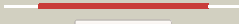



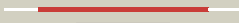


















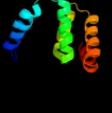









Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2429_(ahpD)_2726816_2727349
Date	Wed Aug 7 12:50:05 BST 2019
Unique Job ID	0c5dad0378cd2480

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1knca_	 Alignment		100.0	100	Fold: AhpD-like Superfamily: AhpD-like Family: AhpD
2	c4g9qA_	 Alignment		99.9	14	PDB header: lyase Chain: A: PDB Molecule: 4-carboxymuconolactone decarboxylase; PDBTitle: crystal structure of a 4-carboxymuconolactone decarboxylase
3	d2q0ta1	 Alignment		99.8	18	Fold: AhpD-like Superfamily: AhpD-like Family: AhpD
4	c3d7iB_	 Alignment		99.7	12	PDB header: lyase Chain: B: PDB Molecule: carboxymuconolactone decarboxylase family protein; PDBTitle: crystal structure of carboxymuconolactone decarboxylase family protein2 possibly involved in oxygen detoxification (1591455) from3 methanococcus jannaschii at 1.75 a resolution
5	c5dipB_	 Alignment		99.7	22	PDB header: oxidoreductase Chain: B: PDB Molecule: alkyl hydroperoxide reductase ahpD; PDBTitle: crystal structure of lpg0406 in reduced form from legionella2 pneumophila
6	c3beyC_	 Alignment		99.7	17	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: conserved protein o27018; PDBTitle: crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural genomics consortium target3 tt217
7	d1vkeb_	 Alignment		99.6	22	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
8	d1vkea_	 Alignment		99.6	20	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
9	c1p8cD_	 Alignment		99.6	20	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of tm1620 (apc4843) from thermotoga2 maritima
10	d2ouwa1	 Alignment		99.6	17	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
11	c2qeua_	 Alignment		99.6	16	PDB header: lyase Chain: A: PDB Molecule: putative carboxymuconolactone decarboxylase; PDBTitle: crystal structure of putative carboxymuconolactone decarboxylase2 (yp_555818.1) from burkholderia xenovorans lb400 at 1.65 a resolution

12	d2cwqa1	Alignment		99.6	16	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
13	d2af7a1	Alignment		99.6	13	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
14	c3lvyB_	Alignment		99.0	14	PDB header: lyase Chain: B: PDB Molecule: carboxymuconolactone decarboxylase family; PDBTitle: crystal structure of carboxymuconolactone decarboxylase2 family protein smu.961 from streptococcus mutans
15	c6ohiA_	Alignment		99.0	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: debrominase bmp8; PDBTitle: crystal structure of the debrominase bmp8 (apo)
16	c3c1B_	Alignment		99.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: putative antioxidant defense protein mlr4105; PDBTitle: crystal structure of an antioxidant defense protein (mlr4105) from2 mesorhizobium loti maff303099 at 2.00 a resolution
17	d2pfxa1	Alignment		99.0	19	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
18	d2oyoal	Alignment		98.9	19	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
19	d2prra1	Alignment		98.9	19	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
20	d2o4da1	Alignment		98.9	24	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
21	d2gmya1	Alignment	not modelled	98.9	26	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
22	c5dj4D_	Alignment	not modelled	97.3	12	PDB header: signaling protein Chain: D: PDB Molecule: sestrin-2; PDBTitle: leucine-bound sestrin2 from homo sapiens
23	c5gzxD_	Alignment	not modelled	97.2	11	PDB header: hydrolase Chain: D: PDB Molecule: (r)-2-haloacid dehalogenase; PDBTitle: the complex structure of d-2-haloacid dehalogenase mutant with d-2-cpa
24	c5aonB_	Alignment	not modelled	63.6	26	PDB header: signaling protein Chain: B: PDB Molecule: peroxin 14; PDBTitle: crystal structure of the conserved n-terminal domain of2 pex14 from trypanosoma brucei
25	c5l87A_	Alignment	not modelled	60.3	28	PDB header: membrane protein Chain: A: PDB Molecule: peroxin 14; PDBTitle: targeting the pex14-pex5 interaction by small molecules provides novel2 therapeutic routes to treat trypanosomiasis.
26	c3ff5B_	Alignment	not modelled	60.1	26	PDB header: protein transport Chain: B: PDB Molecule: peroxisomal biogenesis factor 14; PDBTitle: crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
27	c2w85A_	Alignment	not modelled	49.4	24	PDB header: protein transport Chain: A: PDB Molecule: peroxisomal membrane anchor protein pex14; PDBTitle: structure of pex14 in complex with pex19
28	c1sg7A_	Alignment	not modelled	29.2	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative cation transport regulator chab; PDBTitle: nmr solution structure of the putative cation transport2 regulator chab
						Fold: ChaB-like

