MATRIX SCIENCE MASCOT Search Results

Protein View: P12960

Contactin-1 OS=Mus musculus OX=10090 GN=Cntn1 PE=1 SV=1

Database:	UP589_M_musculus
Score:	144
Monoisotopic mass (M_r):	113317
Calculated pI:	5.80

Sequence similarity is available as **an NCBI BLAST search of P12960 against nr**.

Search parameters

MS data file:	masA79.tmp
Enzyme:	Trypsin: cuts C-term side of KR unless next residue is P.
Variable modifications:	**Carbamidomethyl (C)**, **Oxidation (M)**

Protein sequence coverage: 10%

Matched peptides shown in ***bold red***.

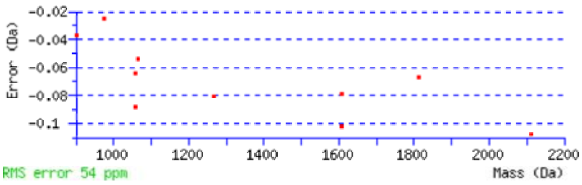
1	MKMPLLVSHL	LLISLTSCLG	DFTWHRRYGH	GVSEEDKGFG	PIFEEQPINT
51	IYPEESLEGK	VSLNCRARAS	PFPVYKWRMN	NGDVDLTNDR	YSMVGGNLVI
101	NNPDKQKDAG	VYYCLASNNY	GMVRSTEATL	SFGYLDPFPP	EERPEVKVKE
151	GKGMVLLCDP	PYHFPDDLSY	RWLLNEFPVF	ITMDKRRFVS	QTNGNLYIAN
201	VESSDRGNYS	CFVSSPSITK	SVFSKFIPLI	PIPER**TTKPY**	**PADIVVQFK**D
251	IYTMMGQNVT	LECFALGNPV	PDIRWRKVLE	PMPSTAEIST	SGAVLKIFNI
301	QLEDEGLYEC	EAENIRGKDK	HQARIYVQAF	PEWVEHINDT	EVDIGSDLYW
351	PCIATGKPIP	TIRWLKNGYS	YHKGELRLYD	VTFENAGMYQ	CIAENAYGSI
401	YANAELKILA	LAPTFEMNPM	KKKILAAKGG	RVIIECKPKA	APKPKFSWSK
451	GTEWLVNSSR	ILIWEDGSLE	INNITRNDGG	IYTCFAENNR	GKANSTGTLV
501	ITNPTRIILA	PINADITVGE	NATMQCAASF	DPALDLTFVW	SFNGYVIDFN
551	KEITHIHYQR	NFMLDANGEL	LIRNAQLKHA	GRYTCTAQTI	VDNSSASADL
601	VVR**GPPGPPG**	**GLR**IEDIRAT	SVALTWSRGS	DNHSPISKYT	IQTK**TILSDD**
651	**WK**DAKTDPPI	IEGNMESAKA	VDLIPWMEYE	FR**VVATNTLG**	**TGEPSIPSNR**
701	**IKTDGAAPNV**	**APSDVGGGGG**	**TNR**ELTITWA	PLSREYHYGN	NFGYIVAFKP
751	FDGEEWKK**VT**	**VTNPDTGR**YV	HKDETMTPST	AFQVKVKAFN	NKGDGPYSLV
801	AVINSAQDAP	SEAPTEVGVK	VLSSSEISVH	WKHVLEKIVE	SYQIRYWAGH
851	DKEAAAHR**VQ**	**VTSQEYSAR**L	ENLLPDTQYF	IEVGACNSAG	CGPSSDVIET
901	FTRKAPPSQP	PRIISSVRSG	SRYIITWDHV	VALSNESTVT	GYKILYRPDG
951	QHDGKLFSTH	KHSIEVPIPR	**DGEYVVEVR**A	HSDGGDGVVS	QVKISGVSTL
1001	SSSLLSLLLP	SLGFLVYSEF			

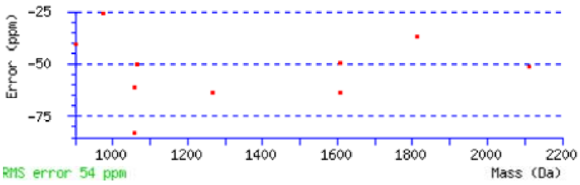
Unformatted sequence string: **1020 residues** (for pasting into other applications).

