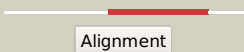

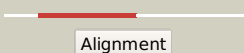

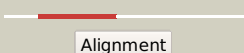

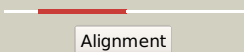

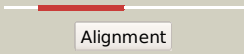

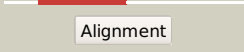

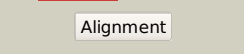

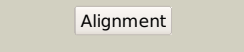

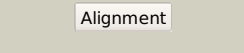



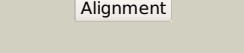












# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD1355c\_(moeY)\_1521891\_1524038  
 Date Wed Jul 31 22:05:45 BST 2019  
 Unique Job ID 4767129b56ca8821

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c2ymvA_</a> |  Alignment   |    | 100.0      | 21     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acg nitroreductase;<br><b>PDBTitle:</b> structure of reduced m smegmatis 5246, a homologue of m.2 tuberculosis acg  |
| 2  | <a href="#">c6h77B_</a> |  Alignment   |    | 100.0      | 17     | <b>PDB header:</b> signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-like modifier-activating enzyme 5;<br><b>PDBTitle:</b> e1 enzyme for ubiquitin like protein activation in complex with ubl   |
| 3  | <a href="#">c4d7aA_</a> |  Alignment   |    | 100.0      | 19     | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> trna threonylcarbamoyladenine dehydratase;<br><b>PDBTitle:</b> crystal structure of e. coli trna n6-threonylcarbamoyladenine2 dehydratase, tcda, in complex with amp at 1.801 angstroem3 resolution |
| 4  | <a href="#">c1zfnA_</a> |  Alignment   |   | 100.0      | 21     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> adenylyltransferase thif;<br><b>PDBTitle:</b> structural analysis of escherichia coli thif   |
| 5  | <a href="#">c3h9gA_</a> |  Alignment |  | 100.0      | 18     | <b>PDB header:</b> transferase/antibiotic<br><b>Chain:</b> A: <b>PDB Molecule:</b> mccb protein;<br><b>PDBTitle:</b> crystal structure of e. coli mccb + mcca-n7isoasn   |
| 6  | <a href="#">d1jw9b_</a> |  Alignment |  | 100.0      | 24     | <b>Fold:</b> Activating enzymes of the ubiquitin-like proteins<br><b>Superfamily:</b> Activating enzymes of the ubiquitin-like proteins<br><b>Family:</b> Molybdenum cofactor biosynthesis protein MoeB  |
| 7  | <a href="#">c5ff5A_</a> |  Alignment |  | 100.0      | 26     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> paaa;<br><b>PDBTitle:</b> crystal structure of semet paaa  |
| 8  | <a href="#">d1yovb1</a> |  Alignment |  | 100.0      | 21     | <b>Fold:</b> Activating enzymes of the ubiquitin-like proteins<br><b>Superfamily:</b> Activating enzymes of the ubiquitin-like proteins<br><b>Family:</b> Ubiquitin activating enzymes (UBA)   |
| 9  | <a href="#">c3gznb_</a> |  Alignment |  | 100.0      | 16     | <b>PDB header:</b> protein binding/ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nedd8-activating enzyme e1 catalytic subunit;<br><b>PDBTitle:</b> structure of nedd8-activating enzyme in complex with nedd8 and mln4924  |
| 10 | <a href="#">c3kycB_</a> |  Alignment |  | 100.0      | 20     | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> sumo-activating enzyme subunit 2;<br><b>PDBTitle:</b> human sumo e1 complex with a sumo1-amp mimic  |
| 11 | <a href="#">c3kydB_</a> |  Alignment |  | 100.0      | 20     | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> sumo-activating enzyme subunit 2;<br><b>PDBTitle:</b> human sumo e1~sumo1-amp tetrahedral intermediate mimic  |

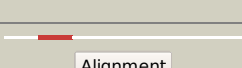
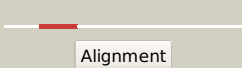
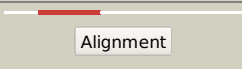
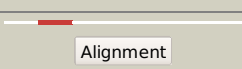

|    |                         |           |   |       |    |   |
|----|-------------------------|-----------|---|-------|----|---|
| 12 | <a href="#">c1y8qD_</a> | Alignment |     | 100.0 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> D: <b>PDB Molecule:</b> ubiquitin-like 2 activating enzyme e1b;<br><b>PDBTitle:</b> sumo e1 activating enzyme sae1-sae2-mg-atp complex   |
| 13 | <a href="#">c3wv9D_</a> | Alignment |    | 100.0 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> hmd co-occurring protein hcge;<br><b>PDBTitle:</b> guanylylpyridinol (gp)- and atp-bound hcge from methanothermobacter2 marburgensis  |
| 14 | <a href="#">c6dc6A_</a> | Alignment |    | 100.0 | 21 | <b>PDB header:</b> signaling protein/ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like modifier-activating enzyme 1;<br><b>PDBTitle:</b> crystal structure of human ubiquitin activating enzyme e1 (uba1) in2 complex with ubiquitin   |
| 15 | <a href="#">c3vh3A_</a> | Alignment |    | 100.0 | 14 | <b>PDB header:</b> metal binding protein/protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like modifier-activating enzyme atg7;<br><b>PDBTitle:</b> crystal structure of atg7ctd-atg8 complex   |
| 16 | <a href="#">c4ii3A_</a> | Alignment |    | 100.0 | 21 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-activating enzyme e1 1;<br><b>PDBTitle:</b> crystal structure of s. pombe ubiquitin activating enzyme 1 (uba1) in2 complex with ubiquitin and atp/mg   |
| 17 | <a href="#">c3cmmA_</a> | Alignment |   | 100.0 | 21 | <b>PDB header:</b> ligase/protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-activating enzyme e1 1;<br><b>PDBTitle:</b> crystal structure of the uba1-ubiquitin complex  |
| 18 | <a href="#">c1y8qA_</a> | Alignment |  | 100.0 | 16 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like 1 activating enzyme e1a;<br><b>PDBTitle:</b> sumo e1 activating enzyme sae1-sae2-mg-atp complex   |
| 19 | <a href="#">c2nvuB_</a> | Alignment |  | 100.0 | 16 | <b>PDB header:</b> protein turnover, ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> maltose binding protein/nedd8-activating enzyme<br><b>PDBTitle:</b> structure of appbp1-uba3~nedd8-nedd8-mgatp-ubc12(c111a), a2 trapped ubiquitin-like protein activation complex                                      |
| 20 | <a href="#">c3vh1A_</a> | Alignment |  | 100.0 | 17 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like modifier-activating enzyme atg7;<br><b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae atg7 (1-595)  |
| 21 | <a href="#">d1yova1</a> | Alignment | not modelled  | 100.0 | 16 | <b>Fold:</b> Activating enzymes of the ubiquitin-like proteins<br><b>Superfamily:</b> Activating enzymes of the ubiquitin-like proteins<br><b>Family:</b> Ubiquitin activating enzymes (UBA)  |
| 22 | <a href="#">c4p22A_</a> | Alignment | not modelled  | 100.0 | 23 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like modifier-activating enzyme 1;<br><b>PDBTitle:</b> crystal structure of n-terminal fragments of e1   |
| 23 | <a href="#">c3gucB_</a> | Alignment | not modelled  | 99.9  | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-like modifier-activating enzyme 5;<br><b>PDBTitle:</b> human ubiquitin-activating enzyme 5 in complex with amppnp   |
