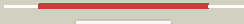



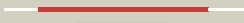














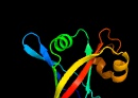




# Phyre2

|               |                              |
|---------------|------------------------------|
| Email         | mdejesus@rockefeller.edu     |
| Description   | RVBD0121c_(-)_147906_148340  |
| Date          | Tue Jul 23 14:50:16 BST 2019 |
| Unique Job ID | 95516eda3fbe8a65             |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|---|---|------------|--------|---|
| 1  | <a href="#">c4zkyB_</a> |  Alignment   |    | 100.0      | 58     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxamine 5-phosphate oxidase;<br><b>PDBTitle:</b> structure of f420 binding protein, msmeg_6526, from mycobacterium2 smegmatis   |
| 2  | <a href="#">d1rfea_</a> |  Alignment   |    | 100.0      | 26     | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like   |
| 3  | <a href="#">c3u0iA_</a> |  Alignment   |    | 100.0      | 17     | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable fad-binding, putative uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of a probable fad-binding, putative uncharacterized2 protein from brucella melitensis                                    |
| 4  | <a href="#">c3f7eB_</a> |  Alignment   |    | 100.0      | 20     | <b>PDB header:</b> unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related, fmn-<br><b>PDBTitle:</b> msmeg_3380 f420 reductase  |
| 5  | <a href="#">c2iabB_</a> |  Alignment |  | 100.0      | 21     | <b>PDB header:</b> unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein;<br><b>PDBTitle:</b> crystal structure of a protein with fmn-binding split barrel fold2 (np_828636.1) from streptomyces avermitilis at 2.00 a resolution  |
| 6  | <a href="#">d2asfa1</a> |  Alignment |  | 100.0      | 22     | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like   |
| 7  | <a href="#">d2hq9a1</a> |  Alignment |  | 100.0      | 19     | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like   |
| 8  | <a href="#">d2fg9a1</a> |  Alignment |  | 100.0      | 14     | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like   |
| 9  | <a href="#">c3fkhB_</a> |  Alignment |  | 99.9       | 17     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative pyridoxamine 5'-phosphate oxidase;<br><b>PDBTitle:</b> crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_601736.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.51 a resolution |
| 10 | <a href="#">d2i02a1</a> |  Alignment |  | 99.9       | 14     | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like   |
| 11 | <a href="#">c3tqvD_</a> |  Alignment |  | 99.9       | 18     | <b>PDB header:</b> heme binding protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> heme-binding protein hutz;<br><b>PDBTitle:</b> crystal structure of hutz,the heme storsge protein from vibrio2 cholerae  |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 12 | <a href="#">c3db0B_</a> | Alignment |              | 99.9 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> lin2891 protein;<br><b>PDBTitle:</b> crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_472219.1) from listeria innocua at 2.00 a resolution                              |
| 13 | <a href="#">d1w9aa_</a> | Alignment |              | 99.9 | 20 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like  |
| 14 | <a href="#">c3ec6A_</a> | Alignment |              | 99.9 | 18 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> general stress protein 26;<br><b>PDBTitle:</b> crystal structure of the general stress protein 26 from bacillus2 anthracis str. sterne                               |
| 15 | <a href="#">c2htiA_</a> | Alignment |              | 99.9 | 15 | <b>PDB header:</b> fmn-binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> bh0577 protein;<br><b>PDBTitle:</b> crystal structure of a flavin-nucleotide-binding protein (bh_0577)2 from bacillus halodurans at 2.50 a resolution                                  |