Sort by ● residue number ○ increasing mass ○ decreasing mass

Show ● matched peptides only ○ predicted peptides also

Query	Start – End	Observed	Mr(expt)	Mr(calc)	Delta	M	Score	Expect	Rank	U	Peptide
411	236 – 249	536.2655	1605.7745	1605.8766	-0.1021	0	23	0.57	1	U	R.TTKPYPADIVVQFK.D
412	236 – 249	536.2732	1605.7977	1605.8766	-0.0789	0	36	0.03	1	U	R.TTKPYPADIVVQFK.D
234	604 – 613	452.7351	903.4556	903.4927	-0.0371	0	27	0.39	1	U	R.GPPGPPGGLR.I
265	645 – 652	489.2380	976.4615	976.4866	-0.0251	0	13	9	1	U	K.TILSDDWK.D
430	683 – 700	906.9426	1811.8707	1811.9377	-0.0671	0	73	5.8e-06	1	U	R.VVATNTLGTGEPSIPSNR.I
441	701 – 723	704.3181	2109.9326	2110.0403	-0.1077	1	26	0.23	1	U	R.IKTDGAAPNVAPSDVGGGGGTNR.E
309	759 – 768	530.2311	1058.4477	1058.5357	-0.0880	0	26	0.46	1	U	K.VTVTNPDTGR.Y
310	759 – 768	530.2429	1058.4712	1058.5357	-0.0644	0	34	0.071	1	U	K.VTVTNPDTGR.Y
370	859 – 869	634.2772	1266.5399	1266.6204	-0.0805	0	48	0.0022	1	U	R.VQVTSQEYSAR.L
312	971 – 979	533.2375	1064.4604	1064.5138	-0.0534	0	43	0.0077	1	U	R.DGEYVVEVR.A