| 24 | <a href="#">c3gr3B_</a> | Alignment | not modelled  | 99.7  | 13 | <b>PDB header:</b> flavoprotein<br><b>Chain:</b> B: <b>PDB Molecule:</b> nitroreductase;<br><b>PDBTitle:</b> crystal structure of a nitroreductase-like family protein (pnba,2 bh06130) from bartonella henselae str. houston-1 at 1.45 a resolution  |
| 25 | <a href="#">c2isiB_</a> | Alignment | not modelled  | 99.5  | 19 | <b>PDB header:</b> flavoprotein<br><b>Chain:</b> B: <b>PDB Molecule:</b> blub;<br><b>PDBTitle:</b> blub bound to reduced flavin (fmnh2) and molecular oxygen.2 (clear crystal form)   |
| 26 | <a href="#">c3kwaA_</a> | Alignment | not modelled  | 99.5  | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative nadh dehydrogenase/nad(p)h nitroreductase;<br><b>PDBTitle:</b> crystal structure of putative nadh dehydrogenase/nad(p)h2 nitroreductase (np_809094.1) from bacteroides thetaiotaomicron vpi-3 5482 at 1.54 a resolution |
| 27 | <a href="#">c3gh8A_</a> | Alignment | not modelled  | 99.5  | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> iodotyrosine dehalogenase 1;<br><b>PDBTitle:</b> crystal structure of mus musculus iodotyrosine deiodinase (iyd) bound2 to fmn and di-iodotyrosine (dit)<br><b>PDB header:</b> unknown function                                  |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 28 | <a href="#">c4xomB_</a> | Alignment | not modelled | 99.5 | 19 | <b>Chain:</b> B: <b>PDB Molecule:</b> coenzyme f420:l-glutamate ligase; <b>PDBTitle:</b> coenzyme f420:l-glutamate ligase (fbib) from mycobacterium2 tuberculosis (c-terminal domain).  |
| 29 | <a href="#">c3eo8A_</a> | Alignment | not modelled | 99.5 | 13 | <b>PDB header:</b> flavoprotein<br><b>Chain:</b> A: <b>PDB Molecule:</b> blub-like flavoprotein; <b>PDBTitle:</b> crystal structure of blub-like flavoprotein (yp_001089088.1) from2 clostridium difficile 630 at 1.74 a resolution   |
| 30 | <a href="#">c3to0A_</a> | Alignment | not modelled | 99.4 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> iodotyrosine deiodinase 1; <b>PDBTitle:</b> crystal structure of mus musculus iodotyrosine deiodinase (yid) c217a,2 c239a bound to fmn   |
| 31 | <a href="#">c3e39A_</a> | Alignment | not modelled | 99.4 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative nitroreductase; <b>PDBTitle:</b> crystal structure of a putative nitroreductase in complex with fmn2 (dde_0787) from desulfovibrio desulfuricans subsp. at 1.70 a3 resolution                                   |
| 32 | <a href="#">c2i7hE_</a> | Alignment | not modelled | 99.4 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> E: <b>PDB Molecule:</b> nitroreductase-like family protein; <b>PDBTitle:</b> crystal structure of the nitroreductase-like family protein from2 bacillus cereus   |
| 33 | <a href="#">c2wzvB_</a> | Alignment | not modelled | 99.4 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nfnb protein; <b>PDBTitle:</b> crystal structure of the fmn-dependent nitroreductase nfnb2 from mycobacterium smegmatis  |
| 34 | <a href="#">c5ko8B_</a> | Alignment | not modelled | 99.4 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of haliscomenobacter hydrossis iodotyrosine2 deiodinase (yid) bound to fmn and mono-iodotyrosine (i-tyr)  |
| 35 | <a href="#">c3ek3A_</a> | Alignment | not modelled | 99.4 | 15 | <b>PDB header:</b> flavoprotein<br><b>Chain:</b> A: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of nitroreductase with bound fmn (yp_211706.1) from2 bacteroides fragilis nctc 9343 at 1.70 a resolution  |
| 36 | <a href="#">d1nox_</a>  | Alignment | not modelled | 99.3 | 15 | <b>Fold:</b> FMN-dependent nitroreductase-like<br><b>Superfamily:</b> FMN-dependent nitroreductase-like<br><b>Family:</b> NADH oxidase/flavin reductase   |
