

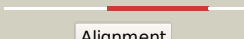
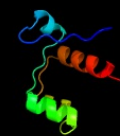
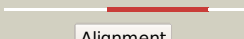










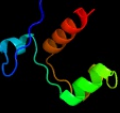








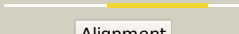

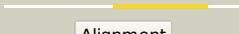



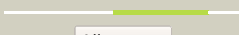

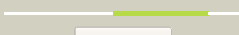





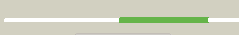

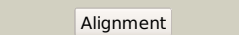
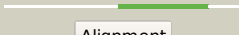
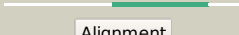



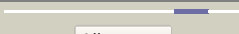
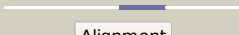


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0807 (-) _901638_902027
Date	Fri Jul 26 01:50:39 BST 2019
Unique Job ID	e2f5af2d599941d9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4nssA_	 Alignment		100.0	66	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
2	d2cfua1	 Alignment		94.6	11	Fold: SCP-like Superfamily: SCP-like Family: Alkylsulfatase C-terminal domain-like
3	c3bn8A_	 Alignment		90.3	18	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
4	d1ikta_	 Alignment		89.7	13	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
5	d1pz4a_	 Alignment		86.9	12	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
6	c3bdqB_	 Alignment		83.9	17	PDB header: lipid transport Chain: B: PDB Molecule: sterol carrier protein 2-like 2; PDBTitle: room tempreture crystal structure of sterol carrier protein-2 2 like-2
7	c4nurB_	 Alignment		82.4	18	PDB header: hydrolase Chain: B: PDB Molecule: psdsa; PDBTitle: crystal structure of thermostable alkylsulfatase sdsap from2 pseudomonas sp. s9
8	c2cfuA_	 Alignment		82.1	11	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.
9	c4pdxB_	 Alignment		79.5	18	PDB header: hydrolase Chain: B: PDB Molecule: putative alkyl/aryl-sulfatase yjcs; PDBTitle: crystal structure of escherchia coli uncharacterized protein yjcs
10	c4jgxB_	 Alignment		78.5	12	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
11	c2yheD_	 Alignment		78.3	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.

12	c2nsfA	 Alignment		78.2	17	PDB header: isomerase Chain: A: PDB Molecule: hypothetical protein cgl3021; PDBTitle: crystal structure of the mycothiol-dependent maleylpyruvate isomerase
13	d1c44a	 Alignment		76.3	15	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
14	c2ozgA	 Alignment		73.6	19	PDB header: transferase Chain: A: PDB Molecule: gcn5-related n-acetyltransferase; PDBTitle: crystal structure of gcn5-related n-acetyltransferase (yp_325469.1)2 from anabaena variabilis atcc 29413 at 2.00 a resolution
15	d2i00a1	 Alignment		70.0	12	Fold: SCP-like Superfamily: SCP-like Family: EF1021 C-terminal domain-like
16	c2hv2D	 Alignment		68.3	15	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of conserved protein of unknown function from2 enterococcus faecalis v583 at 2.4 a resolution, probable n-3 acyltransferase
17	d2ozga1	 Alignment		65.6	15	Fold: SCP-like Superfamily: SCP-like Family: EF1021 C-terminal domain-like
18	d2hv2a1	 Alignment		60.4	20	Fold: SCP-like Superfamily: SCP-like Family: EF1021 C-terminal domain-like
19	c3bkrA	 Alignment		57.9	16	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
20	c2i00D	 Alignment		56.1	11	PDB header: transferase Chain: D: PDB Molecule: acetyltransferase, gnat family; PDBTitle: crystal structure of acetyltransferase (gnat family) from enterococcus2 faecalis
21	c3n7zD	 Alignment	not modelled	55.7	10	PDB header: transferase Chain: D: PDB Molecule: acetyltransferase, gnat family; PDBTitle: crystal structure of acetyltransferase from bacillus anthracis
22	c4ueiA	 Alignment	not modelled	51.2	10	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 helioverpa armigera
23	d1wfra	 Alignment	not modelled	41.7	22	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
24	c4e0iC	 Alignment	not modelled	26.2	28	PDB header: oxidoreductase Chain: C: PDB Molecule: mitochondrial fad-linked sulfhydryl oxidase erv1; PDBTitle: crystal structure of the c30s/c133s mutant of erv1 from saccharomyces2 cerevisiae
25	c6o2uB	 Alignment	not modelled	22.8	26	PDB header: signaling protein Chain: B: PDB Molecule: store-operated calcium entry-associated regulatory factor; PDBTitle: crystal structure of the saraf luminal domain
26	d1w96c1	 Alignment	not modelled	17.7	38	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
27	c4yh8B	 Alignment	not modelled	16.8	23	PDB header: splicing Chain: B: PDB Molecule: splicing factor u2af 59 kda subunit; PDBTitle: structure of yeast u2af complex
28	c4qpgA	 Alignment	not modelled	14.7	23	PDB header: virus Chain: A: PDB Molecule: capsid protein vp1; PDBTitle: crystal structure of empty hepatitis a virus

