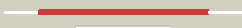



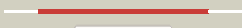










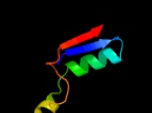





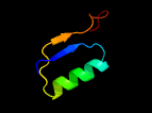
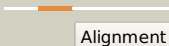

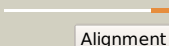
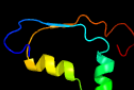
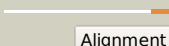

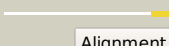

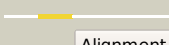
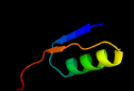
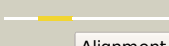

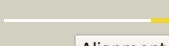

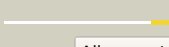


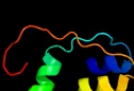
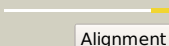

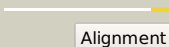
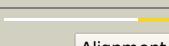
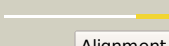
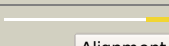
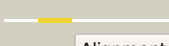



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3261_(fbiA)_3640540_3641535
 Date Thu Aug 8 16:20:46 BST 2019
 Unique Job ID aebf9a21f4242782

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ffea1	 Alignment		100.0	28	Fold: CofD-like Superfamily: CofD-like Family: CofD-like
2	c2ppvA	 Alignment		100.0	20	PDB header: transferase Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein belonging to the upf0052 (se_0549) from2 staphylococcus epidermidis atcc 12228 at 2.00 a resolution
3	d2hzba1	 Alignment		100.0	23	Fold: CofD-like Superfamily: CofD-like Family: CofD-like
4	c2q7xA	 Alignment		100.0	21	PDB header: transferase Chain: A; PDB Molecule: upf0052 protein sp_1565; PDBTitle: crystal structure of a putative phospho transferase (sp_1565) from2 streptococcus pneumoniae tigr4 at 2.00 a resolution
5	c2p0yA	 Alignment		100.0	22	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein lp_0780; PDBTitle: crystal structure of q88yi3_lacpl from lactobacillus plantarum.2 northeast structural genomics consortium target lpr6
6	c3n8kG	 Alignment		86.4	26	PDB header: lyase Chain: G; PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: type ii dehydroquinase from mycobacterium tuberculosis complexed with2 citrazinic acid
7	c1nhqA	 Alignment		85.5	32	PDB header: oxidoreductase (h2o2(a)) Chain: A; PDB Molecule: nadh peroxidase; PDBTitle: crystallographic analyses of nadh peroxidase cys42ala and cys42ser2 mutants: active site structure, mechanistic implications, and an3 unusual environment of arg303
8	c5er0D	 Alignment		84.1	19	PDB header: oxidoreductase Chain: D; PDB Molecule: nadh oxidase; PDBTitle: water-forming nadh oxidase from lactobacillus brevis (lbnox)
9	c3oc4A	 Alignment		83.6	8	PDB header: oxidoreductase Chain: A; PDB Molecule: oxidoreductase, pyridine nucleotide-disulfide family; PDBTitle: crystal structure of a pyridine nucleotide-disulfide family2 oxidoreductase from the enterococcus faecalis v583
10	c2uyqF	 Alignment		83.0	22	PDB header: lyase Chain: F; PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: crystallographic structure of the typeii 3-dehydroquinase from thermus2 thermophilus
11	d1fmta2	 Alignment		82.9	21	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase

12	c2cduB	 Alignment		81.7	19	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh oxidase; PDBTitle: the crystal structure of water-forming nad(p)h oxidase from2 lactobacillus sanfranciscensis
13	d1uqra	 Alignment		81.4	30	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinatase Family: Type II 3-dehydroquinatase
14	d1h05a	 Alignment		80.7	26	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinatase Family: Type II 3-dehydroquinatase
15	d1gqoa	 Alignment		79.3	26	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinatase Family: Type II 3-dehydroquinatase
16	d1s3ia2	 Alignment		78.5	17	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
17	c5tueB	 Alignment		77.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: tetracycline destructase tet(50); PDBTitle: crystal structure of tetracycline destructase tet(50)
18	c3lwzC	 Alignment		76.8	28	PDB header: lyase Chain: C: PDB Molecule: 3-dehydroquinatase; PDBTitle: 1.65 angstrom resolution crystal structure of type ii 3-dehydroquinatase2 dehydratase (aroq) from yersinia pestis
19	c3kipU	 Alignment		76.3	24	PDB header: lyase Chain: U: PDB Molecule: 3-dehydroquinase, type ii; PDBTitle: crystal structure of type-ii 3-dehydroquinase from c. albicans
20	d2c4va1	 Alignment		76.2	27	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinatase Family: Type II 3-dehydroquinatase
21	c4l8lA	 Alignment	not modelled	75.9	30	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinatase 1; PDBTitle: crystal structure of the type ii dehydroquinase from pseudomonas2 aeruginosa
22	d2bw0a2	 Alignment	not modelled	75.7	20	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
23	c6cv6L	 Alignment	not modelled	75.1	30	PDB header: lyase Chain: L: PDB Molecule: 3-dehydroquinatase; PDBTitle: crystal structure of 3-dehydroquinatase dehydratase, type ii, from2 burkholderia phymatum stm815
24	d1pjqa2	 Alignment	not modelled	75.0	19	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
25	c2nnpA	 Alignment	not modelled	74.7	19	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
26	c2e0kA	 Alignment	not modelled	74.5	22	PDB header: transferase Chain: A: PDB Molecule: precorrin-2 c20-methyltransferase; PDBTitle: crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
27	c5n1tA	 Alignment	not modelled	72.8	30	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin-binding subunit of sulfide dehydrogenase; PDBTitle: crystal structure of complex between flavocytochrome c and copper2 chaperone copc from t. paradoxus
28	c3cndB	 Alignment	not modelled	72.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridine nucleotide-disulfide oxidoreductase, class i;

28	c3c9ub	Alignment	not modelled	72.7	13	PDBTitle: pyridine nucleotide complexes with bacillus anthracis coenzyme a-2 disulfide reductase: a structural analysis of dual nad(p)h3 specificity
29	c3tqqa	Alignment	not modelled	71.7	20	PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: structure of the methionyl-trna formyltransferase (fmt) from coxiella2 burnetii
30	c4rhcH	Alignment	not modelled	71.5	25	PDB header: lyase Chain: H: PDB Molecule: 3-dehydroquininate dehydratase; PDBTitle: crystal structure of 3-dehydroquininate dehydratase from acinetobacter2 baumannii at 2.68 a resolution
31	d1gtza	Alignment	not modelled	71.3	30	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquininate dehydratase Family: Type II 3-dehydroquininate dehydratase
32	c1yrwA	Alignment	not modelled	71.0	32	PDB header: transferase Chain: A: PDB Molecule: protein arna; PDBTitle: crystal structure of e.coli arna transformylase domain
33	d2blna2	Alignment	not modelled	70.8	32	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
34	c3ezxA	Alignment	not modelled	70.8	13	PDB header: transferase Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
35	c3tqrA	Alignment	not modelled	70.3	21	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
36	c2ywjA	Alignment	not modelled	69.8	22	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
37	c3cwcB	Alignment	not modelled	69.2	20	PDB header: transferase Chain: B: PDB Molecule: putative glycerate kinase 2; PDBTitle: crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
38	c4lxuB	Alignment	not modelled	68.9	8	PDB header: transferase Chain: B: PDB Molecule: wlard, a sugar 3n-formyl transferase; PDBTitle: dtdp-fuc3n and 5-n-formyl-thf
39	c5jwcA	Alignment	not modelled	68.7	32	PDB header: membrane protein Chain: A: PDB Molecule: nadh dehydrogenase, putative; PDBTitle: structure of ndh2 from plasmodium falciparum in complex with ryl-552
40	c1s3iA	Alignment	not modelled	66.1	18	PDB header: hydrolase, oxidoreductase Chain: A: PDB Molecule: 10-formyltetrahydrofolate dehydrogenase; PDBTitle: crystal structure of the n terminal hydrolase domain of 10-2 formyltetrahydrofolate dehydrogenase
41	c3rfoA	Alignment	not modelled	65.2	17	PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: crystal structure of methionyl-trna formyltransferase from bacillus2 anthracis
42	c4dgkA	Alignment	not modelled	64.2	38	PDB header: oxidoreductase Chain: A: PDB Molecule: phytoene dehydrogenase; PDBTitle: crystal structure of phytoene desaturase crti from pantoea ananatis
43	c3u80A	Alignment	not modelled	64.0	14	PDB header: unknown function Chain: A: PDB Molecule: 3-dehydroquininate dehydratase, type ii; PDBTitle: 1.60 angstrom resolution crystal structure of a 3-dehydroquininate2 dehydratase-like protein from bifidobacterium longum
44	c1fcdB	Alignment	not modelled	63.9	40	PDB header: electron transport(flavocytochrome) Chain: B: PDB Molecule: flavocytochrome c sulfide dehydrogenase (flavin- PDBTitle: the structure of flavocytochrome c sulfide dehydrogenase2 from a purple phototrophic bacterium chromatium vinosum at3 2.5 angstroms resolution
45	d1p3da1	Alignment	not modelled	62.9	21	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
46	d1fcda1	Alignment	not modelled	62.2	40	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
47	c2e4gB	Alignment	not modelled	61.8	19	PDB header: biosynthetic protein, flavoprotein Chain: B: PDB Molecule: tryptophan halogenase; PDBTitle: rebh with bound l-trp
48	c1fmtA	Alignment	not modelled	60.8	23	PDB header: formyltransferase Chain: A: PDB Molecule: methionyl-trna fmet formyltransferase; PDBTitle: methionyl-trnafmet formyltransferase from escherichia coli
49	d2nv0a1	Alignment	not modelled	60.0	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
50	c1zx9A	Alignment	not modelled	59.1	21	PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: crystal structure of tn501 mera
51	d1hyha1	Alignment	not modelled	58.8	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
52	d1ep3b2	Alignment	not modelled	58.1	19	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Dihydroorotate dehydrogenase B, PyrK subunit
53	d1nx4a2	Alignment	not modelled	57.5	20	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked

53	d1qx9d2	Alignment	not modelled	57.5	29	domain Family: Reductases
54	d1ndha2	Alignment	not modelled	57.4	29	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
55	c5m5jA	Alignment	not modelled	57.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: thioredoxin reductase from giardia duodenalis
56	c3uteB	Alignment	not modelled	57.0	24	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of aspergillus fumigatus udp galactopyranose mutase2 sulfate complex
57	c5twcA	Alignment	not modelled	57.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: oxidoreductase iruo in the oxidized form
58	c6fqbE	Alignment	not modelled	56.4	7	PDB header: ligase Chain: E: PDB Molecule: coobyric acid synthase; PDBTitle: murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
59	c3ef6A	Alignment	not modelled	56.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: toluene 1,2-dioxygenase system ferredoxin--nad(+) PDBTitle: crystal structure of toluene 2,3-dioxygenase reductase
60	d1txga2	Alignment	not modelled	56.2	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
61	c3zeuE	Alignment	not modelled	55.9	27	PDB header: hydrolase Chain: E: PDB Molecule: probable trna threonylcarbamoyladenosine biosynthesis PDBTitle: structure of a salmonella typhimurium ygjd-yeaz heterodimer bound to2 atpgammas
62	d1qfja2	Alignment	not modelled	55.4	19	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
63	c3kd9B	Alignment	not modelled	55.3	32	PDB header: oxidoreductase Chain: B: PDB Molecule: coenzyme a disulfide reductase; PDBTitle: crystal structure of pyridine nucleotide disulfide oxidoreductase from2 pyrococcus horikoshii
64	c3lrxC	Alignment	not modelled	55.3	10	PDB header: oxidoreductase Chain: C: PDB Molecule: putative hydrogenase; PDBTitle: crystal structure of the c-terminal domain (residues 78-226) of pf19112 hydrogenase from pyrococcus furiosus, northeast structural genomics3 consortium target pfr246a
65	c3en0A	Alignment	not modelled	55.0	8	PDB header: hydrolase Chain: A: PDB Molecule: cyanophycinase; PDBTitle: the structure of cyanophycinase
66	c3i4tA	Alignment	not modelled	54.8	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: diphthine synthase; PDBTitle: crystal structure of putative diphthine synthase from entamoeba2 histolytica
67	c3l4eA	Alignment	not modelled	54.7	26	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized peptidase lmo0363; PDBTitle: 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
68	c3icrA	Alignment	not modelled	54.5	24	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a-disulfide reductase; PDBTitle: crystal structure of oxidized bacillus anthracis coadr-rhd
69	c2bcpA	Alignment	not modelled	54.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh oxidase; PDBTitle: structural analysis of streptococcus pyogenes nadh oxidase: c44s nox2 with azide
70	c2eq8E	Alignment	not modelled	53.9	31	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
71	c5uaoA	Alignment	not modelled	53.9	34	PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophane-5-halogenase; PDBTitle: crystal structure of mibh, a lathipeptide tryptophan 5-halogenase
72	c6bz5B	Alignment	not modelled	53.8	21	PDB header: oxidoreductase Chain: B: PDB Molecule: salicylate hydroxylase; PDBTitle: structure and mechanism of salicylate hydroxylase from pseudomonas2 putida g7
73	c2weuD	Alignment	not modelled	53.4	32	PDB header: antifungal protein Chain: D: PDB Molecule: tryptophan 5-halogenase; PDBTitle: crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
74	c3iwaA	Alignment	not modelled	53.2	23	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: crystal structure of a fad-dependent pyridine nucleotide-disulphide2 oxidoreductase from desulfovibrio vulgaris
75	c5uaiA	Alignment	not modelled	53.2	21	PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: crystal structure of methionyl-trna formyltransferase from pseudomonas2 aeruginosa
76	c3kpgA	Alignment	not modelled	52.8	29	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfide-quinone reductase, putative; PDBTitle: crystal structure of sulfide:quinone oxidoreductase from2 acidithiobacillus ferrooxidans in complex with decylubiquinone
77	d1q7ra	Alignment	not modelled	52.7	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
