











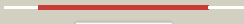



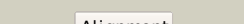

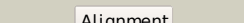

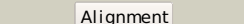












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1lopa_	 Alignment		100.0	99	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
2	c3s6mA_	 Alignment		100.0	66	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: the structure of a peptidyl-prolyl cis-trans isomerase from2 burkholderia pseudomallei
3	d1v9ta_	 Alignment		100.0	57	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
4	c2k7nA_	 Alignment		100.0	31	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
5	d2fu0a1	 Alignment		100.0	32	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
6	d2a2na1	 Alignment		100.0	35	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
7	c3bo7D_	 Alignment		100.0	30	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
8	d2b71a1	 Alignment		100.0	33	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
9	c2b71A_	 Alignment		100.0	33	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin-like protein; PDBTitle: plasmodium yoelii cyclophilin-like protein
10	d2ok3a1	 Alignment		100.0	32	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
11	c1ihgA_	 Alignment		100.0	29	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin 40; PDBTitle: bovine cyclophilin 40, monoclinic form

12	dlzkca1	Alignment		100.0	34	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
13	c2hq6A_	Alignment		100.0	30	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
14	dlxwna1	Alignment		100.0	31	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
15	dlw74a_	Alignment		100.0	38	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
16	c2qerA_	Alignment		100.0	32	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
17	dlihga2	Alignment		100.0	28	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
18	c2he9B_	Alignment		100.0	30	PDB header: isomerase Chain: B: PDB Molecule: nk-tumor recognition protein; PDBTitle: structure of the peptidylprolyl isomerase domain of the2 human nk-tumour recognition protein
19	dlxo7a_	Alignment		100.0	38	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
20	dlcyna_	Alignment		100.0	32	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
21	c3k2cA_	Alignment	not modelled	100.0	32	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of peptidyl-prolyl cis-trans isomerase2 from encephalitozoon cuniculi at 1.9 a resolution
22	d2esla1	Alignment	not modelled	100.0	30	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
23	c3bkpA_	Alignment	not modelled	100.0	33	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin; PDBTitle: crystal structure of the toxoplasma gondii cyclophilin, 49.m03261
24	c2poyB_	Alignment	not modelled	100.0	30	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
25	clz81A_	Alignment	not modelled	100.0	29	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin; PDBTitle: crystal structure of cyclophilin from plasmodium yoelii.
26	dlz81a1	Alignment	not modelled	100.0	29	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
27	d2rmca_	Alignment	not modelled	100.0	34	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
28	c2ck1A_	Alignment	not modelled	100.0	35	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase e; PDBTitle: the structure of oxidised cyclophilin a from s. mansoni
						Fold: Cyclophilin-like

29	d1qnga_	Alignment	not modelled	100.0	29	Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
30	d1vdna1	Alignment	not modelled	100.0	32	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
31	d1w8ma_	Alignment	not modelled	100.0	26	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
32	d1a33a_	Alignment	not modelled	100.0	33	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
33	d1h0pa_	Alignment	not modelled	100.0	33	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
34	d2z6wa1	Alignment	not modelled	100.0	30	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
35	d2igva1	Alignment	not modelled	100.0	30	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
36	d2r99a1	Alignment	not modelled	100.0	30	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
37	d1qoia_	Alignment	not modelled	100.0	33	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
38	c2oseA_	Alignment	not modelled	100.0	22	PDB header: isomerase Chain: A: PDB Molecule: probable peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of the mimivirus cyclophilin
39	d2cfeal	Alignment	not modelled	100.0	36	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
40	d2c3ba1	Alignment	not modelled	100.0	34	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
41	c2nnzA_	Alignment	not modelled	96.1	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: solution structure of the hypothetical protein af2241 from2 archaeoglobus fulgidus
42	c3kopB_	Alignment	not modelled	95.9	18	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
43	d1zx8a1	Alignment	not modelled	93.5	16	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: TM1367-like
44	c2khfA_	Alignment	not modelled	15.9	50	PDB header: antimicrobial protein Chain: A: PDB Molecule: plnj; PDBTitle: plantaricin j in dpc-micelles
45	c2khgA_	Alignment	not modelled	13.8	50	PDB header: antimicrobial protein Chain: A: PDB Molecule: plnj; PDBTitle: plantaricin j in tfe
46	c3ipfA_	Alignment	not modelled	12.3	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the q251q8_deshy protein from desulfotobacterium2 hafniense. northeast structural genomics consortium target dhr8c.