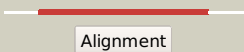

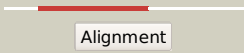



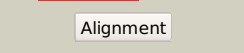
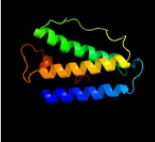


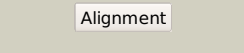
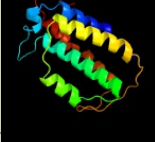
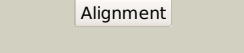
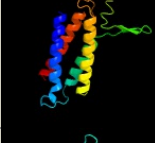

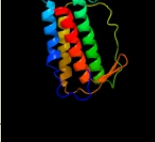
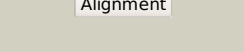
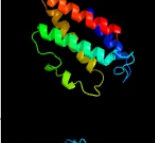
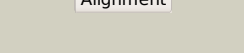
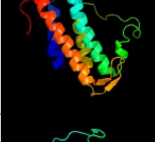
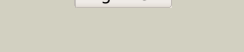
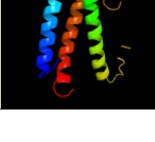





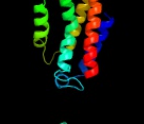

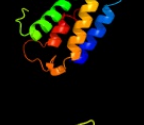
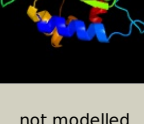


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0332 (-)_397442_398227
Date	Tue Jul 23 14:50:40 BST 2019
Unique Job ID	c179317711037f59

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2nsfA_	 Alignment		100.0	16	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		98.4	8	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	c5civA_	 Alignment		98.4	15	PDB header: unknown function Chain: A: PDB Molecule: sibling bacteriocin; PDBTitle: sibling lethal factor precursor - dfsb
5	c5cogB_	 Alignment		98.3	6	PDB header: unknown function Chain: B: PDB Molecule: irc4; PDBTitle: crystal structure of yeast irc4
6	c6iz2A_	 Alignment		98.3	15	PDB header: unknown function Chain: A: PDB Molecule: dinb/yfiT family protein; PDBTitle: crystal structure of dinb/yfiT protein dr0053 from d. radiodurans r1
7	c2yqyB_	 Alignment		98.2	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein ttha0303; PDBTitle: crystal structure of tt2238, a four-helix bundle protein
8	d1rxqa_	 Alignment		98.0	14	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: YfiT-like putative metal-dependent hydrolases
9	c3cexB_	 Alignment		97.8	13	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
10	c3dkaA_	 Alignment		97.7	14	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
11	c4n6cB_	 Alignment		97.7	6	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	d2ou6a1	Alignment		97.5	13	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
13	c3e4xB	Alignment		97.3	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: apc36150; PDBTitle: crystal structure of putative metal-dependent hydrolases2 apc36150
14	c3di5A	Alignment		97.3	14	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
15	d2hkva1	Alignment		97.2	11	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
16	c2qe9B	Alignment		97.2	6	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
17	d2p1aa1	Alignment		97.2	13	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
18	c5cqVB	Alignment		96.6	7	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein q8dvw2 from streptococcus2 agalactiae
19	c5cofA	Alignment		96.4	6	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterised protein q1r1x2 from escherichia2 coli uti89
20	c3bdqB	Alignment		96.4	22	PDB header: lipid transport Chain: B: PDB Molecule: sterol carrier protein 2-like 2; PDBTitle: room temprature crystal structure of sterol carrier protein-2 2 like-2
21	d1c44a	Alignment	not modelled	96.3	12	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
22	c6h6pA	Alignment	not modelled	96.0	19	PDB header: lipid binding protein Chain: A: PDB Molecule: ubiquinone biosynthesis protein ubij; PDBTitle: ubij-scp2 ubiquinone synthesis protein
23	c6anrA	Alignment	not modelled	96.0	10	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
24	d1ikta	Alignment	not modelled	95.7	13	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
25	c4ueiA	Alignment	not modelled	95.6	11	PDB header: transferase Chain: A: PDB Molecule: sterol carrier protein 2/3-oxoacyl-coa thiolase; PDBTitle: solution structure of the sterol carrier protein domain 22 of helicoverpa armigera
26	d2cfua1	Alignment	not modelled	94.4	11	Fold: SCP-like Superfamily: SCP-like Family: Alkylsulfatase C-terminal domain-like
27	d1pz4a	Alignment	not modelled	93.8	11	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
28	d2nsfa2	Alignment	not modelled	91.5	14	Fold: SCP-like Superfamily: SCP-like Family: Micthiol-dependent maleylpyruvate isomerase C-terminal domain-like PDB header: lipid binding protein