| 16 | <a href="#">d2htia1</a> | Alignment |              | 99.9 | 15 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like  |
| 17 | <a href="#">c6eciQ_</a> | Alignment |              | 99.9 | 24 | <b>PDB header:</b> fad-binding protein<br><b>Chain:</b> Q: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related, fmn-binding<br><b>PDBTitle:</b> structure of the fad binding protein msmeq_5243 from mycobacterium2 smegmatis                               |
| 18 | <a href="#">d2fhqa1</a> | Alignment |              | 99.9 | 18 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like  |
| 19 | <a href="#">c2re7A_</a> | Alignment |              | 99.9 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase related2 protein (psyc_0186) from psychrobacter arcticus 273-4 at 2.50 a3 resolution  |
| 20 | <a href="#">d2fura1</a> | Alignment |              | 99.9 | 14 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like  |
| 21 | <a href="#">c3cp3A_</a> | Alignment | not modelled | 99.9 | 24 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of conserved protein of unknown function dip18742 from corynebacterium diphtheriae                    |
| 22 | <a href="#">d2hq7a1</a> | Alignment | not modelled | 99.9 | 13 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like  |
| 23 | <a href="#">d1vl7a_</a> | Alignment | not modelled | 99.9 | 15 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like  |
| 24 | <a href="#">c5escD_</a> | Alignment | not modelled | 99.9 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> hupz;<br><b>PDBTitle:</b> crystal structure of group a streptococcus hupz   |
| 25 | <a href="#">c6rk0A_</a> | Alignment | not modelled | 99.9 | 18 | <b>PDB header:</b> flavoprotein<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> structure of the flavocytochrome anf3 from azotobacter vinelandii  |
| 26 | <a href="#">c4ybnB_</a> | Alignment | not modelled | 99.9 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> flavin-nucleotide-binding protein;<br><b>PDBTitle:</b> structure of the fad and heme binding protein msmeq_4975 from2 mycobacterium smegmatis   |
| 27 | <a href="#">d2vpaa1</a> | Alignment | not modelled | 99.9 | 22 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like  |
| 28 | <a href="#">c3u34D_</a> | Alignment | not modelled | 99.9 | 13 | <b>PDB header:</b> protein binding<br><b>Chain:</b> D: <b>PDB Molecule:</b> general stress protein;<br><b>PDBTitle:</b> crystal structure of the general stress fmn/fad binding protein from2 the phytopathogen xanthomonas citri<br><b>PDB header:</b> oxidoreductase |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 29 | <a href="#">c3dmbA_</a> | Alignment | not modelled | 99.9 | 11 | <b>Chain:</b> A: <b>PDB Molecule:</b> putative general stress protein 26 with a pnp-oxidase like<br><b>PDBTitle:</b> crystal structure of a putative general stress family protein2 (xcc2264) from xanthomonas campestris pv. campestris at 2.30 a3 resolution   |
| 30 | <a href="#">c2ig6B_</a> | Alignment | not modelled | 99.9 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nimc/nima family protein;<br><b>PDBTitle:</b> crystal structure of a nimc/nima family protein (ca_c2569) from2 clostridium acetobutylicum at 1.80 a resolution  |
| 31 | <a href="#">d2arza1</a> | Alignment | not modelled | 99.9 | 20 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like  |
| 32 | <a href="#">c2htdB_</a> | Alignment | not modelled | 99.9 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> predicted flavin-nucleotide-binding protein from cog3576<br><b>PDBTitle:</b> crystal structure of a putative pyridoxamine 5'-phosphate oxidase2 (ldb0262) from lactobacillus delbrueckii subsp. at 1.60 a resolution        |
| 33 | <a href="#">c2hhzA_</a> | Alignment | not modelled | 99.8 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related;<br><b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase-related2 protein (ssuidraft_2804) from streptococcus suis 89/1591 at 2.00 a3 resolution             |
