

**Protein View: ADT2\_YEAST**

**ADP,ATP carrier protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PET9 PE=1 SV=2**

**Database:** SwissProt  
**Score:** 84  
**Expect:** 3.1e-05  
**Monoisotopic mass (M<sub>r</sub>):** 34632  
**Calculated pI:** 9.80  
**Taxonomy:** Saccharomyces cerevisiae S288C

Sequence similarity is available as [an NCBI BLAST search of ADT2\\_YEAST 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)  
**Mass values searched:** 45  
**Mass values matched:** 13

**Protein sequence coverage: 31%**

Matched peptides shown in **bold red**.

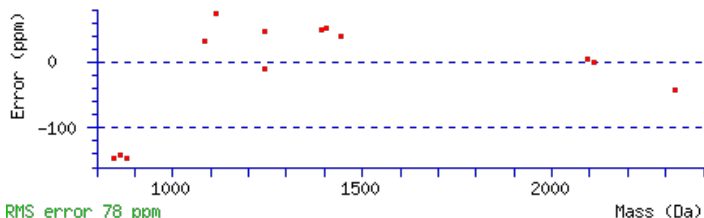
1 **MSSNAQVK**TP LPPAPAP**KE** **SNFLIDFLMG** **GVSAAVAK**TA ASPIERVKLL  
 51 IQNQDEMLKQ GTLDR**KYAGI** **LDCFKRTATQ** **EGVISFWRGN** TANVIR**YFPT**  
 101 **QALNFAFK**DK IK**AMFGFKKE** EGYAKWFAGN LASGGAAGAL SLLFVYSLDY  
 151 ARTRLAADSK SSKKGGARQF NGLIDVYKKT LK**SDGVAGLY** **RGFLPSVVGI**  
 201 **VVYR**GLYFGM YDSLKPLLLT GSLEGSFLAS FLLGWVTTG ASTCSYPLDT  
 251 VRRRMMMTSG QAVK**YDGAFD** **CLRK**IVAEAG VGSLFKGCGA NILRGVAGAG  
 301 VISMYDQLQM ILFGK**KKF**K

Unformatted sequence string: **318 residues** (for pasting into other applications).

Sort by  residue number  increasing mass  decreasing mass  
 Show  matched peptides only  predicted peptides also

Start – End	Observed	Mr(expt)	Mr(calc)	ppm	M	Peptide
1 – 8	<b>864.3020</b>	863.2947	863.4171	-142	0	<b>-.MSSNAQVK.T</b>
1 – 8	<b>880.2910</b>	879.2837	879.4120	-146	0	<b>-.MSSNAQVK.T</b> + Oxidation (M)
19 – 38	<b>2097.1120</b>	2096.1047	2096.0976	3.40	1	<b>K.KESNFLIDFLMGVSAAVAK.T</b>
19 – 38	<b>2113.0970</b>	2112.0897	2112.0925	-1.32	1	<b>K.KESNFLIDFLMGVSAAVAK.T</b> + Oxidation (M)
67 – 75	<b>1086.5620</b>	1085.5547	1085.5216	30.6	0	<b>K.YAGILDCFK.R</b>
67 – 76	<b>1242.6890</b>	1241.6817	1241.6227	47.6	1	<b>K.YAGILDCFKR.T</b>
77 – 88	<b>1394.7730</b>	1393.7657	1393.6990	47.9	0	<b>R.TATQEGVISFWR.G</b>
97 – 108	<b>1446.7990</b>	1445.7917	1445.7343	39.7	0	<b>R.YFPTQALNFAFK.D</b>
113 – 119	<b>844.3150</b>	843.3077	843.4313	-147	1	<b>K.AMFGFKK.E</b> + Oxidation (M)
183 – 204	<b>2324.1760</b>	2323.1687	2323.2689	-43.1	1	<b>K.SDGVAGLYRGFLPSVVGIVVYR.G</b>
192 – 204	<b>1405.8930</b>	1404.8857	1404.8129	51.8	0	<b>R.GFLPSVVGIVVYR.G</b>
265 – 273	<b>1116.5590</b>	1115.5517	1115.4706	72.7	0	<b>K.YDGAFDCLR.K</b>
265 – 274	<b>1244.5610</b>	1243.5537	1243.5656	-9.51	1	<b>K.YDGAFDCLRK.I</b>

**No match to:** 802.3060, 804.3110, 805.3780, 806.3490, 821.3580, 823.3790, 826.3310, 833.1200, 836.3120, 842.3030, 848.3430, 849.3860, 855.0920, 871.0770, 975.3810, 1019.4100, 1060.0910, 1102.5150, 1378.7500, 1468.8000, 1480.8380, 1484.7770, 1497.8610, 1518.7970, 1727.8300, 1775.9570, 1777.9880, 1884.8850, 2109.1780, 2196.0930, 2864.3830, 3084.4840



ID ADT2\_YEAST Reviewed; 318 AA.  
AC P18239; D6VPW9;  
DT 01-NOV-1990, integrated into UniProtKB/Swiss-Prot.  
DT 01-OCT-1994, sequence version 2.  
DT 29-SEP-2021, entry version 192.  
DE RecName: Full=ADP,ATP carrier protein 2;  
DE AltName: Full=ADP/ATP translocase 2;  
DE AltName: Full=Adenine nucleotide translocator 2;  
DE Short=ANT 2;  
DE AltName: Full=Petite colonies protein 9;  
GN Name=PET9; Synonyms=AAC2; OrderedLocusNames=YBL030C; ORFNames=YBL0421;  
OS *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) (Baker's yeast).  
OC Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=559292;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX PubMed=2844786;  
RA Lawson J.E., Douglas M.G.;  
RT "Separate genes encode functionally equivalent ADP/ATP carrier proteins in  
RT *Saccharomyces cerevisiae*. Isolation and analysis of AAC2.";  
RL J. Biol. Chem. 263:14812-14818(1988).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX PubMed=2165073;  
RA Kolarov J., Kolarova N., Nelson N.;  
RT "A third ADP/ATP translocator gene in yeast.";  
RL J. Biol. Chem. 265:12711-12716(1990).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC STRAIN=ATCC 204508 / S288c;  
RA Trezeguet V., le Saux A., Lauquin G.;  
RL Submitted (AUG-1993) to the EMBL/GenBank/DDBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC STRAIN=ATCC 204508 / S288c;  
RX PubMed=7725803; DOI=10.1002/yea.320101217;  
RA van Dyck L., Jonniaux J.-L., Barreiros T.D.M., Kleine K., Goffeau A.;  
RT "Analysis of a 17.4 kb DNA segment of yeast chromosome II encompassing the  
RT ribosomal protein L19 as well as proteins with homologies to components of  
RT the hnRNP and snRNP complexes and to the human proliferation-associated  
RT p120 antigen.";  
RL Yeast 10:1663-1673(1994).  
RN [5]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=ATCC 204508 / S288c;  
RX PubMed=7813418; DOI=10.1002/j.1460-2075.1994.tb06923.x;  
RA Feldmann H., Aigle M., Aljinovic G., Andre B., Baclet M.C., Barthe C.,  
RA Baur A., Becam A.-M., Biteau N., Boles E., Brandt T., Brendel M.,  
RA Brueckner M., Bussereau F., Christiansen C., Contreras R., Crouzet M.,  
RA Cziepluch C., Demolis N., Delaveau T., Doignon F., Domdey H.,  
RA Duesterhus S., Dubois E., Dujon B., El Bakkoury M., Entian K.-D.,  
RA Feuermann M., Fiers W., Fobo G.M., Fritz C., Gassenhuber J., Glansdorff N.,  
RA Goffeau A., Grivell L.A., de Haan M., Hein C., Herbert C.J.,  
RA Hollenberg C.P., Holmstroem K., Jacq C., Jacquet M., Jauniaux J.-C.,  
RA Jonniaux J.-L., Kallesoe T., Kiesau P., Kirchrath L., Koetter P.,  
RA Korol S., Liebl S., Logghe M., Lohan A.J.E., Louis E.J., Li Z.Y.,  
RA Maat M.J., Mallet L., Mannhaupt G., Messenguy F., Miosga T., Molemans F.,  
RA Mueller S., Nasr F., Obermaier B., Perea J., Pierard A., Piravandi E.,  
RA Pohl F.M., Pohl T.M., Potier S., Proft M., Purnelle B., Ramezani Rad M.,  
RA Rieger M., Rose M., Schaaff-Gerstenschlaeger I., Scherens B.,  
RA Schwarzlose C., Skala J., Slonimski P.P., Smits P.H.M., Souciet J.-L.,  
RA Steensma H.Y., Stucka R., Urrestarazu L.A., van der Aart Q.J.M.,  
RA Van Dyck L., Vassarotti A., Vetter I., Vierendeels F., Vissers S.,  
RA Wagner G., de Wergifosse P., Wolfe K.H., Zagulski M., Zimmermann F.K.,  
RA Mewes H.-W., Kleine K.;  
RT "Complete DNA sequence of yeast chromosome II.";  
RL EMBO J. 13:5795-5809(1994).  
RN [6]  
RP GENOME REANNOTATION.  
RC STRAIN=ATCC 204508 / S288c;  
RX PubMed=24374639; DOI=10.1534/g3.113.008995;  
RA Engel S.R., Dietrich F.S., Fisk D.G., Binkley G., Balakrishnan R.,  
RA Costanzo M.C., Dwight S.S., Hitz B.C., Karra K., Nash R.S., Weng S.,  
RA Wong E.D., Lloyd P., Skrzypek M.S., Miyasato S.R., Simison M., Cherry J.M.;  
RT "The reference genome sequence of *Saccharomyces cerevisiae*: Then and now.";  
RL G3 (Bethesda) 4:389-398(2014).  
RN [7]  
RP SUBCELLULAR LOCATION.  
RX PubMed=795470; DOI=10.1016/s0300-9084(76)80120-4;  
RA Lauquin G., Lunardi J., Vignais P.V.;  
RT "Effect of genetic and physiological manipulations on the kinetic and  
RT binding parameters of the adenine nucleotide translocator in *Saccharomyces*  
RT *cerevisiae* and *Candida utilis*.";