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ID   CNTN1_MOUSE             Reviewed;        1020 AA.
AC   P12960; Q6NXV7; Q8BR42; Q8C6A0;
DT   01-JAN-1990, integrated into UniProtKB/Swiss-Prot.
DT   01-JAN-1990, sequence version 1.
DT   08-NOV-2023, entry version 216.
DE   RecName: Full=Contactin-1;
DE   AltName: Full=Neural cell surface protein F3;
DE   Flags: Precursor;
GN   Name=Cntn1;
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OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae;
OC   Murinae; Mus; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RX   PubMed=2474555; DOI=10.1083/jcb.109.2.775;
RA   Gennarini G., Cibelli G., Rougon G., Mattei M.-G., Goridis C.;
RT   "The mouse neuronal cell surface protein F3: a phosphatidylinositol-
RT   anchored member of the immunoglobulin superfamily related to chicken
RT   contactin.";
RL   J. Cell Biol. 109:775-788(1989).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=CD-1; TISSUE=Neural stem cell;
RX   PubMed=15489334; DOI=10.1101/gr.2596504;
RG   The MGC Project Team;
RT   "The status, quality, and expansion of the NIH full-length cDNA project:
RT   the Mammalian Gene Collection (MGC).";
RL   Genome Res. 14:2121-2127(2004).
RN   [3]
RP   PROTEIN SEQUENCE OF 79-90; 226-249; 604-613; 619-628; 759-768 AND 859-869,
RP   AND IDENTIFICATION BY MASS SPECTROMETRY.
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RA   Lubec G., Kang S.U.;
RL   Submitted (APR-2007) to UniProtKB.
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 574-1020.
RC   STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina, and Skin;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J.,
RA   Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impiombato A., Apweiler R.,
RA   Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T.,
RA   Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A.,
RA   Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B.,
RA   Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagiolini M.,
RA   Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S.,
RA   Gariboldi M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D.,
RA   Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M.,
RA   Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H.,
RA   Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V.,
RA   Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S.,
RA   Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H.,
RA   Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N.,
RA   Nakauchi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F.,
RA   Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G.,
RA   Pesole G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z.,
RA   Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schoenbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S.,
RA   Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K., Tammoja K.,
RA   Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R.,
RA   van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamanishi H.,
RA   Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M.,
RA   Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C.,
RA   Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S.,
RA   Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K.,
RA   Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M.,
RA   Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C.,
RA   Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A.,
RA   Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [5]
RP   INTERACTION WITH TNR, AND FUNCTION.
RX   PubMed=7678967; DOI=10.1016/0896-6273(93)90243-k;
RA   Pesheva P., Gennarini G., Goridis C., Schachner M.;
RT   "The F3/11 cell adhesion molecule mediates the repulsion of neurons by the
RT   extracellular matrix glycoprotein J1-160/180.";
RL   Neuron 10:69-82(1993).
RN   [6]
RP   IDENTIFICATION IN A COMPLEX WITH NRCAM AND PTPRB.
RX   PubMed=11564762; DOI=10.1083/jcb.200104122;
RA   Sakurai T., Lustig M., Babiarz J., Furley A.J., Tait S., Brophy P.J.,
RA   Brown S.A., Brown L.Y., Mason C.A., Grumet M.;
RT   "Overlapping functions of the cell adhesion molecules Nr-CAM and L1 in
RT   cerebellar granule cell development.";
RL   J. Cell Biol. 154:1259-1273(2001).
RN   [7]
RP   FUNCTION.
RX   PubMed=11395001; DOI=10.1016/s0896-6273(01)00296-3;
RA   Boyle M.E., Berglund E.O., Murai K.K., Weber L., Peles E., Ranscht B.;
RT   "Contactin orchestrates assembly of the septate-like junctions at the
RT   paranode in myelinated peripheral nerve.";
RL   Neuron 30:385-397(2001).
RN   [8]
RP   FUNCTION, AND INTERACTION WITH NOTCH1.
RX   PubMed=14567914; DOI=10.1016/s0092-8674(03)00810-9;
RA   Hu Q.-D., Ang B.-T., Karsak M., Hu W.-P., Cui X.-Y., Duka T., Takeda Y.,
