




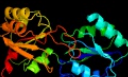
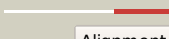

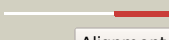















Phyre2

Email: mdejesus@rockefeller.edu
 Description: RVBD0511_(hemD)_602822_604519
 Date: Fri Jul 26 01:50:06 BST 2019
 Unique Job ID: 6e2fcab47eaa2bf6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1pjtB_	 Alignment		100.0	29	PDB header: transferase/oxidoreductase/lyase Chain: B: PDB Molecule: siroheme synthase; PDBTitle: the structure of the ser128ala point-mutant variant of cysg, the2 multifunctional methyltransferase/dehydrogenase/ferrochelatae for3 siroheme synthesis
2	d1s4da_	 Alignment		100.0	28	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
3	c2yboA_	 Alignment		100.0	31	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: the x-ray structure of the sam-dependent uroporphyrinogen2 iii methyltransferase nire from pseudomonas aeruginosa in3 complex with sah
4	c4es6A_	 Alignment		100.0	23	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: crystal structure of hemd (pa5259) from pseudomonas aeruginosa (pao1)2 at 2.22 a resolution
5	c3re1B_	 Alignment		100.0	22	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen-iii synthetase; PDBTitle: crystal structure of uroporphyrinogen iii synthase from pseudomonas syringae pv. tomato dc3000
6	d1pjqa2	 Alignment		100.0	29	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
7	d1wd7a_	 Alignment		100.0	20	Fold: HemD-like Superfamily: HemD-like Family: HemD-like
8	d1jr2a_	 Alignment		100.0	21	Fold: HemD-like Superfamily: HemD-like Family: HemD-like
9	c1jr2A_	 Alignment		100.0	21	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: structure of uroporphyrinogen iii synthase
10	d1cbfa_	 Alignment		100.0	26	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
11	c1cbfA_	 Alignment		100.0	26	PDB header: methyltransferase Chain: A: PDB Molecule: cobalt-precorrin-4 transmethyase; PDBTitle: the x-ray structure of a cobalamin biosynthetic enzyme, cobalt2 precorrin-4 methyltransferase, cbif

12	c3d8tB_	Alignment		100.0	21	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: thermus thermophilus uroporphyrinogen iii synthase
13	c4e16A_	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: precorrin-4 c(11)-methyltransferase; PDBTitle: precorrin-4 c(11)-methyltransferase from clostridium difficile
14	c3mw8A_	Alignment		100.0	23	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: crystal structure of an uroporphyrinogen-iii synthase (sama_3255) from2 shewanella amazonensis sb2b at 1.65 a resolution
15	c3kwpA_	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: predicted methyltransferase; PDBTitle: crystal structure of putative methyltransferase from lactobacillus2 brevis
16	d1ve2a1	Alignment		100.0	26	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
17	c3ndcB_	Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: precorrin-4 c(11)-methyltransferase; PDBTitle: crystal structure of precorrin-4 c11-methyltransferase from2 rhodobacter capsulatus
18	c5n0sA_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: peptide n-methyltransferase; PDBTitle: crystal structure of opha-delta6 mutant y98a in complex with sam
19	c5hw4C_	Alignment		100.0	25	PDB header: transferase Chain: C: PDB Molecule: ribosomal rna small subunit methyltransferase i; PDBTitle: crystal structure of escherichia coli 16s rrna methyltransferase rsmi2 in complex with adomet
20	d1va0a1	Alignment		100.0	29	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
21	c2zvba_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A: PDB Molecule: precorrin-3 c17-methyltransferase; PDBTitle: crystal structure of tt0207 from thermus thermophilus hb8
22	d1wyza1	Alignment	not modelled	100.0	12	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
23	d1wdea_	Alignment	not modelled	100.0	20	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
24	c3nutC_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: C: PDB Molecule: precorrin-3 methylase; PDBTitle: crystal structure of the methyltransferase cobj
25	d2deka1	Alignment	not modelled	100.0	22	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
26	d1vhva_	Alignment	not modelled	100.0	16	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
27	c2e0kA_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: precorrin-2 c20-methyltransferase; PDBTitle: crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
28	c3i4tA_	Alignment	not modelled	100.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: diphthine synthase; PDBTitle: crystal structure of putative diphthine synthase from entamoeba2 histolytica
29	c2ghuA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: precorrin-2 methyltransferase;