| 37 | <a href="#">c3pxvD_</a> | Alignment | not modelled | 99.3 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of a nitroreductase with bound fmn (dhaf_2018) from2 desulfitobacterium hafniense dcb-2 at 2.30 a resolution  |
| 38 | <a href="#">c3bm2B_</a> | Alignment | not modelled | 99.3 | 12 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein ydja; <b>PDBTitle:</b> crystal structure of a minimal nitroreductase ydja from escherichia2 coli k12 with and without fmn cofactor   |
| 39 | <a href="#">c3m5kA_</a> | Alignment | not modelled | 99.3 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative nadh dehydrogenase/nad(p)h nitroreductase; <b>PDBTitle:</b> crystal structure of putative nadh dehydrogenase/nad(p)h2 nitroreductase (bdi_1728) from parabacteroides distasonis atcc 85033 at 1.86 a resolution |
| 40 | <a href="#">d1bkja_</a> | Alignment | not modelled | 99.3 | 18 | <b>Fold:</b> FMN-dependent nitroreductase-like<br><b>Superfamily:</b> FMN-dependent nitroreductase-like<br><b>Family:</b> NADH oxidase/flavin reductase   |
| 41 | <a href="#">d1vfra_</a> | Alignment | not modelled | 99.3 | 13 | <b>Fold:</b> FMN-dependent nitroreductase-like<br><b>Superfamily:</b> FMN-dependent nitroreductase-like<br><b>Family:</b> NADH oxidase/flavin reductase   |
| 42 | <a href="#">d1kqba_</a> | Alignment | not modelled | 99.3 | 16 | <b>Fold:</b> FMN-dependent nitroreductase-like<br><b>Superfamily:</b> FMN-dependent nitroreductase-like<br><b>Family:</b> NADH oxidase/flavin reductase   |
| 43 | <a href="#">d1f5va_</a> | Alignment | not modelled | 99.3 | 18 | <b>Fold:</b> FMN-dependent nitroreductase-like<br><b>Superfamily:</b> FMN-dependent nitroreductase-like<br><b>Family:</b> NADH oxidase/flavin reductase   |
| 44 | <a href="#">c3n2sD_</a> | Alignment | not modelled | 99.3 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> nadph-dependent nitro/flavin reductase; <b>PDBTitle:</b> structure of nfra1 nitroreductase from b. subtilis  |
| 45 | <a href="#">c3g14B_</a> | Alignment | not modelled | 99.2 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nitroreductase family protein; <b>PDBTitle:</b> crystal structure of nitroreductase family protein (yp_877874.1) from2 clostridium novyi nt at 1.75 a resolution   |
| 46 | <a href="#">d1zcha1</a> | Alignment | not modelled | 99.2 | 16 | <b>Fold:</b> FMN-dependent nitroreductase-like<br><b>Superfamily:</b> FMN-dependent nitroreductase-like<br><b>Family:</b> NADH oxidase/flavin reductase   |
| 47 | <a href="#">c4eo3A_</a> | Alignment | not modelled | 99.2 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> bacterioferritin comigratory protein/nadh dehydrogenase; <b>PDBTitle:</b> peroxiredoxin nitroreductase fusion enzyme   |
| 48 | <a href="#">d1ykia1</a> | Alignment | not modelled | 99.2 | 11 | <b>Fold:</b> FMN-dependent nitroreductase-like<br><b>Superfamily:</b> FMN-dependent nitroreductase-like<br><b>Family:</b> NADH oxidase/flavin reductase   |
| 49 | <a href="#">c5hdjA_</a> | Alignment | not modelled | 99.2 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nfra1; <b>PDBTitle:</b> structure of b. megaterium nfra1   |
| 50 | <a href="#">c3gfaB_</a> | Alignment | not modelled | 99.2 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative nitroreductase; <b>PDBTitle:</b> crystal structure of a putative nitroreductase in complex with fmn2 (cd3205) from clostridium difficile 630 at 1.35 a resolution   |
| 51 | <a href="#">c5heiE_</a> | Alignment | not modelled | 99.2 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> E: <b>PDB Molecule:</b> nfra2; <b>PDBTitle:</b> structure of b. megaterium nfra2   |
