



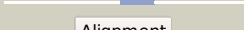

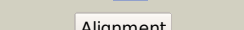

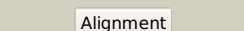


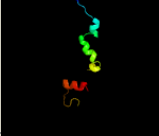

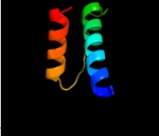
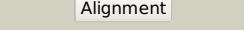

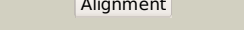

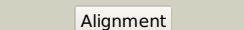


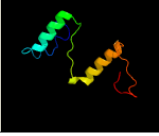

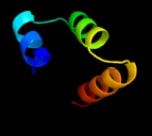





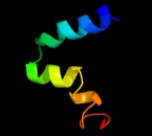
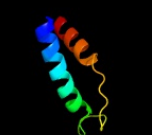


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0826 (-)_919637_920692
Date	Fri Jul 26 01:50:41 BST 2019
Unique Job ID	6e5512f2dc3218bc

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o1mA_	 Alignment		99.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: rubber oxygenase; PDBTitle: structure of latex clearing protein lcp in the closed state
2	c2ru8A_	 Alignment		39.1	13	PDB header: replication Chain: A: PDB Molecule: primosomal protein 1; PDBTitle: dnat c-terminal domain
3	c4ou6A_	 Alignment		27.9	13	PDB header: replication/dna Chain: A: PDB Molecule: primosomal protein 1; PDBTitle: crystal structure of dnat84-153-dt10 ssdna complex form 1
4	c5cuvB_	 Alignment		20.4	20	PDB header: metal binding protein Chain: B: PDB Molecule: acidocalcisomal pyrophosphatase; PDBTitle: crystal structure of trypanosoma cruzi vacuolar soluble2 pyrophosphatases in apo form
5	d1g73a_	 Alignment		16.2	4	Fold: Spectrin repeat-like Superfamily: Smac/diablo Family: Smac/diablo
6	c4plaA_	 Alignment		14.8	27	PDB header: transferase,hydrolase Chain: A: PDB Molecule: chimera protein of phosphatidylinositol 4-kinase type 2- PDBTitle: crystal structure of phosphatidyl inositol 4-kinase ii alpha in2 complex with atp
7	c1unhD_	 Alignment		14.0	6	PDB header: cell cycle Chain: D: PDB Molecule: cyclin-dependent kinase 5 activator 1; PDBTitle: structural mechanism for the inhibition of cdk5-p25 by2 roscovitine, aloisine and indirubin.
8	d1unld_	 Alignment		13.6	6	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin
9	c4nk1B_	 Alignment		13.0	16	PDB header: oxygen binding Chain: B: PDB Molecule: hemoglobin-like protein; PDBTitle: crystal structure of phosphate-bound hell's gate globin iv
10	c2e8mA_	 Alignment		12.3	22	PDB header: signaling protein Chain: A: PDB Molecule: epidermal growth factor receptor kinase PDBTitle: solution structure of the c-terminal sam-domain of2 epidermal growth receptor pathway substrate 8
11	c4wiuA_	 Alignment		11.0	18	PDB header: lyase,transferase Chain: A: PDB Molecule: phosphoenolpyruvate carboxykinase [gtp]; PDBTitle: crystal structure of pepck (rv0211) from mycobacterium tuberculosis in2 complex with oxalate and mn2+

12	d1fewa_	Alignment		10.5	4	Fold: Spectrin repeat-like Superfamily: Smac/diablo Family: Smac/diablo
13	d1u7ka_	Alignment		9.9	10	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
14	c6fviA_	Alignment		8.5	46	PDB header: cell cycle Chain: A: PDB Molecule: centrosomal protein of 192 kda; PDBTitle: ash / papd-like domain of human cep192 (papd-like domain 7)
15	c2jspA_	Alignment		8.2	14	PDB header: gene regulation Chain: A: PDB Molecule: transcriptional regulatory protein ros; PDBTitle: the prokaryotic cys2his2 zinc finger adopts a novel fold as2 revealed by the nmr structure of a. tumefaciens ros dna3 binding domain
16	c1nexC_	Alignment		7.8	12	PDB header: ligase, cell cycle Chain: C: PDB Molecule: centromere dna-binding protein complex cbf3 PDBTitle: crystal structure of scskp1-sccd4-cpd peptide complex
17	d1v7ba2	Alignment		7.8	9	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
18	c1mk2B_	Alignment		7.7	44	PDB header: transcription Chain: B: PDB Molecule: madh-interacting protein; PDBTitle: smad3 sbd complex
19	c4do7B_	Alignment		7.6	23	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase 2; PDBTitle: crystal structure of an amidohydrolase (cog3618) from burkholderia2 multivorans (target efi-500235) with bound zn, space group c2
20	c6alyA_	Alignment		7.4	13	PDB header: transcription Chain: A: PDB Molecule: mediator of rna polymerase ii transcription subunit 15; PDBTitle: solution structure of yeast med15 abd2 residues 277-368
21	c3m20A_	Alignment	not modelled	7.3	17	PDB header: isomerase Chain: A: PDB Molecule: 4-oxalocrotonate tautomerase, putative; PDBTitle: crystal structure of dmpi from archaeoglobus fulgidus determined to 2.37 angstroms resolution
22	c3ucsB_	Alignment	not modelled	7.3	8	PDB header: chaperone Chain: B: PDB Molecule: chaperone-modulator protein cbpm; PDBTitle: crystal structure of the complex between cbpa j-domain and cbpm
23	c4umoB_	Alignment	not modelled	7.1	26	PDB header: signaling protein Chain: B: PDB Molecule: potassium voltage-gated channel subfamily kqt member 1; PDBTitle: crystal structure of the kv7.1 proximal c-terminal domain in complex2 with calmodulin
24	d16vpa_	Alignment	not modelled	7.0	13	Fold: Conserved core of transcriptional regulatory protein vp16 Superfamily: Conserved core of transcriptional regulatory protein vp16 Family: Conserved core of transcriptional regulatory protein vp16
25	d1xg7a_	Alignment	not modelled	6.6	56	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: AgoG-like
26	c3a08C_	Alignment	not modelled	6.5	41	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclin, twinned crystal
27	c2glwA_	Alignment	not modelled	6.4	15	PDB header: transcription Chain: A: PDB Molecule: 92aa long hypothetical protein; PDBTitle: the solution structure of phs018 from pyrococcus horikoshii
28	c2ovqA_	Alignment	not modelled	6.3	14	PDB header: transcription/cell cycle Chain: A: PDB Molecule: s-phase kinase-associated protein 1a; PDBTitle: structure of the skp1-fbw7-cyclinedegc complex

29	d1iwma_	Alignment	not modelled	6.1	33	Fold: LoLA-like prokaryotic lipoproteins and lipoprotein localization factors Superfamily: Prokaryotic lipoproteins and lipoprotein localization factors Family: Outer membrane lipoprotein receptor LolB
30	c4fdxB_	Alignment	not modelled	5.9	19	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonase tautomerase isozyme; PDBTitle: kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozymes from methylbium petroleiphilum
31	c3a08F_	Alignment	not modelled	5.9	50	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
32	c4okmA_	Alignment	not modelled	5.8	19	PDB header: transferase Chain: A: PDB Molecule: terpene synthase metal-binding domain-containing protein; PDBTitle: selinadiene synthase apo and in complex with diphosphate
33	c2bmmA_	Alignment	not modelled	5.7	9	PDB header: oxygen storage/transport Chain: A: PDB Molecule: thermostable hemoglobin from thermobifida fusca; PDBTitle: x-ray structure of a novel thermostable hemoglobin from the2 actinobacterium thermobifida fusca
34	c3zs9D_	Alignment	not modelled	5.6	53	PDB header: hydrolase/transport protein Chain: D: PDB Molecule: golgi to er traffic protein 2; PDBTitle: s. cerevisiae get3-adi-4- complex with a cytosolic get2 fragment
35	d2gica1	Alignment	not modelled	5.5	26	Fold: Rhabdovirus nucleoprotein-like Superfamily: Rhabdovirus nucleoprotein-like Family: Rhabdovirus nucleocapsid protein
36	c5k21C_	Alignment	not modelled	5.5	71	PDB header: oxidoreductase Chain: C: PDB Molecule: pyocyanin demethylase; PDBTitle: pyocyanin demethylase
37	d1q3ma_	Alignment	not modelled	5.5	31	Fold: GLA-domain Superfamily: GLA-domain Family: GLA-domain
38	d2g3ba2	Alignment	not modelled	5.4	9	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
39	c3a08E_	Alignment	not modelled	5.3	50	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
40	c2d3hF_	Alignment	not modelled	5.3	50	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptides (pro-pro-gly)4-hyp-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4
41	c5yo8B_	Alignment	not modelled	5.3	22	PDB header: lyase Chain: B: PDB Molecule: tetraprenyl-beta-curcumene synthase; PDBTitle: crystal structure of beta-c25/c30/c35-prene synthase
42	c2zc2A_	Alignment	not modelled	5.2	17	PDB header: replication Chain: A: PDB Molecule: dnad-like replication protein; PDBTitle: crystal structure of dnad-like replication protein from streptococcus2 mutans ua159, gi 24377835, residues 127-199
43	d1eyxa_	Alignment	not modelled	5.1	13	Fold: Globin-like Superfamily: Globin-like Family: Phycocyanin-like phycobilisome proteins
44	c4ue8B_	Alignment	not modelled	5.1	39	PDB header: translation Chain: B: PDB Molecule: 4e-binding protein thor; PDBTitle: complex of d. melanogaster eif4e with the 4e binding protein thor
45	d1nb4a_	Alignment	not modelled	5.1	13	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
46	c2d3hC_	Alignment	not modelled	5.1	43	PDB header: structural protein Chain: C: PDB Molecule: collagen model peptides (pro-pro-gly)4-hyp-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4