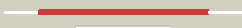



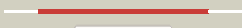





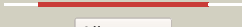



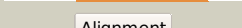

















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2065_(cobH)_2322560_2323186
Date	Mon Aug 5 13:25:17 BST 2019
Unique Job ID	2fb6930fa44eb45b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1f2va_</a>	 Alignment		100.0	55	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Precorrin-8X methylmutase CbiC/CobH <b>Family:</b> Precorrin-8X methylmutase CbiC/CobH
2	<a href="#">c3e7dC_</a>	 Alignment		100.0	57	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> cobh, precorrin-8x methylmutase; <b>PDBTitle:</b> crystal structure of precorrin-8x methyl mutase cbic/cobh from2 brucella melitensis
3	<a href="#">c4au1A_</a>	 Alignment		100.0	51	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> precorrin-8x methylmutase; <b>PDBTitle:</b> crystal structure of cobh (precorrin-8x methyl mutase)2 complexed with c5 desmethyl-hba
4	<a href="#">c2afvB_</a>	 Alignment		100.0	29	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> cobalamin biosynthesis precorrin isomerase; <b>PDBTitle:</b> the crystal structure of putative precorrin isomerase cbic2 in cobalamin biosynthesis
5	<a href="#">d1ou0a_</a>	 Alignment		100.0	34	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Precorrin-8X methylmutase CbiC/CobH <b>Family:</b> Precorrin-8X methylmutase CbiC/CobH
6	<a href="#">d1v9ca_</a>	 Alignment		100.0	36	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Precorrin-8X methylmutase CbiC/CobH <b>Family:</b> Precorrin-8X methylmutase CbiC/CobH
7	<a href="#">d1miob_</a>	 Alignment		88.5	9	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
8	<a href="#">c5kojD_</a>	 Alignment		88.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nitrogenase femo beta subunit protein nifk; <b>PDBTitle:</b> nitrogenase mofep protein in the ids oxidized state
9	<a href="#">d2ji7a1</a>	 Alignment		85.9	22	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
10	<a href="#">d1ovma1</a>	 Alignment		85.9	12	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
11	<a href="#">d1ybha1</a>	 Alignment		83.5	21	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain

12	<a href="#">d1zpdal</a>	Alignment		82.3	13	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
13	<a href="#">d1ozhal</a>	Alignment		82.0	17	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
14	<a href="#">d2djia1</a>	Alignment		79.9	19	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
15	<a href="#">d1pvda1</a>	Alignment		79.8	16	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
16	<a href="#">d1qh8b_</a>	Alignment		78.0	14	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
17	<a href="#">d2ihtal</a>	Alignment		74.6	23	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
18	<a href="#">c3aerB_</a>	Alignment		74.4	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit b; <b>PDBTitle:</b> structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
19	<a href="#">d2ez9a1</a>	Alignment		70.6	18	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
20	<a href="#">d1m1nb_</a>	Alignment		68.6	16	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
21	<a href="#">c2ynmD_</a>	Alignment	not modelled	66.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit b; <b>PDBTitle:</b> structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4 protochlorophyllide a
22	<a href="#">d1t9ba1</a>	Alignment	not modelled	65.7	15	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
23	<a href="#">c3cf4G_</a>	Alignment	not modelled	58.1	4	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G; <b>PDB Molecule:</b> acetyl-coa decarboxylase/synthase epsilon subunit; <b>PDBTitle:</b> structure of the codh component of the m. barkeri acds complex
24	<a href="#">c5n6yE_</a>	Alignment	not modelled	56.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E; <b>PDB Molecule:</b> nitrogenase vanadium-iron protein beta chain; <b>PDBTitle:</b> azotobacter vinelandii vanadium nitrogenase
25	<a href="#">d1q6za1</a>	Alignment	not modelled	49.5	22	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
26	<a href="#">c2rnjA_</a>	Alignment	not modelled	41.4	8	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> response regulator protein vrrar; <b>PDBTitle:</b> nmr structure of the s. aureus vrrar dna binding domain
27	<a href="#">d3bofa1</a>	Alignment	not modelled	39.0	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Methyltetrahydrofolate-utilizing methyltransferases
						<b>Fold:</b> Chelatase-like