29	d1ulza1	Alignment	not modelled	14.2	50	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
30	d1w96a1	Alignment	not modelled	14.0	38	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
31	d2j9ga1	Alignment	not modelled	13.6	63	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
32	d1ss6a	Alignment	not modelled	13.1	29	Fold: NSFL1 (p97 ATPase) cofactor p47, SEP domain Superfamily: NSFL1 (p97 ATPase) cofactor p47, SEP domain Family: NSFL1 (p97 ATPase) cofactor p47, SEP domain
33	c3sxnC	Alignment	not modelled	12.6	13	PDB header: transferase Chain: C: PDB Molecule: enhanced intracellular survival protein; PDBTitle: mycobacterium tuberculosis eis protein initiates modulation of host2 immune responses by acetylation of dusp16/mkp-7
34	c6rftB	Alignment	not modelled	12.3	11	PDB header: antibiotic Chain: B: PDB Molecule: uncharacterized n-acetyltransferase d2e36_21790; PDBTitle: crystal structure of eis2 from mycobacterium abscessus bound to2 acetyl-coa
35	c2hj3A	Alignment	not modelled	10.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfhydryl oxidase erv1p; PDBTitle: structure of the arabidopsis thaliana erv1 thiol oxidase
36	c4e0iA	Alignment	not modelled	10.2	35	PDB header: oxidoreductase Chain: A: PDB Molecule: mitochondrial fad-linked sulfhydryl oxidase erv1; PDBTitle: crystal structure of the c30s/c133s mutant of erv1 from saccharomyces2 cerevisiae
37	d1oqca	Alignment	not modelled	9.8	20	Fold: Four-helical up-and-down bundle Superfamily: FAD-dependent thiol oxidase Family: FAD-dependent thiol oxidase
38	c2xueB	Alignment	not modelled	9.7	32	PDB header: oxidoreductase Chain: B: PDB Molecule: lysine-specific demethylase 6b; PDBTitle: crystal structure of jmj3
39	d1s7ia	Alignment	not modelled	9.3	56	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: DGPF domain (Pfam 04946)
40	c3r1kA	Alignment	not modelled	9.2	9	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
41	c5ntbB	Alignment	not modelled	9.1	12	PDB header: protease inhibitor Chain: B: PDB Molecule: papain inhibitor; PDBTitle: streptomyces papain inhibitor (spi)
42	c5k2yB	Alignment	not modelled	8.7	14	PDB header: transport protein Chain: B: PDB Molecule: probable periplasmic sugar-binding lipoprotein uspc; PDBTitle: crystal structure of m. tuberculosis uspc (monoclinic crystal form)
43	d1m7xa2	Alignment	not modelled	8.7	31	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
44	c4g68A	Alignment	not modelled	8.6	11	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: biochemical and structural insights into xylan utilization by the2 thermophilic bacteriumcaldanaerobius polysaccharolyticus
45	c1uebB	Alignment	not modelled	8.4	21	PDB header: rna binding protein Chain: B: PDB Molecule: elongation factor p; PDBTitle: crystal structure of translation elongation factor p from2 thermus thermophilus hb8
46	c3vxbA	Alignment	not modelled	8.2	12	PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar-binding lipoprotein; PDBTitle: crystal structure of bxl from streptomyces thermoviolaceus opc-520
47	d1pbaa	Alignment	not modelled	7.6	27	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
48	c4eccB	Alignment	not modelled	7.5	37	PDB header: lyase Chain: B: PDB Molecule: chorismate synthase; PDBTitle: 2.5 angstrom resolution crystal structure of bifidobacterium longum2 chorismate synthase
49	c4pmkA	Alignment	not modelled	7.4	17	PDB header: plant protein Chain: A: PDB Molecule: kiwellin; PDBTitle: crystal structure of kiwellin
50	c5mkbF	Alignment	not modelled	7.4	11	PDB header: sugar binding protein Chain: F: PDB Molecule: male1; PDBTitle: maltodextrin binding protein male1 from l. casei bl23 without ligand
51	c4qpiA	Alignment	not modelled	7.2	23	PDB header: virus Chain: A: PDB Molecule: capsid protein vp1; PDBTitle: crystal structure of hepatitis a virus
52	d1yrxa1	Alignment	not modelled	7.2	25	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: BLUF domain
53	c3mbgC	Alignment	not modelled	7.2	24	PDB header: flavoprotein Chain: C: PDB Molecule: fad-linked sulfhydryl oxidase alr; PDBTitle: crystal structure of human augmenter of liver regeneration (alr)
54	c4avrA	Alignment	not modelled	7.1	33	PDB header: unknown function Chain: A: PDB Molecule: pa4485;

