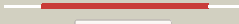



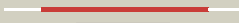


















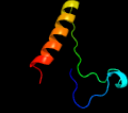



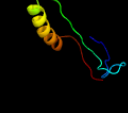





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2393 (-) _2687138_2687983
Date	Mon Aug 5 13:25:55 BST 2019
Unique Job ID	4ea7908f046c9755

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5zt7A_	 Alignment		100.0	26	PDB header: biosynthetic protein Chain: A; PDB Molecule: sirhydrochlorin ferrochelatase; PDBTitle: sirb from bacillus subtilis with co2+
2	c2xvzA_	 Alignment		100.0	18	PDB header: metal binding protein Chain: A; PDB Molecule: chelatase, putative; PDBTitle: cobalt chelatase cbik (periplasmatic) from desulfovrio2 vulgaris hildenborough (co-crystallized with cobalt)
3	d1qgoa_	 Alignment		100.0	19	Fold: Chelatase-like Superfamily: Chelatase Family: Cobalt chelatase CbiK
4	c2jh3C_	 Alignment		100.0	24	PDB header: ribosomal protein Chain: C; PDB Molecule: ribosomal protein s2-related protein; PDBTitle: the crystal structure of dr2241 from deinococcus2 radiodurans at 1.9 a resolution reveals a multi-domain3 protein with structural similarity to chelatases but also4 with two additional novel domains
5	c4ccsA_	 Alignment		100.0	22	PDB header: unknown function Chain: A; PDB Molecule: cbix; PDBTitle: the structure of cbix, the terminal enzyme for biosynthesis2 of siroheme in denitrifying bacteria
6	d2hk6a1	 Alignment		99.9	16	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelatase
7	d1tjna_	 Alignment		99.9	21	Fold: Chelatase-like Superfamily: Chelatase Family: CbiX-like
8	c1tjnA_	 Alignment		99.9	21	PDB header: lyase Chain: A; PDB Molecule: sirhydrochlorin cobaltochelatase; PDBTitle: crystal structure of hypothetical protein af0721 from archaeoglobus2 fulgidus
9	d2hrca1	 Alignment		99.9	12	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelatase
10	c3lyhB_	 Alignment		99.9	32	PDB header: lyase Chain: B; PDB Molecule: cobalamin (vitamin b12) biosynthesis cbix protein; PDBTitle: crystal structure of putative cobalamin (vitamin b12) biosynthesis2 cbix protein (yp_958415.1) from marinobacter aquaeolei vt8 at 1.60 a3 resolution
11	d1lbqa_	 Alignment		99.7	14	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelatase

12	d2p10a1	Alignment		47.6	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Mll9387-like
13	c2qieA	Alignment		47.4	12	PDB header: transferase Chain: A: PDB Molecule: molybdopterin-converting factor subunit 2; PDBTitle: staphylococcus aureus molybdopterin synthase in complex with precursor2 z
14	d1vmia	Alignment		47.3	22	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Phosphotransacetylase
15	c1vmiA	Alignment		47.3	22	PDB header: transferase Chain: A: PDB Molecule: putative phosphate acetyltransferase; PDBTitle: crystal structure of putative phosphate acetyltransferase2 (np_416953.1) from escherichia coli k12 at 2.32 a resolution
16	c1r8jB	Alignment		44.0	15	PDB header: circadian clock protein Chain: B: PDB Molecule: kaia; PDBTitle: crystal structure of circadian clock protein kaia from2 synechococcus elongatus
17	c3rpfB	Alignment		44.0	6	PDB header: transferase Chain: B: PDB Molecule: molybdopterin synthase catalytic subunit; PDBTitle: protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
18	c5e38D	Alignment		40.6	24	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structural basis of mapping the spontaneous mutations with 5-2 flourouracil in uracil phosphoribosyltransferase from mycobacterium3 tuberculosis
19	c2v9cA	Alignment		39.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: fmn-dependent nadh-azoreductase 1; PDBTitle: x-ray crystallographic structure of a pseudomonas2 aeruginosa azoreductase in complex with methyl red.
20	c2hvpA	Alignment		38.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: fmn-dependent nadh-azoreductase; PDBTitle: crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
21	c2p10D	Alignment	not modelled	37.5	17	PDB header: hydrolase Chain: D: PDB Molecule: mll9387 protein; PDBTitle: crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
22	d3beda1	Alignment	not modelled	37.1	20	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: EIIA-man component-like
23	d1v9sa1	Alignment	not modelled	34.8	29	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
24	d1tj1a2	Alignment	not modelled	33.6	15	Fold: TIM beta/alpha-barrel Superfamily: FAD-linked oxidoreductase Family: Proline dehydrogenase domain of bifunctional PutA protein
25	d1o94c	Alignment	not modelled	31.3	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
26	c6fahB	Alignment	not modelled	29.5	10	PDB header: flavoprotein Chain: B: PDB Molecule: caffeyl-coa reductase-etf complex subunit card; PDBTitle: molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
27	c2wp4A	Alignment	not modelled	27.6	16	PDB header: transferase Chain: A: PDB Molecule: molybdopterin-converting factor subunit 2 1; PDBTitle: crystal structure of rv3119 from mycobacterium tuberculosis
28	d1fm0e	Alignment	not modelled	27.0	11	Fold: alpha/beta-Hammerhead Superfamily: Molybdopterin synthase subunit MoaE

						Family: Molybdopterin synthase subunit MoaE
29	d1efpb_	Alignment	not modelled	25.2	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
30	d1r5ja_	Alignment	not modelled	24.1	20	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Phosphotransacetylase
31	d1vkma_	Alignment	not modelled	24.0	13	Fold: Indigoidine synthase A-like Superfamily: Indigoidine synthase A-like Family: Indigoidine synthase A-like
32	d1tcaa_	Alignment	not modelled	24.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
33	c4gijC_	Alignment	not modelled	23.9	19	PDB header: hydrolase Chain: C: PDB Molecule: pseudouridine-5'-phosphate glycosidase; PDBTitle: crystal structure of pseudouridine monophosphate glycosidase complexed2 with sulfate
34	c6jc0D_	Alignment	not modelled	23.3	11	PDB header: transferase Chain: D: PDB Molecule: putative molybdenum cofactor biosynthesis protein; PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
35	c3t4cD_	Alignment	not modelled	23.2	20	PDB header: transferase Chain: D: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase 1; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia ambifaria
36	d1efvb_	Alignment	not modelled	22.2	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
37	c2w9xA_	Alignment	not modelled	21.5	14	PDB header: hydrolase Chain: A: PDB Molecule: putative acetyl xylan esterase; PDBTitle: the active site of a carbohydrate esterase displays2 divergent3 catalytic and non-catalytic binding functions
38	d1o5oa_	Alignment	not modelled	21.1	23	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
39	c5wb4H_	Alignment	not modelled	19.5	15	PDB header: transferase Chain: H: PDB Molecule: n-acetylglucosaminylidiphosphoundecaprenol n-acetyl-beta-d- PDBTitle: crystal structure of the tara wall teichoic acid glycosyltransferase
40	d1nvja_	Alignment	not modelled	19.2	11	Fold: alpha/beta-Hammerhead Superfamily: Molybdopterin synthase subunit MoaE Family: Molybdopterin synthase subunit MoaE
41	c2ehjA_	Alignment	not modelled	19.1	16	PDB header: transferase Chain: A: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of uracil phosphoribosyl transferase
42	d1u7na_	Alignment	not modelled	18.8	26	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: PlsX-like
43	d1s0aa_	Alignment	not modelled	18.6	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
44	c6jzbC_	Alignment	not modelled	18.4	16	PDB header: transferase Chain: C: PDB Molecule: molybdenum cofactor biosynthesis protein e; PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
45	d2nlya1	Alignment	not modelled	17.8	8	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: Divergent polysaccharide deacetylase
46	c5ow0B_	Alignment	not modelled	17.7	14	PDB header: electron transport Chain: B: PDB Molecule: electron transfer flavoprotein, beta subunit; PDBTitle: crystal structure of an electron transfer flavoprotein from2 geobacillus metallireducens
47	d7reqa2	Alignment	not modelled	16.9	12	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
48	d3clsc1	Alignment	not modelled	16.2	12	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
49	d1olta_	Alignment	not modelled	16.2	19	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
50	d1t5ba_	Alignment	not modelled	16.1	12	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
51	c2e55D_	Alignment	not modelled	15.8	20	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of aq2163 protein from aquifex aeolicus
52	c4ap8A_	Alignment	not modelled	15.5	11	PDB header: transferase Chain: A: PDB Molecule: molybdopterin synthase catalytic subunit; PDBTitle: crystal structure of human molybdopterin synthase catalytic subunit2 (mocs2b)
53	d1xg8a_	Alignment	not modelled	15.4	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: YuzD-like
						Fold: PRTase-like

