
















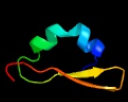


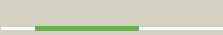
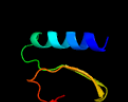
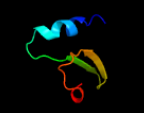
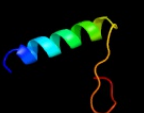
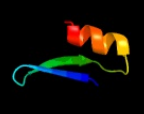


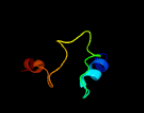
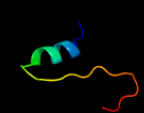
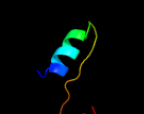
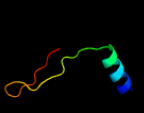


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1962A_RVBD1962A_2205284_2205556
Date	Mon Aug 5 13:25:06 BST 2019
Unique Job ID	c819535196f7adcd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2odkD	 Alignment		99.4	14	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein; PDBTitle: putative prevent-host-death protein from nitrosomonas europaea
2	d2odka1	 Alignment		99.3	14	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
3	c3hryA	 Alignment		99.1	33	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		99.1	33	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	d2a6qb1	 Alignment		98.7	12	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
6	c3g5oA	 Alignment		98.7	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
7	d2a6qa1	 Alignment		98.5	12	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
8	c3oeiB	 Alignment		97.8	18	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		97.7	18	PDB header: toxin inhibitor Chain: A: PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
10	c3k6qB	 Alignment		90.6	13	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		58.4	18	PDB header: signaling protein Chain: A: PDB Molecule: mitogen-activated protein kinase kinase 1 PDBTitle: mp1-p14 complex

12	d3cpta1	Alignment		53.0	17	Fold: Profilin-like Superfamily: Roadblock/LC7 domain Family: Roadblock/LC7 domain
13	d2ns0a1	Alignment		22.3	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like
14	d2ifqa1	Alignment		20.8	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
15	c2wtoB_	Alignment		14.1	28	PDB header: metal binding protein Chain: B: PDB Molecule: orf131 protein; PDBTitle: crystal structure of apo-form czce from c. metallidurans ch34
16	c1gk7A_	Alignment		13.5	19	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 1a fragment (1a)
17	c4ewvB_	Alignment		13.4	32	PDB header: ligase Chain: B: PDB Molecule: 4-substituted benzoates-glutamate ligase gh3.12; PDBTitle: crystal structure of gh3.12 in complex with ampcpp
18	d1logda_	Alignment		13.0	26	Fold: RbsD-like Superfamily: RbsD-like Family: RbsD-like
19	c2wcvl_	Alignment		12.6	30	PDB header: isomerase Chain: I: PDB Molecule: l-fucose mutarotase; PDBTitle: crystal structure of bacterial fucu
20	d2hq7a1	Alignment		10.9	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
21	d1x6va1	Alignment	not modelled	10.4	15	Fold: PUA domain-like Superfamily: PUA domain-like Family: ATP sulfurylase N-terminal domain
22	c3e7nB_	Alignment	not modelled	10.3	25	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
23	c3s4rB_	Alignment	not modelled	9.8	19	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1a/1b fragment with a stabilizing2 mutation
24	c3p13B_	Alignment	not modelled	9.8	26	PDB header: isomerase Chain: B: PDB Molecule: d-ribose pyranase; PDBTitle: complex structure of d-ribose pyranase sa240 with d-ribose
25	c4a34L_	Alignment	not modelled	9.1	23	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
26	c2wcuB_	Alignment	not modelled	8.9	35	PDB header: isomerase Chain: B: PDB Molecule: protein fucu homolog; PDBTitle: crystal structure of mammalian fucu
27	c2oe0B_	Alignment	not modelled	8.6	29	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin-3; PDBTitle: crystal structure of mitochondrial thioredoxin 3 from2 saccharomyces cerevisiae
28	c4heoA_	Alignment	not modelled	8.1	35	PDB header: viral protein Chain: A: PDB Molecule: phosphoprotein; PDBTitle: hendra virus phosphoprotein c terminal domain
						PDB header: isomerase

29	c3mvkA_	Alignment	not modelled	8.1	19	Chain: A: PDB Molecule: protein fucu; PDBTitle: the crystal structure of fucu from bifidobacterium longum to 1.65a
30	d1y8xb1	Alignment	not modelled	7.2	21	Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Ubiquitin activating enzymes (UBA)
31	d1bifa2	Alignment	not modelled	7.1	21	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
32	d1tipa_	Alignment	not modelled	6.9	21	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
33	d2ob5a1	Alignment	not modelled	6.9	15	Fold: RbsD-like Superfamily: RbsD-like Family: RbsD-like
34	c4u4cB_	Alignment	not modelled	6.8	40	PDB header: hydrolase Chain: B: PDB Molecule: protein air2,poly(a) rna polymerase protein 2; PDBTitle: the molecular architecture of the tramp complex reveals the2 organization and interplay of its two catalytic activities
35	d1xfla_	Alignment	not modelled	6.6	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
36	c2vm2C_	Alignment	not modelled	6.6	7	PDB header: oxidoreductase Chain: C: PDB Molecule: thioredoxin h isoform 1.; PDBTitle: crystal structure of barley thioredoxin h isoform 1 crystallized using2 peg as precipitant
37	c5jy5A_	Alignment	not modelled	6.4	21	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin 1 from cryptococcus neoformans at 1.82 angstroms resolution
38	d1k6ma2	Alignment	not modelled	6.3	21	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
39	c4cw9A_	Alignment	not modelled	5.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: entamoeba histolytica thioredoxin c34s mutant
40	d1ep7a_	Alignment	not modelled	5.7	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
41	c5ldda_	Alignment	not modelled	5.7	40	PDB header: protein transport Chain: A: PDB Molecule: mon1; PDBTitle: crystal structure of the heterodimeric gef mon1-ccz1 in complex with2 ypt7
42	d1ti3a_	Alignment	not modelled	5.4	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
43	d1y7ma1	Alignment	not modelled	5.4	14	Fold: L,D-transpeptidase catalytic domain-like Superfamily: L,D-transpeptidase catalytic domain-like Family: L,D-transpeptidase catalytic domain-like
44	d1xwaa_	Alignment	not modelled	5.4	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
45	c3l32B_	Alignment	not modelled	5.4	33	PDB header: viral protein Chain: B: PDB Molecule: phosphoprotein; PDBTitle: structure of the dimerisation domain of the rabies virus2 phosphoprotein
46	c3v62C_	Alignment	not modelled	5.3	50	PDB header: protein binding/dna binding protein Chain: C: PDB Molecule: atp-dependent dna helicase srs2; PDBTitle: structure of the s. cerevisiae srs2 c-terminal domain in complex with2 pcna conjugated to sumo on lysine 164
47	c3v62F_	Alignment	not modelled	5.3	50	PDB header: protein binding/dna binding protein Chain: F: PDB Molecule: atp-dependent dna helicase srs2; PDBTitle: structure of the s. cerevisiae srs2 c-terminal domain in complex with2 pcna conjugated to sumo on lysine 164
48	c6c5rF_	Alignment	not modelled	5.2	25	PDB header: cytosolic protein Chain: F: PDB Molecule: calcium uniporter; PDBTitle: crystal structure of the soluble domain of the mitochondrial calcium2 uniporter
49	d1qx4a1	Alignment	not modelled	5.2	17	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
50	d1syra_	Alignment	not modelled	5.1	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase