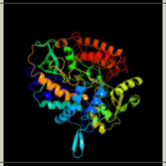
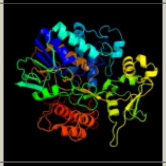
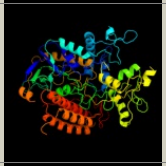
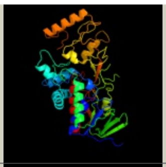
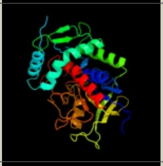
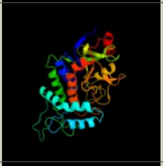
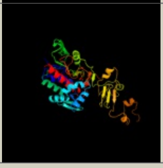
Email	l.a.kelley@imperial.ac.uk
Description	P10902
Date	Thu Jan 5 11:32:21 GMT 2012
Unique Job ID	d37252e5d99cf7a3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1yq4A_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate dehydrogenase flavoprotein subunit; **PDBTitle:** avian respiratory complex ii with 3-nitropropionate and ubiquinone
2	c1kf6A_	Alignment		100.0	34	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fumarate reductase flavoprotein; **PDBTitle:** e. coli quinol-fumarate reductase with bound inhibitor hqno
3	c3p4rM_	Alignment		100.0	34	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**fumarate reductase flavoprotein subunit; **PDBTitle:** crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
4	c2bs3A_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinol-fumarate reductase flavoprotein subunit a; **PDBTitle:** glu c180 -> gln variant quinol:fumarate reductase from2 wolinella succinogenes
5	c2aczA_	Alignment		100.0	31	**PDB header:**oxidoreductase/electron transport **Chain:** A: **PDB Molecule:**succinate dehydrogenase flavoprotein subunit; **PDBTitle:** complex ii (succinate dehydrogenase) from e. coli with atpenin a52 inhibitor co-crystallized at the ubiquinone binding site
6	c1chuA_	Alignment		100.0	98	**PDB header:**flavoenzyme **Chain:** A: **PDB Molecule:**protein (l-aspartate oxidase); **PDBTitle:** structure of l-aspartate oxidase: implications for the2 succinate dehydrogenase/ fumarate reducatse family
7	c2e5vA_	Alignment		100.0	37	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-aspartate oxidase; **PDBTitle:** crystal structure of l-aspartate oxidase from2 hyperthermophilic archaeon sulfolobus tokodaii
8	c2fjaC_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**adenylylsulfate reductase, subunit a; **PDBTitle:** adenosine 5'-phosphosulfate reductase in complex with2 substrate
9	c3gyxA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**adenylylsulfate reductase; **PDBTitle:** crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
10	c1qo8A_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c3 fumarate reductase; **PDBTitle:** the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
11	c1d4cB_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**flavocytochrome c fumarate reductase; **PDBTitle:** crystal structure of the uncomplexed form of the2 flavocytochrome c fumarate reductase of shewanella3 putrefaciens strain mr-1

12	c1jrxA_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c; **PDBTitle:** crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
13	d1chua2	Alignment		100.0	97	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
14	d1kf6a2	Alignment		100.0	35	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
15	d1y0pa2	Alignment		100.0	29	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
16	d1qo8a2	Alignment		100.0	30	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
17	d1neka2	Alignment		100.0	33	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
18	d1d4ca2	Alignment		100.0	29	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
19	c2gqfA_	Alignment		100.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0933; **PDBTitle:** crystal structure of flavoprotein hi0933 from haemophilus influenzae2 rd
20	c2i0zA_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad(fad)-utilizing dehydrogenases; **PDBTitle:** crystal structure of a fad binding protein from bacillus2 cereus, a putative nad(fad)-utilizing dehydrogenases
21	d2bs2a2	Alignment	not modelled	100.0	30	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
22	d1jnra2	Alignment	not modelled	100.0	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
23	c3g05B_	Alignment	not modelled	100.0	21	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl modification enzyme **PDBTitle:** crystal structure of n-terminal domain (2-550) of e.coli mnmg
24	c3cesB_	Alignment	not modelled	99.9	20	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl modification enzyme **PDBTitle:** crystal structure of e.coli mnmg (gida), a highly-conserved trna2 modifying enzyme
25	d1neka1	Alignment	not modelled	99.9	20	**Fold:**Spectrin repeat-like **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
26	d1chua1	Alignment	not modelled	99.9	100	**Fold:**Spectrin repeat-like **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
27	d2bs2a1	Alignment	not modelled	99.9	24	**Fold:**Spectrin repeat-like **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein

						C-terminal domain
28	d1kf6a1	Alignment	not modelled	99.9	26	**Fold:**Spectrin repeat-like **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
29	d1jnra1	Alignment	not modelled	99.9	26	**Fold:**Spectrin repeat-like **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