28	<a href="#">d1qh8a_</a>	Alignment	not modelled	38.9	21	<b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
29	<a href="#">c4grdA_</a>	Alignment	not modelled	37.8	23	<b>PDB header:</b> lyase, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase catalytic subunit; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
30	<a href="#">c4wzzA_</a>	Alignment	not modelled	37.8	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative sugar abc transporter, substrate-binding protein; <b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein2 (ipr025997) from clostridium phytofermentas (cphy_0583, target efi-3 511148) with bound l-rhamnose
31	<a href="#">d1mioa_</a>	Alignment	not modelled	36.5	27	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
32	<a href="#">d1jcea1</a>	Alignment	not modelled	36.3	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
33	<a href="#">c1zljE_</a>	Alignment	not modelled	34.6	11	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> dormancy survival regulator; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
34	<a href="#">c4rjB_</a>	Alignment	not modelled	34.4	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> acetolactate synthase; <b>PDBTitle:</b> acetolactate synthase from bacillus subtilis bound to thdp - crystal2 form ii
35	<a href="#">c2xdqB_</a>	Alignment	not modelled	34.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit b; <b>PDBTitle:</b> dark operative protochlorophyllide oxidoreductase (chl-chlb)2 complex
36	<a href="#">d1m1na_</a>	Alignment	not modelled	34.1	18	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
37	<a href="#">d1a9xa2</a>	Alignment	not modelled	34.1	16	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
38	<a href="#">c1zpdA_</a>	Alignment	not modelled	32.2	13	<b>PDB header:</b> alcohol fermentation <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate decarboxylase; <b>PDBTitle:</b> pyruvate decarboxylase from zymomonas mobilis
39	<a href="#">c1ozhD_</a>	Alignment	not modelled	31.6	17	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> acetolactate synthase, catabolic; <b>PDBTitle:</b> the crystal structure of klebsiella pneumoniae acetolactate2 synthase with enzyme-bound cofactor and with an unusual3 intermediate.
40	<a href="#">c2krfB_</a>	Alignment	not modelled	30.8	5	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein coma; <b>PDBTitle:</b> nmr solution structure of the dna binding domain of competence protein2 a
41	<a href="#">c2vbgB_</a>	Alignment	not modelled	30.5	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> branched-chain alpha-ketoacid decarboxylase; <b>PDBTitle:</b> the complex structure of the branched-chain keto acid2 decarboxylase (kdca) from lactococcus lactis with 2r-1-3 hydroxyethyl-deazathdp
42	<a href="#">c1powA_</a>	Alignment	not modelled	29.8	20	<b>PDB header:</b> oxidoreductase(oxygen as acceptor) <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate oxidase; <b>PDBTitle:</b> the refined structures of a stabilized mutant and of wild-type2 pyruvate oxidase from lactobacillus plantarum
43	<a href="#">c6o55B_</a>	Alignment	not modelled	28.9	25	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> n5-carboxyaminoimidazole ribonucleotide mutase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 (pure) from legionella pneumophila
44	<a href="#">d1a04a1</a>	Alignment	not modelled	28.3	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
45	<a href="#">c2ji6B_</a>	Alignment	not modelled	28.2	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> oxalyl-coa decarboxylase; <b>PDBTitle:</b> x-ray structure of oxalyl-coa decarboxylase in complex with 3-deaza-2 thdp and oxalyl-coa
46	<a href="#">c1ovmC_</a>	Alignment	not modelled	27.7	11	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> indole-3-pyruvate decarboxylase; <b>PDBTitle:</b> crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
47	<a href="#">c5z2fA_</a>	Alignment	not modelled	27.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> nadph/pda bound dihydrodipicolinate reductase from paenisporosarcina2 sp. tg-14
48	<a href="#">d1p4wa_</a>	Alignment	not modelled	27.0	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
49	<a href="#">c4ww4B_</a>	Alignment	not modelled	26.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ruvb-like 2; <b>PDBTitle:</b> double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
50	<a href="#">c3sftA_</a>	Alignment	not modelled	25.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis response regulator protein-glutamate <b>PDBTitle:</b> crystal structure of thermotoga maritima cheb methylesterase catalytic2 domain
51	<a href="#">d1o4va_</a>	Alignment	not modelled	25.4	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) <b>Family:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)

