
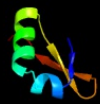




















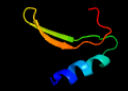



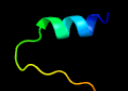


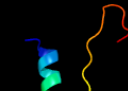
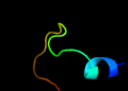


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3407_(-)_3826432_3826731
Date	Fri Aug 9 18:20:07 BST 2019
Unique Job ID	091669e240039355

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2odkD	 Alignment		99.1	17	PDB header: structural genomics, unknown function Chain: D; PDB Molecule: hypothetical protein; PDBTitle: putative prevent-host-death protein from nitrosomonas europaea
2	d2odka1	 Alignment		99.1	18	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
3	c3hryA	 Alignment		98.9	37	PDB header: antitoxin Chain: A; PDB Molecule: prevent host death protein; PDBTitle: crystal structure of phd in a trigonal space group and partially2 disordered
4	c3hs2H	 Alignment		98.9	32	PDB header: antitoxin Chain: H; PDB Molecule: prevent host death protein; PDBTitle: crystal structure of phd truncated to residue 57 in an orthorhombic2 space group
5	c3g5oA	 Alignment		98.5	19	PDB header: toxin/antitoxin Chain: A; PDB Molecule: uncharacterized protein rv2865; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
6	d2a6qb1	 Alignment		98.4	16	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
7	d2a6qa1	 Alignment		98.3	18	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
8	c3oeiB	 Alignment		97.4	19	PDB header: toxin, protein binding Chain: B; PDB Molecule: relj (antitoxin rv3357); PDBTitle: crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
9	c3d55A	 Alignment		97.2	19	PDB header: toxin inhibitor Chain: A; PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
10	c3k6qB	 Alignment		80.7	19	PDB header: ligand binding protein Chain: B; PDB Molecule: putative ligand binding protein; PDBTitle: crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
11	c1skoA	 Alignment		69.2	22	PDB header: signaling protein Chain: A; PDB Molecule: mitogen-activated protein kinase kinase 1 PDBTitle: mp1-p14 complex

12	d3cpta1	Alignment		61.8	24	Fold: Profilin-like Superfamily: Roadblock/LC7 domain Family: Roadblock/LC7 domain
13	c1gk7A_	Alignment		28.8	26	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 1a fragment (1a)
14	c3s4rB_	Alignment		22.6	19	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1a/1b fragment with a stabilizing2 mutation
15	d2ns0a1	Alignment		18.6	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like
16	d1ogda_	Alignment		18.5	22	Fold: RbsD-like Superfamily: RbsD-like Family: RbsD-like
17	c2wcvl_	Alignment		18.0	15	PDB header: isomerase Chain: I: PDB Molecule: l-fucose mutarotase; PDBTitle: crystal structure of bacterial fucu
18	c3e7nB_	Alignment		15.7	22	PDB header: transport protein Chain: B: PDB Molecule: d-ribose high-affinity transport system; PDBTitle: crystal structure of d-ribose high-affinity transport system from2 salmonella typhimurium lt2
19	c3p13B_	Alignment		14.6	22	PDB header: isomerase Chain: B: PDB Molecule: d-ribose pyranase; PDBTitle: complex structure of d-ribose pyranase sa240 with d-ribose
20	d1y8xb1	Alignment		14.0	30	Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Ubiquitin activating enzymes (UBA)
21	c4a34L_	Alignment	not modelled	13.7	12	PDB header: isomerase Chain: L: PDB Molecule: rbsd/fucu transport protein family protein; PDBTitle: crystal structure of the fucose mutarotase in complex with2 l-fucose from streptococcus pneumoniae
22	c2wcuB_	Alignment	not modelled	13.2	23	PDB header: isomerase Chain: B: PDB Molecule: protein fucu homolog; PDBTitle: crystal structure of mammalian fucu
23	c3mvaA_	Alignment	not modelled	12.4	12	PDB header: isomerase Chain: A: PDB Molecule: protein fucu; PDBTitle: the crystal structure of fucu from bifidobacterium longum to 1.65a
24	c2wtoB_	Alignment	not modelled	12.2	28	PDB header: metal binding protein Chain: B: PDB Molecule: orf131 protein; PDBTitle: crystal structure of apo-form czce from c. metallidurans ch34
25	d1x6va1	Alignment	not modelled	11.1	23	Fold: PUA domain-like Superfamily: PUA domain-like Family: ATP sulfurylase N-terminal domain
26	d1bifa2	Alignment	not modelled	11.0	18	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
27	d2ob5a1	Alignment	not modelled	10.5	15	Fold: RbsD-like Superfamily: RbsD-like Family: RbsD-like
28	c3ju0A_	Alignment	not modelled	10.3	20	PDB header: dna binding protein Chain: A: PDB Molecule: phage integrase; PDBTitle: structure of the arm-type binding domain of hai7 integrase Fold: Phosphoglycerate mutase-like