29	c2qbuA	Alignment	not modelled	100.0	20	PDBTitle: crystal structure of methanothermobacter thermautotrophicus cbil PDB header: transferase Chain: A: PDB Molecule: putative cobalamin synthesis related protein; PDBTitle: crystal structure of putative cobalamin synthesis related protein2 (cobf) from corynebacterium diphtheriae PDB header: transferase Chain: B: PDB Molecule: precorrin-6a synthase/cobf protein; PDBTitle: crystal structure of precorrin-6a synthase from rhodobacter capsulatus
30	c2nnpA	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: uroporphyrinogen iii cosynthase (hemd); PDBTitle: crystal structure of uroporphyrinogen-iii synthetase from helicobacter2 pylori 26695 PDB header: transferase Chain: B: PDB Molecule: cobalamin biosynthesis precorrin-6y methylase (cbie); PDBTitle: crystal structure of cobalamin biosynthesis precorrin-6y methylase2 (cbie) from archaeoglobus fulgidus
31	c3nd1B	Alignment	not modelled	100.0	15	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
32	c3p9zA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: D: PDB Molecule: tetrapyrrole methylase family protein; PDBTitle: the structure of a tetrapyrrole methylase family protein domain from2 chlorobium tepidum t1s
33	c2bb3B	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: the crystal structure of a methyltransferase domain from bacteroides2 thetaiotaomicron vpi
34	d2bb3a1	Alignment	not modelled	100.0	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: 457aa long hypothetical protein; PDBTitle: crystal structure of ph0766 from pyrococcus horikoshii ot3
35	c3hh1D	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
36	c3fq6A	Alignment	not modelled	99.2	13	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 pseudomonas aeruginosa complexed with adenine, k+ and zn2+ cations
37	c2csuB	Alignment	not modelled	97.5	11	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
38	c3d64A	Alignment	not modelled	95.5	16	PDB header: membrane protein Chain: G: PDB Molecule: ktr system potassium uptake protein a,ktr system potassium PDBTitle: crystal structure of inactive conformation of ktrab k+ transporter
39	c6f3oC	Alignment	not modelled	95.4	15	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha- subunit from2 aeropyrum pernix
40	c6aphA	Alignment	not modelled	95.4	16	PDB header: ligase Chain: A: PDB Molecule: alpha subunit of acetyl-coenzyme a synthetase PDBTitle: ca. korarchaeum cryptofilum dinucleotide forming acetyl- coenzyme a2 synthetase 1 (apo form)
41	c5butG	Alignment	not modelled	95.2	13	PDB header: ligase Chain: B: PDB Molecule: phosphopantothenate--cysteine ligase; PDBTitle: crystal structure of the c-terminal ctp-binding domain of a2 phosphopantothenylylcysteine decarboxylase/phosphopantothenate-3 cysteine ligase with bound ctp from mycobacterium smegmatis
42	c2yxbA	Alignment	not modelled	95.2	18	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: a thermophilic s-adenosylhomocysteine hydrolase
43	c4yajA	Alignment	not modelled	95.1	12	PDB header: hydrolase Chain: A: PDB Molecule: s-adenosyl-l-homocysteine hydrolase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 naegleria fowleri with bound nad and adenosine
44	c4qj1B	Alignment	not modelled	95.0	24	PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s- 2 adenosylhomocysteine hydrolase
45	c3x2fA	Alignment	not modelled	94.2	13	PDB header: isomerase Chain: D: PDB Molecule: 2-hydroxyisobutyryl-coa mutase small subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
46	c5v96A	Alignment	not modelled	94.2	15	PDB header: hydrolase Chain: D: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
47	c1d4fD	Alignment	not modelled	93.8	16	Fold: Ribokinase-like Superfamily: CoaB-like Family: CoaB-like
48	c4r3uD	Alignment	not modelled	93.6	17	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
49	c3n58D	Alignment	not modelled	93.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
50	d1u7za	Alignment	not modelled	93.3	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family
51	d1m1nb	Alignment	not modelled	93.1	10	
52	c2rirA	Alignment	not modelled	93.1	14	

53	c3k9cA_	Alignment	not modelled	93.0	11	protein; PDBTitle: crystal structure of laci transcriptional regulator from rhodococcus2 species.
54	c3pdiB_	Alignment	not modelled	92.9	14	PDB header: protein binding Chain: B: PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nifn; PDBTitle: precursor bound nifen
55	c4njmA_	Alignment	not modelled	92.4	10	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase, putative; PDBTitle: crystal structure of phosphoglycerate bound 3-phosphoglycerate2 dehydrogenase in entamoeba histolytica
56	d7rega2	Alignment	not modelled	92.1	19	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
57	d1ccwa_	Alignment	not modelled	91.9	13	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
58	c3brqA_	Alignment	not modelled	91.8	10	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator ascg; PDBTitle: crystal structure of the escherichia coli transcriptional repressor2 ascg
59	c3dhyC_	Alignment	not modelled	91.5	19	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and 3 inhibitors
60	c4rk1F_	Alignment	not modelled	91.2	9	PDB header: transcription regulator Chain: F: PDB Molecule: ribose transcriptional regulator; PDBTitle: crystal structure of laci family transcriptional regulator from2 enterococcus faecium, target efi-512930, with bound ribose
61	c3clkB_	Alignment	not modelled	91.1	10	PDB header: transcription regulator Chain: B: PDB Molecule: transcription regulator; PDBTitle: crystal structure of a transcription regulator from lactobacillus2 plantarum
62	c5intB_	Alignment	not modelled	90.8	21	PDB header: ligase Chain: B: PDB Molecule: phosphopantothenate--cysteine ligase; PDBTitle: crystal structure of the c-terminal domain of coenzyme a biosynthesis2 bifunctional protein coabc
63	c3d8uA_	Alignment	not modelled	90.4	9	PDB header: transcription regulator Chain: A: PDB Molecule: purr transcriptional regulator; PDBTitle: the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
64	d1xu9a_	Alignment	not modelled	90.1	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
65	c3qk7C_	Alignment	not modelled	89.8	8	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
66	d1zema1	Alignment	not modelled	89.2	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
67	c5bt9B_	Alignment	not modelled	88.9	23	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of folm alternative dihydrofolate reductase 1 from2 brucella canis complexed with nadp
68	c5tchG_	Alignment	not modelled	88.9	16	PDB header: lyase Chain: G: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
69	c3gvpB_	Alignment	not modelled	88.9	17	PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sah-like domain of human adenosylhomocysteinase 3
70	c3oneA_	Alignment	not modelled	88.9	16	PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
71	c4n7bA_	Alignment	not modelled	88.8	9	PDB header: oxidoreductase Chain: A: PDB Molecule: lytb; PDBTitle: structure of the e-1-hydroxy-2-methyl-but-2-enyl-4-diphosphate2 reductase from plasmodium falciparum
72	c3q2oB_	Alignment	not modelled	88.2	9	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
73	d1fmfa_	Alignment	not modelled	88.1	12	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
74	d1ys7a2	Alignment	not modelled	88.0	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
75	c3ek2D_	Alignment	not modelled	87.6	11	PDB header: oxidoreductase Chain: D: PDB Molecule: enoyl-(acyl-carrier-protein) reductase (nadh); PDBTitle: crystal structure of enoyl-(acyl carrier protein) reductase from2 burkholderia pseudomallei 1719b
76	c4nbtA_	Alignment	not modelled	87.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of fabg from acholeplasma laidlawii
77	c3h5oB_	Alignment	not modelled	87.3	10	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator gntr; PDBTitle: the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
78	d2o8ra3	Alignment	not modelled	87.0	18	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease

						Family: Polyphosphate kinase C-terminal domain
79	c5v1tA_	Alignment	not modelled	86.7	15	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam; PDBTitle: crystal structure of streptococcus suis suib bound to precursor2 peptide suia
80	c3ke8A_	Alignment	not modelled	86.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; PDBTitle: crystal structure of isph:hmbpp-complex
81	c3ksmA_	Alignment	not modelled	86.4	10	PDB header: transport protein Chain: A: PDB Molecule: abc-type sugar transport system, periplasmic component; PDBTitle: crystal structure of abc-type sugar transport system, periplasmic2 component from haehella chejuensis
82	c4zgwB_	Alignment	not modelled	86.2	24	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase; PDBTitle: short-chain dehydrogenase/reductase from serratia marcescens bcrc2 10948
83	c4weoD_	Alignment	not modelled	86.2	18	PDB header: oxidoreductase Chain: D: PDB Molecule: putative acetoin(diacetyl) reductase; PDBTitle: crystal structure of a putative acetoin(diacetyl) reductase2 burkholderia cenocepacia
84	c6hyhA_	Alignment	not modelled	85.7	10	PDB header: sugar binding protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of msmeg_1712 from mycobacterium smegmatis in2 complex with beta-d-fucofuranose
85	c5hm8C_	Alignment	not modelled	85.5	16	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: 2.85 angstrom crystal structure of s-adenosylhomocysteinase from2 cryptosporidium parvum in complex with adenosine and nad.
86	c1v8bA_	Alignment	not modelled	85.5	14	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of a hydrolase
87	c4g2nA_	Alignment	not modelled	85.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase, nad-binding; PDBTitle: crystal structure of putative d-isomer specific 2-hydroxyacid2 dehydrogenase, nad-binding from polaromonas sp. js6 66
88	c4imrA_	Alignment	not modelled	85.3	29	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of 3-oxoacyl (acyl-carrier-protein) reductase2 (target efi-506442) from agrobacterium tumefaciens c58 with nadp3 bound
89	c5unlA_	Alignment	not modelled	85.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-ketoacyl-acp reductase; PDBTitle: crystal structure of a d-beta-hydroxybutyrate dehydrogenase from2 burkholderia multivorans
90	c3k4hA_	Alignment	not modelled	85.0	9	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator laci from2 bacillus cereus subsp. cytotoxis nvh 391-98
91	c3g85A_	Alignment	not modelled	85.0	9	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (laci family); PDBTitle: crystal structure of laci family transcription regulator from2 clostridium acetobutylicum
92	c2qq5A_	Alignment	not modelled	84.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase/reductase sdr family member 1; PDBTitle: crystal structure of human sdr family member 1
93	c4yt2A_	Alignment	not modelled	84.7	21	PDB header: metal binding protein Chain: A: PDB Molecule: h(2)-forming methylenetetrahydromethanopterin PDBTitle: hmd ii from methanocaldococcus jannaschii
94	d1mvoa_	Alignment	not modelled	84.7	9	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
95	c5jydA_	Alignment	not modelled	84.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a putative short chain dehydrogenase from2 burkholderia cenocepacia
96	c6huxA_	Alignment	not modelled	84.4	21	PDB header: oxidoreductase Chain: A: PDB Molecule: h(2)-forming methylenetetrahydromethanopterin PDBTitle: hmdii from methanocaldococcus jannaschii reconstituted with fe-2 guanylylpyridinol (fegg) cofactor and co-crystallized with methenyl-3 tetrahydromethanopterin at 2.5 a resolution
97	d1ja9a_	Alignment	not modelled	84.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
98	c4b79B_	Alignment	not modelled	83.6	19	PDB header: oxidoreductase Chain: B: PDB Molecule: probable short-chain dehydrogenase; PDBTitle: the aeropath project and pseudomonas aeruginosa high-throughput2 crystallographic studies for assessment of potential targets in3 early stage drug discovery.
99	c3c3kA_	Alignment	not modelled	83.6	11	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: crystal structure of an uncharacterized protein from actinobacillus2 succinogenes
100	d1e01a_	Alignment	not modelled	83.5	22	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
101	c2o8rA_	Alignment	not modelled	83.0	19	PDB header: transferase Chain: A: PDB Molecule: polyphosphate kinase; PDBTitle: crystal structure of polyphosphate kinase from porphyromonas2 gingivalis
						PDB header: oxidoreductase Chain: B: PDB Molecule: putative short-chain