52	<a href="#">c4ja0A</a>	Alignment	not modelled	25.2	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase; <b>PDBTitle:</b> crystal structure of the invertebrate bi-functional purine2 biosynthesis enzyme paics at 2.8 a resolution
53	<a href="#">c2nxwB</a>	Alignment	not modelled	25.2	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phenyl-3-pyruvate decarboxylase; <b>PDBTitle:</b> crystal structure of phenylpyruvate decarboxylase of azospirillum2 brasillense
54	<a href="#">c3pdiB</a>	Alignment	not modelled	24.3	24	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> nitrogenase mofe cofactor biosynthesis protein nifn; <b>PDBTitle:</b> precursor bound nifen
55	<a href="#">c3ib7A</a>	Alignment	not modelled	23.9	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> icc protein; <b>PDBTitle:</b> crystal structure of full length rv0805
56	<a href="#">c5tenH</a>	Alignment	not modelled	23.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> structure of 4-hydroxy-tetrahydrodipicolinate reductase from vibrio2 vulnificus with 2,5 furan dicarboxylic and nadh with intact3 polyhistidine tag
57	<a href="#">d1l3la1</a>	Alignment	not modelled	23.6	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
58	<a href="#">c2fw9A</a>	Alignment	not modelled	23.0	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> n5-carboxyaminoimidazole ribonucleotide mutase; <b>PDBTitle:</b> structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
59	<a href="#">c2vbif</a>	Alignment	not modelled	22.8	19	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> pyruvate decarboxylase; <b>PDBTitle:</b> holostructure of pyruvate decarboxylase from acetobacter pasteurianus
60	<a href="#">c2w93A</a>	Alignment	not modelled	22.8	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate decarboxylase isozyme 1; <b>PDBTitle:</b> crystal structure of the saccharomyces cerevisiae pyruvate2 decarboxylase variant e477q in complex with the surrogate pyruvamide
61	<a href="#">d1u11a</a>	Alignment	not modelled	22.7	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) <b>Family:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
62	<a href="#">c2h31A</a>	Alignment	not modelled	21.5	20	<b>PDB header:</b> ligase, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> multifunctional protein ade2; <b>PDBTitle:</b> crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
63	<a href="#">d2fsja2</a>	Alignment	not modelled	20.6	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Ta0583-like
64	<a href="#">c2yvqA</a>	Alignment	not modelled	20.6	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carbamoyl-phosphate synthase; <b>PDBTitle:</b> crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
65	<a href="#">c6gcsK</a>	Alignment	not modelled	20.6	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> psst subunit (nukm); <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
66	<a href="#">c2panF</a>	Alignment	not modelled	20.4	17	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> glyoxylate carboligase; <b>PDBTitle:</b> crystal structure of e. coli glyoxylate carboligase
67	<a href="#">d1d7ya1</a>	Alignment	not modelled	20.3	20	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
68	<a href="#">d2hk6a1</a>	Alignment	not modelled	20.1	20	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> Chelatase <b>Family:</b> Ferrochelatase
69	<a href="#">c3rggD</a>	Alignment	not modelled	19.6	19	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, pure protein; <b>PDBTitle:</b> crystal structure of treponema denticola pure bound to air
70	<a href="#">c1yi1A</a>	Alignment	not modelled	18.9	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetolactate synthase; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, tribenuron methyl
71	<a href="#">c2pgnA</a>	Alignment	not modelled	18.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclohexane-1,2-dione hydrolase (cdh); <b>PDBTitle:</b> the crystal structure of fad and thdp-dependent cyclohexane-1,2-dione2 hydrolase in complex with cyclohexane-1,2-dione
72	<a href="#">c1upaC</a>	Alignment	not modelled	18.1	23	<b>PDB header:</b> synthase <b>Chain:</b> C: <b>PDB Molecule:</b> carboxyethylarginine synthase; <b>PDBTitle:</b> carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
73	<a href="#">c2djiA</a>	Alignment	not modelled	18.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate oxidase; <b>PDBTitle:</b> crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
74	<a href="#">c4e21B</a>	Alignment	not modelled	18.1	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase (decarboxylating); <b>PDBTitle:</b> the crystal structure of 6-phosphogluconate dehydrogenase from2 geobacter metallireducens
						<b>Fold:</b> Methylesterase CheB, C-terminal domain

