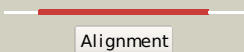
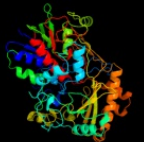
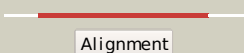
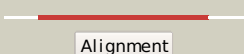
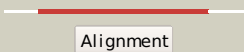
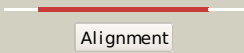
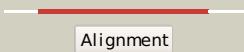
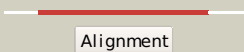
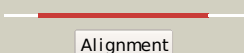
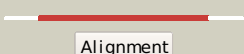
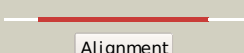
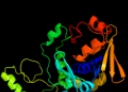


Detailed template information

| #  | Template                | Alignment Coverage                                                                            | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                                              |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c3fimB_</a> |  Alignment   |    | 100.0      | 26     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B; <b>PDB Molecule:</b> aryl-alcohol oxidase;<br><b>PDBTitle:</b> crystal structure of aryl-alcohol-oxidase from pleurotus eryngii                                                                             |
| 2  | <a href="#">c1cf3A_</a> |  Alignment   |    | 100.0      | 29     | <b>PDB header:</b> oxidoreductase(flavoprotein)<br><b>Chain:</b> A; <b>PDB Molecule:</b> protein (glucose oxidase);<br><b>PDBTitle:</b> glucose oxidase from aspergillus niger                                                                                    |
| 3  | <a href="#">c2jbvA_</a> |  Alignment   |    | 100.0      | 38     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> choline oxidase;<br><b>PDBTitle:</b> crystal structure of choline oxidase reveals insights into the catalytic mechanism                                                                |
| 4  | <a href="#">c1gpeA_</a> |  Alignment   |   | 100.0      | 26     | <b>PDB header:</b> oxidoreductase(flavoprotein)<br><b>Chain:</b> A; <b>PDB Molecule:</b> protein (glucose oxidase);<br><b>PDBTitle:</b> glucose oxidase from penicillium amagasakiense                                                                            |
| 5  | <a href="#">c3q9tB_</a> |  Alignment |  | 100.0      | 26     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B; <b>PDB Molecule:</b> choline dehydrogenase and related flavoproteins;<br><b>PDBTitle:</b> crystal structure analysis of formate oxidase                                                                     |
| 6  | <a href="#">c1naaB_</a> |  Alignment |  | 100.0      | 23     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B; <b>PDB Molecule:</b> cellobiose dehydrogenase;<br><b>PDBTitle:</b> cellobiose dehydrogenase flavoprotein fragment in complex with cellobionolactam                                                          |
| 7  | <a href="#">c1ju2A_</a> |  Alignment |  | 100.0      | 25     | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> hydroxynitrile lyase;<br><b>PDBTitle:</b> crystal structure of the hydroxynitrile lyase from almond                                                                                             |
| 8  | <a href="#">c2gewA_</a> |  Alignment |  | 100.0      | 19     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> cholesterol oxidase;<br><b>PDBTitle:</b> atomic resolution structure of cholesterol oxidase @ pH 9.02 (streptomyces sp. sa-coo)                                                        |
| 9  | <a href="#">c1coyA_</a> |  Alignment |  | 100.0      | 17     | <b>PDB header:</b> oxidoreductase(oxygen receptor)<br><b>Chain:</b> A; <b>PDB Molecule:</b> cholesterol oxidase;<br><b>PDBTitle:</b> crystal structure of cholesterol oxidase complexed with a steroid substrate. implications for fad dependent alcohol oxidases |
| 10 | <a href="#">d1cf3a1</a> |  Alignment |  | 100.0      | 34     | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> FAD-linked reductases, N-terminal domain                                                                                                                |
| 11 | <a href="#">c2igoG_</a> |  Alignment |  | 100.0      | 14     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> G; <b>PDB Molecule:</b> pyranose oxidase;<br><b>PDBTitle:</b> crystal structure of pyranose 2-oxidase h167a mutant with 2-2 fluoro-2-deoxy-d-glucose                                                           |

|    |                         |           |                                                                                     |       |    |                                                                                                                                                                                                                                                                                             |
|----|-------------------------|-----------|-------------------------------------------------------------------------------------|-------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">c2f5vA</a>  | Alignment |    | 100.0 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pyranose 2-oxidase;<br><b>PDBTitle:</b> reaction geometry and thermostability mutant of pyranose 2-oxidase2 from the white-rot fungus peniophora sp.                                                             |
| 13 | <a href="#">dlgpea1</a> | Alignment |    | 100.0 | 34 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> FAD-linked reductases, N-terminal domain                                                                                                                                          |
| 14 | <a href="#">dlkdga1</a> | Alignment |    | 100.0 | 28 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> FAD-linked reductases, N-terminal domain                                                                                                                                          |
| 15 | <a href="#">dln4wa1</a> | Alignment |    | 100.0 | 25 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> FAD-linked reductases, N-terminal domain                                                                                                                                          |
| 16 | <a href="#">d3coxa1</a> | Alignment |    | 100.0 | 23 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> FAD-linked reductases, N-terminal domain                                                                                                                                          |
| 17 | <a href="#">d2f5va1</a> | Alignment |    | 100.0 | 20 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> FAD-linked reductases, N-terminal domain                                                                                                                                          |
| 18 | <a href="#">dlju2a1</a> | Alignment |  | 100.0 | 27 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> FAD-linked reductases, N-terminal domain                                                                                                                                          |
| 19 | <a href="#">dlgpea2</a> | Alignment |  | 99.7  | 17 | <b>Fold:</b> FAD-linked reductases, C-terminal domain<br><b>Superfamily:</b> FAD-linked reductases, C-terminal domain<br><b>Family:</b> GMC oxidoreductases                                                                                                                                 |
| 20 | <a href="#">dlcf3a2</a> | Alignment |  | 99.6  | 19 | <b>Fold:</b> FAD-linked reductases, C-terminal domain<br><b>Superfamily:</b> FAD-linked reductases, C-terminal domain<br><b>Family:</b> GMC oxidoreductases                                                                                                                                 |
| 21 | <a href="#">c1yq4A</a>  | Alignment | not modelled                                                                        | 99.6  | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> succinate dehydrogenase flavoprotein subunit;<br><b>PDBTitle:</b> avian respiratory complex ii with 3-nitropropionate and ubiquinone                                                                             |
| 22 | <a href="#">c3p4rM</a>  | Alignment | not modelled                                                                        | 99.6  | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> M: <b>PDB Molecule:</b> fumarate reductase flavoprotein subunit;<br><b>PDBTitle:</b> crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate                                                                  |
| 23 | <a href="#">c1kf6A</a>  | Alignment | not modelled                                                                        | 99.6  | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fumarate reductase flavoprotein;<br><b>PDBTitle:</b> e. coli quinol-fumarate reductase with bound inhibitor hqno                                                                                                 |
| 24 | <a href="#">d1d5ta1</a> | Alignment | not modelled                                                                        | 99.5  | 10 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> GDI-like N domain                                                                                                                                                                 |
| 25 | <a href="#">c1qo8A</a>  | Alignment | not modelled                                                                        | 99.5  | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> flavocytochrome c3 fumarate reductase;<br><b>PDBTitle:</b> the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase                                                                    |
| 26 | <a href="#">c1d4cB</a>  | Alignment | not modelled                                                                        | 99.5  | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> flavocytochrome c fumarate reductase;<br><b>PDBTitle:</b> crystal structure of the uncomplexed form of the2 flavocytochrome c fumarate reductase of shewanella3 putrefaciens strain mr-1                         |
| 27 | <a href="#">c2aczA</a>  | Alignment | not modelled                                                                        | 99.5  | 21 | <b>PDB header:</b> oxidoreductase/electron transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> succinate dehydrogenase flavoprotein subunit;<br><b>PDBTitle:</b> complex ii (succinate dehydrogenase) from e. coli with atpenin a52 inhibitor co-crystallized at the ubiquinone binding site |
|    |                         |           |                                                                                     |       |    | <b>PDB header:</b> oxidoreductase                                                                                                                                                                                                                                                           |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                                                     |
|----|-------------------------|-----------|--------------|------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 28 | <a href="#">c1jrxA_</a> | Alignment | not modelled | 99.5 | 18 | <b>Chain:</b> A: <b>PDB Molecule:</b> flavocytochrome c;<br><b>PDBTitle:</b> crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina                                                                                                                                |
