

MASCOT Search Results

Protein View: F1MMD7

Inter-alpha-trypsin inhibitor heavy chain H4 OS=Bos taurus OX=9913
GN=ITIH4 PE=4 SV=3

Database: Uniprot_bovine
Score: 74
Expect: 0.005
Nominal mass (M_r): 101620
Calculated pI: 6.22

Sequence similarity is available as [an NCBI BLAST search of F1MMD7 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: 12%

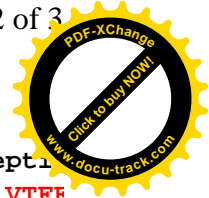
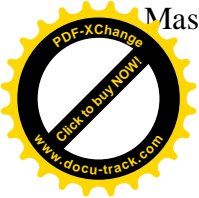
Matched peptides shown in **bold red**.

1	MKTPAPGRIH	SIVLVLLSLA	VLQTSKAQKV	QNDIDIYSLT	VDSKVSSRFA
51	HTVITSRVVN	KADAVREATF	QMELPKKAFI	TNFSMVIDGV	TYPGNIKEKA
101	AAQEYQYSAAV	ARGESAGLVR	ATGRKTEQFQ	VSVSVAPAAK	VTFELVYEEL
151	LAR HLAGAYEL	LLKVRPQQLV	KHLQMDIHIF	EPQGISFLET	ESTFMTNKLA
201	EALTTSQNKI	KAHVRFKPTL	SQQQKYPEKQ	DTVLDGSFIV	RYDVRPLSG
251	GSIQIENGYF	VHYFAPDSL	TIPKNVIFVI	DKSGSMMGRK	IKQTREALIK
301	ILDDLSPHDQ	FDLISFSSEA	TTWKPLLVPA	STENVNEAKS	YATGIQAQGG
351	TNINDAMLMA	VQLEKANQE	ELLPEGSITL	IILLTDGDPT	VGETNPLNIQ
401	KNVRKAINGQ	HSLFCLGFGF	DVSYAFLEKM	ALENGGLARR	IYEDSDSALQ
451	LQDFYQEVAN	PLMTSVAFEY	PSNAVESVTQ	DTFRVFFKGS	ELVVAGK LRE
501	QSPDVLLAQI	RGQLHRENIT	YMMMSHVAEQ	EEMFRSPKYI	FHSFIERLWA
551	YLTIQQLLEQ	MVSALDAEKQ	ALEARALSLS	LSYSFVTPLT	SMVITKPEGQ
601	EQSQVAEKPV	EDES RSRVY	LGPMR FGHSV	GDRTSRKPGG	GLKLLNGTPL
651	FGPPGPPAAA	SPFHRMTSRL	VLPELMSPLA	PASAPSPTSG	PGGASHDTDF
701	RIKGTTP TAL	PFAPVQAPSV	ILPLPGQSVD	RLCVDLRRPQ	ELVNLLSDPD
751	QGVEVTGHFE	TAKARFSWIE	VTFENPQVQI	HASPEHVMT	RNRNSAYKW
801	KETLYSVMPG	LKVTMDKEGL	LLLSRPDRVT	IGLLFWDGPG	KGLRLLLQNT
851	DRFSSHVSGT	LGQFYQDVLW	GPLDTADDSK	RTLKVQGRDY	SATRELKLDY
901	QESPPGKEIS	CWSVEL			

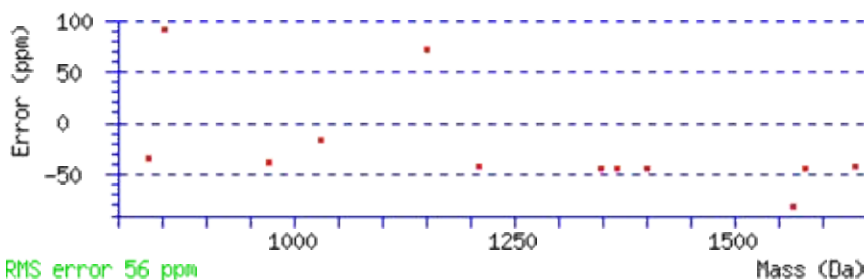
Unformatted sequence string: [916 residues](#) (for pasting into other applications).

