
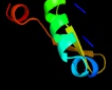




















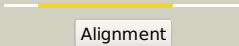



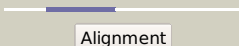

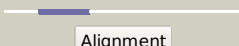

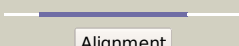

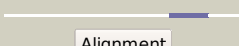

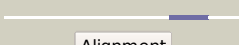


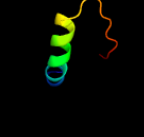

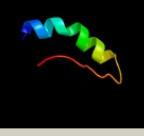


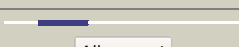

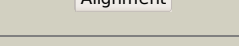
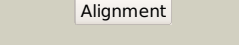
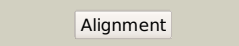




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0596c (-)_695231_695488
Date	Fri Jul 26 01:50:15 BST 2019
Unique Job ID	fc659531cb6c8f6e

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2odkD_	 Alignment		99.3	20	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	20	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
3	c3hryA_	 Alignment		98.9	38	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	38	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		98.5	14	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
6	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
7	d2a6qa1	 Alignment		98.2	15	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
8	c3oeiB_	 Alignment		98.0	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		97.8	13	PDB header: toxin inhibitor Chain: A; PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
10	c3k6qB_	 Alignment		92.4	21	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		73.1	21	PDB header: signaling protein Chain: A; PDB Molecule: mitogen-activated protein kinase kinase 1 PDBTitle: mp1-p14 complex

12	d3cpta1	 Alignment		70.2	20	Fold: Profilin-like Superfamily: Roadblock/LC7 domain Family: Roadblock/LC7 domain
13	d2ns0a1	 Alignment		37.0	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like
14	d1x6va1	 Alignment		16.5	19	Fold: PUA domain-like Superfamily: PUA domain-like Family: ATP sulfurylase N-terminal domain
15	c4heoA_	 Alignment		14.0	35	PDB header: viral protein Chain: A; PDB Molecule: phosphoprotein; PDBTitle: hendra virus phosphoprotein c terminal domain
16	c2wcvl_	 Alignment		14.0	19	PDB header: isomerase Chain: I; PDB Molecule: l-fucose mutarotase; PDBTitle: crystal structure of bacterial fucu
17	c3vepX_	 Alignment		11.6	44	PDB header: membrane protein/transcription Chain: X; PDB Molecule: uncharacterized protein rv3413c/mt3522; PDBTitle: crystal structure of sigd4 in complex with its negative regulator rsda
18	c3vepC_	 Alignment		11.5	44	PDB header: membrane protein/transcription Chain: C; PDB Molecule: uncharacterized protein rv3413c/mt3522; PDBTitle: crystal structure of sigd4 in complex with its negative regulator rsda
19	d1bifa2	 Alignment		10.3	18	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
20	d1k6ma2	 Alignment		10.1	18	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
21	d1ogda_	 Alignment	not modelled	9.7	25	Fold: RbsD-like Superfamily: RbsD-like Family: RbsD-like
22	d2hq7a1	 Alignment	not modelled	9.1	6	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
23	c5xtaC_	 Alignment	not modelled	9.0	21	PDB header: oxidoreductase Chain: C; PDB Molecule: virk protein; PDBTitle: crystal structure of lpg1832, a virk family protein from legionella2 pneumophila
24	c2wtoB_	 Alignment	not modelled	8.5	28	PDB header: metal binding protein Chain: B; PDB Molecule: orf131 protein; PDBTitle: crystal structure of apo-form czce from c. metallidurans ch34
25	c4a34L_	 Alignment	not modelled	8.2	20	PDB header: isomerase Chain: L; PDB Molecule: rbsd/fucu transport protein family protein; PDBTitle: crystal structure of the fucose mutarotase in complex with 2 l-fucose from streptococcus pneumoniae
26	d1tipa_	 Alignment	not modelled	8.2	18	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
27	c3daiA_	 Alignment	not modelled	8.0	28	PDB header: signaling protein Chain: A; PDB Molecule: atpase family aaa domain-containing protein 2; PDBTitle: crystal structure of the bromodomain of the human atad2
28	c6c5rF_	 Alignment	not modelled	8.0	21	PDB header: cytosolic protein Chain: F; PDB Molecule: calcium uniporter; PDBTitle: crystal structure of the soluble domain of the mitochondrial calcium2 uniporter
		 Alignment				PDB header: isomerase

29	c3p13B_	Alignment	not modelled	7.9	8	Chain: B: PDB Molecule: d-ribose pyranase; PDBTitle: complex structure of d-ribose pyranase sa240 with d-ribose
30	d1y7ma1	Alignment	not modelled	7.6	15	Fold: L,D-transpeptidase catalytic domain-like Superfamily: L,D-transpeptidase catalytic domain-like Family: L,D-transpeptidase catalytic domain-like
31	d1y8xb1	Alignment	not modelled	7.6	22	Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Ubiquitin activating enzymes (UBA)
32	d1xbra_	Alignment	not modelled	7.4	36	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: T-box
33	c5ldda_	Alignment	not modelled	6.7	10	PDB header: protein transport Chain: A: PDB Molecule: mon1; PDBTitle: crystal structure of the heterodimeric gef mon1-ccz1 in complex with2 ypt7
34	d1pdoa_	Alignment	not modelled	6.4	10	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: EIIA-man component-like
35	c4a04B_	Alignment	not modelled	6.3	45	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
36	c1gk7A_	Alignment	not modelled	6.3	18	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 1a fragment (1a)
37	c5ghaF_	Alignment	not modelled	6.1	17	PDB header: transferase/transport protein Chain: F: PDB Molecule: sulfur carrier ttub; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
38	c4x3iA_	Alignment	not modelled	5.9	40	PDB header: signaling protein Chain: A: PDB Molecule: activity-regulated cytoskeleton-associated protein; PDBTitle: the crystal structure of arc n-lobe complexed with camk2a fragment
39	c5o1uB_	Alignment	not modelled	5.7	17	PDB header: hydrolase Chain: B: PDB Molecule: phosphodiesterase; PDBTitle: structure of wildtype t.maritima pde (tm1595) with amp and mn2+
40	d1dwka2	Alignment	not modelled	5.6	21	Fold: Cyanase C-terminal domain Superfamily: Cyanase C-terminal domain Family: Cyanase C-terminal domain
41	d1v47a1	Alignment	not modelled	5.4	25	Fold: PUA domain-like Superfamily: PUA domain-like Family: ATP sulfurylase N-terminal domain
42	c2iv1J_	Alignment	not modelled	5.4	21	PDB header: lyase Chain: J: PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the catalytic2 mechanism of cyanase
43	c3zvkg_	Alignment	not modelled	5.4	19	PDB header: antitoxin/toxin/dna Chain: G: PDB Molecule: antitoxin of toxin-antitoxin system vapb; PDBTitle: crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
44	c3iprC_	Alignment	not modelled	5.2	14	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	d1riea_	Alignment	not modelled	5.2	14	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
46	d1h6fa_	Alignment	not modelled	5.0	36	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: T-box