| 52 | <a href="#">d2b67a1</a> | Alignment | not modelled | 99.2 | 12 | <b>Fold:</b> FMN-dependent nitroreductase-like<br><b>Superfamily:</b> FMN-dependent nitroreductase-like<br><b>Family:</b> NADH oxidase/flavin reductase   |
|    |                         |           |              |      |    | <b>PDB header:</b> oxidoreductase   |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 53 | <a href="#">c3bemA</a>  | Alignment | not modelled | 99.2 | 16 | <b>Chain:</b> A: <b>PDB Molecule:</b> putative nad(p)h nitroreductase ydfn;<br><b>PDBTitle:</b> crystal structure of putative nitroreductase ydfn (2632848) from2 bacillus subtilis at 1.65 a resolution  |
| 54 | <a href="#">c3e10B</a>  | Alignment | not modelled | 99.2 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative nadh oxidase;<br><b>PDBTitle:</b> crystal structure of putative nadh oxidase (np_348178.1) from2 clostridium acetobutylicum at 1.40 a resolution  |
| 55 | <a href="#">c3ge5A</a>  | Alignment | not modelled | 99.2 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative nad(p)h:fmn oxidoreductase;<br><b>PDBTitle:</b> crystal structure of a putative nad(p)h:fmn oxidoreductase (pg0310)2 from porphyromonas gingivalis w83 at 1.70 a resolution   |
| 56 | <a href="#">c4qlyB</a>  | Alignment | not modelled | 99.1 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> enone reductase cla-er;<br><b>PDBTitle:</b> crystal structure of cla-er, a novel enone reductase catalyzing a key2 step of a gut-bacterial fatty acid saturation metabolism,3 biohydrogenation                                 |
| 57 | <a href="#">c4dn2A</a>  | Alignment | not modelled | 99.1 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nitroreductase;<br><b>PDBTitle:</b> crystal structure of putative nitroreductase from geobacter2 metallireducens gs-15   |
| 58 | <a href="#">c3k6hB</a>  | Alignment | not modelled | 99.1 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nitroreductase family protein;<br><b>PDBTitle:</b> crystal structure of a nitroreductase family protein from2 agrobacterium tumefaciens str. c58   |
| 59 | <a href="#">c3koqC</a>  | Alignment | not modelled | 99.1 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> nitroreductase family protein;<br><b>PDBTitle:</b> crystal structure of a nitroreductase family protein (cd3355) from2 clostridium difficile 630 at 1.58 a resolution  |
| 60 | <a href="#">c5j6cA</a>  | Alignment | not modelled | 99.1 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative reductase;<br><b>PDBTitle:</b> fmn-dependent nitroreductase (cdr20291_0767) from clostridium2 difficile r20291  |
| 61 | <a href="#">c6czpH</a>  | Alignment | not modelled | 99.1 | 12 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> H: <b>PDB Molecule:</b> oxygen-insensitive nad(p)h nitroreductase;<br><b>PDBTitle:</b> 2.2 angstrom resolution crystal structure oxygen-insensitive nad(p)h-2 dependent nitroreductase nfsb from vibrio vulnificus in complex with3 fmn                |
| 62 | <a href="#">c3of4A</a>  | Alignment | not modelled | 99.1 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nitroreductase;<br><b>PDBTitle:</b> crystal structure of a fmn/fad- and nad(p)h-dependent nitroreductase2 (nfnb, il2077) from idiomarina loihiensis l2tr at 1.90 a resolution  |
| 63 | <a href="#">c3eofB</a>  | Alignment | not modelled | 99.1 | 12 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase;<br><b>PDBTitle:</b> crystal structure of putative oxidoreductase (yp_213212.1) from2 bacteroides fragilis nctc 9343 at 1.99 a resolution  |
