

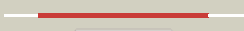





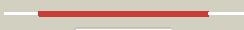
























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2aczA_</a>	 Alignment		100.0	100	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> succinate dehydrogenase flavoprotein subunit; <b>PDBTitle:</b> complex ii (succinate dehydrogenase) from e. coli with atpenin a52 inhibitor co-crystallized at the ubiquinone binding site
2	<a href="#">c1yq4A_</a>	 Alignment		100.0	54	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> succinate dehydrogenase flavoprotein subunit; <b>PDBTitle:</b> avian respiratory complex ii with 3-nitropropionate and ubiquinone
3	<a href="#">c2bs3A_</a>	 Alignment		100.0	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> quinol-fumarate reductase flavoprotein subunit a; <b>PDBTitle:</b> glu c180 -> gln variant quinol:fumarate reductase from2 wolfinella succinogenes
4	<a href="#">c1kf6A_</a>	 Alignment		100.0	44	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fumarate reductase flavoprotein; <b>PDBTitle:</b> e. coli quinol-fumarate reductase with bound inhibitor hqno
5	<a href="#">c3p4rM_</a>	 Alignment		100.0	44	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> fumarate reductase flavoprotein subunit; <b>PDBTitle:</b> crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
6	<a href="#">c2fjaC_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> adenylylsulfate reductase, subunit a; <b>PDBTitle:</b> adenosine 5'-phosphosulfate reductase in complex with2 substrate
7	<a href="#">c3gyxA_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylylsulfate reductase; <b>PDBTitle:</b> crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
8	<a href="#">c1chuA_</a>	 Alignment		100.0	31	<b>PDB header:</b> flavoenzyme <b>Chain:</b> A: <b>PDB Molecule:</b> protein (l-aspartate oxidase); <b>PDBTitle:</b> structure of l-aspartate oxidase: implications for the2 succinate dehydrogenase/ fumarate reductase family
9	<a href="#">c2e5vA_</a>	 Alignment		100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-aspartate oxidase; <b>PDBTitle:</b> crystal structure of l-aspartate oxidase from2 hyperthermophilic archaeon sulfolobus tokodaii
10	<a href="#">c1qo8A_</a>	 Alignment		100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavocytochrome c3 fumarate reductase; <b>PDBTitle:</b> the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
11	<a href="#">c1jrxA_</a>	 Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavocytochrome c; <b>PDBTitle:</b> crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina

12	<a href="#">c1d4cB</a>	Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> flavocytochrome c fumarate reductase; <b>PDBTitle:</b> crystal structure of the uncomplexed form of the2 flavocytochrome c fumarate reductase of shewanella3 putrefaciens strain mr-1
13	<a href="#">d1chua2</a>	Alignment		100.0	39	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
14	<a href="#">d1neka2</a>	Alignment		100.0	100	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
15	<a href="#">d1y0pa2</a>	Alignment		100.0	32	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
16	<a href="#">d1qo8a2</a>	Alignment		100.0	31	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
17	<a href="#">d1kf6a2</a>	Alignment		100.0	45	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
18	<a href="#">c3v76A</a>	Alignment		100.0	20	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> flavoprotein; <b>PDBTitle:</b> the crystal structure of a flavoprotein from sinorhizobium meliloti
19	<a href="#">d1neka1</a>	Alignment		100.0	100	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
20	<a href="#">c2gqfA</a>	Alignment		100.0	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein hi0933; <b>PDBTitle:</b> crystal structure of flavoprotein hi0933 from haemophilus influenzae2 rd
21	<a href="#">c2i0zA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad(fad)-utilizing dehydrogenases; <b>PDBTitle:</b> crystal structure of a fad binding protein from bacillus2 cereus, a putative nad(fad)-utilizing dehydrogenases
22	<a href="#">d2bs2a1</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
23	<a href="#">d1d4ca2</a>	Alignment	not modelled	100.0	35	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
24	<a href="#">d2bs2a2</a>	Alignment	not modelled	100.0	39	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
25	<a href="#">d1jnra2</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
26	<a href="#">d1kf6a1</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
27	<a href="#">d1jnra1</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
28	<a href="#">c3cesB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl modification enzyme

						<b>PDBTitle:</b> crystal structure of e.coli mnmG (gida), a highly-conserved trna2 modifying enzyme
29	<a href="#">c3g05B_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> trna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl modification enzyme <b>PDBTitle:</b> crystal structure of n-terminal domain (2-550) of e.coli mnmG
30	<a href="#">c3nlcA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein vp0956; <b>PDBTitle:</b> crystal structure of the vp0956 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr147
31	<a href="#">d2gqfa1</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> HI0933 N-terminal domain-like
32	<a href="#">d1neka3</a>	Alignment	not modelled	99.9	100	<b>Fold:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
33	<a href="#">c2zxiC_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> fad-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl <b>PDBTitle:</b> structure of aquifex aeolicus gida in the form ii crystal
34	<a href="#">d2bs2a3</a>	Alignment	not modelled	99.9	45	<b>Fold:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
35	<a href="#">c3cp8C_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl <b>PDBTitle:</b> crystal structure of gida from chlorobium tepidum
36	<a href="#">d1chua1</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
37	<a href="#">d1kf6a3</a>	Alignment	not modelled	99.9	50	<b>Fold:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
38	<a href="#">d1chua3</a>	Alignment	not modelled	99.9	35	<b>Fold:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
39	<a href="#">d2i0za1</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> HI0933 N-terminal domain-like
40	<a href="#">c2rghA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glycerophosphate oxidase; <b>PDBTitle:</b> structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
41	<a href="#">c2rgoA_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glycerophosphate oxidase; <b>PDBTitle:</b> structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
42	<a href="#">c2r4jA_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aerobic glycerol-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of escherichia coli semet substituted2 glycerol-3-phosphate dehydrogenase in complex with dhap
43	<a href="#">c3dgaA_</a>	Alignment	not modelled	99.8	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase 2; <b>PDBTitle:</b> crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
44	<a href="#">c3da1A_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase; <b>PDBTitle:</b> x-ray structure of the glycerol-3-phosphate dehydrogenase2 from bacillus halodurans complexed with fad. northeast3 structural genomics consortium target bhr167.
45	<a href="#">c1zkqA_</a>	Alignment	not modelled	99.8	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase 2, mitochondrial; <b>PDBTitle:</b> crystal structure of mouse thioredoxin reductase type 2
46	<a href="#">c2gmhA_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> electron transfer flavoprotein-ubiquinone <b>PDBTitle:</b> structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
47	<a href="#">c2c3dB_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxopropyl-com reductase; <b>PDBTitle:</b> 2.15 angstrom crystal structure of 2-ketopropyl coenzyme m2 oxidoreductase carboxylase with a coenzyme m disulfide3 bound at the active site
48	<a href="#">d1jnra3</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
49	<a href="#">c1v59B_</a>	Alignment	not modelled	99.8	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
						<b>PDB header:</b> oxidoreductase

50	<a href="#">c2eq8E</a>	Alignment	not modelled	99.8	29	<b>Chain:</b> E: <b>PDB Molecule:</b> pyruvate dehydrogenase complex, dihydrolipoamide <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
51	<a href="#">c1zmcG</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
52	<a href="#">c2v6oA</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin glutathione reductase; <b>PDBTitle:</b> structure of schistosoma mansoni thioredoxin-gluthathione2 reductase (smtgr)
53	<a href="#">c1hyuA</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alkyl hydroperoxide reductase subunit f; <b>PDBTitle:</b> crystal structure of intact ahpf
54	<a href="#">d2gmha1</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
55	<a href="#">c3atrA</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> conserved archaeal protein; <b>PDBTitle:</b> geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
56	<a href="#">d1ryia1</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
57	<a href="#">c2nvkX</a>	Alignment	not modelled	99.7	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of thioredoxin reductase from drosophila2 melanogaster
58	<a href="#">c1geuA</a>	Alignment	not modelled	99.7	34	<b>PDB header:</b> oxidoreductase(flavoenzyme) <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> anatomy of an engineered nad-binding site
59	<a href="#">c2gewA</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cholesterol oxidase; <b>PDBTitle:</b> atomic resolution structure of cholesterol oxidase @ ph 9.02 (streptomyces sp. sa-coo)
60	<a href="#">c2zbwA</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hb8
61	<a href="#">c3urhB</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
62	<a href="#">c1ojtA</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> surface protein; <b>PDBTitle:</b> structure of dihydrolipoamide dehydrogenase
63	<a href="#">c2cfyB</a>	Alignment	not modelled	99.7	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase 1; <b>PDBTitle:</b> crystal structure of human thioredoxin reductase 1
64	<a href="#">c3o0hA</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> crystal structure of glutathione reductase from bartonella henselae
65	<a href="#">c1bwcA</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (glutathione reductase); <b>PDBTitle:</b> structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate
66	<a href="#">c3jskN</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> N: <b>PDB Molecule:</b> cypbp37 protein; <b>PDBTitle:</b> thiazole synthase from neurospora crassa
67	<a href="#">c3ic9D</a>	Alignment	not modelled	99.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> the structure of dihydrolipoamide dehydrogenase from colwellia2 psychrerythraea 34h.
68	<a href="#">c3i3lA</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alkylhalidase cmls; <b>PDBTitle:</b> crystal structure of cmls, a flavin-dependent halogenase
69	<a href="#">c2hqmB</a>	Alignment	not modelled	99.7	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae
70	<a href="#">c1dxcC</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> dihydrolipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum
71	<a href="#">c3dmeB</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> conserved exported protein; <b>PDBTitle:</b> crystal structure of conserved exported protein from2 bordetella pertussis. northeast structural genomics target3 ber141
72	<a href="#">c1pj6A</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> n,n-dimethylglycine oxidase; <b>PDBTitle:</b> crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid
73	<a href="#">d3grsa1</a>	Alignment	not modelled	99.7	24	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
74	<a href="#">c2a8xA</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis
75	<a href="#">c1lpfB</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> three-dimensional structure of lipoamide dehydrogenase from2 pseudomonas fluorescens at 2.8 angstroms resolution.3 analysis of redox and thermostability properties