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

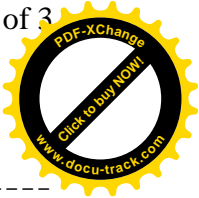
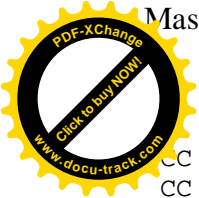
☐ Show predicted peptides also



Query	Start - End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Peptide
59	141 - 153	1581.7833	1580.7760	1580.8450	-43.6	0		K.VTFF
60	141 - 153	1581.7833	1580.7761	1580.8450	-43.6	0	35	K.VTFF
48	230 - 241	1349.6478	1348.6405	1348.6987	-43.1	0		K.QDTV
5	283 - 290	853.4803	852.4730	852.3946	92.0	1		K.SGSM
6	283 - 290	853.4804	852.4731	852.3946	92.1	1		K.SGSM
22	430 - 439	1031.5133	1030.5060	1030.5229	-16.4	0		K.MALE
63	498 - 511	1637.8650	1636.8577	1636.9260	-41.7	1		K.LREQ
49	500 - 511	1368.6882	1367.6809	1367.7409	-43.8	0		R.EQSF
38	539 - 547	1211.5695	1210.5622	1210.6135	-42.3	0		K.YIFF
33	616 - 625	1151.6821	1150.6748	1150.5917	72.2	1		R.GSRV
								+
								Oxidat:
								(M)
1	619 - 625	835.4214	834.4141	834.4422	-33.6	0		R.VYLG
58	800 - 812	1567.6902	1566.6829	1566.8116	-82.1	1		K.WKET
								+
								Oxidat:
								(M)
51	829 - 841	1402.7100	1401.7027	1401.7657	-44.9	0		R.VTIC
15	845 - 852	972.5108	971.5035	971.5400	-37.5	0		R.LLLQ



