

MASCOT Search Results

Protein View: V6F7X3

Apolipoprotein A-IV OS=Bos taurus OX=9913 GN=APOA4 PE=3 SV=1

Database: Uniprot_bovine
Score: 283
Expect: 6.7e-024
Nominal mass (M_r): 42963
Calculated pI: 5.30

Sequence similarity is available as [an NCBI BLAST search of V6F7X3 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: 41%

Matched peptides shown in **bold red**.

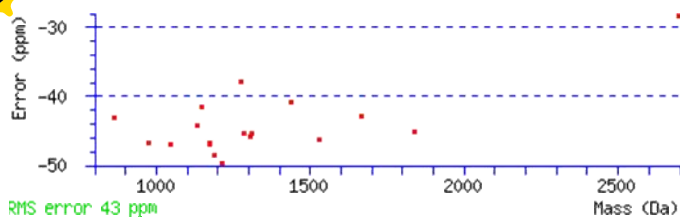
1 MFLKAVVLSL ALVAVTGAEA EVNADQVATV IWDYFSQLGN NAKKAVEHIQ
51 **KSEL****TQQLNT** **LPQDK**LGEVS TYTDDLQKKL **VPFATELHER** LTKDSEKLKE
101 EIRKELEDLR ARLLPHATEV SQKIGDNVRE LQQR**LGPYAE** **ELRTQVDTQA**
151 **QQLRRQLTPY** **AERMEKVMRQ** **NLDQLQASLA** **PYAEELQATV** **NQRVEELKGR**
201 **LTPYADQLQT** **KIEENVEELR** RSLAPYAQDV QGK**LNHQLEG** **LAFQMKKHAE**
251 ELKAKISAKA EELRQGLVPL VNSVHGSQLG NAEDLQK**SLA** **ELSSRLDQQV**
301 **EDFRRTVG****PGY** **GETFNKAMVQ** **QLDTLRQKLG** **PLAGDVEDHL** **SFLEKDLRDK**
351 VSSFFNTLKE KESQAPALPA QEEMPVPLGG

Unformatted sequence string: [380 residues](#) (for pasting into other applications).

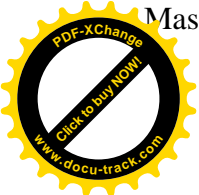
Sort peptides by ☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Show predicted peptides also

Query	Start - End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Peptide
61	52 - 65	1664.7775	1663.7702	1663.8417	-43.0	0		K.SELTQQLNTLFPQDK.L
56	79 - 90	1439.7417	1438.7344	1438.7932	-40.9	1		K.KLVVPFATELHER.L
52	80 - 90	1311.6462	1310.6389	1310.6983	-45.3	0		K.LVPFATELHER.L
53	80 - 90	1311.6462	1310.6390	1310.6983	-45.2	0	14	K.LVPFATELHER.L
26	135 - 143	1047.4978	1046.4905	1046.5396	-46.9	0		R.LGPYAEELR.T
27	135 - 143	1047.4978	1046.4905	1046.5396	-46.9	0	20	R.LGPYAEELR.T
48	144 - 154	1287.6068	1286.5995	1286.6579	-45.4	0		R.TQVDTQAQQLR.R
49	144 - 154	1287.6068	1286.5995	1286.6579	-45.3	0	14	R.TQVDTQAQQLR.R
31	155 - 163	1133.5562	1132.5489	1132.5989	-44.1	1		R.RQLTPYAER.M
18	156 - 163	977.4595	976.4522	976.4978	-46.6	0		R.QLTPYAER.M
19	156 - 163	977.4595	976.4523	976.4978	-46.6	0	15	R.QLTPYAER.M
75	170 - 193	2700.2822	2699.2749	2699.3514	-28.3	0		R.QNLDQLQASLAPYAEELQATVNQR.V
76	170 - 193	2700.2822	2699.2750	2699.3514	-28.3	0	36	R.QNLDQLQASLAPYAEELQATVNQR.V
47	201 - 211	1277.6251	1276.6178	1276.6663	-38.0	0		R.LTPYADQLQTK.I
59	234 - 246	1528.7235	1527.7162	1527.7868	-46.2	0		K.LNHQLEGLAFQMK.K
7	288 - 295	862.4257	861.4184	861.4556	-43.1	0		K.SLAELSSR.L
32	296 - 304	1149.5057	1148.4984	1148.5462	-41.6	0		R.LDQQVEDFR.R
33	296 - 304	1149.5057	1148.4985	1148.5462	-41.6	0	20	R.LDQQVEDFR.R
51	296 - 305	1305.5947	1304.5874	1304.6473	-45.9	1		R.LDQQVEDFR.T
45	306 - 316	1212.5294	1211.5221	1211.5823	-49.6	0		R.TVGPYGETFNK.A
38	317 - 326	1174.5699	1173.5626	1173.6176	-46.8	0		K.AMVQQLDTLR.Q
39	317 - 326	1174.5700	1173.5627	1173.6176	-46.8	0	50	K.AMVQQLDTLR.Q
43	317 - 326	1190.5620	1189.5547	1189.6125	-48.6	0		K.AMVQQLDTLR.Q + Oxidation (M)
66	329 - 345	1839.8657	1838.8584	1838.9414	-45.1	0		K.LGPLAGDVEDHLSFLEK.D



