

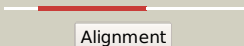
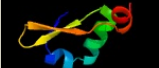
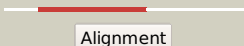







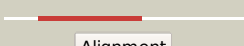









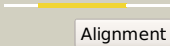

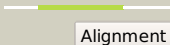

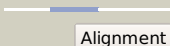


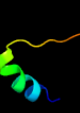
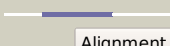
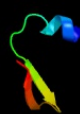
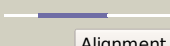
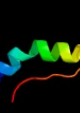
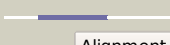

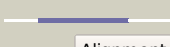
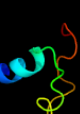

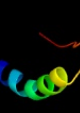
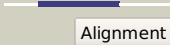
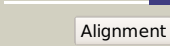
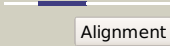

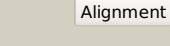

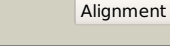
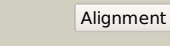


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0626 (-) _718028_718288
Date	Fri Jul 26 01:50:19 BST 2019
Unique Job ID	265a59f2a7f5129a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2odkD	 Alignment		99.4	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		99.4	17	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
3	c3hryA	 Alignment		99.2	35	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		99.2	35	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		98.8	15	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
6	c3g5oA	 Alignment		98.7	23	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		98.6	16	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
8	c3oeiB	 Alignment		97.9	22	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		97.9	22	PDB header: toxin inhibitor Chain: A: PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
10	c3dboA	 Alignment		94.8	100	PDB header: toxin/antitoxin Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a member of the vapbc family of toxin-antitoxin2 systems, vapbc-5, from mycobacterium tuberculosis
11	c3k6qB	 Alignment		94.3	11	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

12	c1skoA	 Alignment		71.5	17	PDB header: signaling protein Chain: A: PDB Molecule: mitogen-activated protein kinase kinase 1 PDBTitle: mp1-p14 complex
13	d3cpta1	 Alignment		62.2	18	Fold: Profilin-like Superfamily: Roadblock/LC7 domain Family: Roadblock/LC7 domain
14	d2ns0a1	 Alignment		29.2	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like
15	c6c5rF	 Alignment		16.0	17	PDB header: cytosolic protein Chain: F: PDB Molecule: calcium uniporter; PDBTitle: crystal structure of the soluble domain of the mitochondrial calcium2 uniporter
16	d1x6va1	 Alignment		14.8	23	Fold: PUA domain-like Superfamily: PUA domain-like Family: ATP sulfurylase N-terminal domain
17	d1k6ma2	 Alignment		14.5	14	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
18	d1bifa2	 Alignment		14.5	14	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
19	c4ewvB	 Alignment		11.0	29	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	d1tipa	 Alignment		10.2	14	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
21	d2hq7a1	 Alignment	not modelled	9.9	9	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
22	c2l2dA	 Alignment	not modelled	9.1	35	PDB header: hydrolase Chain: A: PDB Molecule: otu domain-containing protein 7a; PDBTitle: solution nmr structure of human uba-like domain of otud7a_11_83, nesg2 target ht6304a/ocsp target otud7a_11_83/sgc-toronto
23	c5xtaC	 Alignment	not modelled	8.7	16	PDB header: oxidoreductase Chain: C: PDB Molecule: virK protein; PDBTitle: crystal structure of lpg1832, a virK family protein from legionella2 pneumophila
24	d1xbra	 Alignment	not modelled	8.3	27	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: T-box
25	c4heoA	 Alignment	not modelled	7.4	40	PDB header: viral protein Chain: A: PDB Molecule: phosphoprotein; PDBTitle: hendra virus phosphoprotein c terminal domain
26	c4a04B	 Alignment	not modelled	7.2	36	PDB header: transcription Chain: B: PDB Molecule: t-box transcription factor tbx1; PDBTitle: structure of the dna-bound t-box domain of human tbx1, a2 transcription factor associated with the digeorge syndrome
27	c3jvoA	 Alignment	not modelled	7.0	0	PDB header: viral protein Chain: A: PDB Molecule: gp6; PDBTitle: crystal structure of bacteriophage hk97 gp6
28	c2wcvl	 Alignment	not modelled	6.5	17	PDB header: isomerase Chain: I: PDB Molecule: !-fucose mutarotase; PDBTitle: crystal structure of bacterial fucu

29	c2wtoB_	Alignment	not modelled	6.5	33	PDB header: metal binding protein Chain: B: PDB Molecule: orf131 protein; PDBTitle: crystal structure of apo-form czce from c. metallidurans ch34
30	c2rt6A_	Alignment	not modelled	6.2	17	PDB header: dna binding protein Chain: A: PDB Molecule: primosomal replication protein n"; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for pric n-2 terminal domain
31	c2x6vB_	Alignment	not modelled	6.2	45	PDB header: transcription/dna Chain: B: PDB Molecule: t-box transcription factor tbx5; PDBTitle: crystal structure of human tbx5 in the dna-bound and dna-2 free form
32	d1ogda_	Alignment	not modelled	6.0	25	Fold: RbsD-like Superfamily: RbsD-like Family: RbsD-like
33	c5t1jB_	Alignment	not modelled	5.9	36	PDB header: transcription/dna Chain: B: PDB Molecule: t-box transcription factor tbx21; PDBTitle: crystal structure of the tbx dna binding domain of the transcription2 factor t-bet
34	c5lddA_	Alignment	not modelled	5.7	20	PDB header: protein transport Chain: A: PDB Molecule: mon1; PDBTitle: crystal structure of the heterodimeric gef mon1-ccc1 in complex with2 ypt7
35	d1h6fa_	Alignment	not modelled	5.7	55	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: T-box
36	c5ghaF_	Alignment	not modelled	5.6	17	PDB header: transferase/transport protein Chain: F: PDB Molecule: sulfur carrier ttub; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
37	c1gk7A_	Alignment	not modelled	5.3	31	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 1a fragment (1a)
38	c2psbA_	Alignment	not modelled	5.1	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: yerb protein; PDBTitle: crystal structure of yerb protein from bacillus subtilis. northeast2 structural genomics target sr586
39	d2psba1	Alignment	not modelled	5.1	29	Fold: YerB-like Superfamily: YerB-like Family: YerB-like
40	d1y8xb1	Alignment	not modelled	5.1	13	Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Ubiquitin activating enzymes (UBA)