78	c2bb3B	Alignment	not modelled	52.5	16	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
79	c3q0iA_	Alignment	not modelled	52.4	23	PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: methionyl-trna formyltransferase from vibrio cholerae
80	c3l4bG_	Alignment	not modelled	51.8	17	PDB header: transport protein Chain: G: PDB Molecule: trka k+ channel protien tm1088b; PDBTitle: crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
81	c2gr2A_	Alignment	not modelled	51.8	35	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin reductase; PDBTitle: crystal structure of ferredoxin reductase, bpha4 (oxidized form)
82	c3allA_	Alignment	not modelled	51.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; PDBTitle: crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a
83	c6du7C_	Alignment	not modelled	51.6	17	PDB header: oxidoreductase Chain: C: PDB Molecule: glutathione reductase; PDBTitle: glutathione reductase from streptococcus pneumoniae
84	c6ib5B_	Alignment	not modelled	51.2	23	PDB header: flavoprotein Chain: B: PDB Molecule: tryptophan 6-halogenase; PDBTitle: mutant of flavin-dependent tryptophan halogenase thal with altered2 regioselectivity (thal-rebh5)
85	c5cjjA_	Alignment	not modelled	51.1	19	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: the crystal structure of phosphoribosylglycinamide formyltransferase2 from campylobacter jejuni subsp. jejuni nctc 11168
86	c2ivoC_	Alignment	not modelled	51.0	23	PDB header: hydrolase Chain: C: PDB Molecule: up1; PDBTitle: structure of up1 protein
87	d1to6a_	Alignment	not modelled	51.0	16	Fold: Glycerate kinase I Superfamily: Glycerate kinase I Family: Glycerate kinase I
88	c3hyxC_	Alignment	not modelled	50.7	37	PDB header: oxidoreductase Chain: C: PDB Molecule: sulfide-quinone reductase; PDBTitle: 3-d x-ray structure of the sulfide:quinone oxidoreductase from aquifex2 aeolicus in complex with aurachin c
89	d1gvha3	Alignment	not modelled	50.4	27	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Flavo-hemoglobin, C-terminal domain
90	c5eowA_	Alignment	not modelled	50.4	32	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-hydroxynicotinate 3-monooxygenase; PDBTitle: crystal structure of 6-hydroxynicotinic acid 3-monooxygenase from2 pseudomonas putida kt2440
91	d1cbfa_	Alignment	not modelled	50.1	17	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
92	c1cbfA_	Alignment	not modelled	50.1	17	PDB header: methyltransferase Chain: A: PDB Molecule: cobalt-precorrin-4 transmethylase; PDBTitle: the x-ray structure of a cobalamin biosynthetic enzyme, cobalt2 precorrin-4 methyltransferase, cbif
93	c3kcgA_	Alignment	not modelled	49.9	18	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum
94	c3fg2P_	Alignment	not modelled	49.9	23	PDB header: oxidoreductase Chain: P: PDB Molecule: putative rubredoxin reductase; PDBTitle: crystal structure of ferredoxin reductase for the cyp199a2 system from2 rhodospseudomonas palustris
95	d2piaa2	Alignment	not modelled	49.8	33	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Aromatic dioxygenase reductase-like
96	d1fdra2	Alignment	not modelled	49.3	19	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
97	c6mp5B_	Alignment	not modelled	49.1	33	PDB header: membrane protein, oxidoreductase Chain: B: PDB Molecule: sulfide:quinone oxidoreductase, mitochondrial; PDBTitle: crystal structure of native human sulfide:quinone oxidoreductase
98	c2ywrA_	Alignment	not modelled	48.8	18	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of gar transformylase from aquifex aeolicus
99	c1s6yA_	Alignment	not modelled	48.7	21	PDB header: hydrolase Chain: A: PDB Molecule: 6-phospho-beta-glucosidase; PDBTitle: 2.3a crystal structure of phospho-beta-glucosidase
100	d1umka2	Alignment	not modelled	48.7	29	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
101	c3kijA_	Alignment	not modelled	48.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: nad(fad)-dependent dehydrogenase, nirb-family (n-terminal) PDBTitle: crystal structure of nadh:rubredoxin oxidoreductase from clostridium2 acetobutylicum
102	c3ktnA_	Alignment	not modelled	48.2	15	PDB header: transferase Chain: A: PDB Molecule: carbohydrate kinase, pfkb family; PDBTitle: crystal structure of a putative 2-keto-3-deoxygluconate2

