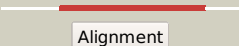



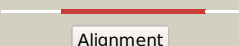





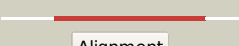












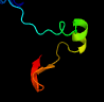
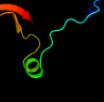



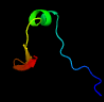
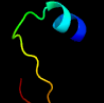
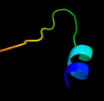


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2873A_(RVBD2873A)_3184673_3184864
 Date Wed Aug 7 12:50:54 BST 2019
 Unique Job ID 47744af9c756f8fb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2odkD_	 Alignment		99.2	10	PDB header: structural genomics, unknown function Chain: D; PDB Molecule: hypothetical protein; PDBTitle: putative prevent-host-death protein from nitrosomonas europaea
2	d2odka1	 Alignment		99.2	10	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
3	c3hryA_	 Alignment		98.9	30	PDB header: antitoxin Chain: A; PDB Molecule: prevent host death protein; PDBTitle: crystal structure of phd in a trigonal space group and partially2 disordered
4	c3hs2H_	 Alignment		98.9	30	PDB header: antitoxin Chain: H; PDB Molecule: prevent host death protein; PDBTitle: crystal structure of phd truncated to residue 57 in an orthorhombic2 space group
5	d2a6qb1	 Alignment		98.3	18	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
6	c3g5oA_	 Alignment		98.3	24	PDB header: toxin/antitoxin Chain: A; PDB Molecule: uncharacterized protein rv2865; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
7	d2a6qa1	 Alignment		98.1	18	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
8	c3oeiB_	 Alignment		97.4	22	PDB header: toxin, protein binding Chain: B; PDB Molecule: relj (antitoxin rv3357); PDBTitle: crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
9	c3d55A_	 Alignment		97.3	22	PDB header: toxin inhibitor Chain: A; PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
10	c3k6qB_	 Alignment		91.1	18	PDB header: ligand binding protein Chain: B; PDB Molecule: putative ligand binding protein; PDBTitle: crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
11	c1skoA_	 Alignment		63.7	19	PDB header: signaling protein Chain: A; PDB Molecule: mitogen-activated protein kinase kinase 1 PDBTitle: mp1-p14 complex

12	d3cpta1	Alignment		52.5	21	Fold: Profilin-like Superfamily: Roadblock/LC7 domain Family: Roadblock/LC7 domain
13	d1v47a1	Alignment		33.3	29	Fold: PUA domain-like Superfamily: PUA domain-like Family: ATP sulfurylase N-terminal domain
14	c1r6xA	Alignment		32.6	19	PDB header: transferase Chain: A: PDB Molecule: atp:sulfate adenyltransferase; PDBTitle: the crystal structure of a truncated form of yeast atp2 sulfurylase, lacking the c-terminal aps kinase-like domain,3 in complex with sulfate
15	d1g8fa1	Alignment		30.1	19	Fold: PUA domain-like Superfamily: PUA domain-like Family: ATP sulfurylase N-terminal domain
16	d2ns0a1	Alignment		26.3	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like
17	c1v47B	Alignment		22.4	32	PDB header: transferase Chain: B: PDB Molecule: atp sulfurylase; PDBTitle: crystal structure of atp sulfurylase from thermophilus hb8 in complex with aps
18	c2qjfB	Alignment		22.1	22	PDB header: transferase Chain: B: PDB Molecule: bifunctional 3'-phosphoadenosine 5'- PDBTitle: crystal structure of atp-sulfurylase domain of human paps2 synthetase 1
19	d1ogda	Alignment		19.4	29	Fold: RbsD-like Superfamily: RbsD-like Family: RbsD-like
20	c3e7nB	Alignment		17.9	13	PDB header: transport protein Chain: B: PDB Molecule: d-ribose high-affinity transport system; PDBTitle: crystal structure of d-ribose high-affinity transport system from2 salmonella typhimurium lt2
21	c3daIA	Alignment	not modelled	17.4	31	PDB header: signaling protein Chain: A: PDB Molecule: atpase family aaa domain-containing protein 2; PDBTitle: crystal structure of the bromodomain of the human atad2
22	c3iprC	Alignment	not modelled	17.2	11	PDB header: transferase Chain: C: PDB Molecule: pts system, iia component; PDBTitle: crystal structure of the enterococcus faecalis gluconate2 specific eiaa phosphotransferase system component
23	c3p13B	Alignment	not modelled	16.2	17	PDB header: isomerase Chain: B: PDB Molecule: d-ribose pyranase; PDBTitle: complex structure of d-ribose pyranase sa240 with d-ribose
24	d1x6va1	Alignment	not modelled	15.9	19	Fold: PUA domain-like Superfamily: PUA domain-like Family: ATP sulfurylase N-terminal domain
25	c2gksB	Alignment	not modelled	15.6	16	PDB header: transferase Chain: B: PDB Molecule: bifunctional sat/aps kinase; PDBTitle: crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
26	d1pdoa	Alignment	not modelled	15.4	6	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: EIIA-man component-like
27	c2wcvI	Alignment	not modelled	14.9	17	PDB header: isomerase Chain: I: PDB Molecule: l-fucose mutarotase; PDBTitle: crystal structure of bacterial fucu
28	d1bifa2	Alignment	not modelled	14.3	7	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
						PDB header: viral protein