29	d1sg7a1	Alignment	not modelled	29.2	26	Superfamily: ChaB-like Family: ChaB-like
30	d2p7vb1	Alignment	not modelled	22.5	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
31	c2k9lA_	Alignment	not modelled	16.8	11	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: structure of the core binding domain of sigma54
32	c2k9mA_	Alignment	not modelled	14.9	11	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: structure of the core binding domain of sigma54
33	c2v79B_	Alignment	not modelled	14.5	9	PDB header: dna binding protein Chain: B: PDB Molecule: dna replication protein dnad; PDBTitle: crystal structure of the n-terminal domain of dnad from bacillus2 subtilis
34	c1t3qD_	Alignment	not modelled	14.0	22	PDB header: oxidoreductase Chain: D: PDB Molecule: quinoline 2-oxidoreductase small subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
35	c4uetA_	Alignment	not modelled	12.7	30	PDB header: retinol-binding protein Chain: A: PDB Molecule: nematode fatty acid retinoid binding protein; PDBTitle: diversity in the structures and ligand binding sites among2 the fatty acid and retinol binding proteins of nematodes3 revealed by na-far-1 from necator americanus
36	c2ekkA_	Alignment	not modelled	12.6	35	PDB header: protein binding Chain: A: PDB Molecule: uba domain from e3 ubiquitin-protein ligase PDBTitle: solution structure of ruh-074, a human uba domain
37	d1zxia1	Alignment	not modelled	11.7	11	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
38	c5tmxA_	Alignment	not modelled	11.4	15	PDB header: transcription regulator Chain: A: PDB Molecule: protein sini; PDBTitle: solution structure of sini, antagonist to the master biofilm-regulator2 sinr in bacillus subtilis
39	d1t56a2	Alignment	not modelled	11.3	25	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
40	d1rm6c1	Alignment	not modelled	10.7	20	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
41	c5y6qA_	Alignment	not modelled	10.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidase small subunit; PDBTitle: crystal structure of an aldehyde oxidase from methylobacillus sp.2 ky4400
42	c4zohC_	Alignment	not modelled	10.5	19	PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase iron-sulfur subunit; PDBTitle: crystal structure of glyceraldehyde oxidoreductase
43	c3t72o_	Alignment	not modelled	10.4	14	PDB header: transcription/dna Chain: O: PDB Molecule: pho box dna (strand 1); PDBTitle: phob(e)-sigma70(4)-(rnap-beta-flap-tip-helix)-dna transcription2 activation sub-complex
44	c3cmwA_	Alignment	not modelled	10.2	22	PDB header: recombination/dna Chain: A: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-ssdna/dsna2 structures
45	d1v97a1	Alignment	not modelled	9.8	22	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
46	c2xgvA_	Alignment	not modelled	9.8	7	PDB header: viral protein Chain: A: PDB Molecule: psiv capsid n-terminal domain; PDBTitle: structure of the n-terminal domain of capsid protein from2 rabbit endogenous lentivirus (relik)
47	d1m9fd_	Alignment	not modelled	9.2	12	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
48	c2mqkA_	Alignment	not modelled	8.7	20	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the mub aaa+ atpase
49	c2jnhA_	Alignment	not modelled	8.6	28	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase cbl-b; PDBTitle: solution structure of the uba domain from cbl-b
50	c2w9yA_	Alignment	not modelled	8.1	14	PDB header: lipid transport Chain: A: PDB Molecule: fatty acid/retinol binding protein protein 7, PDBTitle: the structure of the lipid binding protein ce-far-7 from2 caenorhabditis elegans
51	c2do6A_	Alignment	not modelled	8.0	28	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase cbl-b; PDBTitle: solution structure of rsgi ruh-065, a uba domain from human2 cdna
52	c1ffuA_	Alignment	not modelled	8.0	11	PDB header: hydrolase Chain: A: PDB Molecule: cuts, iron-sulfur protein of carbon monoxide PDBTitle: carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
53	d1dxsa_	Alignment	not modelled	7.8	18	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
54	c2d9sA_	Alignment	not modelled	7.8	28	PDB header: ligase Chain: A: PDB Molecule: cbl e3 ubiquitin protein ligase; PDBTitle: solution structure of rsgi ruh-049, a uba domain from

