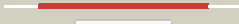



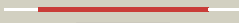














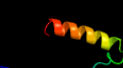




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3609c_foIE_4050156_4050764
 Date Fri Aug 9 18:20:29 BST 2019
 Unique Job ID a31d887668ff2b8b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4uqfB_	 Alignment		100.0	57	PDB header: hydrolase Chain: B; PDB Molecule: gtp cyclohydrolase 1; PDBTitle: crystal structure of listeria monocytogenes gtp cyclohydrolase i
2	d1wpla_	 Alignment		100.0	48	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
3	d1wural	 Alignment		100.0	48	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
4	c1wm9D_	 Alignment		100.0	48	PDB header: hydrolase Chain: D; PDB Molecule: gtp cyclohydrolase i; PDBTitle: structure of gtp cyclohydrolase i from thermus thermophilus hb8
5	c1is7F_	 Alignment		100.0	48	PDB header: hydrolase/protein binding Chain: F; PDB Molecule: gtp cyclohydrolase i; PDBTitle: crystal structure of rat gtpchi/gfrp stimulatory complex
6	d1a8ra_	 Alignment		100.0	37	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
7	c5jyxB_	 Alignment		100.0	22	PDB header: transferase Chain: B; PDB Molecule: archaeosine synthase quef-like; PDBTitle: crystal structure of the covalent thioimide intermediate of the2 archaeosine synthase quef-like
8	c4f8bE_	 Alignment		99.8	19	PDB header: oxidoreductase Chain: E; PDB Molecule: nadph-dependent 7-cyano-7-deazaguanine reductase; PDBTitle: crystal structure of the covalent thioimide intermediate of unimodular2 nitrile reductase quef
9	c3bp1A_	 Alignment		91.4	15	PDB header: oxidoreductase Chain: A; PDB Molecule: nadph-dependent 7-cyano-7-deazaguanine reductase; PDBTitle: crystal structure of putative 7-cyano-7-deazaguanine reductase quef2 from vibrio cholerae o1 biovar eltor
10	c3pg6D_	 Alignment		54.6	19	PDB header: ligase Chain: D; PDB Molecule: e3 ubiquitin-protein ligase dtx3l; PDBTitle: the carboxyl terminal domain of human deltex 3-like
11	c6em34_	 Alignment		28.7	24	PDB header: ribosome Chain: 4; PDB Molecule: ribosomal rna-processing protein 1; PDBTitle: state a architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes

12	d1oz9a_	Alignment		27.6	15	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Predicted metal-dependent hydrolase
13	d1o6ca_	Alignment		27.0	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
14	c3iraA_	Alignment		26.8	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein; PDBTitle: the crystal structure of one domain of the conserved protein from2 methanosarcina mazeri go1
15	d1dpta_	Alignment		25.5	20	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
16	c2xczA_	Alignment		24.5	13	PDB header: immune system Chain: A: PDB Molecule: possible atls1-like light-inducible protein; PDBTitle: crystal structure of macrophage migration inhibitory factor homologue2 from prochlorococcus marinus
17	c3ugsB_	Alignment		23.9	19	PDB header: transferase Chain: B: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
18	d1uiza_	Alignment		23.8	17	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
19	c4g6cA_	Alignment		22.6	16	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase 1; PDBTitle: crystal structure of beta-hexosaminidase 1 from burkholderia2 cenocepacia j2315
20	c2d2rA_	Alignment		21.9	32	PDB header: transferase Chain: A: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
21	c5l0uA_	Alignment	not modelled	21.7	17	PDB header: transferase Chain: A: PDB Molecule: protein o-glucosyltransferase 1; PDBTitle: human poglut1 in complex with egf(+) and udp-phosphono-glucose
22	c5z3gX_	Alignment	not modelled	19.4	25	PDB header: ribosome Chain: X: PDB Molecule: ribosomal rna-processing protein 1; PDBTitle: cryo-em structure of a nucleolar pre-60s ribosome (rpf1-tap)
23	c5enzA_	Alignment	not modelled	18.9	16	PDB header: isomerase Chain: A: PDB Molecule: udp-glcna2-epimerase; PDBTitle: s. aureus mnaa-udp co-structure
24	d2veaa1	Alignment	not modelled	18.5	7	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
25	c1jp3A_	Alignment	not modelled	18.0	48	PDB header: transferase Chain: A: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: structure of e.coli undecaprenyl pyrophosphate synthase
26	c2l9vA_	Alignment	not modelled	17.9	19	PDB header: rna binding protein Chain: A: PDB Molecule: pre-mrna-processing factor 40 homolog a; PDBTitle: nmr structure of the ff domain l24a mutant's folding transition state
27	c6emfA_	Alignment	not modelled	17.0	25	PDB header: ribosome Chain: A: PDB Molecule: g0s4m2; PDBTitle: crystal structure of rrp1 from chaetomium thermophilum in space group2 c2
28	d1vqoj1	Alignment	not modelled	16.8	26	Fold: Ribosomal protein L13 Superfamily: Ribosomal protein L13 Family: Ribosomal protein L13
						PDB header: ribosome