| 29 | <a href="#">d1kf6a2</a> | Alignment | not modelled | 99.5 | 16 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain                                                                                                                 |
| 30 | <a href="#">c2bs3A_</a> | Alignment | not modelled | 99.4 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> quinol-fumarate reductase flavoprotein subunit a;<br><b>PDBTitle:</b> glu c180 -> gln variant quinol:fumarate reductase from2 wolinnella succinogenes                                                                    |
| 31 | <a href="#">c2fjaC_</a> | Alignment | not modelled | 99.4 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> adenyllysulfate reductase, subunit a;<br><b>PDBTitle:</b> adenosine 5'-phosphosulfate reductase in complex with2 substrate                                                                                               |
| 32 | <a href="#">d1ju2a2</a> | Alignment | not modelled | 99.4 | 17 | <b>Fold:</b> FAD-linked reductases, C-terminal domain<br><b>Superfamily:</b> FAD-linked reductases, C-terminal domain<br><b>Family:</b> GMC oxidoreductases                                                                                                                                         |
| 33 | <a href="#">d1y0pa2</a> | Alignment | not modelled | 99.4 | 18 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain                                                                                                                 |
| 34 | <a href="#">c2rghA_</a> | Alignment | not modelled | 99.4 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glycerophosphate oxidase;<br><b>PDBTitle:</b> structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase                         |
| 35 | <a href="#">c2rgoA_</a> | Alignment | not modelled | 99.4 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glycerophosphate oxidase;<br><b>PDBTitle:</b> structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase                         |
| 36 | <a href="#">d1qo8a2</a> | Alignment | not modelled | 99.3 | 15 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain                                                                                                                 |
| 37 | <a href="#">d2bcgg1</a> | Alignment | not modelled | 99.3 | 11 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> GDI-like N domain                                                                                                                                                                         |
| 38 | <a href="#">d2bs2a2</a> | Alignment | not modelled | 99.3 | 12 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain                                                                                                                 |
| 39 | <a href="#">d1neka2</a> | Alignment | not modelled | 99.3 | 15 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain                                                                                                                 |
| 40 | <a href="#">d2i0za1</a> | Alignment | not modelled | 99.3 | 21 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> HI0933 N-terminal domain-like                                                                                                                                                             |
| 41 | <a href="#">c2r4jA_</a> | Alignment | not modelled | 99.3 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aerobic glycerol-3-phosphate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of escherichia coli semet substituted2 glycerol-3-phosphate dehydrogenase in complex with dhap                                         |
| 42 | <a href="#">c1gndA_</a> | Alignment | not modelled | 99.2 | 12 | <b>PDB header:</b> gtpase activation<br><b>Chain:</b> A: <b>PDB Molecule:</b> guanine nucleotide dissociation inhibitor;<br><b>PDBTitle:</b> guanine nucleotide dissociation inhibitor, alpha-isoform                                                                                               |
| 43 | <a href="#">d2gf3a1</a> | Alignment | not modelled | 99.2 | 15 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> FAD-linked reductases, N-terminal domain                                                                                                                                                  |
| 44 | <a href="#">c1zkqA_</a> | Alignment | not modelled | 99.2 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase 2, mitochondrial;<br><b>PDBTitle:</b> crystal structure of mouse thioredoxin reductase type 2                                                                                                      |
| 45 | <a href="#">c3dgaA_</a> | Alignment | not modelled | 99.2 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase 2;<br><b>PDBTitle:</b> crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation                                                                           |
| 46 | <a href="#">d2gqfa1</a> | Alignment | not modelled | 99.2 | 20 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> HI0933 N-terminal domain-like                                                                                                                                                             |
| 47 | <a href="#">c3da1A_</a> | Alignment | not modelled | 99.2 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase;<br><b>PDBTitle:</b> x-ray structure of the glycerol-3-phosphate dehydrogenase2 from bacillus halodurans complexed with fad. northeast3 structural genomics consortium target bhr167. |