RL Biochimie 58:1213-1220(1976).  
 RN [8]  
 RP FUNCTION.  
 RX PubMed=2167309;  
 RA Gawaz M., Douglas M.G., Klingenberg M.;  
 RT "Structure-function studies of adenine nucleotide transport in  
 RT mitochondria. II. Biochemical analysis of distinct AAC1 and AAC2 proteins  
 RT in yeast.";  
 RL J. Biol. Chem. 265:14202-14208(1990).  
 RN [9]  
 RP MUTAGENESIS.  
 RX PubMed=8487299; DOI=10.1006/jmbi.1993.1233;  
 RA Nelson D.R., Lawson J.E., Klingenberg M., Douglas M.G.;  
 RT "Site-directed mutagenesis of the yeast mitochondrial ADP/ATP translocator.  
 RT Six arginines and one lysine are essential.";  
 RL J. Mol. Biol. 230:1159-1170(1993).  
 RN [10]  
 RP TOPOLOGY.  
 RX PubMed=7683726; DOI=10.1006/jmbi.1993.1234;  
 RA Nelson D.R., Douglas M.G.;  
 RT "Function-based mapping of the yeast mitochondrial ADP/ATP translocator by  
 RT selection for second site revertants.";  
 RL J. Mol. Biol. 230:1171-1182(1993).  
 RN [11]  
 RP IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].  
 RC STRAIN=ATCC 76625 / YPH499;  
 RX PubMed=17761666; DOI=10.1074/mcp.m700098-mcp200;  
 RA Reinders J., Wagner K., Zahedi R.P., Stojanovski D., Eyrich B.,  
 RA van der Laan M., Rehling P., Sickmann A., Pfanner N., Meisinger C.;  
 RT "Profiling phosphoproteins of yeast mitochondria reveals a role of  
 RT phosphorylation in assembly of the ATP synthase.";  
 RL Mol. Cell. Proteomics 6:1896-1906(2007).  
 RN [12] {ECO:0007744|PDB:4C9G, ECO:0007744|PDB:4C9H}  
 RP X-RAY CRYSTALLOGRAPHY (2.49 ANGSTROMS) IN COMPLEX WITH  
 RP CARBOXYATRACYLOSIDE, FUNCTION, CATALYTIC ACTIVITY, ACTIVITY REGULATION,  
 RP TOPOLOGY, AND MUTAGENESIS OF ASP-109; LYS-112; ASP-212; LYS-215; ASP-306  
 RP AND GLN-309.  
 RX PubMed=24474793; DOI=10.1073/pnas.1320692111;  
 RA Ruprecht J.J., Hellowell A.M., Harding M., Crichton P.G., McCoy A.J.,  
 RA Kunji E.R.;  
 RT "Structures of yeast mitochondrial ADP/ATP carriers support a domain-based  
 RT alternating-access transport mechanism.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 111:E426-E434(2014).  
 CC -!- FUNCTION: ADP:ATP antiporter that mediates import of ADP into the  
 CC mitochondrial matrix for ATP synthesis, and export of ATP out to fuel  
 CC the cell (PubMed:24474793). Cycles between the cytoplasmic-open state  
 CC (c-state) and the matrix-open state (m-state): operates by the  
 CC alternating access mechanism with a single substrate-binding site  
 CC intermittently exposed to either the cytosolic (c-state) or matrix (m-  
 CC state) side of the inner mitochondrial membrane (By similarity).  
 CC {ECO:0000250|UniProtKB:G2QNH0, ECO:0000269|PubMed:24474793}.  
 CC -!- CATALYTIC ACTIVITY:  
 CC Reaction=ADP(in) + ATP(out) = ADP(out) + ATP(in); Xref=Rhea:RHEA:34999,  
 CC ChEBI:CHEBI:30616, ChEBI:CHEBI:456216;  
 CC Evidence={ECO:0000269|PubMed:24474793};  
 CC PhysiologicalDirection=left-to-right; Xref=Rhea:RHEA:35000;  
 CC Evidence={ECO:0000269|PubMed:24474793};  
 CC -!- ACTIVITY REGULATION: The matrix-open state (m-state) is inhibited by  
 CC the membrane-permeable bongkreikic acid (BKA) (PubMed:24474793). The  
 CC cytoplasmic-open state (c-state) is inhibited by the membrane-  
 CC impermeable toxic inhibitor carboxyatractyloside (CATR)  
 CC (PubMed:24474793). {ECO:0000269|PubMed:24474793}.  
 CC -!- SUBUNIT: Monomer. {ECO:0000250|UniProtKB:G2QNH0}.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrion inner membrane  
 CC {ECO:0000269|PubMed:795470}; Multi-pass membrane protein  
 CC {ECO:0000269|PubMed:24474793}.  
 CC -!- DOMAIN: The transmembrane helices are not perpendicular to the plane of  
 CC the membrane, but cross the membrane at an angle. At least 2 of the  
 CC odd-numbered transmembrane helices exhibit a sharp kink, due to the  
 CC presence of a conserved proline residue. {ECO:0000269|PubMed:24474793}.  
 CC -!- SIMILARITY: Belongs to the mitochondrial carrier (TC 2.A.29) family.  
 CC {ECO:0000305}.  
 CC -----  
 CC Copyrighted by the UniProt Consortium, see <https://www.uniprot.org/terms>  
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 CC -----  
 DR EMBL; X77291; CAA54501.1; -; Genomic\_DNA.  
 DR EMBL; J04021; AAA34381.1; -; Genomic\_DNA.  
 DR EMBL; M34075; AAA97484.1; -; Genomic\_DNA.  
 DR EMBL; X74427; CAA52446.1; -; Genomic\_DNA.  
 DR EMBL; Z35791; CAA84850.1; -; Genomic\_DNA.  
 DR EMBL; BK006936; DAA07089.1; -; Genomic\_DNA.  
 DR PIR; A31978; A31978.  
 DR RefSeq; NP\_009523.1; NM\_001178270.1.  
 DR PDB; 4C9G; X-ray; 2.49 A; A=1-318.

DR PDB; 4C9H; X-ray; 3.20 A; A/B=1-318.  
 DR PDBsum; 4C9G; -.  
 DR PDBsum; 4C9H; -.  
 DR SMR; P18239; -.  
 DR BioGRID; 32667; 209.  
 DR DIP; DIP-2917N; -.  
 DR IntAct; P18239; 70.  
 DR MINT; P18239; -.  
 DR STRING; 4932.YBL030C; -.  
 DR TCDB; 2.A.29.1.7; the mitochondrial carrier (mc) family.  
 DR iPTMnet; P18239; -.  
 DR MaxQB; P18239; -.  
 DR PaxDb; P18239; -.  
 DR PRIDE; P18239; -.  
 DR EnsemblFungi; YBL030C\_mRNA; YBL030C; YBL030C.  
 DR GeneID; 852250; -.  
 DR KEGG; sce:YBL030C; -.  
 DR SGD; S000000126; PET9.  
 DR VEuPathDB; FungiDB:YBL030C; -.  
 DR eggNOG; KOG0749; Eukaryota.  
 DR GeneTree; ENSGT00940000176325; -.  
 DR HOGENOM; CLU\_015166\_12\_0\_1; -.  
 DR InParanoid; P18239; -.  
 DR OMA; YDGIVEC; -.  
 DR Reactome; R-SCE-1268020; Mitochondrial protein import.  
 DR Reactome; R-SCE-83936; Transport of nucleosides and free purine and pyrimidine bases across the plasma membrane.  
 DR PRO; PR:P18239; -.  
 DR Proteomes; UP00002311; Chromosome II.  
 DR RNAct; P18239; protein.  
 DR GO; GO:0016021; C:integral component of membrane; IDA:UniProtKB.  
 DR GO; GO:0005743; C:mitochondrial inner membrane; IDA:SGD.  
 DR GO; GO:0005739; C:mitochondrion; HDA:SGD.  
 DR GO; GO:0005471; F:ATP:ADP antiporter activity; IDA:UniProtKB.  
 DR GO; GO:0015866; P:ADP transport; IDA:SGD.  
 DR GO; GO:0009060; P:aerobic respiration; IMP:SGD.  
 DR GO; GO:0009061; P:anaerobic respiration; IGI:SGD.  
 DR GO; GO:0006915; P:apoptotic process; IMP:SGD.  
 DR GO; GO:0015867; P:ATP transport; IDA:SGD.  
 DR GO; GO:0015886; P:heme transport; IMP:SGD.  
 DR GO; GO:0140021; P:mitochondrial ADP transmembrane transport; IEA:InterPro.  
 DR GO; GO:1990544; P:mitochondrial ATP transmembrane transport; IEA:InterPro.  
 DR GO; GO:0006839; P:mitochondrial transport; IMP:SGD.  
 DR GO; GO:0055085; P:transmembrane transport; IDA:SGD.  
 DR Gene3D; 1.50.40.10; -; 1.  
 DR InterPro; IPR002113; ADT\_euk\_type.  
 DR InterPro; IPR002067; Mit\_carrier.  
 DR InterPro; IPR018108; Mitochondrial\_sb/sol\_carrier.  
 DR InterPro; IPR023395; Mt\_carrier\_dom\_sf.  
 DR PANTHER; PTHR45635; PTHR45635; 1.  
 DR Pfam; PF00153; Mito\_carr; 3.  
 DR PRINTS; PR00927; ADPTRNSLCASE.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR SUPFAM; SSF103506; SSF103506; 1.  
 DR PROSITE; PS50920; SOLCAR; 3.  
 PE 1: Evidence at protein level;  
 KW 3D-structure; Antiport; Membrane; Mitochondrion;  
 KW Mitochondrion inner membrane; Reference proteome; Repeat; Transmembrane;  
 KW Transmembrane helix; Transport.  
 FT CHAIN 1..318  
 FT /note="ADP,ATP carrier protein 2"  
 FT /id="PRO\_0000090594"  
 FT TRANSMEM 23..50  
 FT /note="Helical; Name=1"  
 FT /evidence="ECO:0000269|PubMed:24474793"  
 FT TRANSMEM 91..115  
 FT /note="Helical; Name=2"  
 FT /evidence="ECO:0000269|PubMed:24474793"  
 FT TRANSMEM 123..143  
 FT /note="Helical; Name=3"  
 FT /evidence="ECO:0000269|PubMed:24474793"  
 FT TRANSMEM 193..214  
 FT /note="Helical; Name=4"  
 FT /evidence="ECO:0000269|PubMed:24474793"  
 FT TRANSMEM 228..248  
 FT /note="Helical; Name=5"  
 FT /evidence="ECO:0000269|PubMed:24474793"  
 FT TRANSMEM 288..308  
 FT /note="Helical; Name=6"  
 FT /evidence="ECO:0000269|PubMed:24474793"  
 FT REPEAT 21..114  
 FT /note="Solcar 1"  
 FT REPEAT 125..217  
 FT /note="Solcar 2"  
 FT REPEAT 225..311  
 FT /note="Solcar 3"

