

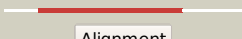






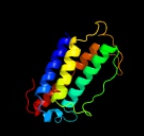



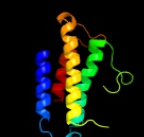

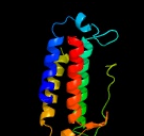
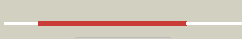
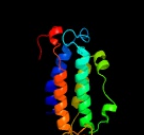







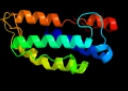







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1727_(-)_1953277_1953846
Date	Fri Aug 2 13:30:33 BST 2019
Unique Job ID	a8c64e1a837c57d6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2nsfA_	 Alignment		100.0	14	PDB header: isomerase Chain: A: PDB Molecule: hypothetical protein cgl3021; PDBTitle: crystal structure of the mycothiol-dependent maleylpyruvate isomerase
2	d2nsfa1	 Alignment		99.9	16	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: Maleylpyruvate isomerase-like
3	c2rd9C_	 Alignment		98.5	10	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
4	c5cogB_	 Alignment		98.5	12	PDB header: unknown function Chain: B: PDB Molecule: irc4; PDBTitle: crystal structure of yeast irc4
5	c6iz2A_	 Alignment		98.4	11	PDB header: unknown function Chain: A: PDB Molecule: dinb/yfiT family protein; PDBTitle: crystal structure of dinb/yfiT protein dr0053 from d. radiodurans r1
6	c5civA_	 Alignment		98.3	14	PDB header: unknown function Chain: A: PDB Molecule: sibling bacteriocin; PDBTitle: sibling lethal factor precursor - dfsb
7	d2ou6a1	 Alignment		98.2	15	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
8	d1rxqa_	 Alignment		98.2	15	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: YfiT-like putative metal-dependent hydrolases
9	c3dkaA_	 Alignment		98.1	16	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
10	c3cexB_	 Alignment		98.0	10	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
11	c4n6cB_	 Alignment		98.0	7	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.

12	d2hkva1	Alignment		97.9	13	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
13	c3di5A	Alignment		97.9	11	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
14	d2p1aa1	Alignment		97.8	7	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
15	c2qe9B	Alignment		97.8	7	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
16	c3e4xB	Alignment		97.7	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: apc36150; PDBTitle: crystal structure of putative metal-dependent hydrolases2 apc36150
17	c5cofA	Alignment		97.6	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterised protein q1r1x2 from escherichia2 coli uti89
18	c6anrA	Alignment		97.5	13	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
19	c2yqyB	Alignment		97.4	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein ttha0303; PDBTitle: crystal structure of tt2238, a four-helix bundle protein
20	c5cqyB	Alignment		97.2	6	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein q8dvw2 from streptococcus2 agalactiae
21	c5wk0A	Alignment	not modelled	88.5	8	PDB header: unknown function Chain: A: PDB Molecule: damage-inducible protein dinb; PDBTitle: crystal structure of the bacillithiol transferase bsta from2 staphylococcus aureus.
22	c2jobA	Alignment	not modelled	21.1	40	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
23	c4idiA	Alignment	not modelled	17.7	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
24	c2qnlA	Alignment	not modelled	12.9	13	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
25	c2dkzA	Alignment	not modelled	11.4	5	PDB header: signaling protein Chain: A: PDB Molecule: hypothetical protein loc64762; PDBTitle: solution structure of the sam_pnt-domain of the2 hypothetical protein loc64762
26	c5uxtA	Alignment	not modelled	9.6	44	PDB header: de novo protein Chain: A: PDB Molecule: coiled-coil trimer with glu:trp:lys triad; PDBTitle: coiled-coil trimer with glu:trp:lys triad
27	d1baa	Alignment	not modelled	9.0	20	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
28	c5uxtC	Alignment	not modelled	8.7	44	PDB header: de novo protein Chain: C: PDB Molecule: coiled-coil trimer with glu:trp:lys triad; PDBTitle: coiled-coil trimer with glu:trp:lys triad

29	c2k9xA_	Alignment	not modelled	7.7	7	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of urm1 from trypanosoma brucei
30	c3v62F_	Alignment	not modelled	6.5	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
31	c3v62C_	Alignment	not modelled	6.5	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
32	d2od5a1	Alignment	not modelled	6.0	40	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Marine metagenome family WH1
33	c2od5A_	Alignment	not modelled	6.0	40	PDB header: dna binding protein Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative nucleic acid binding protein2 (jcvl_pep_1096688149193) from uncultured marine organism at 1.79 a3 resolution
34	c5xfsB_	Alignment	not modelled	5.7	14	PDB header: protein transport Chain: B: PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
35	c2damA_	Alignment	not modelled	5.5	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: etea protein; PDBTitle: solution structure of the novel identified uba-like domain2 in the n-terminal of human etea protein