

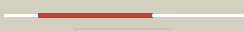












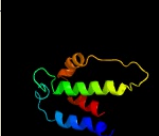



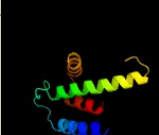

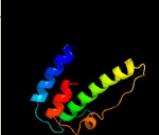
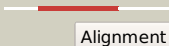

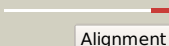

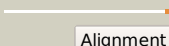
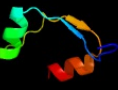
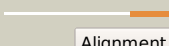

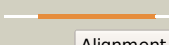
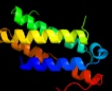
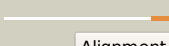

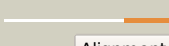





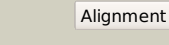
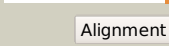
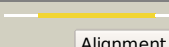
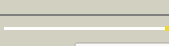
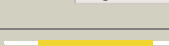
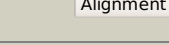
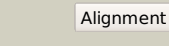
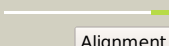


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1929c_(-)_2181269_2181913
Date	Fri Aug 2 13:30:55 BST 2019
Unique Job ID	8050f4f913c98679

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2nsfA_	 Alignment		100.0	15	PDB header: isomerase Chain: A: PDB Molecule: hypothetical protein cgl3021; PDBTitle: crystal structure of the mycothiol-dependent maleylpyruvate isomerase
2	d2nsfa1	 Alignment		99.8	15	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: Maleylpyruvate isomerase-like
3	c5cogB_	 Alignment		97.7	7	PDB header: unknown function Chain: B: PDB Molecule: irc4; PDBTitle: crystal structure of yeast irc4
4	d2nsfa2	 Alignment		97.6	15	Fold: SCP-like Superfamily: SCP-like Family: Microthiol-dependent maleylpyruvate isomerase C-terminal domain-like
5	c5civA_	 Alignment		97.2	12	PDB header: unknown function Chain: A: PDB Molecule: sibling bacteriocin; PDBTitle: sibling lethal factor precursor - dfsb
6	c2yqyB_	 Alignment		97.2	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein ttha0303; PDBTitle: crystal structure of tt2238, a four-helix bundle protein
7	c4n6cB_	 Alignment		96.8	8	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.
8	d1rxqa_	 Alignment		96.4	7	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: YfiT-like putative metal-dependent hydrolases
9	c2rd9C_	 Alignment		96.1	12	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
10	c5cofA_	 Alignment		95.4	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterised protein q1r1x2 from escherichia2 coli uti89
11	c6anrA_	 Alignment		93.7	18	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