| 64 | <a href="#">c3qdID</a>  | Alignment | not modelled | 99.1 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> oxygen-insensitive nadph nitroreductase;<br><b>PDBTitle:</b> crystal structure of rdxa from helicobacter pylori  |
| 65 | <a href="#">c3gagB</a>  | Alignment | not modelled | 99.0 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative nadh dehydrogenase, nadph nitroreductase;<br><b>PDBTitle:</b> crystal structure of a nitroreductase-like protein (smu.346) from2 streptococcus mutans at 1.70 a resolution  |
| 66 | <a href="#">d2frea1</a> | Alignment | not modelled | 99.0 | 23 | <b>Fold:</b> FMN-dependent nitroreductase-like<br><b>Superfamily:</b> FMN-dependent nitroreductase-like<br><b>Family:</b> NADH oxidase/flavin reductase   |
| 67 | <a href="#">c3ge6B</a>  | Alignment | not modelled | 99.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nitroreductase;<br><b>PDBTitle:</b> crystal structure of a putative nitroreductase in complex with fmn2 (exig_2970) from exiguobacterium sibiricum 255-15 at 1.85 a3 resolution  |
| 68 | <a href="#">c3gbhC</a>  | Alignment | not modelled | 99.0 | 10 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> nad(p)h-flavin oxidoreductase;<br><b>PDBTitle:</b> crystal structure of a putative nad(p)h:fmn oxidoreductase (se1966)2 from staphylococcus epidermidis atcc 12228 at 2.00 a resolution  |
| 69 | <a href="#">c2r01A</a>  | Alignment | not modelled | 99.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nitroreductase family protein;<br><b>PDBTitle:</b> crystal structure of a putative fmn-dependent nitroreductase (ct0345)2 from chlorobium tepidum t1s at 1.15 a resolution   |
| 70 | <a href="#">c2hayD</a>  | Alignment | not modelled | 99.0 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> putative nad(p)h-flavin oxidoreductase;<br><b>PDBTitle:</b> the crystal structure of the putative nad(p)h-flavin oxidoreductase2 from streptococcus pyogenes m1 gas  |
| 71 | <a href="#">c2wqfA</a>  | Alignment | not modelled | 98.9 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> copper induced nitroreductase d;<br><b>PDBTitle:</b> crystal structure of the nitroreductase cind from2 lactococcus lactis in complex with fmn   |
| 72 | <a href="#">c2h0uA</a>  | Alignment | not modelled | 98.9 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nadph-flavin oxidoreductase;<br><b>PDBTitle:</b> crystal structure of nad(p)h-flavin oxidoreductase from helicobacter2 pylori  |
| 73 | <a href="#">d2ifaa1</a> | Alignment | not modelled | 98.8 | 15 | <b>Fold:</b> FMN-dependent nitroreductase-like<br><b>Superfamily:</b> FMN-dependent nitroreductase-like<br><b>Family:</b> NADH oxidase/flavin reductase   |
| 74 | <a href="#">c3hoiA</a>  | Alignment | not modelled | 98.8 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fmn-dependent nitroreductase bf3017;<br><b>PDBTitle:</b> crystal structure of fmn-dependent nitroreductase bf3017 from2 bacteroides fragilis nctc 9343 (yp_212631.1) from bacteroides3 fragilis nctc 9343 at 1.55 a resolution |
| 75 | <a href="#">d1ywqa1</a> | Alignment | not modelled | 98.7 | 16 | <b>Fold:</b> FMN-dependent nitroreductase-like<br><b>Superfamily:</b> FMN-dependent nitroreductase-like<br><b>Family:</b> NADH oxidase/flavin reductase   |
| 76 | <a href="#">c4urpB</a>  | Alignment | not modelled | 98.7 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid repression mutant protein 2;<br><b>PDBTitle:</b> the crystal structure of nitroreductase from   |

