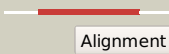

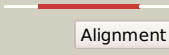
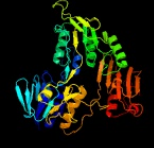
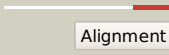
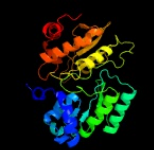
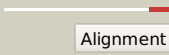

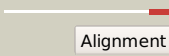

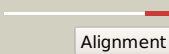

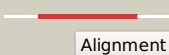

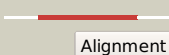

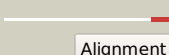

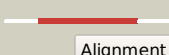





# Phyre2

|               |                               |
|---------------|-------------------------------|
| Email         | mdejesus@rockefeller.edu      |
| Description   | RVBD0252_(nirB)_302866_305427 |
| Date          | Tue Jul 23 14:50:31 BST 2019  |
| Unique Job ID | d8aa5c185c006b63              |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c3ntaA_</a> |  Alignment   |    | 100.0      | 25     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fad-dependent pyridine nucleotide-disulphide<br><b>PDBTitle:</b> structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase  |
| 2  | <a href="#">c3icrA_</a> |  Alignment   |    | 100.0      | 24     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme a-disulfide reductase;<br><b>PDBTitle:</b> crystal structure of oxidized bacillus anthracis coadr-rhd  |
| 3  | <a href="#">c1zj8B_</a> |  Alignment   |    | 100.0      | 19     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable ferredoxin-dependent nitrite reductase nira;<br><b>PDBTitle:</b> structure of mycobacterium tuberculosis nira protein  |
| 4  | <a href="#">c3b0nA_</a> |  Alignment   |   | 100.0      | 19     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nitrite reductase;<br><b>PDBTitle:</b> q448k mutant of assimilatory nitrite reductase (nii3) from tobacco2 leaf   |
| 5  | <a href="#">c2akjA_</a> |  Alignment |  | 100.0      | 19     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nitrite reductase, chloroplast;<br><b>PDBTitle:</b> structure of spinach nitrite reductase  |
| 6  | <a href="#">c5h92A_</a> |  Alignment |  | 100.0      | 24     | <b>PDB header:</b> oxidoreductase/electron transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase [ferredoxin], chloroplastic;<br><b>PDBTitle:</b> crystal structure of the complex between maize sulfite reductase and2 ferredoxin in the form-3 crystal  |
| 7  | <a href="#">c1qv4A_</a> |  Alignment |  | 100.0      | 18     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> programed cell death protein 8;<br><b>PDBTitle:</b> murine apoptosis-inducing factor (aif)  |
| 8  | <a href="#">c2gr2A_</a> |  Alignment |  | 100.0      | 27     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin reductase;<br><b>PDBTitle:</b> crystal structure of ferredoxin reductase, bpha4 (oxidized form)  |
| 9  | <a href="#">c2v4jE_</a> |  Alignment |  | 100.0      | 20     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> E: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit<br><b>PDBTitle:</b> the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration |
| 10 | <a href="#">c3lxdA_</a> |  Alignment |  | 100.0      | 26     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fad-dependent pyridine nucleotide-disulphide<br><b>PDBTitle:</b> crystal structure of ferredoxin reductase arr from novosphingobium2 aromaticivorans  |
| 11 | <a href="#">c1q1wA_</a> |  Alignment |  | 100.0      | 25     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putidaredoxin reductase;<br><b>PDBTitle:</b> crystal structure of putidaredoxin reductase from2 pseudomonas putida  |