12	c5cqvb_	 Alignment		91.4	11	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein q8dvw2 from streptococcus2 agalactiae
13	d1ikta_	 Alignment		90.2	12	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
14	c3bdqB_	 Alignment		89.6	19	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
15	d2cfua1	 Alignment		89.3	13	Fold: SCP-like Superfamily: SCP-like Family: Alkylsulfatase C-terminal domain-like
16	c6iz2A_	 Alignment		89.3	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
17	d1pz4a_	 Alignment		86.3	16	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
18	c6h6pA_	 Alignment		86.3	17	PDB header: lipid binding protein Chain: A: PDB Molecule: ubiquinone biosynthesis protein ubij; PDBTitle: ubij-scp2 ubiquinone synthesis protein
19	d2hkva1	 Alignment		86.1	9	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
20	d1c44a_	 Alignment		81.6	11	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
21	c3cexB_	 Alignment	not modelled	81.0	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
22	c3bkrA_	 Alignment	not modelled	80.3	14	PDB header: lipid binding protein 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
23	c3dkaA_	 Alignment	not modelled	75.2	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
24	c4jgxB_	 Alignment	not modelled	75.2	21	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
25	c3di5A_	 Alignment	not modelled	73.3	18	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
26	c3e4xB_	 Alignment	not modelled	71.1	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: apc36150; PDBTitle: crystal structure of putative metal-dependent hydrolases2 apc36150
27	c4ueiA_	 Alignment	not modelled	69.4	14	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 heliconia2 armigera
28	c3bn8A_	 Alignment	not modelled	69.3	14	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
29	d2ou6a1	Alignment	not modelled	62.2	16	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
30	d2p1aa1	Alignment	not modelled	60.5	8	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
31	c2qe9B	Alignment	not modelled	57.2	13	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
32	c2jobA	Alignment	not modelled	46.9	60	PDB header: lipid binding protein Chain: A: PDB Molecule: antilipoplysaccharide factor; PDBTitle: solution structure of an antilipoplysaccharide factor from2 shrimp and its possible lipid a binding site
33	c4nssA	Alignment	not modelled	44.8	24	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
34	d1lbaa	Alignment	not modelled	18.0	0	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
35	c4pdxB	Alignment	not modelled	17.6	12	PDB header: hydrolase Chain: B: PDB Molecule: putative alkyl/aryl-sulfatase yjcs; PDBTitle: crystal structure of escherchia coli uncharacterized protein yjcs
36	c2cfuA	Alignment	not modelled	13.2	13	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.
37	c2yheD	Alignment	not modelled	12.8	9	PDB header: hydrolase Chain: D: PDB Molecule: sec-alkyl sulfatase; PDBTitle: structure determination of the stereoselective inverting sec-2 alkylsulfatase pisa1 from pseudomonas sp.
38	c2n2sA	Alignment	not modelled	12.7	25	PDB header: signaling protein Chain: A: PDB Molecule: pheromone ep-1; PDBTitle: nmr solution structure of the pheromone ep-1 from euplotes petzi
39	c2k9xA	Alignment	not modelled	11.0	12	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of urm1 from trypanosoma brucei
40	c2dkzA	Alignment	not modelled	8.7	4	PDB header: signaling protein Chain: A: PDB Molecule: hypothetical protein loc64762; PDBTitle: solution structure of the sam_pnt-domain of the2 hypothetical protein loc64762
41	c2hu9B	Alignment	not modelled	7.5	10	PDB header: metal transport Chain: B: PDB Molecule: mercuric transport protein periplasmic component; PDBTitle: x-ray structure of the archaeoglobus fulgidus copz n-2 terminal domain
42	c4idiA	Alignment	not modelled	6.8	16	PDB header: protein binding Chain: A: PDB Molecule: oryza sativa rum1-related; PDBTitle: crystal structure of oryza sativa rum1-related protein from plasmodium yoelii,2 py06420
43	c4nurB	Alignment	not modelled	6.8	6	PDB header: hydrolase Chain: B: PDB Molecule: psdsa; PDBTitle: crystal structure of thermostable alkylsulfatase sdsap from2 pseudomonas sp. s9
44	c2k35A	Alignment	not modelled	5.8	9	PDB header: antimicrobial protein Chain: A: PDB Molecule: hydramacin-1; PDBTitle: hydramacin-1: structure and antibacterial activity of a2 peptide from the basal metazoan hydra
45	d1tc3c	Alignment	not modelled	5.6	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
46	c2qjIA	Alignment	not modelled	5.4	35	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin-related modifier 1; PDBTitle: crystal structure of urm1
47	c3lx4B	Alignment	not modelled	5.3	33	PDB header: oxidoreductase Chain: B: PDB Molecule: fe-hydrogenase; PDBTitle: stepwise [fefe]-hydrogenase h-cluster assembly revealed in the2 structure of hyda(deltaefg)
48	d3c8ya1	Alignment	not modelled	5.3	33	Fold: Fe-only hydrogenase Superfamily: Fe-only hydrogenase Family: Fe-only hydrogenase
49	c5uc2C	Alignment	not modelled	5.1	38	PDB header: hydrolase Chain: C: PDB Molecule: domain of unknown function duf1849; PDBTitle: crystal structure of beta-barrel-like, putative atp binding protein of2 domain of unknown function duf1849 from brucella abortus