| 34 | <a href="#">c5bncB_</a> | Alignment | not modelled | 99.8 | 27 | <b>PDB header:</b> heme binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> heme binding protein msmeg_6519;<br><b>PDBTitle:</b> structure of heme binding protein msmeg_6519 from mycobacterium2 smegmatis   |
| 35 | <a href="#">c3gasA_</a> | Alignment | not modelled | 99.8 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> heme oxygenase;<br><b>PDBTitle:</b> crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme  |
| 36 | <a href="#">c2qeaB_</a> | Alignment | not modelled | 99.8 | 12 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative general stress protein 26;<br><b>PDBTitle:</b> crystal structure of a putative general stress protein 26 (jann_0955)2 from jannaschia sp. ccs1 at 2.46 a resolution  |
| 37 | <a href="#">c3dnhB_</a> | Alignment | not modelled | 99.8 | 19 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein atu2129;<br><b>PDBTitle:</b> the crystal structure of the protein atu2129 (unknown function) from2 agrobacterium tumefaciens str. c58  |
| 38 | <a href="#">d1flma_</a> | Alignment | not modelled | 99.8 | 24 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like  |
| 39 | <a href="#">c2q9kA_</a> | Alignment | not modelled | 99.8 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of a putative oxidoreductase (exig_1997) from2 exiguobacterium sibiricum 255-15 at 1.59 a resolution   |
| 40 | <a href="#">c2ol5B_</a> | Alignment | not modelled | 99.7 | 11 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> pai 2 protein;<br><b>PDBTitle:</b> crystal structure of a protease synthase and sporulation negative2 regulatory protein pai 2 from bacillus stearothermophilus  |
| 41 | <a href="#">d1nrga_</a> | Alignment | not modelled | 99.7 | 24 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like  |
| 42 | <a href="#">c1nrgA_</a> | Alignment | not modelled | 99.7 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxine 5'-phosphate oxidase;<br><b>PDBTitle:</b> structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase   |
| 43 | <a href="#">d1dnla_</a> | Alignment | not modelled | 99.7 | 20 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like  |
| 44 | <a href="#">d1t9ma_</a> | Alignment | not modelled | 99.7 | 24 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like  |
| 45 | <a href="#">d1ty9a_</a> | Alignment | not modelled | 99.7 | 25 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like  |
| 46 | <a href="#">c2a2jA_</a> | Alignment | not modelled | 99.7 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase;<br><b>PDBTitle:</b> crystal structure of a putative pyridoxine 5'-phosphate oxidase2 (rv2607) from mycobacterium tuberculosis  |
| 47 | <a href="#">c4hmwB_</a> | Alignment | not modelled | 99.7 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase;<br><b>PDBTitle:</b> crystal structure of phz3 from burkholderia lata 383   |
| 48 | <a href="#">d2a2ja1</a> | Alignment | not modelled | 99.7 | 20 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like  |
| 49 | <a href="#">c2ou5B_</a> | Alignment | not modelled | 99.6 | 19 | <b>PDB header:</b> flavoprotein<br><b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related, fmn-binding;<br><b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase-related fmn-2 binding protein (jann_0254) from jannaschia sp. ccs1 at 1.60 a3 resolution |
| 50 | <a href="#">d1xhna1</a> | Alignment | not modelled | 99.6 | 18 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like  |
| 51 | <a href="#">c4n7rD_</a> | Alignment | not modelled | 99.4 | 21 | <b>PDB header:</b> oxidoreductase/protein binding<br><b>Chain:</b> D: <b>PDB Molecule:</b> genomic dna, chromosome 3, p1 clone: mxl8;<br><b>PDBTitle:</b> crystal structure of arabidopsis glutamyl-trna reductase in complex2 with its binding protein  |
| 52 | <a href="#">d1ci0a_</a> | Alignment | not modelled | 99.4 | 13 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> PNP-oxidase like  |
