




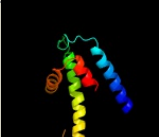















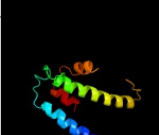




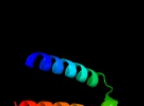






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2036 (-)_2282107_2282748
Date	Mon Aug 5 13:25:14 BST 2019
Unique Job ID	f018313e2e7ab61e

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2nsfA_	 Alignment		100.0	18	PDB header: isomerase Chain: A; PDB Molecule: hypothetical protein cgl3021; PDBTitle: crystal structure of the mycothiol-dependent maleylpyruvate isomerase
2	d2nsfa1	 Alignment		99.9	17	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: Maleylpyruvate isomerase-like
3	c5cogB_	 Alignment		98.7	11	PDB header: unknown function Chain: B; PDB Molecule: irc4; PDBTitle: crystal structure of yeast irc4
4	c5civA_	 Alignment		98.5	14	PDB header: unknown function Chain: A; PDB Molecule: sibling bacteriocin; PDBTitle: sibling lethal factor precursor - dfsb
5	c4n6cB_	 Alignment		98.2	11	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the b1rzq2 protein from streptococcus pneumoniae.2 northeast structural genomics consortium (nesg) target spr36.
6	c2rd9C_	 Alignment		98.1	19	PDB header: hydrolase Chain: C; PDB Molecule: bh0186 protein; PDBTitle: crystal structure of a putative yfiT-like metal-dependent hydrolase2 (bh0186) from bacillus halodurans c-125 at 2.30 a resolution
7	d1rxqa_	 Alignment		98.0	18	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: YfiT-like putative metal-dependent hydrolases
8	c6iz2A_	 Alignment		97.7	7	PDB header: unknown function Chain: A; PDB Molecule: dinb/yfiT family protein; PDBTitle: crystal structure of dinb/yfiT protein dr0053 from d. radiodurans r1
9	c5cofA_	 Alignment		97.6	14	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterised protein q1r1x2 from escherichia2 coli uti89
10	c6anrA_	 Alignment		97.2	19	PDB header: hydrolase Chain: A; PDB Molecule: colibactin self-protection protein clbs; PDBTitle: crystal structure of a self resistance protein clbs from colibactin2 biosynthetic gene cluster
11	c5cqvb_	 Alignment		97.2	9	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein q8dww2 from streptococcus2 agalactiae

12	c3cexB	Alignment		97.1	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the conserved protein of locus ef_3021 from2 enterococcus faecalis
13	d2hkva1	Alignment		96.9	11	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
14	d2ou6a1	Alignment		96.8	13	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
15	c3e4xB	Alignment		96.7	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: apc36150; PDBTitle: crystal structure of putative metal-dependent hydrolases2 apc36150
16	c2yqyB	Alignment		96.6	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein ttha0303; PDBTitle: crystal structure of tt2238, a four-helix bundle protein
17	c2qe9B	Alignment		96.3	11	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein yiza; PDBTitle: crystal structure of a putative metal-dependent hydrolase (yiza,2 bsu10800) from bacillus subtilis at 1.90 a resolution
18	c3di5A	Alignment		96.3	13	PDB header: metal binding protein Chain: A: PDB Molecule: dinb-like protein; PDBTitle: crystal structure of a dinb-like protein (bce_4655) from bacillus2 cereus atcc 10987 at 2.01 a resolution
19	c3dkaA	Alignment		96.0	12	PDB header: unknown function Chain: A: PDB Molecule: dinb-like protein; PDBTitle: crystal structure of a dinb-like protein (yjoa, bsu12410) from2 bacillus subtilis at 2.30 a resolution
20	d2p1aa1	Alignment		96.0	14	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
21	d2nsfa2	Alignment	not modelled	89.4	19	Fold: SCP-like Superfamily: SCP-like Family: Microthiol-dependent maleylpyruvate isomerase C-terminal domain-like
22	c5wk0A	Alignment	not modelled	87.2	10	PDB header: unknown function Chain: A: PDB Molecule: damage-inducible protein dinb; PDBTitle: crystal structure of the bacillithiol transferase bsta from2 staphylococcus aureus.
23	c2jobA	Alignment	not modelled	32.2	60	PDB header: lipid binding protein Chain: A: PDB Molecule: antilipopolsaccharide factor; PDBTitle: solution structure of an antilipopolsaccharide factor from2 shrimp and its possible lipid a binding site
24	d1lbaa	Alignment	not modelled	18.2	20	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
25	c4idiA	Alignment	not modelled	16.1	5	PDB header: protein binding Chain: A: PDB Molecule: oryza sativa rum1-related; PDBTitle: crystal structure of rum1-related protein from plasmodium yoelii,2 py06420
26	c2dkzA	Alignment	not modelled	13.5	32	PDB header: signaling protein Chain: A: PDB Molecule: hypothetical protein loc64762; PDBTitle: solution structure of the sam_pnt-domain of the2 hypothetical protein loc64762
27	c2k9xA	Alignment	not modelled	10.9	12	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of urm1 from trypanosoma brucei
28	c6h6pA	Alignment	not modelled	9.0	14	PDB header: lipid binding protein Chain: A: PDB Molecule: ubiquinone biosynthesis protein ubij; PDBTitle: ubij-scp2 ubiquinone synthesis protein
						PDB header: oxidoreductase

29	c3lfmA_	Alignment	not modelled	8.7	14	Chain: A: PDB Molecule: protein fto; PDBTitle: crystal structure of the fat mass and obesity associated (fto) protein2 reveals basis for its substrate specificity
30	c2n2sA_	Alignment	not modelled	8.0	75	PDB header: signaling protein Chain: A: PDB Molecule: pheromone ep-1; PDBTitle: nmr solution structure of the pheromone ep-1 from euplotes petzi
31	c3bdqB_	Alignment	not modelled	7.7	24	PDB header: lipid transport Chain: B: PDB Molecule: sterol carrier protein 2-like 2; PDBTitle: room temperture crystal structure of sterol carrier protein-2 2 like-2
32	c1yypA_	Alignment	not modelled	7.3	21	PDB header: replication/transferase Chain: A: PDB Molecule: dna polymerase processivity factor; PDBTitle: crystal structure of cytomegalovirus ul44 bound to c-terminal peptide2 from cmv ul54
33	c2od5A_	Alignment	not modelled	6.8	40	PDB header: dna binding protein Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative nucleic acid binding protein2 (jcvi_pep_1096688149193) from uncultured marine organism at 1.79 a3 resolution
34	d2od5a1	Alignment	not modelled	6.8	40	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Marine metagenome family WH1
35	d1pz4a_	Alignment	not modelled	6.4	21	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
36	c2qjIA_	Alignment	not modelled	5.5	18	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin-related modifier 1; PDBTitle: crystal structure of urm1
37	c2qnlA_	Alignment	not modelled	5.4	10	PDB header: signaling protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative dna damage-inducible protein2 (chu_0679) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
38	d2cfua1	Alignment	not modelled	5.2	26	Fold: SCP-like Superfamily: SCP-like Family: Alkylsulfatase C-terminal domain-like