102	c5k9zB_	Alignment	not modelled	83.0	18	dehydrogenase/reductase; PDBTitle: crystal structure of putative short-chain dehydrogenase/reductase from <i>Burkholderia xenovorans</i> lb400
103	c5fydB_	Alignment	not modelled	82.9	26	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase PDBTitle: structural and biochemical insights into 7beta-2 hydroxysteroid dehydrogenase stereoselectivity
104	c3crnA_	Alignment	not modelled	82.9	18	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver domain protein, chey-like; PDBTitle: crystal structure of response regulator receiver domain protein (chey-2 like) from <i>Methanospirillum hungatei</i> jf-1
105	d1geea_	Alignment	not modelled	82.7	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
106	c3rfqC_	Alignment	not modelled	82.7	22	PDB header: biosynthetic protein Chain: C: PDB Molecule: pterin-4-alpha-carbinolamine dehydratase moab2; PDBTitle: crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from <i>Mycobacterium marinum</i>
107	c2mswA_	Alignment	not modelled	82.6	9	PDB header: transferase Chain: A: PDB Molecule: response regulator/sensor histidine kinase; PDBTitle: ligand-induced folding of a receiver domain
108	d2d1ya1	Alignment	not modelled	82.5	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
109	d1qh8b_	Alignment	not modelled	82.4	11	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
110	d1krwa_	Alignment	not modelled	82.4	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
111	c5th5C_	Alignment	not modelled	82.3	8	PDB header: lyase Chain: C: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from <i>Bacillus subtilis</i> with 6-carboxypterin-2 5'-deoxyadenosyl ester bound
112	c4h2dB_	Alignment	not modelled	82.2	10	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-dependent diflavin oxidoreductase 1; PDBTitle: crystal structure of ndor1
113	d2ayxa1	Alignment	not modelled	82.0	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
114	c3fbtB_	Alignment	not modelled	81.8	11	PDB header: oxidoreductase, lyase Chain: B: PDB Molecule: chorismate mutase and shikimate 5-dehydrogenase fusion PDBTitle: crystal structure of a chorismate mutase/shikimate 5-dehydrogenase2 fusion protein from <i>Clostridium acetobutylicum</i>
115	d1hxha_	Alignment	not modelled	81.8	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
116	d1fmca_	Alignment	not modelled	81.7	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
117	c6c8vA_	Alignment	not modelled	81.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme pqq synthesis protein e; PDBTitle: x-ray structure of pqqe from <i>Methylobacterium extorquens</i>
118	c4fn4A_	Alignment	not modelled	81.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: short-chain nad(h)-dependent dehydrogenase/reductase from <i>Sulfolobus2 acidocaldarius</i>
119	c2hrzA_	Alignment	not modelled	81.5	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: the crystal structure of the nucleoside-diphosphate-sugar epimerase2 from <i>Agrobacterium tumefaciens</i>
120	c3gv0A_	Alignment	not modelled	81.3	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of laci family transcription regulator from <i>Agrobacterium tumefaciens</i>