|    |                         |           |              |      |    | <b>PDB header:</b> flavoprotein<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized conserved protein of  |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 53 | <a href="#">c2i51B</a>  | Alignment | not modelled | 99.3 | 17 | cog5135;<br><b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase-related, fmn2 binding protein (npun_f5749) from nostoc punctiforme pcc 73102 at3 1.40 a resolution  |
| 54 | <a href="#">c3r5zB</a>  | Alignment | not modelled | 98.8 | 19 | <b>PDB header:</b> unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420   |
| 55 | <a href="#">c3r5yC</a>  | Alignment | not modelled | 98.8 | 25 | <b>PDB header:</b> unknown function<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> structure of a deazaflavin-dependent nitroreductase from nocardia2 farcinica, with co-factor f420  |
| 56 | <a href="#">c3r5wO</a>  | Alignment | not modelled | 98.7 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> O: <b>PDB Molecule:</b> deazaflavin-dependent nitroreductase;<br><b>PDBTitle:</b> structure of ddn, the deazaflavin-dependent nitroreductase from2 mycobacterium tuberculosis involved in bioreductive activation of pa-3 824, with co-factor f420   |
| 57 | <a href="#">c4y9iA</a>  | Alignment | not modelled | 98.7 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> mycobacterium tuberculosis paralogous family 11;<br><b>PDBTitle:</b> structure of f420-h2 dependent reductase (fdr-a) msmeg_2027   |
| 58 | <a href="#">c3ba3A</a>  | Alignment | not modelled | 98.6 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-like protein;<br><b>PDBTitle:</b> crystal structure of pyridoxamine 5'-phosphate oxidase-like protein2 (np_783940.1) from lactobacillus plantarum at 1.55 a resolution                     |
| 59 | <a href="#">c3h96B</a>  | Alignment | not modelled | 98.6 | 18 | <b>PDB header:</b> flavoprotein<br><b>Chain:</b> B: <b>PDB Molecule:</b> f420-h2 dependent reductase a;<br><b>PDBTitle:</b> msmeg_3358 f420 reductase   |
| 60 | <a href="#">d2ptfa1</a> | Alignment | not modelled | 96.8 | 23 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> MTH863-like  |
| 61 | <a href="#">c2ptfB</a>  | Alignment | not modelled | 96.3 | 21 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein mth_863;<br><b>PDBTitle:</b> crystal structure of protein mth_863 from methanobacterium2 thermoautotrophicum bound to fmn   |
| 62 | <a href="#">c3fgeA</a>  | Alignment | not modelled | 95.7 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative flavin reductase with split barrel domain;<br><b>PDBTitle:</b> crystal structure of putative flavin reductase with split barrel2 domain (yp_750721.1) from shewanella frigidimarina ncimb 400 at 1.743 a resolution |
| 63 | <a href="#">d2imla1</a> | Alignment | not modelled | 95.3 | 23 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> MTH863-like  |
| 64 | <a href="#">c3b5mD</a>  | Alignment | not modelled | 94.6 | 16 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of conserved uncharacterized protein from2 rhodopirellula baltica  |
| 65 | <a href="#">c3bpkB</a>  | Alignment | not modelled | 94.5 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nitrilotriacetate monooxygenase component b;<br><b>PDBTitle:</b> crystal structure of nitrilotriacetate monooxygenase component b from2 bacillus cereus  |
| 66 | <a href="#">c3e4vA</a>  | Alignment | not modelled | 94.4 | 15 | <b>PDB header:</b> flavoprotein<br><b>Chain:</b> A: <b>PDB Molecule:</b> nadh:fmn oxidoreductase like protein;<br><b>PDBTitle:</b> crystal structure of nadh:fmn oxidoreductase like protein in complex2 with fmn (yp_544701.1) from methylobacillus flagellatus kt at 1.40 a3 resolution               |
| 67 | <a href="#">c4z85A</a>  | Alignment | not modelled | 94.1 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 2-nitrobenzoate nitroreductase;<br><b>PDBTitle:</b> crystal structur of pseudomonas fluorescens 2-nitrobenzoate 2-2 nitroreductase nbaa  |