54	c4aviA	Alignment	not modelled	7.1	55	PDBTitle: crystal structure of the hypothetical protein pa4485 from <i>Pseudomonas aeruginosa</i> PDB header: transport protein Chain: A; PDB Molecule: carbohydrate abc transporter substrate-binding protein
55	c4ua8A	Alignment	not modelled	7.0	7	PDBTitle: eur_01830 (maltotriose-binding protein) complexed with maltotriose
56	d1pcaa1	Alignment	not modelled	6.9	38	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
57	d1k0ha	Alignment	not modelled	6.7	63	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: gpFII-like
58	c1q15A	Alignment	not modelled	6.6	20	PDB header: biosynthetic protein Chain: A; PDB Molecule: cara; PDBTitle: carbapenam synthetase
59	d1nsaa2	Alignment	not modelled	6.5	23	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
60	c3k6wA	Alignment	not modelled	6.4	15	PDB header: transport protein Chain: A; PDB Molecule: solute-binding protein ma_0280; PDBTitle: apo and ligand bound structures of moda from the archaeon <i>Methanosarcina acetivorans</i>
61	c3cfxA	Alignment	not modelled	6.3	15	PDB header: transport protein Chain: A; PDB Molecule: upf0100 protein ma_0280; PDBTitle: crystal structure of <i>M. acetivorans</i> periplasmic binding protein2 moda/wtpa with bound tungstate
62	d1fdra1	Alignment	not modelled	6.3	40	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
63	c2xxzA	Alignment	not modelled	6.3	33	PDB header: oxidoreductase Chain: A; PDB Molecule: lysine-specific demethylase 6b; PDBTitle: crystal structure of the human jmj3 jumonji domain
64	d2buna1	Alignment	not modelled	6.2	25	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: BLUF domain
65	c5kwpA	Alignment	not modelled	6.2	44	PDB header: de novo protein Chain: A; PDB Molecule: designed peptide nc_eeh_d2; PDBTitle: nmr solution structure of designed peptide nc_eeh_d2
66	c6fpgH	Alignment	not modelled	6.1	21	PDB header: cell invasion Chain: H; PDB Molecule: ripening-related protein 3; PDBTitle: structure of the ustilago maydis chorismate mutase 1 in complex with a2 zea mays kiwellin
67	c3gitA	Alignment	not modelled	6.0	21	PDB header: transferase Chain: A; PDB Molecule: carbon monoxide dehydrogenase/acetyl-coa synthase subunit PDBTitle: crystal structure of a truncated acetyl-coa synthase
68	c4uzmA	Alignment	not modelled	5.8	78	PDB header: structural protein Chain: A; PDB Molecule: putative membrane protein igaa homolog; PDBTitle: shotgun proteolysis: a practical application
69	d1kwma2	Alignment	not modelled	5.7	23	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
70	c3t69A	Alignment	not modelled	5.6	18	PDB header: transferase Chain: A; PDB Molecule: putative 2-dehydro-3-deoxygalactonokinase; PDBTitle: crystal structure of a putative 2-dehydro-3-deoxygalactonokinase2 protein from <i>Sinorhizobium meliloti</i>
71	c4gdxB	Alignment	not modelled	5.5	19	PDB header: hydrolase Chain: B; PDB Molecule: gamma-glutamyltranspeptidase 1 light chain; PDBTitle: crystal structure of human gamma-glutamyl transpeptidase--glutamate2 complex
72	d1pyta	Alignment	not modelled	5.5	38	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
73	d2boaa2	Alignment	not modelled	5.4	23	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
74	c4ebjB	Alignment	not modelled	5.3	24	PDB header: transferase Chain: B; PDB Molecule: aminoglycoside nucleotidyltransferase; PDBTitle: crystal structure of aminoglycoside 4'-o-adenylyltransferase ant(4)-2 iib, apo
75	d1x0pa1	Alignment	not modelled	5.3	38	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: BLUF domain
76	c4ezhA	Alignment	not modelled	5.3	33	PDB header: oxidoreductase Chain: A; PDB Molecule: lysine-specific demethylase 6b; PDBTitle: the crystal structure of kdm6b bound with h3k27me3 peptide
77	c2hfnJ	Alignment	not modelled	5.2	25	PDB header: electron transport Chain: J; PDB Molecule: synechocystis photoreceptor (slr1694); PDBTitle: crystal structures of the synechocystis photoreceptor slr1694 reveal 2 distinct structural states related to signaling