75	<a href="#">d1chda_</a>	Alignment	not modelled	18.0	21	<b>Superfamily:</b> Methylesterase CheB, C-terminal domain <b>Family:</b> Methylesterase CheB, C-terminal domain
76	<a href="#">c3sztB_</a>	Alignment	not modelled	17.8	6	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> quorum-sensing control repressor; <b>PDBTitle:</b> quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
77	<a href="#">c3sajB_</a>	Alignment	not modelled	17.8	12	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate receptor 1; <b>PDBTitle:</b> crystal structure of glutamate receptor glua1 amino terminal domain
78	<a href="#">c2zfa_</a>	Alignment	not modelled	17.8	23	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> replicase polyprotein 1ab; <b>PDBTitle:</b> nmr conformer closest to the mean coordinates of the domain 513-651 of2 the sars-cov nonstructural protein nsp3
79	<a href="#">c4oaqa_</a>	Alignment	not modelled	16.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> r-specific carbonyl reductase; <b>PDBTitle:</b> crystal structure of the r-specific carbonyl reductase from candida2 parapsilosis atcc 7330
80	<a href="#">c6humK_</a>	Alignment	not modelled	16.7	24	<b>PDB header:</b> proton transport <b>Chain:</b> K: <b>PDB Molecule:</b> nad(p)h-quinone oxidoreductase subunit k; <b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus
81	<a href="#">c3q3ha_</a>	Alignment	not modelled	16.4	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hmw1c-like glycosyltransferase; <b>PDBTitle:</b> crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
82	<a href="#">c4b4kK_</a>	Alignment	not modelled	16.3	21	<b>PDB header:</b> isomerase <b>Chain:</b> K: <b>PDB Molecule:</b> n5-carboxyaminoimidazole ribonucleotide mutase; <b>PDBTitle:</b> crystal structure of bacillus anthracis pure <b>Fold:</b> Flavodoxin-like
83	<a href="#">d1xmpa_</a>	Alignment	not modelled	16.0	21	<b>Superfamily:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) <b>Family:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
84	<a href="#">d2hrca1</a>	Alignment	not modelled	15.5	15	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> Chelatase <b>Family:</b> Ferrochelatase
85	<a href="#">c6ioxB_</a>	Alignment	not modelled	15.2	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphotransacetylase; <b>PDBTitle:</b> crystal structure of porphyromonas gingivalis phosphotransacetylase in2 complex with acetyl-coa
86	<a href="#">d1zfa1</a>	Alignment	not modelled	14.7	26	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
87	<a href="#">c5yw2D_</a>	Alignment	not modelled	14.6	16	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> adenine phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of adenine phosphoribosyltransferase from2 francisella tularensis.
88	<a href="#">d1qcza_</a>	Alignment	not modelled	14.3	25	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) <b>Family:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
89	<a href="#">c4cpdA_</a>	Alignment	not modelled	14.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> alcohol dehydrogenase tadh from thermus sp. atn1
90	<a href="#">c2kqvA_</a>	Alignment	not modelled	13.9	16	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> non-structural protein 3; <b>PDBTitle:</b> sars coronavirus-unique domain (sud): three-domain molecular2 architecture in solution and rna binding. i: structure of the sud-m3 domain of sud-mc
91	<a href="#">c4ifuA_</a>	Alignment	not modelled	13.5	6	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein sdia; <b>PDBTitle:</b> crystal structure of escherichia coli sdia in the space group c2
92	<a href="#">d1k4ia_</a>	Alignment	not modelled	13.5	16	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
93	<a href="#">d1zcha1</a>	Alignment	not modelled	13.4	28	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
94	<a href="#">d1vm6a3</a>	Alignment	not modelled	13.4	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
95	<a href="#">c3lp6D_</a>	Alignment	not modelled	13.4	23	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase catalytic subunit; <b>PDBTitle:</b> crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
96	<a href="#">c4ffjA_</a>	Alignment	not modelled	13.3	33	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin biosynthesis protein ribba; <b>PDBTitle:</b> the crystal structure of spdhpbs from s.pneumoniae
97	<a href="#">c1m6vE_</a>	Alignment	not modelled	13.3	17	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> carbamoyl phosphate synthetase large chain; <b>PDBTitle:</b> crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
98	<a href="#">d3bzka5</a>	Alignment	not modelled	13.2	26	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Tex RuvX-like domain-like
99	<a href="#">d1snna_</a>	Alignment	not modelled	13.2	33	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB