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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1w74a_	 Alignment		100.0	100	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
2	c2k7nA_	 Alignment		100.0	48	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase-like 1; PDBTitle: solution structure of the ppi1 bound to a fragment of skip
3	c1ihgA_	 Alignment		100.0	36	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin 40; PDBTitle: bovine cyclophilin 40, monoclinic form
4	c2hq6A_	 Alignment		100.0	44	PDB header: isomerase Chain: A: PDB Molecule: serologically defined colon cancer antigen 10; PDBTitle: structure of the cyclophilin_cecyp16-like domain of the serologically2 defined colon cancer antigen 10 from homo sapiens
5	c5jheA_	 Alignment		100.0	38	PDB header: chaperone Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase cyp7; PDBTitle: the crystal structure of the saccharomyces cerevisiae co-chaperone2 cpr7
6	c4r3fA_	 Alignment		100.0	46	PDB header: isomerase Chain: A: PDB Molecule: spliceosomal protein cwc27; PDBTitle: structure of the spliceosomal peptidyl-prolyl cis-trans isomerase2 cwc27 from chaetomium thermophilum
7	d2fu0a1	 Alignment		100.0	45	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
8	d2a2na1	 Alignment		100.0	50	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
9	d1ihga2	 Alignment		100.0	33	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
10	c3bo7D_	 Alignment		100.0	36	PDB header: isomerase/immunosuppressant Chain: D: PDB Molecule: peptidyl-prolyl cis-trans isomerase cyclophilin-type; PDBTitle: crystal structure of toxoplasma gondii peptidyl-prolyl cis-trans2 isomerase, 541.m00136
11	d1z81a1	 Alignment		100.0	35	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)

12	c1z81A_	Alignment		100.0	35	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin; PDBTitle: crystal structure of cyclophilin from plasmodium yoelii.
13	d1xwna1	Alignment		100.0	48	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
14	d1zkca1	Alignment		100.0	45	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
15	d2rmca_	Alignment		100.0	47	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
16	c2b71A_	Alignment		100.0	40	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin-like protein; PDBTitle: plasmodium yoelii cyclophilin-like protein
17	d2b71a1	Alignment		100.0	40	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
18	d2ok3a1	Alignment		100.0	49	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
19	d2esla1	Alignment		100.0	47	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
20	c2he9B_	Alignment		100.0	36	PDB header: isomerase Chain: B: PDB Molecule: nk-tumor recognition protein; PDBTitle: structure of the peptidylprolyl isomerase domain of the human nk-2 tumour recognition protein
21	d1xo7a_	Alignment	not modelled	100.0	43	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
22	c3jb9d_	Alignment	not modelled	100.0	52	PDB header: rna binding protein/rna Chain: D: PDB Molecule: small nuclear ribonucleoprotein sm d3; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
23	d1qoia_	Alignment	not modelled	100.0	38	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
24	d1cyna_	Alignment	not modelled	100.0	43	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
25	c3bkpA_	Alignment	not modelled	100.0	37	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin; PDBTitle: crystal structure of the toxoplasma gondii cyclophilin, 49.m03261
26	c5ybaC_	Alignment	not modelled	100.0	39	PDB header: isomerase Chain: C: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: dimeric cyclophilin from t.vaginalis in complex with myb1 peptide
27	d1a33a_	Alignment	not modelled	100.0	39	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
28	c5ex1E_	Alignment	not modelled	100.0	29	PDB header: isomerase Chain: E: PDB Molecule: peptidyl-prolyl cis-trans isomerase cyclophilin type; PDBTitle: crystal structure of cyclophilin aquacyp300 from hirschia baltica

29	d1h0pa_	Alignment	not modelled	100.0	43	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
30	d1v9ta_	Alignment	not modelled	100.0	34	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
31	c2poyB_	Alignment	not modelled	100.0	37	PDB header: isomerase/immunosuppressant Chain: B: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: cryptosporidium parvum cyclophilin type peptidyl-prolyl cis-trans2 isomerase cgd2_4120 in complex with cyclosporin a
32	c2qerA_	Alignment	not modelled	100.0	42	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin-like protein, putative; PDBTitle: crystal structure of cryptosporidium parvum cyclophilin type peptidyl-2 prolyl cis-trans isomerase cgd2_1660 in the presence of dipeptide3 ala-pro
33	c3k2cA_	Alignment	not modelled	100.0	39	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of peptidyl-prolyl cis-trans isomerase from2 encephalitozoon cuniculi at 1.9 a resolution
34	c5ex2A_	Alignment	not modelled	100.0	27	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of cyclophilin aquacyp293 from hirschia baltica
35	d2iqva1	Alignment	not modelled	100.0	32	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
36	d2r99a1	Alignment	not modelled	100.0	37	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
37	c4i9yC_	Alignment	not modelled	100.0	31	PDB header: transport protein Chain: C: PDB Molecule: e3 sumo-protein ligase ranbp2; PDBTitle: structure of the c-terminal domain of nup358
38	c3s6mA_	Alignment	not modelled	100.0	38	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: the structure of a peptidyl-prolyl cis-trans isomerase from2 burkholderia pseudomallei
39	d1w8ma_	Alignment	not modelled	100.0	38	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
40	d2z6wa1	Alignment	not modelled	100.0	38	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
41	d1lopa_	Alignment	not modelled	100.0	38	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
42	c2ck1A_	Alignment	not modelled	100.0	34	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase e; PDBTitle: the structure of oxidised cyclophilin a from s. mansoni
43	d1qnga_	Alignment	not modelled	100.0	38	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
44	d1vdna1	Alignment	not modelled	100.0	36	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
45	d2cfea1	Alignment	not modelled	100.0	45	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
46	c2oseA_	Alignment	not modelled	100.0	23	PDB header: isomerase Chain: A: PDB Molecule: probable peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of the mimivirus cyclophilin
47	c2mvzA_	Alignment	not modelled	100.0	39	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: solution structure for cyclophilin a from geobacillus kaustophilus
48	c5mqfo_	Alignment	not modelled	100.0	38	PDB header: splicing Chain: O: PDB Molecule: crooked neck-like protein 1; PDBTitle: cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
49	d2c3ba1	Alignment	not modelled	100.0	42	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
50	c3rfyA_	Alignment	not modelled	100.0	32	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase cyp38, chloroplastic; PDBTitle: crystal structure of arabidopsis thaliana cyclophilin 38 (atcyp38)
51	c2nnzA_	Alignment	not modelled	95.6	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: solution structure of the hypothetical protein af2241 from2 archaeoglobus fulgidus
52	c3kopB_	Alignment	not modelled	89.3	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein with a cyclophilin-like fold2 (yp_831253.1) from arthrobacter sp. fb24 at 1.90 a resolution
53	d1zx8a1	Alignment	not modelled	78.0	15	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: TM1367-like
54	d1x7fa1	Alignment	not modelled	64.0	16	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Outer surface protein, C-terminal domain
55	c2p0aA_	Alignment	not modelled	46.1	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein duf871;

55	c2p00A	Alignment	not modelled	40.1	10	PDBTitle: crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function
56	c1x7fA	Alignment	not modelled	38.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: outer surface protein; PDBTitle: crystal structure of an uncharacterized b. cereus protein
57	c5xumA	Alignment	not modelled	27.9	29	PDB header: transferase Chain: A: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: crystal structure of thermotoga maritima holo-[acyl-carrier-protein]2 synthase (acps)
58	d1v58a2	Alignment	not modelled	12.7	20	Fold: Cystatin-like Superfamily: DsbC/DsbG N-terminal domain-like Family: DsbC/DsbG N-terminal domain-like
59	c4eo0A	Alignment	not modelled	11.5	15	PDB header: viral protein Chain: A: PDB Molecule: attachment protein g3p; PDBTitle: crystal structure of the pilus binding domain of the filamentous phage2 ike
60	c4r11F	Alignment	not modelled	9.7	31	PDB header: cell adhesion/protein binding Chain: F: PDB Molecule: cadherin-related hmr-1; PDBTitle: a conserved phosphorylation switch controls the interaction between2 cadherin and beta-catenin in vitro and in vivo
61	c6bo0A	Alignment	not modelled	7.8	0	PDB header: oxidoreductase Chain: A: PDB Molecule: mdba protein; PDBTitle: mdba protein, a thiol-disulfide oxidoreductase from corynebacterium2 matruchoitii
62	c4r11D	Alignment	not modelled	7.4	28	PDB header: cell adhesion/protein binding Chain: D: PDB Molecule: cadherin-related hmr-1; PDBTitle: a conserved phosphorylation switch controls the interaction between2 cadherin and beta-catenin in vitro and in vivo
63	c2khfA	Alignment	not modelled	6.1	14	PDB header: antimicrobial protein Chain: A: PDB Molecule: plnj; PDBTitle: plantaricin j in dpc-micelles
64	c2khgA	Alignment	not modelled	5.4	14	PDB header: antimicrobial protein Chain: A: PDB Molecule: plnj; PDBTitle: plantaricin j in tfe