|    |                         |           |              |       |    |  |
|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | <a href="#">c3iwaA_</a> | Alignment |              | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fad-dependent pyridine nucleotide-disulphide<br><b>PDBTitle:</b> crystal structure of a fad-dependent pyridine nucleotide-disulphide2 oxidoreductase from desulfovibrio vulgaris  |
| 13 | <a href="#">c3fg2P_</a> | Alignment |              | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> P: <b>PDB Molecule:</b> putative rubredoxin reductase;<br><b>PDBTitle:</b> crystal structure of ferredoxin reductase for the cyp199a2 system from2 rhodospseudomonas palustris  |
| 14 | <a href="#">c3c7bE_</a> | Alignment |              | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> E: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit beta;<br><b>PDBTitle:</b> structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus   |
| 15 | <a href="#">c3oc4A_</a> | Alignment |              | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, pyridine nucleotide-disulfide family;<br><b>PDBTitle:</b> crystal structure of a pyridine nucleotide-disulfide family2 oxidoreductase from the enterococcus faecalis v583   |
| 16 | <a href="#">c2v3aA_</a> | Alignment |              | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> rubredoxin reductase;<br><b>PDBTitle:</b> crystal structure of rubredoxin reductase from pseudomonas2 aeruginosa.   |
| 17 | <a href="#">c3ef6A_</a> | Alignment |              | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> toluene 1,2-dioxygenase system ferredoxin--nad(+)<br><b>PDBTitle:</b> crystal structure of toluene 2,3-dioxygenase reductase  |
| 18 | <a href="#">c3kd9B_</a> | Alignment |              | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> coenzyme a disulfide reductase;<br><b>PDBTitle:</b> crystal structure of pyridine nucleotide disulfide oxidoreductase from2 pyrococcus horikoshii   |
| 19 | <a href="#">c1yqzA_</a> | Alignment |              | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme a disulfide reductase;<br><b>PDBTitle:</b> structure of coenzyme a-disulfide reductase from2 staphylococcus aureus refined at 1.54 angstrom resolution   |
| 20 | <a href="#">c5jciA_</a> | Alignment |              | 100.0 | 23 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> os09g0567300 protein;<br><b>PDBTitle:</b> structure and catalytic mechanism of monodehydroascorbate reductase,2 mdhar, from oryza sativa l. japonica   |
| 21 | <a href="#">c3c7bA_</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit alpha;<br><b>PDBTitle:</b> structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus  |
| 22 | <a href="#">c2bcpA_</a> | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nadh oxidase;<br><b>PDBTitle:</b> structural analysis of streptococcus pyogenes nadh oxidase: c44s nox2 with azide  |
| 23 | <a href="#">c2v4jA_</a> | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit<br><b>PDBTitle:</b> the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration |
| 24 | <a href="#">c1m6iA_</a> | Alignment | not modelled | 100.0 | 17 | <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)   |
| 25 | <a href="#">c1nhqA_</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> oxidoreductase (h2o2(a))<br><b>Chain:</b> A: <b>PDB Molecule:</b> nadh peroxidase;<br><b>PDBTitle:</b> crystallographic analyses of nadh peroxidase cys42ala and cys42ser2 mutants: active site structure, mechanistic implications, and an3 unusual environment of arg303                  |
| 26 | <a href="#">c3kjiA_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nad(fad)-dependent dehydrogenase, nirb-family (n-terminal)<br><b>PDBTitle:</b> crystal structure of nadh:rubredoxin oxidoreductase from clostridium2 acetobutylicum   |
| 27 | <a href="#">c5aopA_</a> | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase hemoprotein;<br><b>PDBTitle:</b> sulfite reductase structure reduced with crii edta, 5-coordinate2 siroheme, siroheme feii, [4fe-4s] +1<br><b>PDB header:</b> oxidoreductase                                      |