|     |                         |           |              |      |    |   |
|-----|-------------------------|-----------|--------------|------|----|---|
|     |                         |           |              |      |    | saccharomyces2 cerevisiae   |
| 77  | <a href="#">c5j62B_</a> | Alignment | not modelled | 98.7 | 11 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative reductase;<br><b>PDBTitle:</b> fmn-dependent nitroreductase (cdr20291_0684) from clostridium2 difficile r20291  |
| 78  | <a href="#">c3hj9A_</a> | Alignment | not modelled | 98.7 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase;<br><b>PDBTitle:</b> crystal structure of a putative nitroreductase (reut_a1228) from2 ralstonia eutropha jmp134 at 2.00 a resolution   |
| 79  | <a href="#">c3eo7A_</a> | Alignment | not modelled | 98.6 | 18 | <b>PDB header:</b> flavoprotein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative nitroreductase;<br><b>PDBTitle:</b> crystal structure of a putative nitroreductase (ava_2154) from2 anabaena variabilis atcc 29413 at 1.80 a resolution   |
| 80  | <a href="#">d1vkwa_</a> | Alignment | not modelled | 98.5 | 25 | <b>Fold:</b> FMN-dependent nitroreductase-like<br><b>Superfamily:</b> FMN-dependent nitroreductase-like<br><b>Family:</b> Putative nitroreductase TM1586  |
| 81  | <a href="#">c5lq4B_</a> | Alignment | not modelled | 98.2 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cyagox;<br><b>PDBTitle:</b> the structure of thcox, the first oxidase protein from the cyanobactin2 pathways   |
| 82  | <a href="#">c2axqA_</a> | Alignment | not modelled | 98.0 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine dehydrogenase;<br><b>PDBTitle:</b> apo histidine-tagged saccharopine dehydrogenase (l-glu forming) from saccharomyces cerevisiae  |
| 83  | <a href="#">c1e5IA_</a> | Alignment | not modelled | 97.9 | 11 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine reductase;<br><b>PDBTitle:</b> apo saccharopine reductase from magnaporthe grisea   |
| 84  | <a href="#">c4rl6A_</a> | Alignment | not modelled | 97.8 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine dehydrogenase;<br><b>PDBTitle:</b> crystal structure of the q04i03_strp2 protein from streptococcus2 pneumoniae. northeast structural genomics consortium target spr105                             |
| 85  | <a href="#">c5l78A_</a> | Alignment | not modelled | 97.5 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alpha-aminoadipic semialdehyde synthase, mitochondrial;<br><b>PDBTitle:</b> crystal structure of human aminoadipate semialdehyde synthase,2 saccharopine dehydrogenase domain (in nad+ bound form)               |
| 86  | <a href="#">d1pjqa1</a> | Alignment | not modelled | 97.4 | 19 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Siroheme synthase N-terminal domain-like  |
| 87  | <a href="#">c2z2vA_</a> | Alignment | not modelled | 97.0 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1688;<br><b>PDBTitle:</b> crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii  |
| 88  | <a href="#">c3ic5A_</a> | Alignment | not modelled | 96.8 | 24 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative saccharopine dehydrogenase;<br><b>PDBTitle:</b> n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroiyi.   |
| 89  | <a href="#">d1vi2a1</a> | Alignment | not modelled | 96.7 | 11 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain   |
| 90  | <a href="#">c4plpB_</a> | Alignment | not modelled | 96.7 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> homospermidine synthase;<br><b>PDBTitle:</b> crystal structure of the homospermidine synthase (hss) from2 blastochloris viridis in complex with nad   |
| 91  | <a href="#">c5ugjC_</a> | Alignment | not modelled | 96.6 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase;<br><b>PDBTitle:</b> crystal structure of htpa reductase from neisseria meningitidis  |
| 92  | <a href="#">c2d3tB_</a> | Alignment | not modelled | 96.6 | 16 | <b>PDB header:</b> lyase, oxidoreductase/transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> fatty oxidation complex alpha subunit;<br><b>PDBTitle:</b> fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v  |
| 93  | <a href="#">c2nloA_</a> | Alignment | not modelled | 96.6 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> shikimate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum   |
| 94  | <a href="#">d1e5qa1</a> | Alignment | not modelled | 96.6 | 11 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain  |
| 95  | <a href="#">c4ywjB_</a> | Alignment | not modelled | 96.6 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase;<br><b>PDBTitle:</b> crystal structure of 4-hydroxy-tetrahydrodipicolinate reductase (htpa2 reductase) from pseudomonas aeruginosa                                    |
| 96  | <a href="#">c1vi2B_</a> | Alignment | not modelled | 96.5 | 11 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> shikimate 5-dehydrogenase 2;<br><b>PDBTitle:</b> crystal structure of shikimate-5-dehydrogenase with nad   |
| 97  | <a href="#">c1pjtb_</a> | Alignment | not modelled | 96.5 | 20 | <b>PDB header:</b> transferase/oxidoreductase/lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> siroheme synthase;<br><b>PDBTitle:</b> the structure of the ser128ala point-mutant variant of cysg, the2 multifunctional methyltransferase/dehydrogenase/ferrochelatae for3 siroheme synthesis |
| 98  | <a href="#">c1drwA_</a> | Alignment | not modelled | 96.5 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase;<br><b>PDBTitle:</b> escherichia coli dhpr/nhdh complex  |
| 99  | <a href="#">c3tozA_</a> | Alignment | not modelled | 96.5 | 7  | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> shikimate dehydrogenase;<br><b>PDBTitle:</b> 2.2 angstrom crystal structure of shikimate 5-dehydrogenase from2 listeria monocytogenes in complex with nad.   |
| 100 | <a href="#">c3mogA_</a> | Alignment | not modelled | 96.4 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable 3-hydroxybutyryl-coa dehydrogenase;<br><b>PDBTitle:</b> crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 escherichia coli k12 substr. mg1655   |