						kinase from enterococcus faecalis
103	d2ivda1	Alignment	not modelled	48.1	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
104	c3ntaA	Alignment	not modelled	48.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
105	c1yqzA	Alignment	not modelled	47.7	30	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a disulfide reductase; PDBTitle: structure of coenzyme a-disulfide reductase from2 staphylococcus aureus refined at 1.54 angstrom resolution
106	c4gudA	Alignment	not modelled	47.6	14	PDB header: transferase Chain: A: PDB Molecule: imidazole glycerol phosphate synthase subunit hish; PDBTitle: crystal structure of amidotransferase hish from vibrio cholerae
107	d1ddga2	Alignment	not modelled	47.2	35	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: NADPH-cytochrome p450 reductase-like
108	d2cnda2	Alignment	not modelled	46.1	19	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
109	c4g6gB	Alignment	not modelled	45.9	25	PDB header: oxidoreductase Chain: B: PDB Molecule: rotenone-insensitive nadh-ubiquinone oxidoreductase, PDBTitle: crystal structure of ndh with trt
110	c2xdoC	Alignment	not modelled	45.7	28	PDB header: oxidoreductase Chain: C: PDB Molecule: tetx2 protein; PDBTitle: structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
111	d1nhpa1	Alignment	not modelled	45.5	30	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
112	d1j20a1	Alignment	not modelled	45.1	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
113	c2ardA	Alignment	not modelled	45.0	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: tryptophan halogenase prna; PDBTitle: the structure of tryptophan 7-halogenase (prna) suggests a mechanism2 for regioselective chlorination
114	c6gehA	Alignment	not modelled	44.9	18	PDB header: metal transport Chain: A: PDB Molecule: fad-binding 9, siderophore-interacting domain protein; PDBTitle: structure and reactivity of a siderophore-interacting protein from the2 marine bacterium shewanella reveals unanticipated functional3 versatility.
115	c2rgjA	Alignment	not modelled	44.8	24	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin-containing monooxygenase; PDBTitle: crystal structure of flavin-containing monooxygenase phzs
116	c2yboA	Alignment	not modelled	44.0	24	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
117	d1a8pa2	Alignment	not modelled	43.7	29	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
118	c2zvba	Alignment	not modelled	43.7	20	PDB header: transferase Chain: A: PDB Molecule: precorrin-3 c17-methyltransferase; PDBTitle: crystal structure of tt0207 from thermus thermophilus hb8
119	c3ihmB	Alignment	not modelled	43.7	21	PDB header: oxidoreductase Chain: B: PDB Molecule: styrene monooxygenase a; PDBTitle: structure of the oxygenase component of a pseudomonas styrene2 monooxygenase
120	d1ka9h	Alignment	not modelled	43.5	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)