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ID      V6F7X3_BOVIN          Unreviewed;      380 AA.
AC      V6F7X3;
DT      10-APR-2019, integrated into UniProtKB/TrEMBL.
DT      10-APR-2019, sequence version 1.
DT      26-FEB-2020, entry version 9.
DE      SubName: Full=Apolipoprotein A-IV {ECO:0000313|EMBL:DAA22387.1};
GN      Name=APOA4 {ECO:0000313|EMBL:DAA22387.1};
GN      ORFNames=BOS_14370 {ECO:0000313|EMBL:DAA22387.1};
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:DAA22387.1, ECO:0000313|Proteomes:UP000321980};
RN      [1] {ECO:0000313|EMBL:DAA22387.1, ECO:0000313|Proteomes:UP000321980}
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX      PubMed=19393038; DOI=10.1186/gb-2009-10-4-r42;
RA      Zimin A.V., Delcher A.L., Florea L., Kelley D.R., Schatz M.C., Puiu D.,
RA      Hanrahan F., Pertea G., Van Tassell C.P., Sonstegard T.S., Marcais G.,
RA      Roberts M., Subramanian P., Yorke J.A., Salzberg S.L.;
RT      "A whole-genome assembly of the domestic cow, Bos taurus.";
RL      Genome Biol. 10:R42.01-R42.10(2009).
CC      -!- SUBCELLULAR LOCATION: Secreted {ECO:0000256|SAAS:SAAS00143437}.
CC      -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
CC      {ECO:0000256|SAAS:SAAS00598075}.
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      EMBL; GJ062397; DAA22387.1; -; Genomic_DNA.
DR      RefSeq; XP_005215912.1; XM_005215855.3.
DR      RefSeq; XP_010810673.1; XM_010812371.2.
DR      RefSeq; XP_015330105.1; XM_015474619.1.
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DR      GeneID; 537301; -.
DR      CTD; 337; -.
DR      OMA; TVVWDYF; -.
DR      OrthoDB; 1299087at2759; -.
DR      Proteomes; UP000321980; Chromosome 15.
DR      GO; GO:0005576; C:extracellular region; IEA:UniProtKB-SubCell.
DR      GO; GO:0008289; F:lipid binding; IEA:InterPro.
DR      GO; GO:0006869; P:lipid transport; IEA:UniProtKB-KW.
DR      GO; GO:0042157; P:lipoprotein metabolic process; IEA:InterPro.
DR      InterPro; IPR000074; ApoA_E.
DR      Pfam; PF01442; Apolipoprotein; 2.
PE      3: Inferred from homology;
KW      Chylomicron {ECO:0000256|SAAS:SAAS01245600};
KW      Coiled coil {ECO:0000256|SAM:Coils};
KW      Lipid transport {ECO:0000256|SAAS:SAAS00143435};
KW      Lipoprotein {ECO:0000313|EMBL:DAA22387.1};
KW      Secreted {ECO:0000256|SAAS:SAAS00143438}; Signal {ECO:0000256|SAM:SignalP};
KW      Transport {ECO:0000256|SAAS:SAAS00143435}.
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FT      REGION          361..380
FT                      /note="Disordered"
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FT      COILED          88..112
FT                      /evidence="ECO:0000256|SAM:Coils"
FT      COILED          246..266
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FT                      /evidence="ECO:0000256|SAM:Coils"
SQ      SEQUENCE      380 AA; 42990 MW; 9D3F49D2A70BE77C CRC64;
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LFQDKLGEVS TYTDDLQKKL VPFATELHER LTKDSEKLKE EIRKELEDLR ARLLPHATEV
SQKIGDNVRE LQQRLLGPYAE ELRTQVDTQA QQLRRQLTPY AERMEKVMRQ NLDQLQASLA
PYAEELQATV NQRVEELKGR LTPYADQLQT KIEENVLELR RSLAPYAQDV QGKLNHQLEG
LAFQMKKHAE ELKAKISAKA EELRQGLVPL VNSVHGSQLG NAEDLQKSLA ELSSRLDQQV
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EDFRRTVGPY GETFNKAMVQ QLDTLRQKLK PLAGDVEDHL SFLEKDLRDK VSSFFNTLKE
KESQAPALPA QEEMPVPLGG

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