|    |                        |           |              |       |    |  |
|----|------------------------|-----------|--------------|-------|----|--|
| 28 | <a href="#">c2cduB</a> | Alignment | not modelled | 100.0 | 22 | <b>Chain:</b> B: <b>PDB Molecule:</b> nadph oxidase;<br><b>PDBTitle:</b> the crystal structure of water-forming nad(p)h oxidase from <i>2 lactobacillus sanfranciscensis</i>   |
| 29 | <a href="#">c1y56A</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1363;<br><b>PDBTitle:</b> crystal structure of l-proline dehydrogenase from <i>p.horikoshii</i>  |
| 30 | <a href="#">c1x31A</a> | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sarcosine oxidase alpha subunit;<br><b>PDBTitle:</b> crystal structure of heterotetrameric sarcosine oxidase from <i>2 corynebacterium sp. u-96</i>   |
| 31 | <a href="#">c3cgbB</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> pyridine nucleotide-disulfide oxidoreductase, class i;<br><b>PDBTitle:</b> pyridine nucleotide complexes with bacillus anthracis coenzyme a-2 disulfide reductase: a structural analysis of dual nad(p)h3 specificity                           |
| 32 | <a href="#">c5er0D</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> nadh oxidase;<br><b>PDBTitle:</b> water-forming nadh oxidase from <i>lactobacillus brevis (lbnx)</i>  |
| 33 | <a href="#">c2v6oA</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin glutathione reductase;<br><b>PDBTitle:</b> structure of schistosoma mansoni thioredoxin-gluthathione2 reductase (smtgr)   |
| 34 | <a href="#">c5w1jA</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin glutathione reductase;<br><b>PDBTitle:</b> echinococcus granulosus thioredoxin glutathione reductas (egtgr)  |
| 35 | <a href="#">c5jwcA</a> | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> nadh dehydrogenase, putative;<br><b>PDBTitle:</b> structure of ndh2 from plasmodium falciparum in complex with ryl-552  |
| 36 | <a href="#">c1xhcA</a> | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nadh oxidase /nitrite reductase;<br><b>PDBTitle:</b> nadh oxidase /nitrite reductase from <i>pyrococcus furiosus pfu-1140779-2 001</i>  |
| 37 | <a href="#">c2c3dB</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><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   |
| 38 | <a href="#">c4dnaA</a> | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable glutathione reductase;<br><b>PDBTitle:</b> crystal structure of putative glutathione reductase from <i>sinorhizobium2 meliloti 1021</i>  |
| 39 | <a href="#">c1xdiA</a> | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> rv3303c-lpda;<br><b>PDBTitle:</b> crystal structure of lpda (rv3303c) from <i>mycobacterium tuberculosis</i>  |
| 40 | <a href="#">c6mp5B</a> | Alignment | not modelled | 100.0 | 11 | <b>PDB header:</b> membrane protein, oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> sulfide:quinone oxidoreductase, mitochondrial;<br><b>PDBTitle:</b> crystal structure of native human sulfide:quinone oxidoreductase   |
| 41 | <a href="#">c4xdbC</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase, membrane protein, flavop<br><b>Chain:</b> C: <b>PDB Molecule:</b> nadh dehydrogenase-like protein saouhsc_00878;<br><b>PDBTitle:</b> nadh:quinone oxidoreductase (ndh-ii) from <i>staphylococcus aureus -2 holoprotein structure</i>  |
| 42 | <a href="#">c3urhB</a> | Alignment | not modelled | 100.0 | 18 | <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 from <i>2 sinorhizobium meliloti 1021</i>  |
| 43 | <a href="#">c1tytA</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> trypanothione reductase, oxidized form;<br><b>PDBTitle:</b> crystal and molecular structure of crithidia fasciculata2 trypanothione reductase at 2.6 angstroms resolution   |
| 44 | <a href="#">c2eq7B</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxoglutarate dehydrogenase e3 component;<br><b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from <i>thermus thermophilus2 hb8</i> with psbdo  |
| 45 | <a href="#">c1fcdB</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> electron transport(flavocytochrome)<br><b>Chain:</b> B: <b>PDB Molecule:</b> flavocytochrome c sulfide dehydrogenase (flavin-<br><b>PDBTitle:</b> the structure of flavocytochrome c sulfide dehydrogenase2 from a purple phototrophic bacterium <i>chromatium vinosum at3</i> 2.5 angstroms resolution |
| 46 | <a href="#">c2qaeA</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase;<br><b>PDBTitle:</b> crystal structure analysis of trypanosoma cruzi lipoamide2 dehydrogenase   |
| 47 | <a href="#">c6du7C</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> glutathione reductase;<br><b>PDBTitle:</b> glutathione reductase from <i>streptococcus pneumoniae</i>   |
| 48 | <a href="#">c6bz0C</a> | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase;<br><b>PDBTitle:</b> 1.83 angstrom resolution crystal structure of dihydrolipoyl2 dehydrogenase from <i>acinetobacter baumannii</i> in complex with fad.  |
| 49 | <a href="#">c1ojtA</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> surface protein;<br><b>PDBTitle:</b> structure of dihydrolipoamide dehydrogenase  |
| 50 | <a href="#">c2eq8E</a> | Alignment | not modelled | 100.0 | 24 | <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 <i>thermus thermophilus2 hb8</i> with psbdp  |
| 51 | <a href="#">c3kpgA</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sulfide-quinone reductase, putative;<br><b>PDBTitle:</b> crystal structure of sulfide:quinone oxidoreductase from <i>2</i>  |

