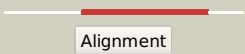



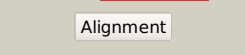

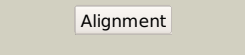

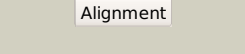
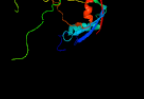
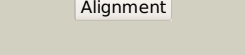

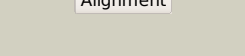

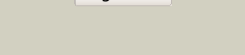


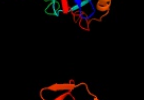


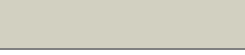












Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2582_(ppiB)_2906824_2907750
 Date Wed Aug 7 12:50:22 BST 2019
 Unique Job ID 9fb21f678e26238a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ex1E_	 Alignment		100.0	21	PDB header: isomerase Chain: E: PDB Molecule: peptidyl-prolyl cis-trans isomerase cyclophilin type; PDBTitle: crystal structure of cyclophilin aquacyp300 from hirschia baltica
2	c4r3fA_	 Alignment		100.0	30	PDB header: isomerase Chain: A: PDB Molecule: spliceosomal protein cwc27; PDBTitle: structure of the spliceosomal peptidyl-prolyl cis-trans isomerase2 cwc27 from chaetomium thermophilum
3	c5ex2A_	 Alignment		100.0	22	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of cyclophilin aquacyp293 from hirschia baltica
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 ppl1 bound to a fragment of skip
5	c3rfyA_	 Alignment		100.0	28	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase cyp38, chloroplastic; PDBTitle: crystal structure of arabidopsis thaliana cyclophilin 38 (atcyp38)
6	d2a2na1	 Alignment		100.0	31	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
7	c3bo7D_	 Alignment		100.0	24	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	d2fu0a1	 Alignment		100.0	30	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
9	d1zkca1	 Alignment		100.0	33	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
10	c1ihgA_	 Alignment		100.0	27	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin 40; PDBTitle: bovine cyclophilin 40, monoclinic form
11	c2hq6A_	 Alignment		100.0	29	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

12	d2b71a1	Alignment		100.0	32	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
13	c2b71A_	Alignment		100.0	32	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin-like protein; PDBTitle: plasmodium yoelii cyclophilin-like protein
14	d1xwna1	Alignment		100.0	31	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
15	c5jheA_	Alignment		100.0	28	PDB header: chaperone Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase cyp7; PDBTitle: the crystal structure of the saccharomyces cerevisiae co-chaperone2 cpr7
16	d1w74a_	Alignment		100.0	39	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
17	d1ihga2	Alignment		100.0	27	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
18	d2ok3a1	Alignment		100.0	35	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
19	d1v9ta_	Alignment		100.0	30	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
20	c3s6mA_	Alignment		100.0	28	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
21	c2qerA_	Alignment	not modelled	100.0	28	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
22	d1xo7a_	Alignment	not modelled	100.0	29	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
23	c3jb9d_	Alignment	not modelled	100.0	32	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
24	d1lopa_	Alignment	not modelled	100.0	29	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
25	d1z81a1	Alignment	not modelled	100.0	29	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
26	c1z81A_	Alignment	not modelled	100.0	29	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin; PDBTitle: crystal structure of cyclophilin from plasmodium yoelii.
27	c2poyB_	Alignment	not modelled	100.0	29	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
28	c3bkpA_	Alignment	not modelled	100.0	30	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin; PDBTitle: crystal structure of the toxoplasma gondii cyclophilin, 49.m03261

29	d2rmca_	Alignment	not modelled	100.0	30	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
30	d2r99a1	Alignment	not modelled	100.0	33	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
31	c2he9B_	Alignment	not modelled	100.0	25	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
32	d1cyna_	Alignment	not modelled	100.0	27	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
33	d2esla1	Alignment	not modelled	100.0	30	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
34	c3k2cA_	Alignment	not modelled	100.0	26	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
35	d2cfea1	Alignment	not modelled	100.0	30	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
36	c2ck1A_	Alignment	not modelled	100.0	29	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase e; PDBTitle: the structure of oxidised cyclophilin a from s. mansoni
37	d2z6wa1	Alignment	not modelled	100.0	30	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
38	d2iqva1	Alignment	not modelled	100.0	29	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
39	d1a33a_	Alignment	not modelled	100.0	29	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
40	d1vdna1	Alignment	not modelled	100.0	28	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
41	c4i9yC_	Alignment	not modelled	100.0	29	PDB header: transport protein Chain: C: PDB Molecule: e3 sumo-protein ligase ranbp2; PDBTitle: structure of the c-terminal domain of nup358
42	d1qnga_	Alignment	not modelled	100.0	29	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
43	d1h0pa_	Alignment	not modelled	100.0	28	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
44	c5ybaC_	Alignment	not modelled	100.0	30	PDB header: isomerase Chain: C: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: dimeric cyclophilin from t.vaginalis in complex with myb1 peptide
45	d1w8ma_	Alignment	not modelled	100.0	28	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
46	d1qoia_	Alignment	not modelled	100.0	31	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
47	c2mvzA_	Alignment	not modelled	100.0	35	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: solution structure for cyclophilin a from geobacillus kaustophilus
48	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
49	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)
50	d2c3ba1	Alignment	not modelled	100.0	24	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
51	c2nnzA_	Alignment	not modelled	95.2	16	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	89.2	15	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	d1x7fa1	Alignment	not modelled	80.7	18	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Outer surface protein, C-terminal domain
54	c2p0oA_	Alignment	not modelled	74.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein duf871; PDBTitle: crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function
55	c1x7fa_	Alignment	not modelled	71.6	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: outer surface protein; PDBTitle: crystal structure of an uncharacterized b. cereus protein