ID F1MMD7_BOVIN Unreviewed; 916 AA.
AC F1MMD7;
DT 03-MAY-2011, integrated into UniProtKB/TrEMBL.
DT 10-APR-2019, sequence version 3.
DT 26-FEB-2020, entry version 60.
DE SubName: Full=Inter-alpha-trypsin inhibitor heavy chain H4 {ECO:0000313|Ensembl:ENSBTAP00000010330, Name=ITIH4 {ECO:0000313|Ensembl:ENSBTAP00000010330, ECO:0000313|VGNC:VGNC:30336};
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|Ensembl:ENSBTAP00000010330, ECO:0000313|Proteomes:UP000009136};
RN [1] {ECO:0000313|Ensembl:ENSBTAP00000010330}
RP IDENTIFICATION.
RC STRAIN=Hereford {ECO:0000313|Ensembl:ENSBTAP00000010330};
RG Ensembl;
RL Submitted (MAR-2016) to UniProtKB.
RN [2] {ECO:0000313|Ensembl:ENSBTAP00000010330, ECO:0000313|Proteomes:UP000009136};
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Hereford {ECO:0000313|Ensembl:ENSBTAP00000010330, ECO:0000313|Proteomes:UP000009136};
RA Rosen B.D., Bickhart D.M., Koren S., Schnabel R.D., Hall R., Zimin A., Dreischer C., Schultheiss S., Schroeder S.G., Elisk C.G., Couldrey C., Liu G.E., Van Tassell C.P., Phillippy A.M., Smith T.P.L., Medrano J.F.;
RT "ARS-UCD1.2.";
RL Submitted (MAR-2018) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR PRIDE; F1MMD7; -.
DR Ensembl; ENSBTAT00000010330; ENSBTAP00000010330; ENSBTAG00000007850.
DR VGNC; VGNC:30336; ITIH4.
DR eggNOG; ENOG410IEJB; Eukaryota.
DR eggNOG; COG2304; LUCA.
DR GeneTree; ENSGT00940000161039; -.
DR HOGENOM; CLU_008101_0_0_1; -.
DR OrthoDB; 955432at2759; -.
DR TreeFam; TF328982; -.
DR Reactome; R-BTA-114608; Platelet degranulation.
DR Proteomes; UP000009136; Chromosome 22.
DR Bgee; ENSBTAG00000007850; Expressed in liver and 8 other tissues.
DR ExpressionAtlas; F1MMD7; baseline.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA:InterPro.
DR GO; GO:0030212; P:hyaluronan metabolic process; IEA:InterPro.
DR Gene3D; 3.40.50.410; -; 1.
DR InterPro; IPR010600; ITI_HC_C.
DR InterPro; IPR013694; VIT.
DR InterPro; IPR002035; VWF_A.
DR InterPro; IPR036465; vWFA_dom_sf.
DR Pfam; PF06668; ITI_HC_C; 1.
DR Pfam; PF08487; VIT; 1.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00609; VIT; 1.
DR SMART; SM00327; VWA; 1.
DR SUPFAM; SSF53300; SSF53300; 1.
DR PROSITE; PS51468; VIT; 1.
DR PROSITE; PS50234; VWFA; 1.
PE 4: Predicted;
KW Coiled coil {ECO:0000256|SAM:Coils};
KW Reference proteome {ECO:0000313|Proteomes:UP000009136};
KW Signal {ECO:0000256|SAM:SignalP}.
FT REGION 597..616
FT /note="Disordered"
FT /evidence="ECO:0000256|SAM:MobiDB-lite"
FT REGION 678..701
FT /note="Disordered"
FT /evidence="ECO:0000256|SAM:MobiDB-lite"
SQ SEQUENCE 916 AA; 101513 MW; C870BDBB3392C46F CRC64;
MKTPAPGRIH SIVLVLLSLA VLQTSKAQKV QNDIDIYSLT VDSKVSSRFA HTVITSRVVN
KADAVREATF QMELPKKAFI TNFSMVIDGV TYPGNIKEKA AAQEQYSAAV ARGESAGLVR
ATGRKTEQFQ VSVSVAPAAK VTFELVYEEL LARHLGAYEL LLKVRPQQLV KHLQMDIHIF
EPQGISFLET ESTFMTNKLA EALTTSQNKI KAHVRFKPTL SQQQKYPEKQ DTVLDGSFIV
RYDVDRPLSG GSIQIENGYF VHYFAPDSLS TIPKNVIFVI DKSGSMMGRK IKQTREALIK
ILDDLSPHDQ FDLISFSSEA TTWKPLLVPA STENVNEAKS YATGIAQGG TNINDAMLMA
VQLLEKANQE ELLPEGSITL IILLTDGDPT VGETNPLNIQ KNVRKAINGQ HSLFCLGFGE
DVSYAFLEKM ALENGGLARR IYEDSDSALQ LQDFYQEVAN PLMTSVAFEY PSNAVESVTQ
DTFRVFFKGS ELVVAGKLRE QSPDVLLAQI RGQLHRENIT YMMMSHVAEQ EEMFRSPKYI
FHSFIERLWA YLTIQQLLEQ MVSALDAEQ ALEARALSLS LSYSFVTPLT SMVITKPEGQ
EQSQVAEKPV EDESRGSRVY LGPMRFGHSV GDRTSRKPGG GLKLLNGTPL FGPPGPPAAA
SPFHRMTSRL VLPPELMSPLA PASAPSPTSG PGGASHDTDF RIKGTTPTAL PFAPVQAPS
ILPLPGQSVD RLCVDLRRPQ ELVNLLSDPD QGVEVTGHFE TAKARFSWIE VTFENPQVQI
HASPEHVMT RNRNSAYKW KETLYSVMPG LKVTMDKEGL LLLSRPDRVT IGLLFDWGGP
KGLRLLQNT DRFSSHVSGT LGQFYQDVLW GPLDTADDSK RTLKVQGRDY SATRELKLDY
QESPPGKEIS CWSVEL
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