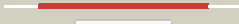

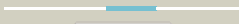

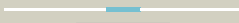




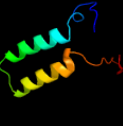














Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0276 (-) _331748_332668
Date	Tue Jul 23 14:50:34 BST 2019
Unique Job ID	b7fb45521f60ba7e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o1mA_	 Alignment		99.1	14	PDB header: oxidoreductase Chain: A; PDB Molecule: rubber oxygenase; PDBTitle: structure of latex clearing protein lcp in the closed state
2	c1unhD_	 Alignment		34.9	13	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.
3	d1unld_	 Alignment		33.5	15	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin
4	c3wkgA_	 Alignment		27.1	14	PDB header: isomerase Chain: A; PDB Molecule: cellobiose 2-epimerase; PDBTitle: crystal structure of cellobiose 2-epimerase in complex with2 glucosylmannose
5	d1nb4a_	 Alignment		26.6	7	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
6	c2ru8A_	 Alignment		26.6	13	PDB header: replication Chain: A; PDB Molecule: primosomal protein 1; PDBTitle: dnat c-terminal domain
7	c2vh3B_	 Alignment		22.0	20	PDB header: unknown function Chain: B; PDB Molecule: ranasmurfin; PDBTitle: ranasmurfin
8	d1u5ta1	 Alignment		19.2	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
9	c4z4IA_	 Alignment		18.9	14	PDB header: isomerase Chain: A; PDB Molecule: cellobiose 2-epimerase; PDBTitle: crystal structure of cellobiose 2-epimerase from caldicellulosiruptor2 saccharolyticus dsm 8903
10	c5cuvB_	 Alignment		17.4	5	PDB header: metal binding protein Chain: B; PDB Molecule: acidocalcisomal pyrophosphatase; PDBTitle: crystal structure of trypanosoma cruzi vacuolar soluble2 pyrophosphatases in apo form
11	c6alyA_	 Alignment		15.8	6	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