56	c5dudA	Alignment	not modelled	54.6	16	PDB header: unknown function Chain: A; PDB Molecule: ybgk; PDBTitle: crystal structure of e. coli ybgjk
57	d1zx8a1	Alignment	not modelled	48.3	18	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: TM1367-like
58	c2khfA	Alignment	not modelled	29.5	36	PDB header: antimicrobial protein Chain: A; PDB Molecule: plnj; PDBTitle: plantaricin j in dpc-micelles
59	c3mmlE	Alignment	not modelled	29.3	19	PDB header: hydrolase Chain: E; PDB Molecule: allophanate hydrolase subunit 2; PDBTitle: allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
60	c2khgA	Alignment	not modelled	26.4	36	PDB header: antimicrobial protein Chain: A; PDB Molecule: plnj; PDBTitle: plantaricin j in tfe
61	c6oegY	Alignment	not modelled	22.8	15	PDB header: translocase Chain: Y; PDB Molecule: type iv secretion system apparatus protein cagx; PDBTitle: structure of cagx from a cryo-em reconstruction of a t4ss
62	c5wstA	Alignment	not modelled	22.7	16	PDB header: motor protein Chain: A; PDB Molecule: unconventional myosin-viia; PDBTitle: crystal structure of myo7a sah
63	c2kimA	Alignment	not modelled	21.0	17	PDB header: transferase Chain: A; PDB Molecule: o6-methylguanine-dna methyltransferase; PDBTitle: 1.7-mm microcryoprobe solution nmr structure of an o6-methylguanine2 dna methyltransferase family protein from vibrio parahaemolyticus.3 northeast structural genomics consortium target vpr247.
64	c3gx4X	Alignment	not modelled	19.7	14	PDB header: dna binding protein/dna Chain: X; PDB Molecule: alkyltransferase-like protein 1; PDBTitle: crystal structure analysis of s. pombe atl in complex with dna
65	c2x5rA	Alignment	not modelled	18.0	40	PDB header: viral protein Chain: A; PDB Molecule: hypothetical protein orf126; PDBTitle: crystal structure of the hypothetical protein orf126 from pyrobaculum2 spherical virus
66	d1sfea1	Alignment	not modelled	17.5	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
67	c5eurC	Alignment	not modelled	16.5	29	PDB header: unknown function Chain: C; PDB Molecule: uncharacterized protein; PDBTitle: hypothetical protein sf216 from shigella flexneri 5a m90t
68	c3x27C	Alignment	not modelled	15.2	10	PDB header: lyase Chain: C; PDB Molecule: cucumopine synthase; PDBTitle: structure of mcbb in complex with tryptophan
69	d1qnta1	Alignment	not modelled	13.2	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
70	c3f5hB	Alignment	not modelled	12.1	18	PDB header: protein binding Chain: B; PDB Molecule: type i polyketide synthase pikaiii, type i polyketide PDBTitle: crystal structure of fused docking domains from pikaiii and pikaiv of2 the pikromycin polyketide synthase
71	c2d46A	Alignment	not modelled	11.8	18	PDB header: metal transport Chain: A; PDB Molecule: calcium channel, voltage-dependent, beta 4 PDBTitle: solution structure of the human beta4a-a domain
72	d1x0ha1	Alignment	not modelled	11.5	21	Fold: RGC domain-like Superfamily: RGC domain-like Family: RGC domain
73	c5nj8D	Alignment	not modelled	11.2	16	PDB header: transcription Chain: D; PDB Molecule: aryl hydrocarbon receptor nuclear translocator; PDBTitle: structural basis for aryl hydrocarbon receptor mediated gene2 activation
74	c1oqyA	Alignment	not modelled	10.1	14	PDB header: replication Chain: A; PDB Molecule: uv excision repair protein rad23 homolog a; PDBTitle: structure of the dna repair protein hhr23a
75	c3oepA	Alignment	not modelled	9.9	17	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative uncharacterized protein ttha0988; PDBTitle: crystal structure of ttha0988 in space group p43212
76	d1xrsb2	Alignment	not modelled	9.5	57	Fold: Dodecin subunit-like Superfamily: D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain Family: D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain
77	c6eu1Q	Alignment	not modelled	8.7	29	PDB header: transcription Chain: Q; PDB Molecule: dna-directed rna polymerase iii subunit rpc7; PDBTitle: rna polymerase iii - open dna complex (oc-pol3)
78	c5zm8A	Alignment	not modelled	8.5	19	PDB header: lipid transport Chain: A; PDB Molecule: oxysterol-binding protein-related protein 2; PDBTitle: crystal structure of orp2-ord in complex with pi(4,5)p2
79	c1z8yl	Alignment	not modelled	7.3	36	PDB header: virus Chain: I; PDB Molecule: spike glycoprotein e1; PDBTitle: mapping the e2 glycoprotein of alphaviruses
80	c1z8yO	Alignment	not modelled	7.3	36	PDB header: virus Chain: O; PDB Molecule: spike glycoprotein e1; PDBTitle: mapping the e2 glycoprotein of alphaviruses

81	c1z8yK_	Alignment	not modelled	7.3	36	PDB header: virus Chain: K: PDB Molecule: spike glycoprotein e1; PDBTitle: mapping the e2 glycoprotein of alphaviruses
82	c1z8yM_	Alignment	not modelled	7.3	36	PDB header: virus Chain: M: PDB Molecule: spike glycoprotein e1; PDBTitle: mapping the e2 glycoprotein of alphaviruses
83	c2kncB_	Alignment	not modelled	7.3	17	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
84	c5z08D_	Alignment	not modelled	6.5	29	PDB header: cell cycle Chain: D: PDB Molecule: cenp-h; PDBTitle: the crystal structure of kinetochore subunits cenp-h/l/k triple2 complex
85	d1m4ma_	Alignment	not modelled	6.5	24	Fold: Inhibitor of apoptosis (IAP) repeat Superfamily: Inhibitor of apoptosis (IAP) repeat Family: Inhibitor of apoptosis (IAP) repeat
86	c2j98A_	Alignment	not modelled	6.3	21	PDB header: rna binding protein Chain: A: PDB Molecule: replicase polyprotein 1ab; PDBTitle: human coronavirus 229e non structural protein 9 cys69ala mutant (nsp9)
87	c2m1aA_	Alignment	not modelled	6.3	42	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 rev arginine-rich motif (arm); PDBTitle: hiv-1 rev arm peptide (residues t34-r50)
88	c2vdaA_	Alignment	not modelled	6.3	29	PDB header: protein transport Chain: A: PDB Molecule: translocase subunit seca; PDBTitle: solution structure of the seca-signal peptide complex
89	c4uaqA_	Alignment	not modelled	6.0	39	PDB header: protein transport Chain: A: PDB Molecule: protein translocase subunit seca 2; PDBTitle: crystal structure of the accessory translocation atpase, seca2, from2 mycobacterium tuberculosis
90	c6qbzA_	Alignment	not modelled	5.9	26	PDB header: ribosomal protein Chain: A: PDB Molecule: ribosome hibernation promoting factor; PDBTitle: solution structure of the n-terminal domain of the staphylococcus2 aureus hibernation promoting factor
91	c1kuzB_	Alignment	not modelled	5.9	33	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: solution structure of the membrane proximal regions of2 alpha-iiB and beta-3 integrins
92	c5mmjy_	Alignment	not modelled	5.8	9	PDB header: ribosome Chain: Y: PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome
93	c2rqlA_	Alignment	not modelled	5.7	30	PDB header: translation Chain: A: PDB Molecule: probable sigma-54 modulation protein; PDBTitle: solution structure of the e. coli ribosome hibernation2 promoting factor hpf
94	c3m0aD_	Alignment	not modelled	5.6	55	PDB header: signaling protein Chain: D: PDB Molecule: baculoviral iap repeat-containing protein 3; PDBTitle: crystal structure of traf2:ciap2 complex
95	c4rgwA_	Alignment	not modelled	5.6	37	PDB header: transferase/transcription Chain: A: PDB Molecule: transcription initiation factor tfiid subunit 1; PDBTitle: crystal structure of a taf1-taf7 complex in human transcription factor2 iid
96	d2qfaa1	Alignment	not modelled	5.5	29	Fold: Inhibitor of apoptosis (IAP) repeat Superfamily: Inhibitor of apoptosis (IAP) repeat Family: Inhibitor of apoptosis (IAP) repeat
97	d1l4sa_	Alignment	not modelled	5.3	35	Fold: Ribosome binding protein Y (YfiA homologue) Superfamily: Ribosome binding protein Y (YfiA homologue) Family: Ribosome binding protein Y (YfiA homologue)
98	d1imua_	Alignment	not modelled	5.2	33	Fold: Ribosome binding protein Y (YfiA homologue) Superfamily: Ribosome binding protein Y (YfiA homologue) Family: Ribosome binding protein Y (YfiA homologue)
99	c4zyeA_	Alignment	not modelled	5.0	27	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: crystal structure of sulfolobus solfataricus o6-methylguanine2 methyltransferase