Phyre^2

Email	l.a.kelley@imperial.ac.uk
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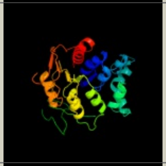
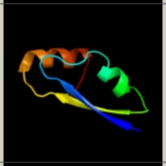
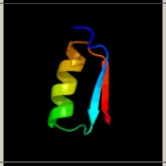
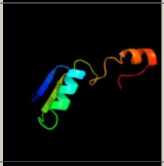
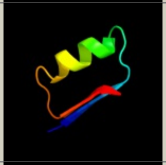
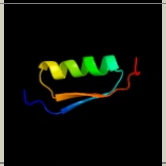
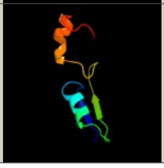
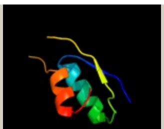
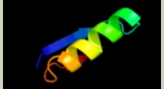
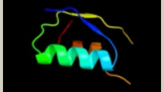
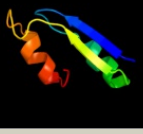
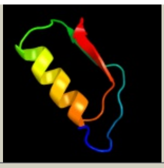
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2hzba1	Alignment		100.0	30	**Fold:**CofD-like **Superfamily:**CofD-like **Family:**CofD-like
2	c2ppvA_	Alignment		100.0	34	**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	c2q7xA_	Alignment		100.0	29	**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
4	d2ffea1	Alignment		100.0	16	**Fold:**CofD-like **Superfamily:**CofD-like **Family:**CofD-like
5	c2p0yA_	Alignment		100.0	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein lp_0780; **PDBTitle:** crystal structure of q88yi3_lacpl from lactobacillus2 plantarum. northeast structural genomics consortium target3 lpr6
6	c3dzcA_	Alignment		88.7	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.35 angstrom resolution structure of wecb (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
7	d1p3da1	Alignment		86.8	21	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
8	c3kljA_	Alignment		86.7	13	**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
9	c3kpgA_	Alignment		86.5	33	**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
10	d2afba1	Alignment		84.9	24	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
11	c1yqzA_	Alignment		84.4	15	**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

12	d2blna2	Alignment		82.9	23	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
13	d1fcda1	Alignment		82.2	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
14	c1yrwA_	Alignment		82.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of e.coli arna transformylase domain
15	c1kyqC_	Alignment		81.5	24	**PDB header:**oxidoreductase, lyase **Chain:** C: **PDB Molecule:**siroheme biosynthesis protein met8; **PDBTitle:** met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis.
16	c1fcdB_	Alignment		81.2	19	**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
17	c3dfzB_	Alignment		81.1	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**precorrin-2 dehydrogenase; **PDBTitle:** sirc, precorrin-2 dehydrogenase
18	c2e4gB_	Alignment		80.9	26	**PDB header:**biosynthetic protein, flavoprotein **Chain:** B: **PDB Molecule:**tryptophan halogenase; **PDBTitle:** rebh with bound l-trp
19	d1fmta2	Alignment		80.9	21	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
20	d1f0ka_	Alignment		80.7	24	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG
21	c3n8kG_	Alignment	not modelled	79.2	25	**PDB header:**lyase **Chain:** G: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** type ii dehydroquinase from mycobacterium tuberculosis complexed with2 citrazinic acid
22	d1sb8a_	Alignment	not modelled	78.9	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
23	c3ia7A_	Alignment	not modelled	77.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calg4; **PDBTitle:** crystal structure of calg4, the calicheamicin glycosyltransferase
24	c2weuD_	Alignment	not modelled	77.0	27	**PDB header:**antifungal protein **Chain:** D: **PDB Molecule:**tryptophan 5-halogenase; **PDBTitle:** crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
25	d1kyqa1	Alignment	not modelled	76.9	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
26	c3allA_	Alignment	not modelled	76.6	19	**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
27	d1pj5a2	Alignment	not modelled	75.7	11	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
28	c3kd9B_	Alignment	not modelled	75.4	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**coenzyme a disulfide reductase; **PDBTitle:** crystal structure of pyridine nucleotide disulfide oxidoreductase from2 pyrococcus horikoshii

29	c2vdcl_	Alignment		75.4	16	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**glutamate synthase [nadph] small chain; **PDBTitle:** the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
30	d1q1ra2	Alignment	not modelled	75.4	25	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
31	c1pjtB_	Alignment	not modelled	74.5	27	**PDB header:**transferase/oxidoreductase/lyase **Chain:** B: **PDB Molecule:**siroheme synthase; **PDBTitle:** the structure of the ser128ala point-mutant variant of cysg,2 the multifunctional3 methyltransferase/dehydrogenase/ferrochelatase for4 siroheme synthesis
32	d1ndha2	Alignment	not modelled	74.1	20	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
33	c3ps9A_	Alignment	not modelled	74.1	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna 5-methylaminomethyl-2-thiouridine biosynthesis **PDBTitle:** crystal structure of mnmc from e. coli
34	c1ps9A_	Alignment	not modelled	73.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,4-dienoyl-coa reductase; **PDBTitle:** the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
35	c2uygF_	Alignment	not modelled	73.6	26	**PDB header:**lyase **Chain:** F: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystallogaphic structure of the typeii 3-dehydroquinase2 from thermus thermophilus
36	d1cjca2	Alignment	not modelled	73.2	17	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
37	c3icrA_	Alignment	not modelled	73.2	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coenzyme a-disulfide reductase; **PDBTitle:** crystal structure of oxidized bacillus anthracis coadr-rhd
38	c3i3lA_	Alignment	not modelled	72.7	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkylhalidase cmls; **PDBTitle:** crystal structure of cmls, a flavin-dependent halogenase
39	c3lxdA_	Alignment	not modelled	72.6	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad-dependent pyridine nucleotide-disulphide **PDBTitle:** crystal structure of ferredoxin reductase arr from novosphingobium2 aromaticivorans
40	d1vdca2	Alignment	not modelled	71.9	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
41	d1b5qa1	Alignment	not modelled	71.7	28	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
42	c1h83A_	Alignment	not modelled	71.1	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**polyamine oxidase; **PDBTitle:** structure of polyamine oxidase in complex with2 1,8-diaminooctane
43	d1h05a_	Alignment	not modelled	70.8	25	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
44	c1c0iA_	Alignment	not modelled	70.5	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-amino acid oxidase; **PDBTitle:** crystal structure of d-amino acid oxidase in complex with2 two anthranylate molecules
45	d1trba2	Alignment	not modelled	70.3	24	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
46	c1k97A_	Alignment	not modelled	70.1	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
47	d2dw4a2	Alignment	not modelled	70.1	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
48	d1fl2a2	Alignment	not modelled	69.9	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
49	d1fdra2	Alignment	not modelled	69.3	20	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
50	c3qj4A_	Alignment	not modelled	69.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**renalase; **PDBTitle:** crystal structure of human renalase (isoform 1)
51	c3ntaA_	Alignment	not modelled	69.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad-dependent pyridine nucleotide-disulphide **PDBTitle:** structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
52	d1uqra_	Alignment	not modelled	69.1	39	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
						Fold: Nucleotide-binding domain

53	d1c0pa1	Alignment	not modelled	68.8	24	**Superfamily:**Nucleotide-binding domain **Family:**D-aminoacid oxidase, N-terminal domain
54	c3g5rA_	Alignment	not modelled	68.8	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylenetetrahydrofolate--trna-(uracil-5-)- **PDBTitle:** crystal structure of thermus thermophilus trmfo in complex with2 tetrahydrofolate
55	c2v3aA_	Alignment	not modelled	68.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin reductase; **PDBTitle:** crystal structure of rubredoxin reductase from pseudomonas2 aeruginosa.
56	c3hyxC_	Alignment	not modelled	68.1	33	**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
57	d1gqoa_	Alignment	not modelled	67.7	25	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
58	c2cmgA_	Alignment	not modelled	67.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**spermidine synthase; **PDBTitle:** crystal structure of spermidine synthase from helicobacter2 pylori
59	d1d7ya2	Alignment	not modelled	67.2	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
60	d1ep3b2	Alignment	not modelled	66.9	21	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Dihydroorotate dehydrogenase B, PyrK subunit
61	d1k92a1	Alignment	not modelled	66.8	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
62	c3djeA_	Alignment	not modelled	66.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fructosyl amine: oxygen oxidoreductase; **PDBTitle:** crystal structure of the deglycating enzyme fructosamine2 oxidase from aspergillus fumigatus (amadoriase ii) in3 complex with fsa
63	c2ardA_	Alignment	not modelled	66.3	29	**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
64	c3ab1B_	Alignment	not modelled	66.0	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin--nadp reductase; **PDBTitle:** crystal structure of ferredoxin nadp+ oxidoreductase
65	c3ihmB_	Alignment	not modelled	65.3	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**styrene monooxygenase a; **PDBTitle:** structure of the oxygenase component of a pseudomonas styrene2 monooxygenase
66	d1onfa2	Alignment	not modelled	65.3	12	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
67	c3k5iB_	Alignment	not modelled	65.3	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosyl-aminoimidazole carboxylase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-3 aminoimadazole ribonucleotide
68	c3k30B_	Alignment	not modelled	65.1	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**histamine dehydrogenase; **PDBTitle:** histamine dehydrogenase from nocardiodes simplex
69	c2gr2A_	Alignment	not modelled	65.1	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin reductase; **PDBTitle:** crystal structure of ferredoxin reductase, bpha4 (oxidized form)
70	c3iwaA_	Alignment	not modelled	65.0	13	**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
71	c3lrxC_	Alignment	not modelled	64.7	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative hydrogenase; **PDBTitle:** crystal structure of the c-terminal domain (residues 78-226)2 of pf1911 hydrogenase from pyrococcus furiosus, northeast3 structural genomics consortium target pfr246a
72	c1djnB_	Alignment	not modelled	64.5	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**trimethylamine dehydrogenase; **PDBTitle:** structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
73	c2b9yA_	Alignment	not modelled	64.4	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aminooxidase; **PDBTitle:** crystal structure of cla-producing fatty acid isomerase2 from p. acnes
74	c3ef6A_	Alignment	not modelled	64.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**toluene 1,2-dioxygenase system ferredoxin--nad(+) **PDBTitle:** crystal structure of toluene 2,3-dioxygenase reductase
75	c1q1wA_	Alignment	not modelled	64.1	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putidaredoxin reductase; **PDBTitle:** crystal structure of putidaredoxin reductase from2 pseudomonas putida
76	d1qx4a2	Alignment	not modelled	63.9	20	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
77	d1seza1	Alignment	not modelled	63.9	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain

						Family:FAD-linked reductases, N-terminal domain
78	c2ivoC_	Alignment	not modelled	63.6	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**up1; **PDBTitle:** structure of up1 protein
79	c3cwcB_	Alignment	not modelled	63.6	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative glycerate kinase 2; **PDBTitle:** crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
80	c1xdiA_	Alignment	not modelled	63.4	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**rv3303c-lpda; **PDBTitle:** crystal structure of lpda (rv3303c) from mycobacterium tuberculosis
81	c3lwzC_	Alignment	not modelled	63.3	33	**PDB header:**lyase **Chain:** C: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.65 angstrom resolution crystal structure of type ii 3-2 dehydroquinate dehydratase (aroq) from yersinia pestis
82	c1fmtA_	Alignment	not modelled	63.2	21	**PDB header:**formyltransferase **Chain:** A: **PDB Molecule:**methionyl-trna fmet formyltransferase; **PDBTitle:** methionyl-trnafmet formyltransferase from escherichia coli
83	c2a87A_	Alignment	not modelled	62.8	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of m. tuberculosis thioredoxin reductase
84	c2ywjA_	Alignment	not modelled	62.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
85	c3q0iA_	Alignment	not modelled	62.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** methionyl-trna formyltransferase from vibrio cholerae
