

MASCOT Search Results

Protein View: A0A1R3UGP4

Kallikrein G OS=Bos taurus OX=9913 GN=KLNG PE=3 SV=1

Database: Uniprot_bovine
Score: 66
Expect: 0.034
Nominal mass (M_r): 28249
Calculated pI: 9.07

Sequence similarity is available as [an NCBI BLAST search of A0A1R3UGP4 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: 42%

Matched peptides shown in **bold red**.

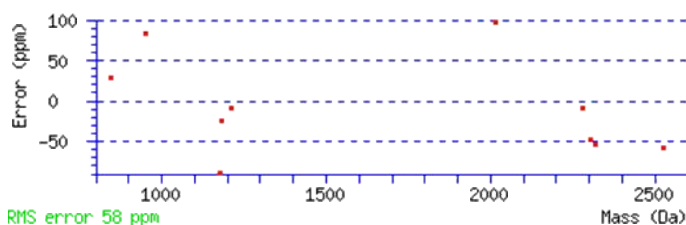
1 **MMTLQLIMFA** **LVTGHVGGET** **RIIK**GYECP HSQPWQAALF QK**TRLLCGAT**
51 **LIAPRWLLTA** AHCRKPR**YVV** **HLGAHSLGRQ** **DGCEQTRTAT** **KSFPHPDFNN**
101 **SLPNKDHRND** **IMLVKMVTPA** HLTWAVRPLT VSPRCVPAGA NCLISGWGTM
151 SSPQLHLPHT LRC**CANVTIIK** **HRECE**DAYPG NITDTMVCAS VRKEGKDSCQ
201 GDSGGPLVCN GSLQGIISWG QDPCAVSK**KP** **GVYTKVCKYV** **DWIK**TMENN

Unformatted sequence string: [250 residues](#) (for pasting into other applications).

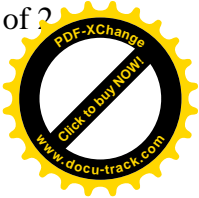
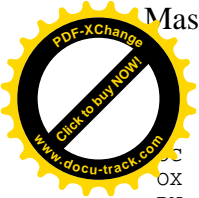
Sort peptides by Residue Number Increasing Mass Decreasing Mass

Show predicted peptides also

Query	Start - End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Peptide
75	1 - 21	2305.0740	2304.0667	2304.1793	-48.8	0		-.MMTLQLIMFALVTGHVGGETR.I
76	1 - 21	2321.0552	2320.0479	2320.1742	-54.4	0		-.MMTLQLIMFALVTGHVGGETR.I + Oxidation (M)
77	2 - 24	2528.2617	2527.2544	2527.4019	-58.3	1		M.MTLQLIMFALVTGHVGGETRIK.G
45	45 - 55	1184.6520	1183.6447	1183.6747	-25.3	0		R.LLCGATLIAPR.W
74	68 - 87	2283.0847	2282.0774	2282.0975	-8.78	1		R.YVVHLGAHSLGRQDGCEQTR.T
72	88 - 105	2015.1949	2014.1876	2013.9908	97.7	1		R.TATKSFPHPDFNNSLPNK.D
6	109 - 115	848.4780	847.4707	847.4473	27.6	0		R.NDIMLVK.M + Oxidation (M)
52	163 - 172	1211.6572	1210.6499	1210.6604	-8.69	1		R.CANVTIIKHR.E
44	229 - 238	1179.5499	1178.5426	1178.6482	-89.5	1		K.KPGVYTKVCK.Y
25	239 - 245	951.5720	950.5647	950.4862	82.7	0		K.YVDWIK.T



ID A0A1R3UGP4_BOVIN Unreviewed; 250 AA.
AC A0A1R3UGP4;
DT 12-APR-2017, integrated into UniProtKB/TrEMBL.
DT 12-APR-2017, sequence version 1.
DT 11-DEC-2019, entry version 7.
DE SubName: Full=Kallikrein G {ECO:0000313|EMBL:SFW93292.1};
GN Name=KLNG {ECO:0000313|EMBL:SFW93292.1};
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Laurasiatheria; Artiodactyla; Ruminantia; Pecora; Bovidae;



OX NCBI_TaxID=9913 {ECO:0000313|EMBL:SFW93292.1};
RN [1] {ECO:0000313|EMBL:SFW93292.1}
RP NUCLEOTIDE SEQUENCE.
RX PubMed=28224083; DOI=10.1016/j.ymgmr.2017.01.009;
RA Premzl M.;
RT "Comparative genomic analysis of eutherian kallikrein genes.";
RL Mol. Genet. Metab. Rep. 10:96-99(2017).
RN [2] {ECO:0000313|EMBL:SFW93292.1}
RP NUCLEOTIDE SEQUENCE.
RX DOI=10.1016/j.genrep.2019.100414;
RA Premzl M.;
RT "Eutherian third-party data gene collections.";
RL Gene Rep 16:0-0(2019).
CC -!- SIMILARITY: Belongs to the peptidase S1 family.
CC {ECO:0000256|SAAS:SAAS00559343}.
CC -----
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CC -----
DR EMBL; LT631645; SFW93292.1; -; Genomic_DNA.
DR RefSeq; XP_010813547.1; XM_010815245.2.
DR RefSeq; XP_010822145.1; XM_010823843.2.
DR GeneID; 526737; -.
DR CTD; 11012; -.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA:InterPro.
DR CDD; cd00190; Tryp_Spc; 1.
DR InterPro; IPR009003; Peptidase_S1_PA.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001254; Trypsin_dom.
DR InterPro; IPR018114; TRYPSIN_HIS.
DR InterPro; IPR033116; TRYPSIN_SER.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR SUPFAM; SSF50494; SSF50494; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
PE 3: Inferred from homology;
KW Disulfide bond {ECO:0000256|SAAS:SAAS00037407};
KW Hydrolase {ECO:0000256|RuleBase:RU363034};
KW Protease {ECO:0000256|RuleBase:RU363034};
KW Serine protease {ECO:0000256|RuleBase:RU363034};
KW Signal {ECO:0000256|SAM:SignalP}.
FT SIGNAL 1..18
FT /evidence="ECO:0000256|SAM:SignalP"
FT CHAIN 19..250
FT /evidence="ECO:0000256|SAM:SignalP"
FT /id="PRO_5010232748"
FT DOMAIN 22..248
FT /note="Peptidase S1"
FT /evidence="ECO:0000259|PROSITE:PS50240"
SQ SEQUENCE 250 AA; 27526 MW; FC0A1E17DA0325D1 CRC64;
MMTLQLIMFA LVTGHVGGET RIIKGYECP HSQPWQAALF QKTRLLCGAT LIAPRWLLTA
AHCRCPRYVV HLGASLGRQ DGCEQTRTAT KSFPHPDFNN SLPNKDHRND IMLVKMVTPTA
HLTWA VRPLT VSPRCVPAGA NCLISGWGT SSPQLHLPHT LRCANVTIHK HRECEAYPG
NITDTMYCAS VRKEGKDSCQ GDSGGPLVCN GSLQGIISWG QDPCAVSKKP GVTYTKVCKYV
DWIQKTMENN

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