54	d2c4ka1	Alignment	not modelled	15.3	21	Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
55	c2qjwA_	Alignment	not modelled	15.1	17	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein xcc1541; PDBTitle: crystal structure of a putative hydrolase of the alpha/beta2 superfamily (xcc1541) from xanthomonas campestris pv. campestris at3 1.35 a resolution
56	c2duwA_	Alignment	not modelled	15.0	20	PDB header: ligand binding protein Chain: A: PDB Molecule: putative coa-binding protein; PDBTitle: solution structure of putative coa-binding protein of2 klebsiella pneumoniae
57	c2q8uA_	Alignment	not modelled	14.9	10	PDB header: hydrolase Chain: A: PDB Molecule: exonuclease, putative; PDBTitle: crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
58	c4e4rA_	Alignment	not modelled	14.3	15	PDB header: transferase Chain: A: PDB Molecule: phosphate acetyltransferase; PDBTitle: eutd phosphotransacetylase from staphylococcus aureus
59	c3p0rA_	Alignment	not modelled	14.2	21	PDB header: oxidoreductase Chain: A: PDB Molecule: azoreductase; PDBTitle: crystal structure of azoreductase from bacillus anthracis str. sterne
60	c4kq9A_	Alignment	not modelled	14.0	9	PDB header: transport protein Chain: A: PDB Molecule: ribose abc transporter, substrate binding protein; PDBTitle: crystal structure of periplasmic ribose abc transporter from2 conexibacter woesei dsm 14684
61	c2gjfF_	Alignment	not modelled	13.8	21	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative cytoplasmic protein; PDBTitle: crystal structure of a protein of unknown function from salmonella2 typhimurium
62	c3ff1B_	Alignment	not modelled	13.4	17	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: structure of glucose 6-phosphate isomerase from staphylococcus aureus
63	d2d59a1	Alignment	not modelled	13.4	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
64	c1tj2A_	Alignment	not modelled	13.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: bifunctional puta protein; PDBTitle: crystal structure of e. coli puta proline dehydrogenase domain2 (residues 86-669) complexed with acetate
65	c3e9kA_	Alignment	not modelled	13.0	9	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
66	d1q6za1	Alignment	not modelled	12.9	26	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
67	d2ji7a1	Alignment	not modelled	12.9	7	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
68	c1pjaA_	Alignment	not modelled	12.7	22	PDB header: hydrolase Chain: A: PDB Molecule: palmitoyl-protein thioesterase 2 precursor; PDBTitle: the crystal structure of palmitoyl protein thioesterase-2 reveals the2 basis for divergent substrate specificities of the two lysosomal3 thioesterases (ppt1 and ppt2)
69	d1pjaa_	Alignment	not modelled	12.7	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
70	c2omdB_	Alignment	not modelled	12.7	18	PDB header: lyase Chain: B: PDB Molecule: molybdopterin-converting factor subunit 2; PDBTitle: crystal structure of molybdopterin converting factor subunit 22 (aq_2181) from aquifex aeolicus vf5
71	c4ry0A_	Alignment	not modelled	12.6	9	PDB header: transport protein Chain: A: PDB Molecule: probable ribose abc transporter, substrate-binding protein; PDBTitle: crystal structure of ribose transporter solute binding protein2 rhe_pf00037 from rhizobium etli cfn 42, target efi-511357, in complex3 with d-ribose
72	d1pdaa1	Alignment	not modelled	12.4	22	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
73	d1ozha1	Alignment	not modelled	12.1	7	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
74	d2qjva1	Alignment	not modelled	12.0	21	Fold: Phage tail protein-like Superfamily: Phage tail protein-like Family: STM4215-like
75	d1u9ya1	Alignment	not modelled	11.8	37	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
76	c3iprC_	Alignment	not modelled	11.8	16	PDB header: transferase Chain: C: PDB Molecule: pts system, iia component; PDBTitle: crystal structure of the enterococcus faecalis gluconate2 specific eiia phosphotransferase system component
77	c3d02A_	Alignment	not modelled	11.7	15	PDB header: sugar binding protein Chain: A: PDB Molecule: putative lacI-type transcriptional regulator; PDBTitle: crystal structure of periplasmic sugar-binding protein2 (yp_001338366.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 1.30 a resolution
78	c4h1xA_	Alignment	not modelled	11.6	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phosphate-binding protein psts 2; PDBTitle: crystal structure of a phosphate abc transporter, phosphate-binding2 protein (sp_2084) from streptococcus pneumoniae tigr4 at 1.77 a3 resolution