						mouse2 cdna
55	c4wxcC_	Alignment	not modelled	7.6	16	PDB header: lyase Chain: C; PDB Molecule: biotin and thiamin synthesis associated; PDBTitle: crystal structure of hydg: a maturase of the [fefe]-hydrogenase
56	c1t3bA_	Alignment	not modelled	6.8	33	PDB header: isomerase Chain: A; PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: x-ray structure of dsbc from haemophilus influenzae
57	d1t33a2	Alignment	not modelled	6.6	12	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
58	c2q0oA_	Alignment	not modelled	6.3	4	PDB header: transcription Chain: A; PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
59	d1dgja1	Alignment	not modelled	6.3	14	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
60	d1otva_	Alignment	not modelled	6.3	15	Fold: Heme oxygenase-like Superfamily: Heme oxygenase-like Family: PqqC-like
61	d1wdka1	Alignment	not modelled	6.3	19	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: HCDH C-domain-like
62	c4om9A_	Alignment	not modelled	6.1	9	PDB header: hydrolase Chain: A; PDB Molecule: serine protease pet; PDBTitle: x-ray crystal structure of the passenger domain of plasmid encoded2 toxin, an autotransporter enterotoxin from enteroaggregative3 escherichia coli (eac)
63	c4r33A_	Alignment	not modelled	6.0	25	PDB header: lyase Chain: A; PDB Molecule: nosl; PDBTitle: x-ray structure of the tryptophan lyase nosl with tryptophan and s-2 adenosyl-l-homocysteine bound
64	d2csba4	Alignment	not modelled	6.0	29	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
65	d1vlba1	Alignment	not modelled	5.9	14	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
66	d3bula1	Alignment	not modelled	5.8	17	Fold: Methionine synthase domain-like Superfamily: Methionine synthase domain Family: Methionine synthase domain
67	c3itcA_	Alignment	not modelled	5.7	15	PDB header: hydrolase Chain: A; PDB Molecule: renal dipeptidase; PDBTitle: crystal structure of sco3058 with bound citrate and glycerol
68	c4wt3A_	Alignment	not modelled	5.5	19	PDB header: chaperone Chain: A; PDB Molecule: rubisco accumulation factor 1, isoform 2; PDBTitle: the n-terminal domain of rubisco accumulation factor 1 from2 arabidopsis thaliana
69	c1rm6F_	Alignment	not modelled	5.4	20	PDB header: oxidoreductase Chain: F; PDB Molecule: 4-hydroxybenzoyl-coa reductase gamma subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
70	c5yisC_	Alignment	not modelled	5.3	56	PDB header: protein binding Chain: C; PDB Molecule: ankyrin-2; PDBTitle: crystal structure of ankb lir/lc3b complex
71	c3cixA_	Alignment	not modelled	5.3	23	PDB header: adomet binding protein Chain: A; PDB Molecule: fefe-hydrogenase maturase; PDBTitle: x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
72	d3orca_	Alignment	not modelled	5.3	27	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
73	c5ui5I_	Alignment	not modelled	5.1	11	PDB header: transcription/dna Chain: I; PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: crystal structure of aquifex aeolicus sigman bound to promoter dna