| 48 | <a href="#">c3dmeB_</a> | Alignment | not modelled | 99.2 | 13 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> conserved exported protein;<br><b>PDBTitle:</b> crystal structure of conserved exported protein from2 bordetella pertussis. northeast structural genomics target3 ber141                          |
| 49 | <a href="#">d1pj5a2</a> | Alignment | not modelled | 99.2 | 19 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> FAD-linked reductases, N-terminal domain                                                                                                                                                  |
| 50 | <a href="#">d1d4ca2</a> | Alignment | not modelled | 99.2 | 19 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain                                                                                                                 |
| 51 | <a href="#">c3gyxA_</a> | Alignment | not modelled | 99.2 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> adenyllysulfate reductase;<br><b>PDBTitle:</b> crystal structure of adenyllysulfate reductase from2 desulfovibrio gigas                                                                                                  |
| 52 | <a href="#">c1pj6A_</a> | Alignment | not modelled | 99.2 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> n,n-dimethylglycine oxidase;<br><b>PDBTitle:</b> crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid                                                                    |
|    |                         |           |              |      |    | <b>PDB header:</b> oxidoreductase                                                                                                                                                                                                                                                                   |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                                     |
|----|-------------------------|-----------|--------------|------|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 53 | <a href="#">c2c3dB_</a> | Alignment | not modelled | 99.1 | 18 | <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxopropyl-com reductase;<br><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                                                   |
| 54 | <a href="#">c1zmcG_</a> | Alignment | not modelled | 99.1 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> G: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase;<br><b>PDBTitle:</b> crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+                                                                            |
| 55 | <a href="#">c2zziC_</a> | Alignment | not modelled | 99.1 | 22 | <b>PDB header:</b> fad-binding protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl<br><b>PDBTitle:</b> structure of aquifex aeolicus gida in the form ii crystal                                                                               |
| 56 | <a href="#">c2nvkX_</a> | Alignment | not modelled | 99.1 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> X: <b>PDB Molecule:</b> thioredoxin reductase;<br><b>PDBTitle:</b> crystal structure of thioredoxin reductase from drosophila2 melanogaster                                                                                      |
| 57 | <a href="#">d1chua2</a> | Alignment | not modelled | 99.1 | 26 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain                                                                                                 |
| 58 | <a href="#">c3ka7A_</a> | Alignment | not modelled | 99.1 | 10 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase;<br><b>PDBTitle:</b> crystal structure of an oxidoreductase from methanosarcina2 mazel. northeast structural genomics consortium target id3 mar208                                        |
| 59 | <a href="#">c3jskN_</a> | Alignment | not modelled | 99.1 | 29 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> N: <b>PDB Molecule:</b> cypbp37 protein;<br><b>PDBTitle:</b> thiazole synthase from neurospora crassa                                                                                                                      |
| 60 | <a href="#">c3cpiH_</a> | Alignment | not modelled | 99.1 | 11 | <b>PDB header:</b> protein transport<br><b>Chain:</b> H: <b>PDB Molecule:</b> rab gdp-dissociation inhibitor;<br><b>PDBTitle:</b> crystal structure of yeast rab-gdi                                                                                                                |
| 61 | <a href="#">c2olnA_</a> | Alignment | not modelled | 99.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nikd protein;<br><b>PDBTitle:</b> nikd, an unusual amino acid oxidase essential for2 nikkomycin biosynthesis: closed form at 1.15 a resolution                                                           |
| 62 | <a href="#">d1ryia1</a> | Alignment | not modelled | 99.0 | 13 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> FAD-linked reductases, N-terminal domain                                                                                                                                  |
| 63 | <a href="#">c3g05B_</a> | Alignment | not modelled | 99.0 | 27 | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl modification enzyme<br><b>PDBTitle:</b> crystal structure of n-terminal domain (2-550) of e.coli mnmg                                                       |
| 64 | <a href="#">c1hyuA_</a> | Alignment | not modelled | 99.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alkyl hydroperoxide reductase subunit f;<br><b>PDBTitle:</b> crystal structure of intact ahpf                                                                                                            |
| 65 | <a href="#">d1rp0a1</a> | Alignment | not modelled | 99.0 | 23 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> Thi4-like                                                                                                                                                                 |
| 66 | <a href="#">c3cp8C_</a> | Alignment | not modelled | 99.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl<br><b>PDBTitle:</b> crystal structure of gida from chlorobium tepidum                                                                                            |
| 67 | <a href="#">c3urhB_</a> | Alignment | not modelled | 99.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase;<br><b>PDBTitle:</b> crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021                                                                 |
| 68 | <a href="#">c3cesB_</a> | Alignment | not modelled | 98.9 | 28 | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl modification enzyme<br><b>PDBTitle:</b> crystal structure of e.coli mnmg (gida), a highly-conserved trna2 modifying enzyme                                  |
| 69 | <a href="#">c2e5vA_</a> | Alignment | not modelled | 98.9 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-aspartate oxidase;<br><b>PDBTitle:</b> crystal structure of l-aspartate oxidase from2 hyperthermophilic archaeon sulfolobus tokodaii                                                                   |
| 70 | <a href="#">c2gahB_</a> | Alignment | not modelled | 98.9 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> heterotetrameric sarcosine oxidase beta-subunit;<br><b>PDBTitle:</b> heterotetrameric sarcosine: structure of a diflavin2 metalloenzyme at 1.85 a resolution                                             |
| 71 | <a href="#">c2i0zA_</a> | Alignment | not modelled | 98.9 | 38 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nad(fad)-utilizing dehydrogenases;<br><b>PDBTitle:</b> crystal structure of a fad binding protein from bacillus2 cereus, a putative nad(fad)-utilizing dehydrogenases                                    |
| 72 | <a href="#">c3fbsB_</a> | Alignment | not modelled | 98.9 | 42 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase;<br><b>PDBTitle:</b> the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens                                                                                          |
| 73 | <a href="#">c1chuA_</a> | Alignment | not modelled | 98.9 | 24 | <b>PDB header:</b> flavoenzyme<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (l-aspartate oxidase);<br><b>PDBTitle:</b> structure of l-aspartate oxidase: implications for the2 succinate dehydrogenase/ fumarate reductase family                                               |
| 74 | <a href="#">c3nlcA_</a> | Alignment | not modelled | 98.9 | 18 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein vp0956;<br><b>PDBTitle:</b> crystal structure of the vp0956 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr147 |
| 75 | <a href="#">c3djeA_</a> | Alignment | not modelled | 98.9 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fructosyl amine: oxygen oxidoreductase;<br><b>PDBTitle:</b> crystal structure of the deglycating enzyme fructosamine2 oxidase from aspergillus fumigatus (amadoriase ii) in3 complex with fsa            |
| 76 | <a href="#">d2cula1</a> | Alignment | not modelled | 98.8 | 27 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> GidA-like                                                                                                                                                                 |
| 77 | <a href="#">c3v76A_</a> | Alignment | not modelled | 98.8 | 19 | <b>PDB header:</b> flavoprotein<br><b>Chain:</b> A: <b>PDB Molecule:</b> flavoprotein;<br><b>PDBTitle:</b> the crystal structure of a flavoprotein from sinorhizobium                                                                                                               |

|     |                         |           |              |      |    |                                                                                                                                                                                                                                                          |
|-----|-------------------------|-----------|--------------|------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|     |                         |           |              |      |    | meliloti                                                                                                                                                                                                                                                 |
| 78  | <a href="#">c3l8kB_</a> | Alignment | not modelled | 98.8 | 35 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase;<br><b>PDBTitle:</b> crystal structure of a dihydrolipoyl dehydrogenase from <i>Sulfolobus solfataricus</i>                                       |
| 79  | <a href="#">c3o0hA_</a> | Alignment | not modelled | 98.8 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase;<br><b>PDBTitle:</b> crystal structure of glutathione reductase from <i>Bartonella henselae</i>                                                         |
| 80  | <a href="#">c2gqfA_</a> | Alignment | not modelled | 98.8 | 36 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein hi0933;<br><b>PDBTitle:</b> crystal structure of flavoprotein hi0933 from <i>Haemophilus influenzae</i> 2 rd                      |
| 81  | <a href="#">c1ltxR_</a> | Alignment | not modelled | 98.8 | 25 | <b>PDB header:</b> transferase/protein binding<br><b>Chain:</b> R: <b>PDB Molecule:</b> rab escort protein 1;<br><b>PDBTitle:</b> structure of rab escort protein-1 in complex with rab2 geranylgeranyl transferase and isoprenoid                       |
| 82  | <a href="#">d1vg0a1</a> | Alignment | not modelled | 98.8 | 25 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> GDI-like N domain                                                                                                                              |
| 83  | <a href="#">c3rhaA_</a> | Alignment | not modelled | 98.8 | 35 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putrescine oxidase;<br><b>PDBTitle:</b> the crystal structure of oxidoreductase from <i>Arthrobacter aureus</i>                                                               |
| 84  | <a href="#">c1m6iA_</a> | Alignment | not modelled | 98.7 | 12 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death protein 8;<br><b>PDBTitle:</b> crystal structure of apoptosis inducing factor (aif)                                                                     |
| 85  | <a href="#">c1ebdB_</a> | Alignment | not modelled | 98.7 | 28 | <b>PDB header:</b> complex (oxidoreductase/transferase)<br><b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase;<br><b>PDBTitle:</b> dihydrolipoamide dehydrogenase complexed with the binding2 domain of the dihydrolipoamide acetylase |
| 86  | <a href="#">c3p1wA_</a> | Alignment | not modelled | 98.7 | 25 | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> rabgdi protein;<br><b>PDBTitle:</b> crystal structure of rab gdi from <i>Plasmodium falciparum</i> , pfl2060c                                                              |
| 87  | <a href="#">c1gv4A_</a> | Alignment | not modelled | 98.7 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death protein 8;<br><b>PDBTitle:</b> murine apoptosis-inducing factor (aif)                                                                                   |
| 88  | <a href="#">d2gmha1</a> | Alignment | not modelled | 98.7 | 37 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> FAD-linked reductases, N-terminal domain                                                                                                       |
| 89  | <a href="#">c2yg4B_</a> | Alignment | not modelled | 98.7 | 38 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putrescine oxidase;<br><b>PDBTitle:</b> structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine                                    |
| 90  | <a href="#">d1jnra2</a> | Alignment | not modelled | 98.7 | 27 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain                                                                      |
| 91  | <a href="#">c3ic9D_</a> | Alignment | not modelled | 98.7 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase;<br><b>PDBTitle:</b> the structure of dihydrolipoamide dehydrogenase from <i>Colwellia2 psychrerythraea</i> 34h.                               |
| 92  | <a href="#">d1ebda1</a> | Alignment | not modelled | 98.7 | 29 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains                                                                                      |
| 93  | <a href="#">c3atrA_</a> | Alignment | not modelled | 98.7 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> conserved archaeal protein;<br><b>PDBTitle:</b> geranylgeranyl reductase (ggr) from <i>Sulfolobus acidocaldarius</i> co-2 crystallized with its ligand                        |
| 94  | <a href="#">c3d8xB_</a> | Alignment | not modelled | 98.7 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase 1;<br><b>PDBTitle:</b> crystal structure of <i>Saccharomyces cerevisiae</i> nadph dependent2 thioredoxin reductase 1                                    |
| 95  | <a href="#">d1onfa1</a> | Alignment | not modelled | 98.7 | 38 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains                                                                                      |
| 96  | <a href="#">c1s3bB_</a> | Alignment | not modelled | 98.7 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> amine oxidase [flavin-containing] b;<br><b>PDBTitle:</b> crystal structure of maob in complex with n-methyl-n-2 propargyl-1(r)-aminoindan                                     |
| 97  | <a href="#">d1lpfa1</a> | Alignment | not modelled | 98.7 | 31 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains                                                                                      |
| 98  | <a href="#">c2vv1D_</a> | Alignment | not modelled | 98.7 | 36 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> monoamine oxidase n;<br><b>PDBTitle:</b> the structure of mao-n-d3, a variant of monoamine oxidase2 from <i>Aspergillus niger</i> .                                           |
| 99  | <a href="#">c2q7vA_</a> | Alignment | not modelled | 98.7 | 38 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase;<br><b>PDBTitle:</b> crystal structure of <i>Deinococcus radiodurans</i> thioredoxin2 reductase                                                         |
| 100 | <a href="#">c2hqmB_</a> | Alignment | not modelled | 98.7 | 38 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glutathione reductase;<br><b>PDBTitle:</b> crystal structure of glutathione reductase glr1 from the yeast2 <i>Saccharomyces cerevisiae</i>                                    |