76	<a href="#">c1ndaD_</a>	Alignment	not modelled	99.7	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> trypanothione oxidoreductase; <b>PDBTitle:</b> the structure of trypanosoma cruzi trypanothione reductase2 in the oxidized and nadph reduced state
77	<a href="#">c2w0hA_</a>	Alignment	not modelled	99.7	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trypanothione reductase; <b>PDBTitle:</b> x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph
78	<a href="#">c1f6mF_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of a complex between thioredoxin2 reductase, thioredoxin, and the nadp+ analog, aadp+
79	<a href="#">c1onfA_</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> crystal structure of plasmodium falciparum glutathione reductase
80	<a href="#">c3e1tA_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> halogenase; <b>PDBTitle:</b> structure and action of the myxobacterial chondrochloren2 halogenase cndh, a new variant of fad-dependent halogenases
81	<a href="#">c3r9uA_</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> thioredoxin-disulfide reductase from campylobacter jejuni.
82	<a href="#">c1tytA_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trypanothione reductase, oxidized form; <b>PDBTitle:</b> crystal and molecular structure of crithidia fasciculata2 trypanothione reductase at 2.6 angstroms resolution
83	<a href="#">c2qaeA_</a>	Alignment	not modelled	99.6	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure analysis of trypanosoma cruzi lipoamide2 dehydrogenase
84	<a href="#">d1rp0a1</a>	Alignment	not modelled	99.6	24	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Thi4-like
85	<a href="#">c2eq7B_</a>	Alignment	not modelled	99.6	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxoglutarate dehydrogenase e3 component; <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
86	<a href="#">d2gf3a1</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
87	<a href="#">c2gahB_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> heterotetrameric sarcosine oxidase beta-subunit; <b>PDBTitle:</b> heterotetrameric sarcosine: structure of a diflavin2 metalloenzyme at 1.85 a resolution
88	<a href="#">d1pj5a2</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
89	<a href="#">c3f8rD_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> thioredoxin reductase (trxb-3); <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules
90	<a href="#">d3coxa1</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
91	<a href="#">c3fbsB_</a>	Alignment	not modelled	99.6	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens
92	<a href="#">c2q0lA_</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> helicobacter pylori thioredoxin reductase reduced by sodium dithionite2 in complex with nadp+
93	<a href="#">c1coyA_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> oxidoreductase(oxygen receptor) <b>Chain:</b> A: <b>PDB Molecule:</b> cholesterol oxidase; <b>PDBTitle:</b> crystal structure of cholesterol oxidase complexed with a2 steroid substrate. implications for fad dependent alcohol3 oxidases
94	<a href="#">c2q7vA_</a>	Alignment	not modelled	99.6	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans thioredoxin2 reductase
95	<a href="#">c1zx9A_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> crystal structure of tn501 mera
96	<a href="#">c1naaB_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cellobiose dehydrogenase; <b>PDBTitle:</b> cellobiose dehydrogenase flavoprotein fragment in complex with2 cellobionolactam
97	<a href="#">d1lpfa1</a>	Alignment	not modelled	99.6	23	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
98	<a href="#">c1s3bB_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> amine oxidase [flavin-containing] b; <b>PDBTitle:</b> crystal structure of maob in complex with n-methyl-n-2 propargyl-1(r)-aminoindan
99	<a href="#">d3lada1</a>	Alignment	not modelled	99.6	24	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
100	<a href="#">c1vdcA_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph dependent thioredoxin reductase; <b>PDBTitle:</b> structure of nadph dependent thioredoxin reductase
						<b>Fold:</b> FAD/NAD(P)-binding domain



101	<a href="#">d1h6va1</a>	Alignment	not modelled	99.6	21	<b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
102	<a href="#">c1gpeA</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> oxidoreductase(flavoprotein) <b>Chain:</b> A: <b>PDB Molecule:</b> protein (glucose oxidase); <b>PDBTitle:</b> glucose oxidase from penicillium amagasakiense
103	<a href="#">c2jbvA</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> choline oxidase; <b>PDBTitle:</b> crystal structure of choline oxidase reveals insights into2 the catalytic mechanism
104	<a href="#">c3ab1B</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> crystal structure of ferredoxin nadp+ oxidoreductase
105	<a href="#">c3djeA</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fructosyl amine: oxygen oxidoreductase; <b>PDBTitle:</b> crystal structure of the deglycating enzyme fructosamine2 oxidase from aspergillus fumigatus (amadoriase ii) in3 complex with fsa
106	<a href="#">c3cgvA</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranyl reductase related protein; <b>PDBTitle:</b> crystal structure of geranylgeranyl bacteriochlorophyll reductase-like2 fixc homolog (np_393992.1) from thermoplasma acidophilum at 1.60 a3 resolution
107	<a href="#">c3ps9A</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna 5-methylaminomethyl-2-thiouridine biosynthesis <b>PDBTitle:</b> crystal structure of mnmC from e. coli
108	<a href="#">d1dxa1</a>	Alignment	not modelled	99.5	26	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
109	<a href="#">c1lvIA</a>	Alignment	not modelled	99.5	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> the refined structure of pseudomonas putida lipoamide dehydrogenase2 complexed with nad+ at 2.45 angstroms resolution
110	<a href="#">c1ltxR</a>	Alignment	not modelled	99.5	12	<b>PDB header:</b> transferase/protein binding <b>Chain:</b> R: <b>PDB Molecule:</b> rab escort protein 1; <b>PDBTitle:</b> structure of rab escort protein-1 in complex with rab2 geranylgeranyl transferase and isoprenoid
111	<a href="#">c2igoG</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> pyranose oxidase; <b>PDBTitle:</b> crystal structure of pyranose 2-oxidase h167a mutant with 2-2 fluoro-2-deoxy-d-glucose
112	<a href="#">c1y56B</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> sarcosine oxidase; <b>PDBTitle:</b> crystal structure of l-proline dehydrogenase from p.horikoshii
113	<a href="#">d1n4wa1</a>	Alignment	not modelled	99.5	18	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
114	<a href="#">d1v59a1</a>	Alignment	not modelled	99.5	21	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
115	<a href="#">c1gthD</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydropyrimidine dehydrogenase; <b>PDBTitle:</b> dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
116	<a href="#">d2bcgg1</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> GDI-like N domain
117	<a href="#">c2f5vA</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyranose 2-oxidase; <b>PDBTitle:</b> reaction geometry and thermostability mutant of pyranose 2-oxidase2 from the white-rot fungus peniophora sp.
118	<a href="#">d1kdga1</a>	Alignment	not modelled	99.5	17	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
119	<a href="#">c2olnA</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nikd protein; <b>PDBTitle:</b> nikd, an unusual amino acid oxidase essential for2 nikkomycin biosynthesis: closed form at 1.15 a resolution
120	<a href="#">c3nixF</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> flavoprotein/dehydrogenase; <b>PDBTitle:</b> crystal structure of flavoprotein/dehydrogenase from cytophaga2 hutchinsonii. northeast structural genomics consortium target chr43.