|     |                        |   |              |      |    |  |
|-----|------------------------|---|--------------|------|----|--|
| 101 | <a href="#">c6iaqA</a> |  Alignment    | not modelled | 96.4 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase n-terminus domain-containing<br><b>PDBTitle:</b> structure of amine dehydrogenase from mycobacterium smegmatis  |
| 102 | <a href="#">c4inaA</a> |  Alignment   | not modelled | 96.4 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine dehydrogenase;<br><b>PDBTitle:</b> crystal structure of the q7mss8_wolsu protein from wolinella2 succinogenes. northeast structural genomics consortium target wsr35                                   |
| 103 | <a href="#">c3fwnB</a> |  Alignment   | not modelled | 96.3 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, decarboxylating;<br><b>PDBTitle:</b> dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate                      |
| 104 | <a href="#">c2dc1A</a> |  Alignment   | not modelled | 96.2 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-aspartate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus   |
| 105 | <a href="#">c3k6jA</a> |  Alignment   | not modelled | 96.2 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein f01g10.3, confirmed by transcript evidence;<br><b>PDBTitle:</b> crystal structure of the dehydrogenase part of multifunctional enzyme 12 from c.elegans   |
| 106 | <a href="#">c4f3yA</a> |  Alignment   | not modelled | 96.1 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase;<br><b>PDBTitle:</b> x-ray crystal structure of dihydrodipicolinate reductase from2 burkholderia thailandensis  |
| 107 | <a href="#">c2hjrK</a> |  Alignment   | not modelled | 96.1 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> K: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of cryptosporidium parvum malate2 dehydrogenase   |
| 108 | <a href="#">c5tenH</a> |  Alignment   | not modelled | 96.1 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> H: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase;<br><b>PDBTitle:</b> structure of 4-hydroxy-tetrahydrodipicolinate reductase from vibrio2 vulnificus with 2,5 furan dicarboxylic and nadh with intact3 polyhistidine tag |
| 109 | <a href="#">c2x58B</a> |  Alignment  | not modelled | 96.1 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal bifunctional enzyme;<br><b>PDBTitle:</b> the crystal structure of mfe1 liganded with coa  |
| 110 | <a href="#">c1u4sA</a> |  Alignment | not modelled | 96.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase;<br><b>PDBTitle:</b> plasmodium falciparum lactate dehydrogenase complexed with 2,6-2 naphthalenedisulphonic acid   |
| 111 | <a href="#">c6hrdD</a> |  Alignment | not modelled | 96.0 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> 3-hydroxybutyryl-coa dehydrogenase;<br><b>PDBTitle:</b> crystal structure of m. tuberculosis fadb2 (rv0468)   |
| 112 | <a href="#">c4om8B</a> |  Alignment | not modelled | 95.9 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxybutyryl-coa dehydrogenase;<br><b>PDBTitle:</b> crystal structure of 5-formyl-3-hydroxy-2-methylpyridine 4-carboxylic2 acid (fhmpc) 5-dehydrogenase, an nad+ dependent dismutase.                           |
| 113 | <a href="#">c4ei8A</a> |  Alignment | not modelled | 95.9 | 15 | <b>PDB header:</b> replication<br><b>Chain:</b> A: <b>PDB Molecule:</b> plasmid replication protein repx;<br><b>PDBTitle:</b> crystal structure of bacillus cereus tubz, apo-form  |
| 114 | <a href="#">c4bgvB</a> |  Alignment | not modelled | 95.8 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> 1.8 a resolution structure of the malate dehydrogenase from2 picrophilus torridus in its apo form   |
| 115 | <a href="#">c6iauB</a> |  Alignment | not modelled | 95.8 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> amine dehydrogenase;<br><b>PDBTitle:</b> amine dehydrogenase from cystobacter fuscus in complex with nadp+ and2 cyclohexylamine   |
| 116 | <a href="#">c1ldbA</a> |  Alignment | not modelled | 95.8 | 18 | <b>PDB header:</b> oxidoreductase(choh(d)-nad(a))<br><b>Chain:</b> A: <b>PDB Molecule:</b> apo-l-lactate dehydrogenase;<br><b>PDBTitle:</b> structure determination and refinement of bacillus2 stearrowthermophilus lactate dehydrogenase   |
| 117 | <a href="#">c3e18A</a> |  Alignment | not modelled | 95.8 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase;<br><b>PDBTitle:</b> crystal structure of nad-binding protein from listeria innocua  |
| 118 | <a href="#">c1zcgA</a> |  Alignment | not modelled | 95.8 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal bifunctional enzyme;<br><b>PDBTitle:</b> crystal structure of 3-hydroxyacyl-coa dehydrogenase   |
| 119 | <a href="#">c4e21B</a> |  Alignment | not modelled | 95.8 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase (decarboxylating);<br><b>PDBTitle:</b> the crystal structure of 6-phosphogluconate dehydrogenase from2 geobacter metallireducens   |
| 120 | <a href="#">c1pzfD</a> |  Alignment | not modelled | 95.7 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> lactate dehydrogenase;<br><b>PDBTitle:</b> t.gondii ldh1 ternary complex with apad+ and oxalate   |