

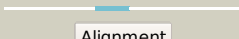
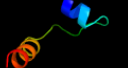
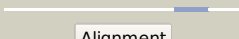



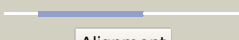


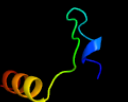

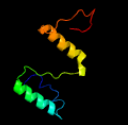
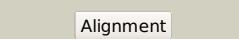

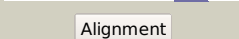


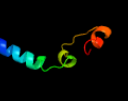




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1645c_(-)_1854406_1855461
Date	Fri Aug 2 13:30:24 BST 2019
Unique Job ID	b84c43f150fbae5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o1mA_	 Alignment		99.2	12	PDB header: oxidoreductase Chain: A: PDB Molecule: rubber oxygenase; PDBTitle: structure of latex clearing protein lcp in the closed state
2	c2ru8A_	 Alignment		31.5	17	PDB header: replication Chain: A: PDB Molecule: primosomal protein 1; PDBTitle: dnat c-terminal domain
3	c6akmA_	 Alignment		24.9	33	PDB header: protein binding Chain: A: PDB Molecule: suppressor of ikbke 1; PDBTitle: crystal structure of slmap-sike1 complex
4	c2e8mA_	 Alignment		22.5	18	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
5	c5xazD_	 Alignment		20.7	12	PDB header: dna binding protein Chain: D: PDB Molecule: gamma-butyrolactone receptor protein; PDBTitle: crystal structure of full length native tylp, a tetr regulator from2 streptomyces fradiae
6	c4ou6A_	 Alignment		17.5	13	PDB header: replication/dna Chain: A: PDB Molecule: primosomal protein 1; PDBTitle: crystal structure of dnat84-153-dt10 ssdna complex form 1
7	c4wiuA_	 Alignment		17.0	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+
8	d1g73a_	 Alignment		14.4	8	Fold: Spectrin repeat-like Superfamily: Smac/diablo Family: Smac/diablo
9	c5fcmB_	 Alignment		13.7	30	PDB header: cell cycle Chain: B: PDB Molecule: basal body protein; PDBTitle: crbld10-n 1-70
10	c1nexC_	 Alignment		13.4	17	PDB header: ligase, cell cycle Chain: C: PDB Molecule: centromere dna-binding protein complex cbf3 PDBTitle: crystal structure of scskp1-sccdc4-cpd peptide complex
11	c1unhD_	 Alignment		13.0	7	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.

12	c2ovqA_	Alignment		12.9	18	PDB header: transcription/cell cycle Chain: A: PDB Molecule: s-phase kinase-associated protein 1a; PDBTitle: structure of the skp1-fbw7-cyclinedegc complex
13	d1unld_	Alignment		12.7	7	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin
14	d1v7ba2	Alignment		11.9	9	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
15	c3m20A_	Alignment		11.7	20	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
16	d1u7ka_	Alignment		11.3	15	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
17	c5cuvB_	Alignment		10.8	18	PDB header: metal binding protein Chain: B: PDB Molecule: acidocalcisomal pyrophosphatase; PDBTitle: crystal structure of trypanosoma cruzi vacuolar soluble2 pyrophosphatases in apo form
18	c4nk1B_	Alignment		10.5	11	PDB header: oxygen binding Chain: B: PDB Molecule: hemoglobin-like protein; PDBTitle: crystal structure of phosphate-bound hell's gate globin iv
19	c3ucsb_	Alignment		10.4	5	PDB header: chaperone Chain: B: PDB Molecule: chaperone-modulator protein cbpm; PDBTitle: crystal structure of the complex between cbpa j-domain and cbpm
20	d1fewa_	Alignment		9.3	8	Fold: Spectrin repeat-like Superfamily: Smac/diablo Family: Smac/diablo
21	d1gyxa_	Alignment	not modelled	9.3	19	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
22	c3mb2J_	Alignment	not modelled	9.0	15	PDB header: isomerase Chain: j: PDB Molecule: 4-oxalocrotonate tautomerase family enzyme - beta subunit; PDBTitle: kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
23	c2jspA_	Alignment	not modelled	9.0	21	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
24	c6alyA_	Alignment	not modelled	8.4	14	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
25	d16vpa_	Alignment	not modelled	8.2	20	Fold: Conserved core of transcriptional regulatory protein vp16 Superfamily: Conserved core of transcriptional regulatory protein vp16 Family: Conserved core of transcriptional regulatory protein vp16
26	c5wyID_	Alignment	not modelled	7.7	50	PDB header: ribosomal protein/nuclear protein Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of chaetomium thermophilum utp10 n-terminal domain2 in complex with utp17 c-terminal helices
27	c4fdxB_	Alignment	not modelled	7.6	16	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonase tautomerase isozyeme; PDBTitle: kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozyemes from methylbium petroleiphilum