| 101 | <a href="#">c3ctyA_</a> | Alignment | not modelled | 98.7 | 34 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase;<br><b>PDBTitle:</b> crystal structure of <i>T. acidophilum</i> thioredoxin reductase                                                                   |
| 102 | <a href="#">c1ojtA_</a> | Alignment | not modelled | 98.7 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> surface protein;<br><b>PDBTitle:</b> structure of dihydrolipoamide dehydrogenase                                                                                              |
| 103 | <a href="#">c2zbwA_</a> | Alignment | not modelled | 98.7 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase;<br><b>PDBTitle:</b> crystal structure of thioredoxin reductase-like protein from <i>Thermus2 thermophilus</i> hb8                                      |



|     |                         |           |              |      |    |                                                                                                                                                                                                                                          |
|-----|-------------------------|-----------|--------------|------|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 104 | <a href="#">c1w4xA_</a> | Alignment | not modelled | 98.7 | 28 | <b>PDB header:</b> oxygenase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phenylacetone monooxygenase;<br><b>PDBTitle:</b> phenylacetone monooxygenase, a baeyer-villiger2 monooxygenase                                                     |
| 105 | <a href="#">d1gesa1</a> | Alignment | not modelled | 98.6 | 35 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains                                                                      |
| 106 | <a href="#">c1dxcC_</a> | Alignment | not modelled | 98.6 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase;<br><b>PDBTitle:</b> dihydrolipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum                               |
| 107 | <a href="#">c2cfyB_</a> | Alignment | not modelled | 98.6 | 33 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase 1;<br><b>PDBTitle:</b> crystal structure of human thioredoxin reductase 1                                                               |
| 108 | <a href="#">c3f8rD_</a> | Alignment | not modelled | 98.6 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> thioredoxin reductase (trxb-3);<br><b>PDBTitle:</b> crystal structure of sulfolobus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules |
| 109 | <a href="#">c1f6mF_</a> | Alignment | not modelled | 98.6 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> F: <b>PDB Molecule:</b> thioredoxin reductase;<br><b>PDBTitle:</b> crystal structure of a complex between thioredoxin2 reductase, thioredoxin, and the nadp+ analog, aadp+            |
| 110 | <a href="#">c3k7tB_</a> | Alignment | not modelled | 98.6 | 40 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 6-hydroxy-l-nicotine oxidase;<br><b>PDBTitle:</b> crystal structure of apo-form 6-hydroxy-l-nicotine oxidase,2 crystal form p3121                             |
| 111 | <a href="#">c2eq8E_</a> | Alignment | not modelled | 98.6 | 39 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> E: <b>PDB Molecule:</b> pyruvate dehydrogenase complex, dihydrolipoamide<br><b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp   |
| 112 | <a href="#">c2w0hA_</a> | Alignment | not modelled | 98.6 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> trypanothione reductase;<br><b>PDBTitle:</b> x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph               |
| 113 | <a href="#">c2a8xA_</a> | Alignment | not modelled | 98.6 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase;<br><b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis                                |
| 114 | <a href="#">c1geuA_</a> | Alignment | not modelled | 98.6 | 34 | <b>PDB header:</b> oxidoreductase(flavoenzyme)<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase;<br><b>PDBTitle:</b> anatomy of an engineered nad-binding site                                                             |
| 115 | <a href="#">c1bwcA_</a> | Alignment | not modelled | 98.6 | 32 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (glutathione reductase);<br><b>PDBTitle:</b> structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate       |
| 116 | <a href="#">d1v59a1</a> | Alignment | not modelled | 98.6 | 31 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains                                                                      |
| 117 | <a href="#">c1v59B_</a> | Alignment | not modelled | 98.6 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase;<br><b>PDBTitle:</b> crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+                                   |
| 118 | <a href="#">d1o5wa1</a> | Alignment | not modelled | 98.6 | 40 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> FAD-linked reductases, N-terminal domain                                                                                       |
| 119 | <a href="#">c2uzzD_</a> | Alignment | not modelled | 98.6 | 35 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> n-methyl-l-tryptophan oxidase;<br><b>PDBTitle:</b> x-ray structure of n-methyl-l-tryptophan oxidase (mtox)                                                    |
| 120 | <a href="#">d3lada1</a> | Alignment | not modelled | 98.6 | 33 | <b>Fold:</b> FAD/NAD(P)-binding domain<br><b>Superfamily:</b> FAD/NAD(P)-binding domain<br><b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains                                                                      |