86	c2bcpA_	Alignment	not modelled	62.1	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh oxidase; **PDBTitle:** structural analysis of streptococcus pyogenes nadh oxidase:2 c44s nox with azide
87	d1ihua1	Alignment	not modelled	61.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
88	d1pjqa1	Alignment	not modelled	61.7	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
89	c2eq8E_	Alignment	not modelled	61.5	17	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
90	c3eagA_	Alignment	not modelled	61.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso- **PDBTitle:** the crystal structure of udp-n-acetylmuramate:l-alanyl-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitides
91	c3c6kC_	Alignment	not modelled	61.0	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**spermine synthase; **PDBTitle:** crystal structure of human spermine synthase in complex2 with spermidine and 5-methylthioadenosine
92	d2piaa2	Alignment	not modelled	61.0	21	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
93	c2xdoC_	Alignment	not modelled	60.9	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**tetx2 protein; **PDBTitle:** structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
94	d1qfja2	Alignment	not modelled	60.8	21	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
95	d1cqxa3	Alignment	not modelled	60.0	24	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
96	d1mo9a2	Alignment	not modelled	59.7	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
97	d2gv8a1	Alignment	not modelled	59.7	12	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
98	d1djqa3	Alignment	not modelled	59.5	19	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
99	d1umka2	Alignment	not modelled	59.3	17	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
100	d1hyha1	Alignment	not modelled	59.1	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
101	c3ouzA_	Alignment	not modelled	59.1	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
102	d2voua1	Alignment	not modelled	59.0	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain

103	c3dhnA_	Alignment	not modelled	58.9	22	**PDB header:**isomerase, lyase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
104	c1f8sA_	Alignment	not modelled	58.8	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-amino acid oxidase; **PDBTitle:** crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
105	c3d8xB_	Alignment	not modelled	58.7	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase 1; **PDBTitle:** crystal structure of saccharomyces cerevisiae nadph dependent2 thioredoxin reductase 1
106	c3bzbA_	Alignment	not modelled	58.7	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein cmq451c from the2 primitive red alga cyanidioschyzon merolae
107	d2iida1	Alignment	not modelled	58.6	20	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
108	d1h6va2	Alignment	not modelled	58.5	14	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
109	c3pvcA_	Alignment	not modelled	58.5	13	**PDB header:**oxidoreductase, transferase **Chain:** A: **PDB Molecule:**trna 5-methylaminomethyl-2-thiouridine biosynthesis **PDBTitle:** crystal structure of apo mnmc from yersinia pestis
110	c3kipU_	Alignment	not modelled	58.4	28	**PDB header:**lyase **Chain:** U: **PDB Molecule:**3-dehydroquinase, type ii; **PDBTitle:** crystal structure of type-ii 3-dehydroquinase from c. albicans
111	d1w4xa2	Alignment	not modelled	58.0	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
112	c3lzxB_	Alignment	not modelled	58.0	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin--nadp reductase 2; **PDBTitle:** crystal structure of ferredoxin-nadp+ oxidoreductase from bacillus2 subtilis (form ii)
113	c3hn7A_	Alignment	not modelled	57.8	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-l-alanine ligase; **PDBTitle:** crystal structure of a murein peptide ligase mpl (psyc_0032) from2 psychrobacter arcticus 273-4 at 1.65 a resolution
114	c3nrnA_	Alignment	not modelled	57.7	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pf1083; **PDBTitle:** crystal structure of pf1083 protein from pyrococcus furiosus,2 northeast structural genomics consortium target pfr223
115	c1vjtA_	Alignment	not modelled	57.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** crystal structure of alpha-glucosidase (tm0752) from thermotoga2 maritima at 2.50 a resolution
116	d1d7ya1	Alignment	not modelled	57.5	27	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
117	d1s3ia2	Alignment	not modelled	57.3	21	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
118	c1v59B_	Alignment	not modelled	57.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
119	c2xagA_	Alignment	not modelled	56.9	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
120	c2v1dA_	Alignment	not modelled	56.9	23	**PDB header:**oxidoreductase/repressor **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** structural basis of lsd1-corest selectivity in histone h32 recognition