12	c3m20A_	Alignment		15.0	3	PDB header: isomerase Chain: A: PDB Molecule: 4-oxalocrotonate tautomerase, putative; PDBTitle: crystal structure of dmpl from archaeoglobus fulgidus determined to 2.37 angstroms resolution
13	c4ou6A_	Alignment		13.7	13	PDB header: replication/dna Chain: A: PDB Molecule: primosomal protein 1; PDBTitle: crystal structure of dnat84-153-dt10 ssdna complex form 1
14	d1v7ba2	Alignment		13.4	10	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
15	d1g73a_	Alignment		12.7	25	Fold: Spectrin repeat-like Superfamily: Smac/diablo Family: Smac/diablo
16	c3s6jC_	Alignment		11.5	3	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the crystal structure of a hydrolase from pseudomonas syringae
17	c5zhhB_	Alignment		11.5	14	PDB header: isomerase Chain: B: PDB Molecule: cellobiose 2-epimerase; PDBTitle: structure of cellobiose 2-epimerase from bacillus thermoamylovorans 2 b4167
18	d16vpa_	Alignment		11.4	33	Fold: Conserved core of transcriptional regulatory protein vp16 Superfamily: Conserved core of transcriptional regulatory protein vp16 Family: Conserved core of transcriptional regulatory protein vp16
19	d1gyxa_	Alignment		10.5	13	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
20	c3mb2j_	Alignment		10.4	10	PDB header: isomerase Chain: j: PDB Molecule: 4-oxalocrotonate tautomerase family enzyme - beta subunit; PDBTitle: kinetic and structural characterization of a heterohexameric 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the 4 tautomerase superfamily
21	d1gx5a_	Alignment	not modelled	10.0	5	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
22	d1x9na1	Alignment	not modelled	10.0	19	Fold: ATP-dependent DNA ligase DNA-binding domain Superfamily: ATP-dependent DNA ligase DNA-binding domain Family: ATP-dependent DNA ligase DNA-binding domain
23	c4zvbD_	Alignment	not modelled	9.8	18	PDB header: signaling protein Chain: D: PDB Molecule: diguanylate cyclase dosc; PDBTitle: crystal structure of globin domain of the e. coli dosc - form ii2 (ferrous)
24	d1lj8a3	Alignment	not modelled	9.7	13	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Mannitol 2-dehydrogenase
25	c2e8mA_	Alignment	not modelled	9.4	12	PDB header: signaling protein Chain: A: PDB Molecule: epidermal growth factor receptor kinase PDBTitle: solution structure of the c-terminal sam-domain of 2 epidermal growth receptor pathway substrate 8
26	c1nexC_	Alignment	not modelled	9.3	9	PDB header: ligase, cell cycle Chain: C: PDB Molecule: centromere dna-binding protein complex cbf3 PDBTitle: crystal structure of scskp1-sccd4-cpd peptide complex
27	c4xboA_	Alignment	not modelled	8.6	12	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine/uridine-2'-o)-methyltransferase trmj; PDBTitle: crystal structure of full length e.coli trmj in complex with sah
28	c4lkbA_	Alignment	not modelled	8.6	6	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 PDB header: transferase Chain: A: PDB Molecule: n-acetylhexosamine 1-phosphate kinase; PDBTitle: n-acetylhexosamine 1-phosphate kinase in complex with glcnac and2 amppnp
29	c4ockA_	Alignment	not modelled	8.3	13	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonase tautomerase isozyyme; PDBTitle: kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozyymes from methylbium petroleiphilum
30	c4fdxB_	Alignment	not modelled	8.1	23	Fold: Spectrin repeat-like Superfamily: Smac/diablo Family: Smac/diablo
31	d1fewa_	Alignment	not modelled	7.9	25	PDB header: oxygen binding Chain: B: PDB Molecule: hemoglobin-like protein; PDBTitle: crystal structure of phosphate-bound hell's gate globin iv
32	c4nk1B_	Alignment	not modelled	7.5	12	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
33	d2fd5a2	Alignment	not modelled	7.3	14	PDB header: toxin Chain: B: PDB Molecule: toxin subunit yena2; PDBTitle: cryo-em structure of yentca in its prepore state
34	c6ogdB_	Alignment	not modelled	7.1	14	PDB header: plant protein Chain: B: PDB Molecule: 2-isopropylmalate synthase, a genome specific 1; PDBTitle: crystal structure of methylthioalkylmalate synthase (bjumam1.1) from2 brassica juncea
35	c6e1jB_	Alignment	not modelled	7.0	12	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
36	d1u7ka_	Alignment	not modelled	7.0	13	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
37	c2jspA_	Alignment	not modelled	6.9	29	Fold: GLA-domain Superfamily: GLA-domain Family: GLA-domain
38	d1q3ma_	Alignment	not modelled	6.8	38	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: Hypothetical protein HI1388.1
39	d1mwwa_	Alignment	not modelled	6.6	3	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase hp0924; PDBTitle: crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori.
40	c2ormA_	Alignment	not modelled	6.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase (gdhb) from thermus2 thermophilus (glu bound form)
41	c3aogA_	Alignment	not modelled	6.3	16	PDB header: oxidoreductase Chain: D: PDB Molecule: nad-specific glutamate dehydrogenase; PDBTitle: crystal structure of gudb1 a decryptified secondary glutamate2 dehydrogenase from b. subtilis
42	c3k8zD_	Alignment	not modelled	6.2	12	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein; PDBTitle: abc transporter solute binding protein from sulfurospirillum2 deleyianum dsm 6946
43	c4pagA_	Alignment	not modelled	6.1	28	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MSAD-like
44	d2aala1	Alignment	not modelled	6.1	14	PDB header: sugar binding protein/ligase Chain: A: PDB Molecule: maltose-binding periplasmic protein, tripartite motif- PDBTitle: crystal structure of rhesus trim5alpha pry/spry domain
45	c4b3nA_	Alignment	not modelled	5.8	20	PDB header: rna binding protein Chain: P: PDB Molecule: splicing factor 3b subunit 1; PDBTitle: 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
46	c2f9jP_	Alignment	not modelled	5.8	33	PDB header: transport protein Chain: C: PDB Molecule: protoglobin; PDBTitle: structure of protoglobin from methanosarcina acetivorans2 c2a
47	c2veeC_	Alignment	not modelled	5.7	14	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase ywhb; PDBTitle: crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
48	c2op8A_	Alignment	not modelled	5.6	13	PDB header: transferase Chain: A: PDB Molecule: sensor protein qsec; PDBTitle: backbone structure of the membrane domain of e. coli histidine kinase2 receptor qsec, center for structures of membrane proteins (csm)3 target 4311c
49	c2kseA_	Alignment	not modelled	5.4	58	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+
50	c4wiuA_	Alignment	not modelled	5.3	17	PDB header: isomerase Chain: C: PDB Molecule: fg41 malonate semialdehyde decarboxylase; PDBTitle: crystal structure of fg41msad inactivated by 3-chloropropiolate
51	c3mlcC_	Alignment	not modelled	5.2	10	