29	c4heoA	Alignment	not modelled	14.2	35	Chain: A: PDB Molecule: phosphoprotein; PDBTitle: hendra virus phosphoprotein c terminal domain
30	d1k6ma2	Alignment	not modelled	14.0	7	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
31	c6fmgC	Alignment	not modelled	13.6	6	PDB header: transferase Chain: C: PDB Molecule: pts system mannose-specific transporter subunit iiaB; PDBTitle: structure of the mannose transporter iia domain from streptococcus2 pneumoniae
32	c4a34L	Alignment	not modelled	13.5	17	PDB header: isomerase Chain: L: PDB Molecule: rbsd/fucu transport protein family protein; PDBTitle: crystal structure of the fucose mutarotase in complex with2 l-fucose from streptococcus pneumoniae
33	c3gx1A	Alignment	not modelled	13.2	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin1832 protein; PDBTitle: crystal structure of a domain of lin1832 from listeria innocua
34	c2wcuB	Alignment	not modelled	12.8	22	PDB header: isomerase Chain: B: PDB Molecule: protein fucu homolog; PDBTitle: crystal structure of mammalian fucu
35	c3mvaA	Alignment	not modelled	12.7	17	PDB header: isomerase Chain: A: PDB Molecule: protein fucu; PDBTitle: the crystal structure of fucu from bifidobacterium longum to 1.65a
36	d2ob5a1	Alignment	not modelled	12.1	22	Fold: RbsD-like Superfamily: RbsD-like Family: RbsD-like
37	d2hq7a1	Alignment	not modelled	11.2	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
38	c1vw48	Alignment	not modelled	11.0	14	PDB header: ribosome Chain: 8: PDB Molecule: 54s ribosomal protein l13, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
39	c1g8gB	Alignment	not modelled	10.9	23	PDB header: transferase Chain: B: PDB Molecule: sulfate adenylyltransferase; PDBTitle: atp sulfurylase from s. cerevisiae: the binary product complex with2 aps
40	d1umka1	Alignment	not modelled	10.2	22	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
41	c1gk7A	Alignment	not modelled	10.1	25	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 1a fragment (1a)
42	d2ifqa1	Alignment	not modelled	9.9	11	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
43	c3ve5D	Alignment	not modelled	9.8	28	PDB header: recombination Chain: D: PDB Molecule: recombination protein recr; PDBTitle: structure of recombination mediator protein recr16-196 deletion mutant
44	d1m8pa1	Alignment	not modelled	9.6	27	Fold: PUA domain-like Superfamily: PUA domain-like Family: ATP sulfurylase N-terminal domain
45	c5t3uA	Alignment	not modelled	9.3	3	PDB header: transport protein Chain: A: PDB Molecule: pts system, iia component; PDBTitle: crystal structure of the pts iia protein associated with the fucose2 utilization operon from streptococcus pneumoniae
46	c5uc2C	Alignment	not modelled	9.2	18	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
47	c3cr8C	Alignment	not modelled	9.0	23	PDB header: transferase Chain: C: PDB Molecule: sulfate adenylyltransferase, adenylylsulfate kinase; PDBTitle: hexameric aps kinase from thiobacillus denitrificans
48	c3emxB	Alignment	not modelled	8.9	21	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from aeropyrum pernix
49	d3beda1	Alignment	not modelled	8.5	16	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: EIIA-man component-like
50	c1m8pB	Alignment	not modelled	8.4	27	PDB header: transferase Chain: B: PDB Molecule: sulfate adenylyltransferase; PDBTitle: crystal structure of p. chrysogenum atp sulfurylase in the t-state
51	d1qx4a1	Alignment	not modelled	8.3	17	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
52	c5z2vB	Alignment	not modelled	8.2	17	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pao1
53	d1ndha1	Alignment	not modelled	8.1	17	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
54	c6o5IA	Alignment	not modelled	7.9	33	PDB header: dna binding protein Chain: A: PDB Molecule: ppra; PDBTitle: crystal structure of ppra filament from deinococcus peraridillitoris
						Fold: Reductase/isomerase/elongation factor common domain