29	c3zf7Y_	Alignment	not modelled	16.6	13	Chain: Y; PDB Molecule: 60s ribosomal protein l24, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
30	c5xk9F_	Alignment	not modelled	15.2	24	PDB header: transferase Chain: F; PDB Molecule: undecaprenyl diphosphate synthase; PDBTitle: crystal structure of isosquilandulyl diphosphate synthase from2 streptomyces sp. strain cnh-189 in complex with gssp and dmapp
31	c5gukA_	Alignment	not modelled	15.1	28	PDB header: biosynthetic protein Chain: A; PDB Molecule: cyclolavandulyl diphosphate synthase; PDBTitle: crystal structure of apo form of cyclolavandulyl diphosphate synthase2 (clds) from streptomyces sp. cl190
32	d1f75a_	Alignment	not modelled	15.0	20	Fold: Undecaprenyl diphosphate synthase Superfamily: Undecaprenyl diphosphate synthase Family: Undecaprenyl diphosphate synthase
33	d2nn6f2	Alignment	not modelled	15.0	29	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
34	c6nuwF_	Alignment	not modelled	14.8	22	PDB header: cell cycle Chain: F; PDB Molecule: inner kinetochore subunit okp1; PDBTitle: yeast ctf19 complex
35	d1j09a2	Alignment	not modelled	13.8	35	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
36	d1ueha_	Alignment	not modelled	13.8	48	Fold: Undecaprenyl diphosphate synthase Superfamily: Undecaprenyl diphosphate synthase Family: Undecaprenyl diphosphate synthase
37	c5hxpA_	Alignment	not modelled	12.7	36	PDB header: transferase Chain: A; PDB Molecule: (2z,6z)-farnesyl diphosphate synthase, chloroplastic; PDBTitle: crystal structure of z,z-farnesyl diphosphate synthase (d71m, e75a and2 h103y mutants) complexed with ipp
38	c5f86A_	Alignment	not modelled	12.3	12	PDB header: transferase/hydrolase Chain: A; PDB Molecule: o-glucosyltransferase rumi; PDBTitle: crystal structure of drosophila poglut1 (rumi) complexed with its2 substrate protein (egf repeat)
39	c2o90A_	Alignment	not modelled	12.3	18	PDB header: lyase Chain: A; PDB Molecule: dihydroneopterin aldolase; PDBTitle: atomic resolution crystal structure of e.coli dihydroneopterin2 aldolase in complex with neopterin
40	c5hg1A_	Alignment	not modelled	12.0	16	PDB header: transferase/transferase inhibitor Chain: A; PDB Molecule: hexokinase-2; PDBTitle: crystal structure of human hexokinase 2 with compd 1, a c-2-substituted2 glucosamine
41	c3f6nA_	Alignment	not modelled	11.9	21	PDB header: viral protein, dna-binding protein Chain: A; PDB Molecule: virion-associated protein; PDBTitle: crystal structure of the virion-associated protein p3 from2 caulimovirus
42	c3k4tB_	Alignment	not modelled	11.6	21	PDB header: viral protein, dna-binding protein Chain: B; PDB Molecule: virion-associated protein; PDBTitle: crystal structure of the virion-associated protein p3 from2 caulimovirus
43	c5ljiA_	Alignment	not modelled	11.6	38	PDB header: oxidoreductase Chain: A; PDB Molecule: flavodoxin; PDBTitle: streptococcus pneumonia tigr4 flavodoxin: structural and biophysical2 characterization of a novel drug target
44	c2lmkA_	Alignment	not modelled	11.5	37	PDB header: signaling protein Chain: A; PDB Molecule: exocrine gland-secreting peptide 1; PDBTitle: solution structure of mouse pheromone esp1
45	c5bzaA_	Alignment	not modelled	11.4	14	PDB header: hydrolase Chain: A; PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of cbsa from thermotoga neapolitana
46	c3aiiA_	Alignment	not modelled	11.4	31	PDB header: ligase Chain: A; PDB Molecule: glutamyl-trna synthetase; PDBTitle: archaeal non-discriminating glutamyl-trna synthetase from2 methanothermobacter thermoautotrophicus
47	d1vhxa_	Alignment	not modelled	11.3	27	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
48	c3tevA_	Alignment	not modelled	11.2	19	PDB header: hydrolase Chain: A; PDB Molecule: glycosyl hydrolase, family 3; PDBTitle: the crystal structure of glycosyl hydrolase from deinococcus2 radiodurans r1
49	c5odcD_	Alignment	not modelled	11.1	18	PDB header: oxidoreductase Chain: D; PDB Molecule: methyl-viologen reducing hydrogenase subunit d; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus at 2.3 a resolution
50	d3eeqa1	Alignment	not modelled	11.0	8	Fold: CobE/GbiG C-terminal domain-like Superfamily: CobE/GbiG C-terminal domain-like Family: CobE/GbiG C-terminal domain-like
51	c5hc7A_	Alignment	not modelled	10.9	28	PDB header: transferase/transferase inhibitor Chain: A; PDB Molecule: prenyltransferase for protein; PDBTitle: crystal structure of lavandulyl diphosphate synthase from lavandula x2 intermedia in complex with s-thioo-isopentenylidiphosphate
52	c3femB_	Alignment	not modelled	10.8	32	PDB header: biosynthetic protein, transferase Chain: B; PDB Molecule: pyridoxine biosynthesis protein snz1; PDBTitle: structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
53	d1b9la_	Alignment	not modelled	10.7	22	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: DHN aldolase/epimerase
54	c4m1aB_	Alignment	not modelled	10.6	10	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: hypothetical protein;