29	d1k6ma2	Alignment	not modelled	10.1	18	Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
30	c4ewvB	Alignment	not modelled	9.6	33	PDB header: ligase Chain: B: PDB Molecule: 4-substituted benzoates-glutamate ligase gh3.12; PDBTitle: crystal structure of gh3.12 in complex with ampcpp
31	c3iprC	Alignment	not modelled	9.4	22	PDB header: transferase Chain: C: PDB Molecule: pts system, iia component; PDBTitle: crystal structure of the enterococcus faecalis gluconate2 specific eiia phosphotransferase system component
32	d1tipa	Alignment	not modelled	8.1	18	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
33	c4heoA	Alignment	not modelled	7.8	50	PDB header: viral protein Chain: A: PDB Molecule: phosphoprotein; PDBTitle: hendra virus phosphoprotein c terminal domain
34	c2ii4C	Alignment	not modelled	7.7	23	PDB header: transferase Chain: C: PDB Molecule: lipoamide acyltransferase component of branched-chain PDBTitle: crystal structure of a cubic core of the dihydrolipoamide2 acyltransferase (e2b) component in the branched-chain alpha-ketoacid3 dehydrogenase complex (bckdc), coenzyme a-bound form
35	d1s29a	Alignment	not modelled	7.6	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: La domain
36	c5iddA	Alignment	not modelled	7.6	20	PDB header: protein transport Chain: A: PDB Molecule: mon1; PDBTitle: crystal structure of the heterodimeric gef mon1-ccz1 in complex with2 ypt7
37	c4h1bA	Alignment	not modelled	7.2	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an alpha-lytic protease prodomain-like protein2 (despig_01740) from desulfovibrio piger atcc 29098 at 1.80 a3 resolution
38	d1umka1	Alignment	not modelled	6.8	22	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
39	d1qx4a1	Alignment	not modelled	6.6	17	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
40	c5o1uB	Alignment	not modelled	6.3	4	PDB header: hydrolase Chain: B: PDB Molecule: phosphodiesterase; PDBTitle: structure of wildtype t.maritima pde (tm1595) with amp and mn2+
41	d2hq7a1	Alignment	not modelled	6.2	3	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
42	c3jvoA	Alignment	not modelled	6.1	13	PDB header: viral protein Chain: A: PDB Molecule: gp6; PDBTitle: crystal structure of bacteriophage hk97 gp6
43	d1j08a2	Alignment	not modelled	5.7	10	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
44	c2ekdD	Alignment	not modelled	5.6	18	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein ph0250; PDBTitle: structural study of project id ph0250 from pyrococcus horikoshii ot3
45	d1v47a1	Alignment	not modelled	5.5	30	Fold: PUA domain-like Superfamily: PUA domain-like Family: ATP sulfurylase N-terminal domain
46	d1ndha1	Alignment	not modelled	5.5	22	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
47	d1t6t1	Alignment	not modelled	5.4	16	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain
48	d2cnda1	Alignment	not modelled	5.4	22	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
49	c6fmgC	Alignment	not modelled	5.3	21	PDB header: transferase Chain: C: PDB Molecule: pts system mannose-specific transporter subunit iiaB; PDBTitle: structure of the mannose transporter iia domain from streptococcus pneumoniae