55	d2cnda1	Alignment	not modelled	7.6	17	Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
56	c5ldda_	Alignment	not modelled	7.6	30	PDB header: protein transport Chain: A: PDB Molecule: mon1; PDBTitle: crystal structure of the heterodimeric gef mon1-ccz1 in complex with2 ypt7
57	d1y8xb1	Alignment	not modelled	7.2	17	Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Ubiquitin activating enzymes (UBA)
58	d1qfja1	Alignment	not modelled	7.0	13	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
59	c3s4rB_	Alignment	not modelled	6.7	31	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1a/1b fragment with a stabilizing2 mutation
60	c1b9xC_	Alignment	not modelled	6.7	9	PDB header: signaling protein Chain: C: PDB Molecule: protein (phosducin); PDBTitle: structural analysis of phosducin and its phosphorylation-2 regulated interaction with transducin
61	c4x3iA_	Alignment	not modelled	6.7	30	PDB header: signaling protein Chain: A: PDB Molecule: activity-regulated cytoskeleton-associated protein; PDBTitle: the crystal structure of arc n-lobe complexed with camk2a fragment
62	d2fhqa1	Alignment	not modelled	6.5	10	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
63	d1y7ma1	Alignment	not modelled	6.5	25	Fold: L,D-transpeptidase catalytic domain-like Superfamily: L,D-transpeptidase catalytic domain-like Family: L,D-transpeptidase catalytic domain-like
64	c5uxmA_	Alignment	not modelled	6.3	24	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: type ii dah7ps from pseudomonas aeruginosa with trp bound
65	c3lfhF_	Alignment	not modelled	6.2	13	PDB header: transferase Chain: F: PDB Molecule: phosphotransferase system, mannose/fructose-specific PDBTitle: crystal structure of manxa from thermoanaerobacter tengcongensis
66	c3dmbA_	Alignment	not modelled	6.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: putative general stress protein 26 with a pnp-oxidase like PDBTitle: crystal structure of a putative general stress family protein2 (xcc2264) from xanthomonas campestris pv. campestris at 2.30 a3 resolution
67	d1qzma_	Alignment	not modelled	6.2	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
68	c2nbsA_	Alignment	not modelled	6.1	14	PDB header: unknown function Chain: A: PDB Molecule: e_1r26; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for designed2 protein e_1r26
69	c2wtoB_	Alignment	not modelled	6.0	31	PDB header: metal binding protein Chain: B: PDB Molecule: orf131 protein; PDBTitle: crystal structure of apo-form czce from c. metallidurans ch34
70	d1tipa_	Alignment	not modelled	6.0	8	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
71	c4gitA_	Alignment	not modelled	5.9	24	PDB header: hydrolase Chain: A: PDB Molecule: lon protease; PDBTitle: crystal structure of alpha sub-domain of lon protease from2 brevibacillus thermoruber
72	c5o1uB_	Alignment	not modelled	5.7	8	PDB header: hydrolase Chain: B: PDB Molecule: phosphodiesterase; PDBTitle: structure of wildtype t.maritima pde (tm1595) with amp and mn2+
73	d2b7oa1	Alignment	not modelled	5.7	24	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class-II DAHP synthetase
74	c1xjqA_	Alignment	not modelled	5.5	19	PDB header: transferase Chain: A: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: adp complex of human paps synthetase 1
75	c2oeOB_	Alignment	not modelled	5.5	10	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin-3; PDBTitle: crystal structure of mitochondrial thioredoxin 3 from2 saccharomyces cerevisiae
76	c3v62F_	Alignment	not modelled	5.4	50	PDB header: protein binding/dna binding protein Chain: F: PDB Molecule: atp-dependent dna helicase srs2; PDBTitle: structure of the s. cerevisiae srs2 c-terminal domain in complex with2 pcna conjugated to sumo on lysine 164
77	c3v62C_	Alignment	not modelled	5.4	50	PDB header: protein binding/dna binding protein Chain: C: PDB Molecule: atp-dependent dna helicase srs2; PDBTitle: structure of the s. cerevisiae srs2 c-terminal domain in complex with2 pcna conjugated to sumo on lysine 164
78	c3i18A_	Alignment	not modelled	5.3	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo2051 protein; PDBTitle: crystal structure of the pdz domain of the sdrC-like protein (lmo2051)2 from listeria monocytogenes, northeast structural genomics consortium3 target lmr166b
79	c2acmA_	Alignment	not modelled	5.2	14	PDB header: structural protein Chain: A: PDB Molecule: mucin-1; PDBTitle: solution structure of the sea domain of human mucin 1 (mu1)

80	d1t6t1_	Alignment	not modelled	5.2	15	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain
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