FT REGION 252..257  
 FT /note="Important for transport activity"  
 FT /evidence="ECO:0000250|UniProtKB:P12235"  
 FT MOTIF 252..257  
 FT /note="Nucleotide carrier signature motif"  
 FT /evidence="ECO:0000250|UniProtKB:P02722"  
 FT BINDING 96  
 FT /note="ADP"  
 FT /evidence="ECO:0000305|PubMed:24474793"  
 FT BINDING 108  
 FT /note="ADP"  
 FT /evidence="ECO:0000305|PubMed:24474793"  
 FT BINDING 252  
 FT /note="ADP"  
 FT /evidence="ECO:0000305|PubMed:24474793"  
 FT MUTAGEN 109  
 FT /note="D->K: Loss of transport activity; when associated  
 FT with K-212 and K-306. Restored transport activity; when  
 FT associated with D-112; K-212; D-215; K-306 and D-309."  
 FT /evidence="ECO:0000269|PubMed:24474793"  
 FT MUTAGEN 112  
 FT /note="K->D: Loss of transport activity; when associated  
 FT with D-215 and D-309. Restored transport activity; when  
 FT associated with K-109; K-212; D-215; K-306 and D-309."  
 FT /evidence="ECO:0000269|PubMed:24474793"  
 FT MUTAGEN 212  
 FT /note="D->K: Loss of transport activity; when associated  
 FT with K-109 and K-306. Restored transport activity; when  
 FT associated with D-109; D-112; D-215; K-306 and D-309."  
 FT /evidence="ECO:0000269|PubMed:24474793"  
 FT MUTAGEN 215  
 FT /note="K->D: Loss of transport activity; when associated  
 FT with D-112 and D-309. Restored transport activity; when  
 FT associated with K-109; D-112; K-212; K-306 and D-309."  
 FT /evidence="ECO:0000269|PubMed:24474793"  
 FT MUTAGEN 306  
 FT /note="D->K: Loss of transport activity; when associated  
 FT with K-109 and K-212. Restored transport activity; when  
 FT associated with D-109; D-112; K-212; D-215 and D-309."  
 FT /evidence="ECO:0000269|PubMed:24474793"  
 FT MUTAGEN 309  
 FT /note="Q->D: Loss of transport activity; when associated  
 FT with D-112 and D-215. Restored transport activity; when  
 FT associated with K-109; D-112; K-212; D-215 and K-306."  
 FT /evidence="ECO:0000269|PubMed:24474793"  
 FT CONFLICT 58  
 FT /note="L -> I (in Ref. 2; AAA97484)"  
 FT /evidence="ECO:0000305"  
 FT CONFLICT 65  
 FT /note="R -> K (in Ref. 2; AAA97484)"  
 FT /evidence="ECO:0000305"  
 FT CONFLICT 68  
 FT /note="A -> S (in Ref. 2; AAA97484)"  
 FT /evidence="ECO:0000305"  
 FT CONFLICT 71  
 FT /note="L -> V (in Ref. 2; AAA97484)"  
 FT /evidence="ECO:0000305"  
 FT CONFLICT 79  
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 FT CONFLICT 83  
 FT /note="V -> L (in Ref. 2; AAA97484)"  
 FT /evidence="ECO:0000305"  
 FT CONFLICT 113  
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 FT /evidence="ECO:0000305"  
 FT CONFLICT 124  
 FT /note="A -> G (in Ref. 2; AAA97484)"  
 FT /evidence="ECO:0000305"  
 FT HELIX 25..52  
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 FT HELIX 54..59  
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 FT HELIX 70..81  
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 FT HELIX 84..87  
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 FT HELIX 90..95  
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FT HELIX 173..183  
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 FT TURN 187..189  
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 FT HELIX 193..213  
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 FT HELIX 229..244  
 FT /evidence="ECO:0007829|PDB:4C9G"  
 FT HELIX 246..257  
 FT /evidence="ECO:0007829|PDB:4C9G"  
 FT TURN 258..260  
 FT /evidence="ECO:0007829|PDB:4C9G"  
 FT HELIX 268..279  
 FT /evidence="ECO:0007829|PDB:4C9G"  
 FT HELIX 281..285  
 FT /evidence="ECO:0007829|PDB:4C9G"  
 FT HELIX 288..308  
 FT /evidence="ECO:0007829|PDB:4C9G"  
 FT STRAND 313..315  
 FT /evidence="ECO:0007829|PDB:4C9H"  
 SQ SEQUENCE 318 AA; 34426 MW; A9805DC33D9E24AC CRC64;  
 MSSNAQVKTP LPPAPAPKKE SNFLIDFLMG GVSAAVAKTA ASPIERVKLL IQNQDEMLKQ  
 GTLDRKYAGI LDCFKRTATQ EGVISFWRGN TANVIRYFPT QALNFAFKDK IKAMFGFKKE  
 EGYAKWFAGN LASGGAAGAL SLLFVYSLDY ARTRLAADSK SSKKGGARQF NGLIDVYKKT  
 LKSDGVAGLY RGFLPSVVGI VVYRGLYFGM YDSLKPLLLT GSLEGSFLAS FLLGWVVTG  
 ASTCSYPLDT VRRRMMMTSG QAVKYDGAFD CLRKIVAAEG VGSLEFKGCGA NILRGVAGAG  
 VISMYDQLQM ILFGKKFK

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