RA   Chia W., Sankar N., Ng Y.-K., Ling E.-A., Maciag T., Small D.,
RA   Trifonova R., Kopan R., Okano H., Nakafuku M., Chiba S., Hirai H.,
RA   Aster J.C., Schachner M., Pallen C.J., Watanabe K., Xiao Z.-C.;
RT   "F3/contactin acts as a functional ligand for Notch during oligodendrocyte
RT   maturation.";
RL   Cell 115:163-175(2003).
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RN   [9]
RP   IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].
RC   TISSUE=Brain;
RX   PubMed=21183079; DOI=10.1016/j.cell.2010.12.001;
RA   Huttlin E.L., Jedrychowski M.P., Elias J.E., Goswami T., Rad R.,
RA   Beausoleil S.A., Villen J., Haas W., Sowa M.E., Gygi S.P.;
RT   "A tissue-specific atlas of mouse protein phosphorylation and expression.";
RL   Cell 143:1174-1189(2010).
RN   [10]
RP   INTERACTION WITH PTPRZ1.
RX   PubMed=20133774; DOI=10.1073/pnas.0911235107;
RA   Bouyain S., Watkins D.J.;
RT   "The protein tyrosine phosphatases PTPRZ and PTPRG bind to distinct members
RT   of the contactin family of neural recognition molecules.";
RL   Proc. Natl. Acad. Sci. U.S.A. 107:2443-2448(2010).
RN   [11]
RP   INTERACTION WITH TASOR, AND TISSUE SPECIFICITY.
RX   PubMed=31112734; DOI=10.1016/j.yexcr.2019.05.018;
RA   Gresakova V., Novosadova V., Prochazkova M., Bhargava S., Jenickova I.,
RA   Prochazka J., Sedlacek R.;
RT   "Fam208a orchestrates interaction protein network essential for early
RT   embryonic development and cell division.";
RL   Exp. Cell Res. 382:111437-111437(2019).
CC   -!- FUNCTION: Contactins mediate cell surface interactions during nervous
CC       system development. Involved in the formation of paranodal axo-glial
CC       junctions in myelinated peripheral nerves and in the signaling between
CC       axons and myelinating glial cells via its association with CNTNAP1.
CC       Participates in oligodendrocytes generation by acting as a ligand of
CC       NOTCH1. Its association with NOTCH1 promotes NOTCH1 activation through
CC       the released notch intracellular domain (NICD) and subsequent
CC       translocation to the nucleus. Interaction with TNR induces a repulsion
CC       of neurons and an inhibition of neurite outgrowth.
CC       {ECO:0000269|PubMed:11395001, ECO:0000269|PubMed:14567914,
CC       ECO:0000269|PubMed:7678967}.
CC   -!- SUBUNIT: Monomer. Interacts with CNTNAP1 in cis form (By similarity).
CC       Binds to the carbonic-anhydrase like domain of PTPRZ1
CC       (PubMed:20133774). Interacts with NOTCH1 and TNR (PubMed:7678967,
CC       PubMed:14567914). Detected in a complex with NRCAM and PTPRB
CC       (PubMed:11564762). Interacts with TASOR (PubMed:31112734).
CC       {ECO:0000250|UniProtKB:Q12860, ECO:0000250|UniProtKB:Q63198,
CC       ECO:0000269|PubMed:14567914, ECO:0000269|PubMed:20133774,
CC       ECO:0000269|PubMed:31112734, ECO:0000269|PubMed:7678967}.
CC   -!- SUBCELLULAR LOCATION: Cell membrane; Lipid-anchor, GPI-anchor.
CC   -!- TISSUE SPECIFICITY: Expressed in the ovary and in Sertoli cells of the
CC       testis. {ECO:0000269|PubMed:31112734}.
CC   -!- MISCELLANEOUS: F3 shares with L1, N-CAM, MAG, and other cell adhesion
CC       molecules from nervous tissue the L2/HNK-1 carbohydrate epitope.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily. Contactin
CC       family. {ECO:0000305}.
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; X14943; CAA33075.1; -; mRNA.
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DR   SMR; P12960; -.
DR   BioGRID; 198797; 25.
DR   IntAct; P12960; 10.
DR   STRING; 10090.ENSMUSP00000000109; -.
DR   GlyConnect; 2224; 19 N-Linked glycans (8 sites).
DR   GlyCosmos; P12960; 9 sites, 19 glycans.
DR   GlyGen; P12960; 11 sites, 19 N-linked glycans (8 sites), 1 O-linked glycan (2 sites).
DR   iPTMnet; P12960; -.
DR   PhosphoSitePlus; P12960; -.
DR   SwissPalm; P12960; -.
DR   CPTAC; non-CPTAC-3642; -.
DR   MaxQB; P12960; -.
DR   PaxDb; 10090-ENSMUSP00000000109; -.
DR   PeptideAtlas; P12960; -.
DR   ProteomicsDB; 285524; -.
DR   ABCD; P12960; 1 sequenced antibody.
DR   Antibodypedia; 25021; 361 antibodies from 40 providers.
DR   DNASU; 12805; -.
DR   Ensembl; ENSMUST00000000109; ENSMUSP00000000109; ENSMUSG00000055022.
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DR   CTD; 1272; -.
DR   MGI; MGI:105980; Cntn1.
DR   VEuPathDB; HostDB:ENSMUSG00000055022; -.
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DR   GeneTree; ENSGT00940000155915; -.
DR   HOGENOM; CLU_005756_0_0_1; -.
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DR   TreeFam; TF351103; -.
DR   BioGRID-ORCS; 12805; 1 hit in 76 CRISPR screens.
DR   ChiTaRS; Cntn1; mouse.
DR   PRO; PR:P12960; -.
DR   Proteomes; UP000000589; Chromosome 15.
DR   RNAct; P12960; Protein.
DR   Bgee; ENSMUSG00000055022; Expressed in lateral geniculate body and 209 other tissues.
