


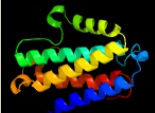




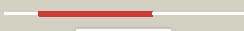
























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3099c_(-)_3468410_3469261
Date	Thu Aug 8 16:20:28 BST 2019
Unique Job ID	bf7cf7011514a1e7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2nsfA_	 Alignment		100.0	13	PDB header: isomerase Chain: A: PDB Molecule: hypothetical protein cgl3021; PDBTitle: crystal structure of the mycothiol-dependent maleylpyruvate isomerase
2	d2nsfa1	 Alignment		100.0	14	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: Maleylpyruvate isomerase-like
3	c5civA_	 Alignment		99.6	16	PDB header: unknown function Chain: A: PDB Molecule: sibling bacteriocin; PDBTitle: sibling lethal factor precursor - dfsb
4	c5cogB_	 Alignment		99.5	15	PDB header: unknown function Chain: B: PDB Molecule: irc4; PDBTitle: crystal structure of yeast irc4
5	d1rxqa_	 Alignment		99.4	15	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: YfiT-like putative metal-dependent hydrolases
6	c4n6cB_	 Alignment		99.4	12	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.
7	c2rd9C_	 Alignment		99.2	15	PDB header: hydrolase Chain: C: PDB Molecule: bh0186 protein; PDBTitle: crystal structure of a putative yfi-like metal-dependent hydrolase2 (bh0186) from bacillus halodurans c-125 at 2.30 a resolution
8	c6iz2A_	 Alignment		99.2	16	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		99.2	14	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterised protein q1r1x2 from escherichia2 coli uti89
10	c3cexB_	 Alignment		99.1	8	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	c6anrA_	 Alignment		99.1	17	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	d2ou6a1	Alignment		99.0	15	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
13	c5cqvb_	Alignment		98.9	9	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein q8dvw2 from streptococcus2 agalactiae
14	c3dkaA_	Alignment		98.8	9	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
15	c2yqyb_	Alignment		98.8	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein ttha0303; PDBTitle: crystal structure of tt2238, a four-helix bundle protein
16	d2p1aa1	Alignment		98.8	13	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
17	c3di5A_	Alignment		98.7	16	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
18	d2hkva1	Alignment		98.6	13	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
19	c3e4xB_	Alignment		98.5	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: apc36150; PDBTitle: crystal structure of putative metal-dependent hydrolases2 apc36150
20	c2qe9B_	Alignment		98.4	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
21	c6h6pA_	Alignment	not modelled	97.7	15	PDB header: lipid binding protein Chain: A: PDB Molecule: ubiquinone biosynthesis protein ubij; PDBTitle: ubij-scp2 ubiquinone synthesis protein
22	c3bdqB_	Alignment	not modelled	97.7	19	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
23	d2cfua1	Alignment	not modelled	97.5	12	Fold: SCP-like Superfamily: SCP-like Family: Alkylsulfatase C-terminal domain-like
24	d1ikta_	Alignment	not modelled	97.2	15	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
25	d1pz4a_	Alignment	not modelled	97.1	15	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
26	d1c44a_	Alignment	not modelled	97.1	14	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
27	c4jgxB_	Alignment	not modelled	96.8	13	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
28	c5wk0A_	Alignment	not modelled	96.8	12	PDB header: unknown function Chain: A: PDB Molecule: damage-inducible protein dinb; PDBTitle: crystal structure of the bacillithiol transferase bsta from2 staphylococcus aureus.
						PDB header: transferase Chain: A: PDB Molecule: sterol carrier protein 2/3-oxoacyl-coa