29	c3bkrA_	Alignment	not modelled	91.4	8	Chain: A: PDB Molecule: sterol carrier protein-2 like-3; PDBTitle: crystal structure of sterol carrier protein-2 like-3 (scp2-2 l3) from aedes aegypti
30	c4jgxB_	Alignment	not modelled	89.4	8	PDB header: lipid binding protein Chain: B: PDB Molecule: fatty acid-binding protein; PDBTitle: the structure of sterol carrier protein 2 from the yeast yarrowia2 lipolytica
31	c3bn8A_	Alignment	not modelled	87.5	5	PDB header: transport protein Chain: A: PDB Molecule: putative sterol carrier protein 2; PDBTitle: crystal structure of a putative sterol carrier protein type 2 (af1534)2 from archaeoglobus fulgidus dsm 4304 at 2.11 a resolution
32	c4nssA_	Alignment	not modelled	79.5	15	PDB header: unknown function Chain: A: PDB Molecule: mycobacterial protein; PDBTitle: a structural and functional investigation of a novel protein from2 mycobacterium smegmatis implicated in mycobacterial macrophage3 survivability
33	c2yheD_	Alignment	not modelled	59.4	20	PDB header: hydrolase Chain: D: PDB Molecule: sec-alkyl sulfatase; PDBTitle: structure determination of the stereoselective inverting sec-2 alkylsulfatase pisa1 from pseudomonas sp.
34	c4pdxB_	Alignment	not modelled	50.6	7	PDB header: hydrolase Chain: B: PDB Molecule: putative alkyl/aryl-sulfatase yjcs; PDBTitle: crystal structure of escherchia coli uncharacterized protein yjcs
35	c4nurB_	Alignment	not modelled	44.6	18	PDB header: hydrolase Chain: B: PDB Molecule: psdsa; PDBTitle: crystal structure of thermostable alkylsulfatase sdsap from2 pseudomonas sp. s9
36	c2jobA_	Alignment	not modelled	31.9	80	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
37	c5wk0A_	Alignment	not modelled	24.5	10	PDB header: unknown function Chain: A: PDB Molecule: damage-inducible protein dinb; PDBTitle: crystal structure of the bacillithiol transferase bsta from2 staphylococcus aureus.
38	c3ssoE_	Alignment	not modelled	16.1	14	PDB header: transferase Chain: E: PDB Molecule: methyltransferase; PDBTitle: myce methyltransferase from the mycinamycin biosynthetic pathway in2 complex with mg and sah, crystal form 2
39	d1v8ca2	Alignment	not modelled	15.0	26	Fold: TBP-like Superfamily: MoaD-related protein, C-terminal domain Family: MoaD-related protein, C-terminal domain
40	c3ssmB_	Alignment	not modelled	14.2	14	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: myce methyltransferase from the mycinamycin biosynthetic pathway in2 complex with mg and sah, crystal form 1
41	c3vx6A_	Alignment	not modelled	11.3	16	PDB header: ligase Chain: A: PDB Molecule: e1; PDBTitle: crystal structure of kluyveromyces marxianus atg7ntd
42	c2cfuA_	Alignment	not modelled	9.0	9	PDB header: hydrolase Chain: A: PDB Molecule: sdsa1; PDBTitle: crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
43	c2k9xA_	Alignment	not modelled	8.5	18	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of urm1 from trypanosoma brucei
44	c3lx4B_	Alignment	not modelled	8.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: fe-hydrogenase; PDBTitle: stepwise [fefe]-hydrogenase h-cluster assembly revealed in the2 structure of hyda(deltaafg)
45	c2i00D_	Alignment	not modelled	7.7	8	PDB header: transferase Chain: D: PDB Molecule: acetyltransferase, gnat family; PDBTitle: crystal structure of acetyltransferase (gnat family) from enterococcus2 faecalis
46	d2od5a1	Alignment	not modelled	7.3	60	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Marine metagenome family WH1
47	c2od5A_	Alignment	not modelled	7.3	60	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
48	c3vx8D_	Alignment	not modelled	7.2	32	PDB header: ligase Chain: D: PDB Molecule: ubiquitin-like modifier-activating enzyme atg7; PDBTitle: crystal structure of arabidopsis thaliana atg7ntd-atg3 complex
49	c2qilA_	Alignment	not modelled	6.9	16	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin-related modifier 1; PDBTitle: crystal structure of urm1
50	d1lbaa_	Alignment	not modelled	5.3	27	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
51	d2i00a1	Alignment	not modelled	5.2	10	Fold: SCP-like Superfamily: SCP-like Family: EF1021 C-terminal domain-like