79	c3cvgD	Alignment	not modelled	11.6	11	PDB header: metal binding protein Chain: D: PDB Molecule: putative metal binding protein; PDBTitle: crystal structure of a periplasmic putative metal binding protein
80	c3ff4A	Alignment	not modelled	11.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412
81	d1pdoa	Alignment	not modelled	11.1	15	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: EIIA-man component-like
82	c4ix1B	Alignment	not modelled	11.0	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of hypothetical protein opag_01669 from rhodococcus2 opacus pd630, target 016205
83	d1r8ja2	Alignment	not modelled	10.9	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: N-terminal domain of the circadian clock protein KaiA
84	d2ihta1	Alignment	not modelled	10.7	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
85	d1xtta1	Alignment	not modelled	10.7	5	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
86	c3ga7A	Alignment	not modelled	10.7	13	PDB header: hydrolase Chain: A: PDB Molecule: acetyl esterase; PDBTitle: 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
87	c4k40B	Alignment	not modelled	10.5	8	PDB header: hydrolase Chain: B: PDB Molecule: gdsl-like lipase/acylhydrolase family protein; PDBTitle: peptidoglycan o-acetylerase in action, 0 min
88	c5f2kA	Alignment	not modelled	10.5	14	PDB header: transferase Chain: A: PDB Molecule: fatty acid o-methyltransferase; PDBTitle: crystal structure of mycobacterial fatty acid o-methyltransferase in2 complex with sah and octanoate
89	d1dkua1	Alignment	not modelled	10.3	26	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
90	c3rotA	Alignment	not modelled	10.0	6	PDB header: transport protein Chain: A: PDB Molecule: abc sugar transporter, periplasmic sugar binding protein; PDBTitle: crystal structure of abc sugar transporter (periplasmic sugar binding2 protein) from legionella pneumophila
91	c6fmgC	Alignment	not modelled	9.9	11	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
92	c4k39A	Alignment	not modelled	9.9	10	PDB header: oxidoreductase Chain: A: PDB Molecule: anaerobic sulfatase-maturing enzyme; PDBTitle: native ansmece with bound adomet and cp18cys peptide
93	d2djia1	Alignment	not modelled	9.7	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
94	d1fnda2	Alignment	not modelled	9.7	8	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
95	d1y81a1	Alignment	not modelled	9.7	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
96	c2fqxA	Alignment	not modelled	9.6	11	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein tmpc; PDBTitle: pnra from treponema pallidum complexed with guanosine
97	d1xgsa1	Alignment	not modelled	9.4	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Methionine aminopeptidase, insert domain
98	c4ltyD	Alignment	not modelled	9.3	8	PDB header: hydrolase Chain: D: PDB Molecule: exonuclease subunit sbcd; PDBTitle: crystal structure of e.coli sbcd at 1.8 a resolution
99	c3lv2A	Alignment	not modelled	9.0	21	PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis 7,8-diaminopelargonic2 acid synthase in complex with substrate analog sinefungin