30	d1chua3	Alignment	not modelled	99.9	100	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
31	c3cp8C_	Alignment	not modelled	99.9	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl **PDBTitle:** crystal structure of gida from chlorobium tepidum
32	c3nlcA_	Alignment	not modelled	99.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein vp0956; **PDBTitle:** crystal structure of the vp0956 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr147
33	d2gqfa1	Alignment	not modelled	99.9	26	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**HI0933 N-terminal domain-like
34	c2zxiC_	Alignment	not modelled	99.9	19	**PDB header:**fad-binding protein **Chain:** C: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl **PDBTitle:** structure of aquifex aeolicus gida in the form ii crystal
35	d2bs2a3	Alignment	not modelled	99.9	38	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
36	c2v6oA_	Alignment	not modelled	99.9	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin glutathione reductase; **PDBTitle:** structure of schistosoma mansoni thioredoxin-glutathione2 reductase (smtgr)
37	d1neka3	Alignment	not modelled	99.8	37	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
38	c3dgzA_	Alignment	not modelled	99.8	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase 2; **PDBTitle:** crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
39	c1zkqA_	Alignment	not modelled	99.8	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase 2, mitochondrial; **PDBTitle:** crystal structure of mouse thioredoxin reductase type 2
40	c2nvkX_	Alignment	not modelled	99.8	20	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of thioredoxin reductase from drosophila2 melanogaster
41	d1kf6a3	Alignment	not modelled	99.8	38	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
42	c1tytA_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**trypanothione reductase, oxidized form; **PDBTitle:** crystal and molecular structure of crithidia fasciculata2 trypanothione reductase at 2.6 angstroms resolution
43	c2c3dB_	Alignment	not modelled	99.8	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-oxopropyl-com reductase; **PDBTitle:** 2.15 angstrom crystal structure of 2-ketopropyl coenzyme m2 oxidoreductase carboxylase with a coenzyme m disulfide3 bound at the active site
44	c2cfyB_	Alignment	not modelled	99.8	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase 1; **PDBTitle:** crystal structure of human thioredoxin reductase 1
45	c1v59B_	Alignment	not modelled	99.8	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
46	d2i0za1	Alignment	not modelled	99.8	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**HI0933 N-terminal domain-like
47	c1zmcG_	Alignment	not modelled	99.8	18	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**dihydrolipoyl dehydrogenase; **PDBTitle:** crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
48	c1hyuA_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alkyl hydroperoxide reductase subunit f; **PDBTitle:** crystal structure of intact ahpf
49	c1ndaD_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**trypanothione oxidoreductase; **PDBTitle:** the structure of trypanosoma cruzi trypanothione reductase2 in the oxidized and nadph reduced state
50	c1ojtA_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**surface protein; **PDBTitle:** structure of dihydrolipoamide dehydrogenase

51	c3urhB_	Alignment	not modelled	99.7	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrolipoyl dehydrogenase; **PDBTitle:** crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
52	c2w0hA_	Alignment	not modelled	99.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**trypanothione reductase; **PDBTitle:** x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph
53	c2eq8E_	Alignment	not modelled	99.7	27	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
54	c1geuA_	Alignment	not modelled	99.7	18	**PDB header:**oxidoreductase(flavoenzyme) **Chain:** A: **PDB Molecule:**glutathione reductase; **PDBTitle:** anatomy of an engineered nad-binding site
55	c2a8xA_	Alignment	not modelled	99.7	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrolipoyl dehydrogenase; **PDBTitle:** crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis
56	c3o0hA_	Alignment	not modelled	99.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione reductase; **PDBTitle:** crystal structure of glutathione reductase from bartonella henselae
57	c1onfA_	Alignment	not modelled	99.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione reductase; **PDBTitle:** crystal structure of plasmodium falciparum glutathione reductase
58	c3atrA_	Alignment	not modelled	99.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**conserved archaeal protein; **PDBTitle:** geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
59	d3grsa1	Alignment	not modelled	99.7	25	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
60	d1jnra3	Alignment	not modelled	99.7	21	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
61	c1lpfB_	Alignment	not modelled	99.7	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** three-dimensional structure of lipoamide dehydrogenase from2 pseudomonas fluorescens at 2.8 angstroms resolution.3 analysis of redox and thermostability properties
62	c1dxlC_	Alignment	not modelled	99.7	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** dihydrolipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum
63	c2rghA_	Alignment	not modelled	99.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alpha-glycerophosphate oxidase; **PDBTitle:** structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
64	d3lada1	Alignment	not modelled	99.7	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
65	c1bwcA_	Alignment	not modelled	99.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (glutathione reductase); **PDBTitle:** structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate
66	d1h6va1	Alignment	not modelled	99.7	25	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
67	c2rgoA_	Alignment	not modelled	99.7	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alpha-glycerophosphate oxidase; **PDBTitle:** structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
68	c2qaeA_	Alignment	not modelled	99.7	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrolipoyl dehydrogenase; **PDBTitle:** crystal structure analysis of trypanosoma cruzi lipoamide2 dehydrogenase
69	c2hqmB_	Alignment	not modelled	99.7	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione reductase; **PDBTitle:** crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae
70	c2zbwA_	Alignment	not modelled	99.7	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hb8
71	c1ebdB_	Alignment	not modelled	99.7	26	**PDB header:**complex (oxidoreductase/transferase) **Chain:** B: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** dihydrolipoamide dehydrogenase complexed with the binding2 domain of the dihydrolipoamide acetylase
72	d1dxla1	Alignment	not modelled	99.7	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
73	d1lpfa1	Alignment	not modelled	99.7	24	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
74	c3da1A_	Alignment	not modelled	99.7	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase; **PDBTitle:** x-ray structure of the glycerol-3-phosphate dehydrogenase2 from bacillus halodurans complexed with fad. northeast3 structural genomics consortium target bhr167.

75	c2eq7B_	Alignment	not modelled	99.7	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-oxoglutarate dehydrogenase e3 component; **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
76	c3jskN_	Alignment	not modelled	99.6	22	**PDB header:**biosynthetic protein **Chain:** N: **PDB Molecule:**cypbp37 protein; **PDBTitle:** thiazole synthase from neurospora crassa
77	c3ic9D_	Alignment	not modelled	99.6	23	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** the structure of dihydrolipoamide dehydrogenase from colwellia2 psychrerythraea 34h.
78	c3l8kB_	Alignment	not modelled	99.6	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrolipoyl dehydrogenase; **PDBTitle:** crystal structure of a dihydrolipoyl dehydrogenase from2 sulfolobus solfataricus
79	c3r9uA_	Alignment	not modelled	99.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** thioredoxin-disulfide reductase from campylobacter jejuni.
80	d1v59a1	Alignment	not modelled	99.6	20	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
81	c1x31A_	Alignment	not modelled	99.6	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sarcosine oxidase alpha subunit; **PDBTitle:** crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
82	c1lvlA_	Alignment	not modelled	99.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** the refined structure of pseudomonas putida lipoamide dehydrogenase2 complexed with nad+ at 2.45 angstroms resolution
83	c2r9zB_	Alignment	not modelled	99.6	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione amide reductase; **PDBTitle:** glutathione amide reductase from chromatium gracile
84	c1f6mF_	Alignment	not modelled	99.6	18	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of a complex between thioredoxin2 reductase, thioredoxin, and the nadp+ analog, aadp+
85	d1ojta1	Alignment	not modelled	99.6	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
86	c2r4jA_	Alignment	not modelled	99.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aerobic glycerol-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of escherichia coli semet substituted2 glycerol-3-phosphate dehydrogenase in complex with dhap
87	c3fbsB_	Alignment	not modelled	99.6	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens
88	c2q0lA_	Alignment	not modelled	99.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** helicobacter pylori thioredoxin reductase reduced by sodium dithionite2 in complex with nadp+
89	c1gthD_	Alignment	not modelled	99.6	22	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
90	d1ryia1	Alignment	not modelled	99.6	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
91	d1feca1	Alignment	not modelled	99.6	24	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
92	c1zx9A_	Alignment	not modelled	99.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** crystal structure of tn501 mera
93	c3f8rD_	Alignment	not modelled	99.6	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**thioredoxin reductase (trxb-3); **PDBTitle:** crystal structure of sulfolobus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules
94	d1lvla1	Alignment	not modelled	99.6	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
95	c2q7vA_	Alignment	not modelled	99.6	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of deinococcus radiodurans thioredoxin2 reductase
96	c3ctyA_	Alignment	not modelled	99.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of t. acidophilum thioredoxin reductase
97	c1xdiA_	Alignment	not modelled	99.6	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**rv3303c-lpda; **PDBTitle:** crystal structure of lpda (rv3303c) from mycobacterium tuberculosis
98	c2gmhA_	Alignment	not modelled	99.6	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**electron transfer flavoprotein-ubiquinone **PDBTitle:** structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
99	c1y56A_	Alignment	not modelled	99.6	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1363; **PDBTitle:** crystal structure of l-proline dehydrogenase from p.horikoshii
						Fold:FAD/NAD(P)-binding domain

100	d1rp0a1	Alignment	not modelled	99.6	25	**Superfamily:**FAD/NAD(P)-binding domain **Family:**Thi4-like
101	c3icrA_	Alignment	not modelled	99.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coenzyme a-disulfide reductase; **PDBTitle:** crystal structure of oxidized bacillus anthracis coadr-rhd
102	d1ebda1	Alignment	not modelled	99.6	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
103	d2gf3a1	Alignment	not modelled	99.5	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
104	c3ab1B_	Alignment	not modelled	99.5	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin--nadp reductase; **PDBTitle:** crystal structure of ferredoxin nadp+ oxidoreductase
105	c1fl2A_	Alignment	not modelled	99.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alkyl hydroperoxide reductase subunit f; **PDBTitle:** catalytic core component of the alkylhydroperoxide reductase ahpf from2 e.coli
106	d1aoga1	Alignment	not modelled	99.5	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
107	c3cgdB_	Alignment	not modelled	99.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pyridine nucleotide-disulfide oxidoreductase, class i; **PDBTitle:** pyridine nucleotide complexes with bacillus anthracis coenzyme a-2 disulfide reductase: a structural analysis of dual nad(p)h3 specificity
108	c1gv4A_	Alignment	not modelled	99.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**programed cell death protein 8; **PDBTitle:** murine apoptosis-inducing factor (aif)
109	c3i3lA_	Alignment	not modelled	99.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkylhalidase cmls; **PDBTitle:** crystal structure of cmls, a flavin-dependent halogenase
110	c1q1wA_	Alignment	not modelled	99.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putidaredoxin reductase; **PDBTitle:** crystal structure of putidaredoxin reductase from2 pseudomonas putida
111	c3e1tA_	Alignment	not modelled	99.5	17	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**halogenase; **PDBTitle:** structure and action of the myxobacterial chondrochloren2 halogenase cndh, a new variant of fad-dependent halogenases
112	c3ntaA_	Alignment	not modelled	99.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad-dependent pyridine nucleotide-disulphide **PDBTitle:** structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
113	c1gpeA_	Alignment	not modelled	99.5	21	**PDB header:**oxidoreductase(flavoprotein) **Chain:** A: **PDB Molecule:**protein (glucose oxidase); **PDBTitle:** glucose oxidase from penicillium amagasakiense
114	c1yqzA_	Alignment	not modelled	99.5	20	**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
115	d1pj5a2	Alignment	not modelled	99.5	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
116	c3dmeB_	Alignment	not modelled	99.5	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved exported protein; **PDBTitle:** crystal structure of conserved exported protein from2 bordetella pertussis. northeast structural genomics target3 ber141
117	c1pj6A_	Alignment	not modelled	99.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**n,n-dimethylglycine oxidase; **PDBTitle:** crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid
118	c2bcpA_	Alignment	not modelled	99.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh oxidase; **PDBTitle:** structural analysis of streptococcus pyogenes nadh oxidase:2 c44s nox with azide
119	c3kd9B_	Alignment	not modelled	99.5	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**coenzyme a disulfide reductase; **PDBTitle:** crystal structure of pyridine nucleotide disulfide oxidoreductase from2 pyrococcus horikoshii
120	c1naaB_	Alignment	not modelled	99.5	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cellobiose dehydrogenase; **PDBTitle:** cellobiose dehydrogenase flavoprotein fragment in complex with2 cellobionolactam