54	c4m1ab_	Alignment	not modelled	10.8	10	PDBTitle: crystal structure of a domain of unknown function (duf1904) from <i>sebadella termitidis</i> atcc 33386 PDB header: hydrolase
55	c6c0dA_	Alignment	not modelled	10.6	18	Chain: A: PDB Molecule: amidase, hydantoinase/carbamoylase family; PDBTitle: crystal structure of an amidase (hydantoinase/carbamoylase family)2 from <i>burkholderia phymatum</i>
56	c3fwtA_	Alignment	not modelled	10.5	10	PDB header: cytokine Chain: A: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: crystal structure of <i>leishmania major</i> mif2
57	c4v19N_	Alignment	not modelled	10.0	20	PDB header: ribosome Chain: N: PDB Molecule: mitoribosomal protein ul13m, mrp13; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
58	c6fsiA_	Alignment	not modelled	9.9	14	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: crystal structure of semiquinone flavodoxin 1 from <i>bacillus cereus</i> 2 (1.32 a resolution)
59	d1u8va1	Alignment	not modelled	9.9	19	Fold: Bromodomain-like Superfamily: Acyl-CoA dehydrogenase C-terminal domain-like Family: Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
60	c6gagB_	Alignment	not modelled	9.7	38	PDB header: electron transport Chain: B: PDB Molecule: flavodoxin; PDBTitle: crystal structure of oxidised flavodoxin 2 from <i>bacillus cereus</i>
61	d1nzja_	Alignment	not modelled	9.7	31	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
62	c5w6yB_	Alignment	not modelled	9.7	12	PDB header: biosynthetic protein, isomerase Chain: B: PDB Molecule: chorismate mutase; PDBTitle: physcomitrella patens chorismate mutase
63	c3lk6A_	Alignment	not modelled	9.5	20	PDB header: hydrolase Chain: A: PDB Molecule: lipoprotein ybbd; PDBTitle: beta-n-hexosaminidase n318d mutant (ybbd_n318d) from <i>bacillus subtilis</i>
64	c3sqlB_	Alignment	not modelled	9.5	18	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 3; PDBTitle: crystal structure of glycoside hydrolase from <i>synechococcus</i>
65	c6hcyA_	Alignment	not modelled	9.2	14	PDB header: membrane protein Chain: A: PDB Molecule: metalloreductase steap4; PDBTitle: human steap4 bound to nadp, fad, heme and fe(iii)-nta.
66	d1j3aa_	Alignment	not modelled	9.2	26	Fold: Ribosomal protein L13 Superfamily: Ribosomal protein L13 Family: Ribosomal protein L13
67	c2zbtB_	Alignment	not modelled	9.2	32	PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from <i>thermus2 thermophilus</i> hb8
68	d1u9da_	Alignment	not modelled	9.1	22	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: VC0714-like
69	c2kduB_	Alignment	not modelled	9.0	67	PDB header: metal binding protein/exocytosis Chain: B: PDB Molecule: protein unc-13 homolog a; PDBTitle: structural basis of the munc13-1/ca2+-calmodulin2 interaction: a novel 1-26 calmodulin binding motif with a3 bipartite binding mode
70	c3gacD_	Alignment	not modelled	8.9	16	PDB header: cytokine Chain: D: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: structure of mif with hpp
71	c3d5bN_	Alignment	not modelled	8.8	29	PDB header: ribosome Chain: N: PDB Molecule: 50s ribosomal protein l13; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
72	d1fima_	Alignment	not modelled	8.8	17	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
73	c4firB_	Alignment	not modelled	8.7	32	PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxal biosynthesis lyase pdxs from <i>pyrococcus</i>
74	d5csma_	Alignment	not modelled	8.7	24	Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Allosteric chorismate mutase
75	d1nbua_	Alignment	not modelled	8.6	22	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: DHN aldolase/epimerase
76	c6gcs8_	Alignment	not modelled	8.5	33	PDB header: oxidoreductase Chain: 8: PDB Molecule: nb8m subunit; PDBTitle: cryo-em structure of respiratory complex i from <i>yarrowia lipolytica</i>
77	d1vmea1	Alignment	not modelled	8.5	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
78	c3b64A_	Alignment	not modelled	8.5	15	PDB header: cytokine Chain: A: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: macrophage migration inhibitory factor (mif) from <i>leishmania major</i>
79	c5t58N_	Alignment	not modelled	8.5	19	PDB header: cell cycle Chain: N: PDB Molecule: klla0c15939p; PDBTitle: structure of the mind complex shows a regulatory focus

						of yeast2 kinetochore assembly
80	c2vfwB_	Alignment	not modelled	8.5	22	PDB header: transferase Chain: B: PDB Molecule: short-chain z-isoprenyl diphosphate synthetase; PDBTitle: rv1086 native
81	d1d8ja_	Alignment	not modelled	8.4	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: The central core domain of TFII E beta
82	c4dh4A_	Alignment	not modelled	8.3	16	PDB header: isomerase Chain: A: PDB Molecule: mif; PDBTitle: macrophage migration inhibitory factor toxoplasma gondii
83	c2nv2U_	Alignment	not modelled	8.2	34	PDB header: lyase/transferase Chain: U: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
84	d1v29a_	Alignment	not modelled	8.2	18	Fold: Nitrile hydratase alpha chain Superfamily: Nitrile hydratase alpha chain Family: Nitrile hydratase alpha chain
85	d1cmca_	Alignment	not modelled	8.2	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Met repressor, MetJ (MetR)
86	c3ngvA_	Alignment	not modelled	8.2	14	PDB header: transport protein Chain: A: PDB Molecule: d7 protein; PDBTitle: crystal structure of anst-d7l1
87	d2o16a3	Alignment	not modelled	8.1	15	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
88	d1lfpa_	Alignment	not modelled	8.1	36	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
89	c3wo8B_	Alignment	not modelled	8.1	19	PDB header: hydrolase Chain: B: PDB Molecule: beta-n-acetylglucosaminidase; PDBTitle: crystal structure of the beta-n-acetylglucosaminidase from thermotoga2 maritima
90	c3cf5G_	Alignment	not modelled	7.9	23	PDB header: ribosome/antibiotic Chain: G: PDB Molecule: 50s ribosomal protein l13; PDBTitle: thiopeptide antibiotic thiostrepton bound to the large ribosomal2 subunit of deinococcus radiodurans
91	d2zjrg1	Alignment	not modelled	7.9	23	Fold: Ribosomal protein L13 Superfamily: Ribosomal protein L13 Family: Ribosomal protein L13
92	c4h3sA_	Alignment	not modelled	7.7	11	PDB header: ligase Chain: A: PDB Molecule: glutamine-trna ligase; PDBTitle: the structure of glutamyl-trna synthetase from saccharomyces2 cerevisiae
93	c1zn1L_	Alignment	not modelled	7.7	33	PDB header: biosynthetic/structural protein/rna Chain: L: PDB Molecule: 30s ribosomal protein s12; PDBTitle: coordinates of rrf fitted into cryo-em map of the 70s post-termination2 complex
94	c2k29A_	Alignment	not modelled	7.6	24	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
95	d2d28c1	Alignment	not modelled	7.6	15	Fold: Alpha-lytic protease prodomain-like Superfamily: EspE N-terminal domain-like Family: GSP II protein E N-terminal domain-like
96	c2yztB_	Alignment	not modelled	7.6	37	PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from2 methanocaldococcus jannaschii
97	c4rn7A_	Alignment	not modelled	7.5	30	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylmuramoyl-l-alanine amidase; PDBTitle: the crystal structure of n-acetylmuramoyl-l-alanine amidase from2 clostridium difficile 630
98	c3uv1B_	Alignment	not modelled	7.5	22	PDB header: allergen Chain: B: PDB Molecule: der f 7 allergen; PDBTitle: crystal structure a major allergen from dust mite
99	c3hlyA_	Alignment	not modelled	7.4	24	PDB header: flavoprotein Chain: A: PDB Molecule: flavodoxin-like domain; PDBTitle: crystal structure of the flavodoxin-like domain from synechococcus sp2 q5mzp6_synp6 protein. northeast structural genomics consortium target3 snr135d.