| 68 | <a href="#">d1ejea</a>  | Alignment | not modelled | 94.1 | 15 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> NADH:FMN oxidoreductase-like   |
| 69 | <a href="#">d2nr4a1</a> | Alignment | not modelled | 91.3 | 16 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> MTH863-like  |
| 70 | <a href="#">c2d5mA</a>  | Alignment | not modelled | 84.9 | 15 | <b>PDB header:</b> electron transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> flavodoxin;<br><b>PDBTitle:</b> flavodoxin of desulfovibrio vulgaris (miyazaki f)  |
| 71 | <a href="#">c3hmzA</a>  | Alignment | not modelled | 74.6 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> flavin reductase domain protein, fmn-binding;<br><b>PDBTitle:</b> crystal structure of a fmn-binding domain of flavin reductases-like2 enzyme (sba1_0626) from shewanella baltica os155 at 1.50 a resolution                 |
| 72 | <a href="#">c3bnkB</a>  | Alignment | not modelled | 69.3 | 16 | <b>PDB header:</b> electron transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> flavodoxin;<br><b>PDBTitle:</b> x-ray crystal structure of flavodoxin from methanosarcina2 acetivorans   |
| 73 | <a href="#">c3pftA</a>  | Alignment | not modelled | 63.7 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> flavin reductase;<br><b>PDBTitle:</b> crystal structure of untagged c54a mutant flavin reductase (dszd) in2 complex with fmn from mycobacterium goodii   |
| 74 | <a href="#">c2r6vA</a>  | Alignment | not modelled | 58.6 | 8  | <b>PDB header:</b> flavoprotein<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ph0856;<br><b>PDBTitle:</b> crystal structure of fmn-binding protein (np_142786.1) from pyrococcus2 horikoshii at 1.35 a resolution  |
| 75 | <a href="#">c4l82D</a>  | Alignment | not modelled | 52.7 | 10 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> rifea.00250.a;<br><b>PDBTitle:</b> structure of a putative oxidoreductase from rickettsia felis  |
| 76 | <a href="#">c4f07A</a>  | Alignment | not modelled | 42.6 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> styrene monooxygenase component 2;<br><b>PDBTitle:</b> structure of the styrene monooxygenase flavin reductase   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
|    |                         |           |              |      |    | (smob) from2 pseudomonas putida s12  |
| 77 | <a href="#">c2qckA_</a> | Alignment | not modelled | 29.1 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> flavin reductase domain protein;<br><b>PDBTitle:</b> crystal structure of flavin reductase domain protein (yp_831077.1)2 from arthrobacter sp. fb24 at 1.90 a resolution                |
| 78 | <a href="#">d1usca_</a> | Alignment | not modelled | 24.7 | 16 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> NADH:FMN oxidoreductase-like  |
| 79 | <a href="#">d1rz0a_</a> | Alignment | not modelled | 23.7 | 19 | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> NADH:FMN oxidoreductase-like  |
| 80 | <a href="#">c3k87B_</a> | Alignment | not modelled | 23.6 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> chlorophenol-4-monooxygenase component 1;<br><b>PDBTitle:</b> crystal structure of nadh:fad oxidoreductase (tfc) - fad2 complex   |
| 81 | <a href="#">c2xi5D_</a> | Alignment | not modelled | 20.5 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> rna polymerase I;<br><b>PDBTitle:</b> n-terminal endonuclease domain of la crosse virus I-protein  |
| 82 | <a href="#">c2xi7B_</a> | Alignment | not modelled | 20.4 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> rna polymerase I;<br><b>PDBTitle:</b> n-terminal endonuclease domain of la crosse virus I-protein  |
| 83 | <a href="#">c3rh7A_</a> | Alignment | not modelled | 20.2 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical oxidoreductase;<br><b>PDBTitle:</b> crystal structure of a putative oxidoreductase (sma0793) from2 sinorhizobium meliloti 1021 at 3.00 a resolution                        |