|    |                         |           |              |       |    |   |
|----|-------------------------|-----------|--------------|-------|----|---|
|    |                         |           |              |       |    | acidithiobacillus ferrooxidans in complex with decylubiquinone<br><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+                            |
| 52 | <a href="#">c1zmcG_</a> | Alignment | not modelled | 100.0 | 17 | <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  |
| 53 | <a href="#">c1hyuA_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> rotenone-insensitive nadh-ubiquinone oxidoreductase,<br><b>PDBTitle:</b> crystal structure of ndh with trt   |
| 54 | <a href="#">c2a8xA_</a> | Alignment | not modelled | 100.0 | 22 | <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   |
| 55 | <a href="#">c4g6gB_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fad-dependent pyridine nucleotide-disulfide oxidoreductase;<br><b>PDBTitle:</b> structure of bacterial type ii nadh dehydrogenase from2 caldalkalibacillus thermarum at 2.5a resolution                                    |
| 56 | <a href="#">c4nwzA_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> mercuric reductase;<br><b>PDBTitle:</b> mercuric reductase from metallosphaera sedula  |
| 57 | <a href="#">c4ywoA_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase;<br><b>PDBTitle:</b> 1.72 angstrom resolution crystal structure of 2-oxoglutarate2 dehydrogenase complex subunit dihydrolipoamide dehydrogenase from3 bordetella pertussis in complex with fad |
| 58 | <a href="#">c6aonB_</a> | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> rotenone-insensitive nadh-ubiquinone oxidoreductase;<br><b>PDBTitle:</b> structure of the ndi1 protein from saccharomyces cerevisiae in complex2 with nad+   |
| 59 | <a href="#">c4gapB_</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> mercuric reductase;<br><b>PDBTitle:</b> crystal structure of tn501 mera  |
| 60 | <a href="#">c1zx9A_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase;<br><b>PDBTitle:</b> the refined structure of pseudomonas putida lipoamide dehydrogenase2 complexed with nad+ at 2.45 angstroms resolution  |
| 61 | <a href="#">c1lvIA_</a> | Alignment | not modelled | 100.0 | 26 | <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  |
| 62 | <a href="#">c1dxIC_</a> | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase;<br><b>PDBTitle:</b> dihydrolipoamide dehydrogenase of pyruvate dehydrogenase from2 escherichia coli   |
| 63 | <a href="#">c4jdrB_</a> | Alignment | not modelled | 100.0 | 18 | <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  |
| 64 | <a href="#">c1ebdB_</a> | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase 2;<br><b>PDBTitle:</b> structure of plasmodium falciparum thioredoxin reductase-thioredoxin2 complex   |
| 65 | <a href="#">c4j56A_</a> | Alignment | not modelled | 100.0 | 16 | <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  |
| 66 | <a href="#">c1geuA_</a> | Alignment | not modelled | 100.0 | 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  |
| 67 | <a href="#">c2w0hA_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> flavin-binding subunit of sulfide dehydrogenase;<br><b>PDBTitle:</b> crystal structure of complex between flavocytochrome c and copper2 chaperone copc from t. paradoxus   |
| 68 | <a href="#">c5n1tA_</a> | Alignment | not modelled | 100.0 | 20 | <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   |
| 69 | <a href="#">c3dgzA_</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> sulfide-quinone reductase;<br><b>PDBTitle:</b> 3-d x-ray structure of the sulfide:quinone oxidoreductase from aquifex2 aeolicus in complex with aurachin c   |
| 70 | <a href="#">c3hyxC_</a> | Alignment | not modelled | 100.0 | 17 | <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  |
| 71 | <a href="#">c1bwcA_</a> | Alignment | not modelled | 100.0 | 16 | <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+  |
| 72 | <a href="#">c1v59B_</a> | Alignment | not modelled | 100.0 | 18 | <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 colwellia2 psychrerythraea 34h.   |
| 73 | <a href="#">c3ic9D_</a> | Alignment | not modelled | 100.0 | 14 | <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  |
| 74 | <a href="#">c2cfyB_</a> | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> hydrolase,oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase;<br><b>PDBTitle:</b> 1.88 angstrom resolution crystal structure of glutathione reductase2 from streptococcus mutans ua159 in complex with fad  |
| 75 | <a href="#">c5v36A_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase;<br><b>PDBTitle:</b> three-dimensional structure of lipoamide dehydrogenase   |
| 76 | <a href="#">c1lpfB_</a> | Alignment | not modelled | 100.0 | 18 |   |