28	c3ivuB_	Alignment	not modelled	7.5	23	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
29	c5wylB_	Alignment	not modelled	7.5	50	PDB header: ribosomal protein/nuclear protein Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of chaetomium thermophilum utp10 n-terminal domain2 in complex with utp17 c-terminal helices
30	d1vfla1	Alignment	not modelled	6.9	30	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenosine/AMP deaminase
31	c6fviA_	Alignment	not modelled	6.8	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)
32	d1iwma_	Alignment	not modelled	6.5	33	Fold: LoIA-like prokaryotic lipoproteins and lipoprotein localization factors Superfamily: Prokaryotic lipoproteins and lipoprotein localization factors Family: Outer membrane lipoprotein receptor LolB
33	c5yo8B_	Alignment	not modelled	6.3	15	PDB header: lyase Chain: B: PDB Molecule: tetraprenyl-beta-curcumen synthase; PDBTitle: crystal structure of beta-c25/c30/c35-prene synthase
34	c2ormA_	Alignment	not modelled	6.2	23	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase hp0924; PDBTitle: crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori.
35	c4plaA_	Alignment	not modelled	6.2	23	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
36	c2glwA_	Alignment	not modelled	6.1	23	PDB header: transcription Chain: A: PDB Molecule: 92aa long hypothetical protein; PDBTitle: the solution structure of phs018 from pyrococcus horikoshii
37	c5hwiA_	Alignment	not modelled	5.9	56	PDB header: transferase Chain: A: PDB Molecule: glutathione-specific gamma-glutamylcyclotransferase; PDBTitle: crystal structure of selenomethionine labelled gamma glutamyl2 cyclotransferase specific to glutathione from yeast
38	d2gica1	Alignment	not modelled	5.9	26	Fold: Rhabdovirus nucleoprotein-like Superfamily: Rhabdovirus nucleoprotein-like Family: Rhabdovirus nucleocapsid protein
39	c3kmiB_	Alignment	not modelled	5.7	19	PDB header: membrane protein Chain: B: PDB Molecule: putative membrane protein cog4129; PDBTitle: crystal structure of putative membrane protein from clostridium2 difficile 630
40	c2op8A_	Alignment	not modelled	5.5	23	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase ywhb; PDBTitle: crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
41	c3bpjD_	Alignment	not modelled	5.5	27	PDB header: translation Chain: D: PDB Molecule: eukaryotic translation initiation factor 3 subunit j; PDBTitle: crystal structure of human translation initiation factor 3, subunit 12 alpha
42	d1lj8a3	Alignment	not modelled	5.5	22	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Mannitol 2-dehydrogenase
43	c6fskA_	Alignment	not modelled	5.4	22	PDB header: oxidoreductase Chain: A: PDB Molecule: dyp-type peroxidase; PDBTitle: f194y mutant of the dye-decolorizing peroxidase (dyp) from pleurotus2 ostreatus
44	c4lkbA_	Alignment	not modelled	5.4	19	PDB header: isomerase Chain: A: PDB Molecule: hypothetical protein alr4568/putative 4-oxalocrotonate PDBTitle: crystal structure of a putative 4-oxalocrotonate tautomerase from2 nostoc sp. pcc 7120
45	c6j9eF_	Alignment	not modelled	5.4	15	PDB header: transcription Chain: F: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: cryo-em structure of xanthomonos oryzae transcription elongation2 complex with nusa and the bacteriophage protein p7
46	c4umoB_	Alignment	not modelled	5.4	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
47	c2rpsA_	Alignment	not modelled	5.4	50	PDB header: immune system Chain: A: PDB Molecule: chemokine; PDBTitle: solution structure of a novel insect chemokine isolated from2 integument
48	c6ogdB_	Alignment	not modelled	5.4	10	PDB header: toxin Chain: B: PDB Molecule: toxin subunit yena2; PDBTitle: cryo-em structure of yentca in its prepore state
49	c3df0C_	Alignment	not modelled	5.4	27	PDB header: hydrolase Chain: C: PDB Molecule: calpastatin; PDBTitle: calcium-dependent complex between m-calpain and calpastatin
50	d1o4ua2	Alignment	not modelled	5.4	9	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
51	c4pagA_	Alignment	not modelled	5.4	15	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein; PDBTitle: abc transporter solute binding protein from sulfurospirillum2 deleyianum dsm 6946
						PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate isomerase protein;

52	c4fazB_	Alignment	not modelled	5.3	23	PDBTitle: kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozymes from methylibium petroleophilum
53	c5uifC_	Alignment	not modelled	5.3	28	PDB header: hydrolase Chain: C: PDB Molecule: ps01740; PDBTitle: crystal structure of native ps01740
54	c3zs9D_	Alignment	not modelled	5.3	53	PDB header: hydrolase/transport protein Chain: D: PDB Molecule: golgi to er traffic protein 2; PDBTitle: s. cerevisiae get3-adp-alf4- complex with a cytosolic get2 fragment
55	c5lhxA_	Alignment	not modelled	5.2	30	PDB header: structural protein Chain: A: PDB Molecule: serine/threonine-protein kinase plk4; PDBTitle: pb3 domain of drosophila melanogaster plk4 (sak)
56	c1mk2B_	Alignment	not modelled	5.1	29	PDB header: transcription Chain: B: PDB Molecule: madh-interacting protein; PDBTitle: smad3 sbd complex
57	c6hwwA_	Alignment	not modelled	5.1	15	PDB header: viral protein Chain: A: PDB Molecule: putative gag polyprotein; PDBTitle: immature mlv capsid hexamer structure in intact virus particles
58	d2aala1	Alignment	not modelled	5.1	21	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MSAD-like
59	d1lmia_	Alignment	not modelled	5.1	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: Antigen MPT63/MPB63 (immunoprotective extracellular protein) Family: Antigen MPT63/MPB63 (immunoprotective extracellular protein)