DR   Genevisible; P12960; MM.
DR   GO; GO:0030424; C:axon; IBA:GO_Central.
DR   GO; GO:0043209; C:myelin sheath; HDA:UniProtKB.
DR   GO; GO:0005886; C:plasma membrane; IBA:GO_Central.
DR   GO; GO:0045211; C:postsynaptic membrane; IDA:SynGO.
DR   GO; GO:0042734; C:presynaptic membrane; IDA:SynGO.
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DR   GO; GO:0042552; P:myelination; IMP:MGI.
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DR   GO; GO:0007219; P:Notch signaling pathway; IEA:UniProtKB-KW.
DR   GO; GO:0010628; P:positive regulation of gene expression; IMP:MGI.
DR   GO; GO:0010976; P:positive regulation of neuron projection development; IGI:MGI.
DR   GO; GO:0050731; P:positive regulation of peptidyl-tyrosine phosphorylation; ISO:MGI.
DR   GO; GO:0010765; P:positive regulation of sodium ion transport; IMP:MGI.
DR   CDD; cd00063; FN3; 4.
DR   CDD; cd05727; Ig2_Contactin-2-like; 1.
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DR   CDD; cd04970; Ig6_Contactin; 1.
DR   CDD; cd05849; IgI_1_Contactin-1; 1.
DR   CDD; cd05851; IgI_3_Contactin-1; 1.
DR   Gene3D; 2.60.40.10; Immunoglobulins; 10.
DR   InterPro; IPR047102; Contactin-1_2_Ig1.
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PE   1: Evidence at protein level;
KW   3D-structure; Cell adhesion; Cell membrane; Direct protein sequencing;
KW   Disulfide bond; Glycoprotein; GPI-anchor; Immunoglobulin domain;
KW   Lipoprotein; Membrane; Notch signaling pathway; Reference proteome; Repeat;
KW   Signal.
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FT   DOMAIN          813..908
FT                   /note="Fibronectin type-III 3"
FT                   /evidence="ECO:0000255|PROSITE-ProRule:PRU00316"
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FT   DOMAIN          909..1002
FT                   /note="Fibronectin type-III 4"
FT                   /evidence="ECO:0000255|PROSITE-ProRule:PRU00316"
FT   REGION          695..719
FT                   /note="Disordered"
FT                   /evidence="ECO:0000256|SAM:MobiDB-lite"
FT   LIPID           1001
FT                   /note="GPI-anchor amidated serine"
FT                   /evidence="ECO:0000255"
FT   CARBOHYD        208
FT                   /note="N-linked (GlcNAc...) asparagine"
FT                   /evidence="ECO:0000255"
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FT                   /note="N-linked (GlcNAc...) asparagine"
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FT   CARBOHYD        338
FT                   /note="N-linked (GlcNAc...) asparagine"
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FT   CARBOHYD        457
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FT   CARBOHYD        935
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FT   DISULFID        65..114
FT                   /evidence="ECO:0000255|PROSITE-ProRule:PRU00114"
FT   DISULFID        158..211
FT                   /evidence="ECO:0000255|PROSITE-ProRule:PRU00114"
FT   DISULFID        263..310
FT                   /evidence="ECO:0000255|PROSITE-ProRule:PRU00114"
FT   DISULFID        352..391
FT                   /evidence="ECO:0000255|PROSITE-ProRule:PRU00114"
FT   DISULFID        436..484
FT                   /evidence="ECO:0000255|PROSITE-ProRule:PRU00114"
FT   DISULFID        526..585
FT                   /evidence="ECO:0000255|PROSITE-ProRule:PRU00114"
FT   CONFLICT        433
FT                   /note="I -> V (in Ref. 2; AAH66864)"
FT                   /evidence="ECO:0000305"
SQ   SEQUENCE   1020 AA;  113388 MW;  9DCDAA40EAA4CBC7 CRC64;
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     VSLNCRARAS PFPVYKWRMN NGDVDLTNDR YSMVGGNLVI NNPDKQKDAG VYYCLASNNY
     GMVRSTEATL SFGYLDPFPP EERPEVKVKE GKGMVLLCDP PYHFPDDLSY RWLLNEFPVF
     ITMDKRRFVS QTNGNLYIAN VESSDRGNYS CFVSSPSITK SVFSKFIPLI PIPERTTKPY
     PADIVVQFKD IYTMMGQNVT LECFALGNPV PDIRWRKVLE PMPSTAEIST SGAVLKIFNI
     QLEDEGLYEC EAENIRGKDK HQARIYVQAF PEWVEHINDT EVDIGSDLYW PCIATGKPIP
     TIRWLKNGYS YHKGELRLYD VTFENAGMYQ CIAENAYGSI YANAELKILA LAPTFEMNPM
     KKKILAAKGG RVIIECKPKA APKPKFSWSK GTEWLVNSSR ILIWEDGSLE INNITRNDGG
     IYTCFAENNR GKANSTGTLV ITNPTRIILA PINADITVGE NATMQCAASF DPALDLTFVW
     SFNGYVIDFN KEITHIHYQR NFMLDANGEL LIRNAQLKHA GRYTCTAQTI VDNSSASADL
     VVRGPPGPPG GLRIEDIRAT SVALTWSRGS DNHSPISKYT IQTKTILSDD WKDAKTDPPI
     IEGNMESAKA VDLIPWMEYE FRVVATNTLG TGEPSIPSNR IKTDGAAPNV APSDVGGGGG
     TNRELTITWA PLSREYHYGN NFGYIVAFKP FDGEEWKKVT VTNPDTGRYV HKDETMTPST
     AFQVKVKAFN NKGDGPYSLV AVINSAQDAP SEAPTEVGVK VLSSSEISVH WKHVLEKIVE
     SYQIRYWAGH DKEAAAHRVQ VTSQEYSARL ENLLPDTQYF IEVGACNSAG CGPSSDVIET
     FTRKAPPSQP PRIISSVRSG SRYIITWDHV VALSNESTVT GYKILYRPDG QHDGKLFSTH
     KHSIEVPIPR DGEYVVEVRA HSDGGDGVVS QVKISGVSTL SSSLLSLLLP SLGFLVYSEF
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