29	c4ueiA_	Alignment	not modelled	96.7	13	thiolase; PDBTitle: solution structure of the sterol carrier protein domain 22 of <i>helicoverpa armigera</i>
30	c3bkrA_	Alignment	not modelled	96.5	18	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 <i>aedes aegypti</i>
31	c3bn8A_	Alignment	not modelled	95.3	11	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 <i>archaeoglobus fulgidus</i> dsm 4304 at 2.11 a resolution
32	c4pdxB_	Alignment	not modelled	95.0	7	PDB header: hydrolase Chain: B: PDB Molecule: putative alkyl/aryl-sulfatase yjcs; PDBTitle: crystal structure of <i>escherchia coli</i> uncharacterized protein yjcs
33	c4nurB_	Alignment	not modelled	87.4	14	PDB header: hydrolase Chain: B: PDB Molecule: psdsa; PDBTitle: crystal structure of thermostable alkylsulfatase sdsap from <i>2 pseudomonas sp. s9</i>
34	c2cfuA_	Alignment	not modelled	87.3	12	PDB header: hydrolase Chain: A: PDB Molecule: sdsa1; PDBTitle: crystal structure of sdsa1, an alkylsulfatase from <i>2 pseudomonas aeruginosa</i> , in complex with 1-decane-sulfonic-3 acid.
35	c2yheD_	Alignment	not modelled	87.0	13	PDB header: hydrolase Chain: D: PDB Molecule: sec-alkyl sulfatase; PDBTitle: structure determination of the stereoselective inverting sec-2 alkylsulfatase pisa1 from <i>pseudomonas sp.</i>
36	c2qnlA_	Alignment	not modelled	85.4	9	PDB header: signaling protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative dna damage-inducible protein2 (chu_0679) from <i>cytophaga hutchinsonii</i> atcc 33406 at 1.50 a3 resolution
37	c2i00D_	Alignment	not modelled	85.0	13	PDB header: transferase Chain: D: PDB Molecule: acetyltransferase, gnat family; PDBTitle: crystal structure of acetyltransferase (gnat family) from <i>enterococcus2 faecalis</i>
38	c4nssA_	Alignment	not modelled	82.6	22	PDB header: unknown function Chain: A: PDB Molecule: mycobacterial protein; PDBTitle: a structural and functional investigation of a novel protein from <i>2 mycobacterium smegmatis</i> implicated in mycobacterial macrophage3 survivability
39	d2nsfa2	Alignment	not modelled	80.6	14	Fold: SCP-like Superfamily: SCP-like Family: Micthiol-dependent maleylpyruvate isomerase C-terminal domain-like
40	c2ozgA_	Alignment	not modelled	58.8	14	PDB header: transferase Chain: A: PDB Molecule: gcn5-related n-acetyltransferase; PDBTitle: crystal structure of gcn5-related n-acetyltransferase (yp_325469.1)2 from <i>anabaena variabilis</i> atcc 29413 at 2.00 a resolution
41	d2i00a1	Alignment	not modelled	51.8	12	Fold: SCP-like Superfamily: SCP-like Family: EF1021 C-terminal domain-like
42	d2ozga1	Alignment	not modelled	50.4	14	Fold: SCP-like Superfamily: SCP-like Family: EF1021 C-terminal domain-like
43	d2hv2a1	Alignment	not modelled	42.4	11	Fold: SCP-like Superfamily: SCP-like Family: EF1021 C-terminal domain-like
44	c6qkja_	Alignment	not modelled	41.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: egtb from <i>chloracidobacterium thermophilum</i> , a type ii sulfoxide2 synthase in complex with n,n,n-trimethyl-histidine
45	d1wfra_	Alignment	not modelled	38.8	24	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
46	d1w2za3	Alignment	not modelled	32.0	15	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
47	c2dkza_	Alignment	not modelled	29.6	22	PDB header: signaling protein Chain: A: PDB Molecule: hypothetical protein loc64762; PDBTitle: solution structure of the sam_pnt-domain of the2 hypothetical protein loc64762
48	c2jobA_	Alignment	not modelled	25.0	60	PDB header: lipid binding protein Chain: A: PDB Molecule: antilipoplysaccharide factor; PDBTitle: solution structure of an antilipoplysaccharide factor from <i>2 shrimp</i> and its possible lipid a binding site
49	c2hv2D_	Alignment	not modelled	24.6	19	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of conserved protein of unknown function from <i>2 enterococcus faecalis v583</i> at 2.4 a resolution, probable n-3 acyltransferase
50	c3n7zD_	Alignment	not modelled	22.7	12	PDB header: transferase Chain: D: PDB Molecule: acetyltransferase, gnat family; PDBTitle: crystal structure of acetyltransferase from <i>bacillus anthracis</i>
51	c4my3A_	Alignment	not modelled	14.3	16	PDB header: transferase Chain: A: PDB Molecule: gcn5-related n-acetyltransferase; PDBTitle: crystal structure of gcn5-related n-acetyltransferase from <i>kribbella2 flavida</i>
52	c6rftB_	Alignment	not modelled	11.3	14	PDB header: antibiotic Chain: B: PDB Molecule: uncharacterized n-acetyltransferase d2e36_21790; PDBTitle: crystal structure of eis2 from <i>mycobacterium abscessus</i> bound to2 acetyl-coa
53	c3sxnC_	Alignment	not modelled	10.9	14	PDB header: transferase Chain: C: PDB Molecule: enhanced intracellular survival protein; PDBTitle: <i>mycobacterium tuberculosis</i> eis protein initiates

						modulation of host2 immune responses by acetylation of dusp16/mkp-7
54	c3r1kA_	Alignment	not modelled	9.3	10	PDB header: transferase Chain: A: PDB Molecule: enhanced intracellular survival protein; PDBTitle: crystal structure of acetyltransferase eis from mycobacterium2 tuberculosis h37rv in complex with coa and an acetamide moiety
55	c4idiA_	Alignment	not modelled	9.2	6	PDB header: protein binding Chain: A: PDB Molecule: oryza sativa rum1-related; PDBTitle: crystal structure of rum1-related protein from plasmodium yoelii,2 py06420
56	d1t8sa_	Alignment	not modelled	7.3	19	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
57	d1iiea_	Alignment	not modelled	6.0	40	Fold: Class II MHC-associated invariant chain ectoplasmic trimerization domain Superfamily: Class II MHC-associated invariant chain ectoplasmic trimerization domain Family: Class II MHC-associated invariant chain ectoplasmic trimerization domain
58	c2iv1j_	Alignment	not modelled	5.9	6	PDB header: lyase Chain: J: PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the catalytic2 mechanism of cyanase
59	d1lbaa_	Alignment	not modelled	5.7	27	Fold: N-acetylMuramoyl-L-alanine amidase-like Superfamily: N-acetylMuramoyl-L-alanine amidase-like Family: N-acetylMuramoyl-L-alanine amidase-like