|     |                         |           |              |       |    |   |
|-----|-------------------------|-----------|--------------|-------|----|---|
|     |                         |           |              |       |    | from2 pseudomonas fluorescens at 2.8 angstroms resolution.3 analysis of redox and thermostability properties  |
| 77  | <a href="#">c6b4oB</a>  | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glutathione reductase;<br><b>PDBTitle:</b> 1.73 angstrom resolution crystal structure of glutathione reductase2 from enterococcus faecalis in complex with fad  |
| 78  | <a href="#">c1zkqA</a>  | Alignment | not modelled | 100.0 | 19 | <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  |
| 79  | <a href="#">c1ndaD</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> trypanothione oxidoreductase;<br><b>PDBTitle:</b> the structure of trypanosoma cruzi trypanothione reductase in the2 oxidized and nadph reduced state  |
| 80  | <a href="#">c2nvkX</a>  | Alignment | not modelled | 100.0 | 17 | <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  |
| 81  | <a href="#">c2r9zB</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glutathione amide reductase;<br><b>PDBTitle:</b> glutathione amide reductase from chromatium gracile   |
| 82  | <a href="#">c5x1yC</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> mercuric reductase;<br><b>PDBTitle:</b> structure of mercuric reductase from lysinibacillus sphaericus   |
| 83  | <a href="#">c1onfA</a>  | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase;<br><b>PDBTitle:</b> crystal structure of plasmodium falciparum glutathione reductase  |
| 84  | <a href="#">c2hqmB</a>  | Alignment | not modelled | 100.0 | 17 | <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 saccharomyces cerevisiae  |
| 85  | <a href="#">c4b1bB</a>  | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase;<br><b>PDBTitle:</b> crystal structure of plasmodium falciparum oxidised2 thioredoxin reductase at 2.9 angstrom  |
| 86  | <a href="#">c3l8kB</a>  | Alignment | not modelled | 100.0 | 17 | <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 sulfolobus2 solfataricus  |
| 87  | <a href="#">c3o0hA</a>  | Alignment | not modelled | 100.0 | 19 | <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 bartonella henselae   |
| 88  | <a href="#">c1gthD</a>  | Alignment | not modelled | 100.0 | 12 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> dihydropyrimidine dehydrogenase;<br><b>PDBTitle:</b> dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil  |
| 89  | <a href="#">d1aopa3</a> | Alignment | not modelled | 100.0 | 19 | <b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like<br><b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like<br><b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like   |
| 90  | <a href="#">c6qkqB</a>  | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> flavoprotein<br><b>Chain:</b> B: <b>PDB Molecule:</b> ncr a;<br><b>PDBTitle:</b> 2-naphthoyl-coa reductase(ncr)  |
| 91  | <a href="#">d1zj8a4</a> | Alignment | not modelled | 100.0 | 21 | <b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like<br><b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like<br><b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like   |
| 92  | <a href="#">d2akja4</a> | Alignment | not modelled | 100.0 | 19 | <b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like<br><b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like<br><b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like   |
| 93  | <a href="#">c5jcaL</a>  | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> L: <b>PDB Molecule:</b> nadh-dependent ferredoxin:nadp oxidoreductase (nfni)<br><b>PDBTitle:</b> nadp(h) bound nadh-dependent ferredoxin:nadp oxidoreductase (nfni)2 from pyrococcus furiosus                              |
| 94  | <a href="#">d2v4jb3</a> | Alignment | not modelled | 100.0 | 18 | <b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like<br><b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like<br><b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like   |
| 95  | <a href="#">d3c7ba3</a> | Alignment | not modelled | 100.0 | 17 | <b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like<br><b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like<br><b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like   |
| 96  | <a href="#">c3k30B</a>  | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> histamine dehydrogenase;<br><b>PDBTitle:</b> histamine dehydrogenase from nocardioides simplex   |
| 97  | <a href="#">d2v4ja3</a> | Alignment | not modelled | 100.0 | 19 | <b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like<br><b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like<br><b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like   |
| 98  | <a href="#">c4yifD</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> dihydropyrimidine dehydrogenase subunit a;<br><b>PDBTitle:</b> insights into flavin-based electron bifurcation via the nadh-dependent2 reduced ferredoxin-nadp oxidoreductase structure            |
| 99  | <a href="#">d3c7bb3</a> | Alignment | not modelled | 100.0 | 15 | <b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like<br><b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like<br><b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like   |
| 100 | <a href="#">c1ps9A</a>  | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 2,4-dienoyl-coa reductase;<br><b>PDBTitle:</b> the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase  |
| 101 | <a href="#">c1djnB</a>  | Alignment | not modelled | 100.0 | 12 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> trimethylamine dehydrogenase;<br><b>PDBTitle:</b> structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1) |
|     |                         |           |              |       |    | <b>PDB header:</b> oxidoreductase   |