| 84 | <a href="#">c5b42A_</a> | Alignment | not modelled | 15.8 | 12 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna mismatch repair protein mutl;<br><b>PDBTitle:</b> crystal structure of the c-terminal endonuclease domain of aquifex2 aeolicus mutl.   |
| 85 | <a href="#">c2r0xA_</a> | Alignment | not modelled | 15.1 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> possible flavin reductase;<br><b>PDBTitle:</b> crystal structure of a putative flavin reductase (ycdh_h5_1225) from2 haemophilus somnus 129pt at 1.06 a resolution                      |
| 86 | <a href="#">c4xhyA_</a> | Alignment | not modelled | 15.0 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> flavin reductase domain protein, fmn-binding protein;<br><b>PDBTitle:</b> nadh:fmn oxidoreductase from paracoccus denitrificans   |
| 87 | <a href="#">d1i0ra_</a> | Alignment | not modelled | 14.7 | 9  | <b>Fold:</b> Split barrel-like<br><b>Superfamily:</b> FMN-binding split barrel<br><b>Family:</b> NADH:FMN oxidoreductase-like  |
| 88 | <a href="#">c2l82A_</a> | Alignment | not modelled | 12.5 | 23 | <b>PDB header:</b> de novo protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> designed protein or32;<br><b>PDBTitle:</b> solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or32               |
| 89 | <a href="#">c3cr8C_</a> | Alignment | not modelled | 11.8 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> sulfate adenylyltransferase, adenylylsulfate kinase;<br><b>PDBTitle:</b> hexameric aps kinase from thiobacillus denitrificans  |
| 90 | <a href="#">c3cb0B_</a> | Alignment | not modelled | 11.6 | 9  | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 4-hydroxyphenylacetate 3-monooxygenase;<br><b>PDBTitle:</b> cobr  |
| 91 | <a href="#">d1zzka1</a> | Alignment | not modelled | 11.5 | 13 | <b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I)<br><b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I)<br><b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)   |
| 92 | <a href="#">c3nfwB_</a> | Alignment | not modelled | 10.8 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> flavin reductase-like, fmn-binding protein;<br><b>PDBTitle:</b> crystal structure of nitrilotriacetate monooxygenase component b2 (a0r521 homolog) from mycobacterium thermoresistibile |
| 93 | <a href="#">c2d38A_</a> | Alignment | not modelled | 10.4 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical nadh-dependent fmn oxidoreductase;<br><b>PDBTitle:</b> the crystal structure of flavin reductase hpac complexed with nadp+   |
| 94 | <a href="#">d1g8fa1</a> | Alignment | not modelled | 9.3  | 19 | <b>Fold:</b> PUA domain-like<br><b>Superfamily:</b> PUA domain-like<br><b>Family:</b> ATP sulfurylase N-terminal domain  |
| 95 | <a href="#">c6igzF_</a> | Alignment | not modelled | 8.7  | 50 | <b>PDB header:</b> plant protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> psaf;<br><b>PDBTitle:</b> structure of psi-lhci  |
| 96 | <a href="#">c4kt0F_</a> | Alignment | not modelled | 8.6  | 50 | <b>PDB header:</b> electron transport<br><b>Chain:</b> F: <b>PDB Molecule:</b> photosystem i subunit iii;<br><b>PDBTitle:</b> crystal structure of a virus like photosystem i from the2 cyanobacterium synechocystis pcc 6803                                      |
| 97 | <a href="#">c3kk4B_</a> | Alignment | not modelled | 8.5  | 19 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein bp1543;<br><b>PDBTitle:</b> uncharacterized protein bp1543 from bordetella pertussis tohama i  |
| 98 | <a href="#">c6ijjF_</a> | Alignment | not modelled | 8.4  | 50 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> psaf;<br><b>PDBTitle:</b> photosystem i of chlamydomonas reinhardtii  |
| 99 | <a href="#">c4b8tA_</a> | Alignment | not modelled | 7.8  | 10 | <b>PDB header:</b> transcription/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> kh-type splicing regulatory protein;<br><b>PDBTitle:</b> rna binding protein solution structure of the third kh2 domain of ksrp in complex with the g-rich target sequence.          |