelet degranulation.
 DR Reactome; R-BTA-6798695; Neutrophil degranulation.
 DR Proteomes; UP000009136; Chromosome 18.
 DR Bgee; ENSBTAG00000009735; Expressed in liver and 4 other tissues.
 DR ExpressionAtlas; Q2KJF1; baseline and differential.
 DR GO; GO:0005576; C:extracellular region; IEA:UniProtKB-SubCell.
 DR Gene3D; 2.60.40.10; -; 5.
 DR InterPro; IPR016332; A1B_glyco/leuk_Ig-like_rcpt.
 DR InterPro; IPR007110; Ig-like_dom.
 DR InterPro; IPR036179; Ig-like_dom_sf.
 DR InterPro; IPR013783; Ig-like_fold.
 DR InterPro; IPR003599; Ig_sub.
 DR InterPro; IPR003598; Ig_sub2.
 DR Pfam; PF13895; Ig_2; 1.
 DR PIRSF; PIRSF001979; Alpha_1B_glycoprot_prd; 1.
 DR SMART; SM00409; IG; 4.
 DR SMART; SM00408; IGC2; 4.
 DR SUPFAM; SSF48726; SSF48726; 5.
 DR PROSITE; PS50835; IG_LIKE; 2.
 PE 1: Evidence at protein level;
 KW Direct protein sequencing; Disulfide bond; Glycoprotein;
 KW Immunoglobulin domain; Reference proteome; Repeat; Secreted; Signal.
 FT SIGNAL 1..21
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 FT CHAIN 22..503
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 FT /evidence="ECO:0000269|PubMed:20116414"
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 FT DOMAIN 27..115
 FT /note="Ig-like V-type 1"
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 FT DOMAIN 117..204
 FT /note="Ig-like V-type 2"



FT DOMAIN /evidence="ECO:0000255"
208..305
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FT /evidence="ECO:0000255"
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FT DISULFID 431..478
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SQ SEQUENCE 503 AA; 53554 MW; 22643DBA75DD4435 CRC64;
MSAWAALLLL WGLSLSPVTE QATFFDPRPS LWAEAGSPLA PWADVTLTCQ SPLPTQEFQL
LKDGVGQEPV HLESPAHEHR FPLGPVTSTT RGLYRCSYKG NNDWISPSNL VEVGTGAEPLP
APSISTSPVS WITPGLNTTL LCLSGLRGVT FLLRLEGEDQ FLEVAEAEPA TQATFPVHRA
GNYSYRTH AAGTPSEPSA TVTIEELDPP PAPTTLVDRE SAKVLRPGSS ASLTCVAPLS
GVDFQLRRGA EEQLVPRAST SPDRVFFRLS ALAAGDGSY TCRYRLRSEL AAWSRDSAPA
ELVLSDGTLA PELSAEPAI LSPTPGALVQ LRCRAPRAGV RFALVRKDAG GRQVQVRLSP
AGPEAQFELR GVSVDGSGNY SCVYVDTSPF FAGSKPSATL ELRVDGGLPR PQLRALWTGA
LTPGRDAVLR CEAEVPDVSF LLLRAGEEEP LAVAWSTHGP ADLVLTSVGP QHAGTYSCRY
RTGGPRSLLS ELSDPVELRV AGS
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