|     |                         |           |              |       |    |   |
|-----|-------------------------|-----------|--------------|-------|----|---|
| 102 | <a href="#">c3d1cA</a>  | Alignment | not modelled | 100.0 | 18 | <b>Chain:</b> A: <b>PDB Molecule:</b> flavin-containing putative monooxygenase;<br><b>PDBTitle:</b> crystal structure of flavin-containing putative monooxygenase2 (np_373108.1) from staphylococcus aureus mu50 at 2.40 a resolution   |
| 103 | <a href="#">c4gcmB</a>  | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase;<br><b>PDBTitle:</b> crystal structure of a thioredoxine reductase (trxb) from2 staphylococcus aureus subsp. aureus mu50 at 1.80 a resolution  |
| 104 | <a href="#">d1zj8a3</a> | Alignment | not modelled | 100.0 | 21 | <b>Fold:</b> Nitrite and sulphite reductase 4Fe-4S domain-like<br><b>Superfamily:</b> Nitrite and sulphite reductase 4Fe-4S domain-like<br><b>Family:</b> Nitrite and sulphite reductase 4Fe-4S domain-like   |
| 105 | <a href="#">c2vdcI</a>  | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> I: <b>PDB Molecule:</b> glutamate synthase [nadph] small chain;<br><b>PDBTitle:</b> the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications. |
| 106 | <a href="#">c2zbwA</a>  | Alignment | not modelled | 100.0 | 18 | <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 thermus2 thermophilus hb8  |
| 107 | <a href="#">c5w4cA</a>  | Alignment | not modelled | 100.0 | 16 | <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 from cryptococcus2 neoformans in complex with fad (fo conformation)  |
| 108 | <a href="#">c3h8lA</a>  | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nadh oxidase;<br><b>PDBTitle:</b> the first x-ray structure of a sulfide:quinone2 oxidoreductase: insights into sulfide oxidation mechanism  |
| 109 | <a href="#">c6de6B</a>  | Alignment | not modelled | 100.0 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> histamine dehydrogenase;<br><b>PDBTitle:</b> 2.1 a resolution structure of histamine dehydrogenase from rhizobium2 sp. 4-9   |
| 110 | <a href="#">c5yggB</a>  | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin--nadp reductase;<br><b>PDBTitle:</b> crystal structure of ferredoxin nadp+ oxidoreductase from2 rhodopseudomonas palustris  |
| 111 | <a href="#">c1lqtB</a>  | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> fpra;<br><b>PDBTitle:</b> a covalent modification of nadp+ revealed by the atomic resolution2 structure of fpra, a mycobacterium tuberculosis oxidoreductase   |
| 112 | <a href="#">c6garB</a>  | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin--nadp reductase;<br><b>PDBTitle:</b> crystal structure of oxidised ferredoxin/flavodoxin nadp+2 oxidoreductase 1 (fnr1) from bacillus cereus  |
| 113 | <a href="#">c5uwvA</a>  | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase;<br><b>PDBTitle:</b> the crystal structure of thioredoxin reductase from streptococcus2 pyogenes mgas5005  |
| 114 | <a href="#">c4fk1D</a>  | Alignment | not modelled | 100.0 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> putative thioredoxin reductase;<br><b>PDBTitle:</b> crystal structure of putative thioredoxin reductase trxb from bacillus2 anthracis  |
| 115 | <a href="#">c1cjcA</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (adrenodoxin reductase);<br><b>PDBTitle:</b> structure of adrenodoxin reductase of mitochondrial p450 systems  |
| 116 | <a href="#">c5twcA</a>  | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nadp reductase;<br><b>PDBTitle:</b> oxidoreductase iruo in the oxidized form   |
| 117 | <a href="#">c3r9uA</a>  | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase;<br><b>PDBTitle:</b> thioredoxin-disulfide reductase from campylobacter jejuni.  |
| 118 | <a href="#">c1vdcA</a>  | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nadh dependent thioredoxin reductase;<br><b>PDBTitle:</b> structure of nadph dependent thioredoxin reductase   |
| 119 | <a href="#">c5jriA</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pyridine nucleotide-disulfide oxidoreductase;<br><b>PDBTitle:</b> structure of an oxidoreductase semet-labelled from synechocystis sp.2 pcc6803  |
| 120 | <a href="#">c4ntdA</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase;<br><b>PDBTitle:</b> crystal structure of hlmi   |