




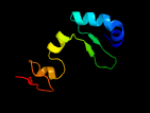
















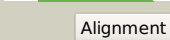

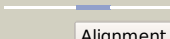


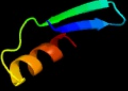

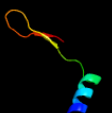
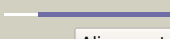
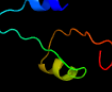





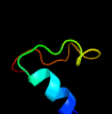


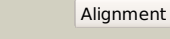
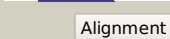
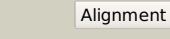
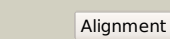
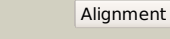
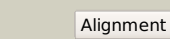

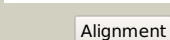


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2830c (-)_3137019_3137234
Date	Wed Aug 7 12:50:49 BST 2019
Unique Job ID	280a4ba12c21c065

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2odka1	 Alignment		99.2	20	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
2	c2odkD	 Alignment		99.2	20	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein; PDBTitle: putative prevent-host-death protein from nitrosomonas europaea
3	c3hryA	 Alignment		99.0	31	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		98.8	30	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		98.4	14	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
6	c3g5oA	 Alignment		98.3	32	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		98.0	14	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
8	c3oeiB	 Alignment		97.7	23	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	23	PDB header: toxin inhibitor Chain: A: PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
10	c3k6qB	 Alignment		90.0	17	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		70.8	20	PDB header: signaling protein Chain: A: PDB Molecule: mitogen-activated protein kinase kinase 1 PDBTitle: mp1-p14 complex

12	d3cpta1	 Alignment		54.7	18	Fold: Profilin-like Superfamily: Roadblock/LC7 domain Family: Roadblock/LC7 domain
13	d2ns0a1	 Alignment		21.6	45	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like
14	c3dmlA	 Alignment		13.5	10	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the periplasmic thioredoxin soxs from paracoccus2 pantotrophus (reduced form)
15	d2hq7a1	 Alignment		13.2	6	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
16	d1ogda	 Alignment		12.6	15	Fold: RbsD-like Superfamily: RbsD-like Family: RbsD-like
17	d1bifa2	 Alignment		11.9	11	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
18	d1k6ma2	 Alignment		10.6	11	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
19	c4ewvB	 Alignment		9.4	35	PDB header: ligase Chain: B: PDB Molecule: 4-substituted benzoates-glutamate ligase gh3.12; PDBTitle: crystal structure of gh3.12 in complex with ampcpp
20	d1x6va1	 Alignment		9.4	20	Fold: PUA domain-like Superfamily: PUA domain-like Family: ATP sulfurylase N-terminal domain
21	d1tipa	 Alignment	not modelled	9.1	11	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
22	c3e7nB	 Alignment	not modelled	8.4	13	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	c6gwjD	 Alignment	not modelled	8.0	28	PDB header: rna binding protein Chain: D: PDB Molecule: ekc/keops complex subunit gon7; PDBTitle: protein complex
24	c3p13B	 Alignment	not modelled	7.5	13	PDB header: isomerase Chain: B: PDB Molecule: d-ribose pyranase; PDBTitle: complex structure of d-ribose pyranase sa240 with d-ribose
25	c2wcvl	 Alignment	not modelled	7.1	25	PDB header: isomerase Chain: I: PDB Molecule: l-fucose mutarotase; PDBTitle: crystal structure of bacterial fucu
26	c5lddA	 Alignment	not modelled	7.1	10	PDB header: protein transport Chain: A: PDB Molecule: mon1; PDBTitle: crystal structure of the heterodimeric gef mon1-ccz1 in complex with2 ypt7
27	c1snaA	 Alignment	not modelled	7.1	40	PDB header: de novo protein Chain: A: PDB Molecule: tetrameric beta-beta-alpha mini-protein; PDBTitle: an oligomeric domain-swapped beta-beta-alpha mini-protein
28	c1snaC	 Alignment	not modelled	7.1	40	PDB header: de novo protein Chain: C: PDB Molecule: tetrameric beta-beta-alpha mini-protein; PDBTitle: an oligomeric domain-swapped beta-beta-alpha mini-protein PDB header: de novo protein

29	c1snaD_	Alignment	not modelled	7.1	40	Chain: D: PDB Molecule: tetrameric beta-beta-alpha mini-protein; PDBTitle: an oligomeric domain-swapped beta-beta-alpha mini-protein
30	c1snaB_	Alignment	not modelled	7.1	40	PDB header: de novo protein Chain: B: PDB Molecule: tetrameric beta-beta-alpha mini-protein; PDBTitle: an oligomeric domain-swapped beta-beta-alpha mini-protein
31	c4heoA_	Alignment	not modelled	7.0	17	PDB header: viral protein Chain: A: PDB Molecule: phosphoprotein; PDBTitle: hendra virus phosphoprotein c terminal domain
32	c6nkID_	Alignment	not modelled	6.9	8	PDB header: antitoxin Chain: D: PDB Molecule: antitoxin vapp1; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
33	c3ve5D_	Alignment	not modelled	6.8	33	PDB header: recombination Chain: D: PDB Molecule: recombination protein recr; PDBTitle: structure of recombination mediator protein recr16-196 deletion mutant
34	d1uwka_	Alignment	not modelled	6.7	17	Fold: Urocanase Superfamily: Urocanase Family: Urocanase
35	c2zqeA_	Alignment	not modelled	6.7	27	PDB header: dna binding protein Chain: A: PDB Molecule: mutS2 protein; PDBTitle: crystal structure of the smr domain of thermus thermophilus mutS2
36	c4nhyc_	Alignment	not modelled	6.5	19	PDB header: oxidoreductase/oxidoreductase inhibitor oxygenase domain- Chain: C: PDB Molecule: 2-oxoglutarate and iron-dependent PDBTitle: crystal structure of human ogfod1, 2-oxoglutarate and iron-dependent2 oxygenase domain containing 1, in complex with pyridine-2,4-3 dicarboxylic acid (2,4-pdca)
37	c6c5rF_	Alignment	not modelled	6.3	27	PDB header: cytosolic protein Chain: F: PDB Molecule: calcium uniporter; PDBTitle: crystal structure of the soluble domain of the mitochondrial calcium2 uniporter
38	d1xbra_	Alignment	not modelled	6.3	45	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: T-box
39	d1pdoa_	Alignment	not modelled	6.2	13	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: EIIA-man component-like
40	c3v62F_	Alignment	not modelled	6.0	42	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
41	c3v62C_	Alignment	not modelled	6.0	42	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
42	d1vm0a_	Alignment	not modelled	5.9	20	Fold: IF3-like Superfamily: AlbA-like Family: Hypothetical protein At2g34160
43	c6qj1A_	Alignment	not modelled	5.8	13	PDB header: cell cycle protein,structural Chain: A: PDB Molecule: structural maintenance of chromosomes protein,structural PDBTitle: crystal structure of the c. thermophilum condensin smc2 atpase head2 (crystal from i)
44	c3iprC_	Alignment	not modelled	5.6	17	PDB header: transferase Chain: C: PDB Molecule: pts system, iia component; PDBTitle: crystal structure of the enterococcus faecalis gluconate2 specific eiiA phosphotransferase system component
45	c1gk7A_	Alignment	not modelled	5.5	18	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 1a fragment (1a)