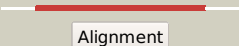



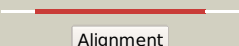





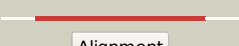













# Phyre2

|               |                                |
|---------------|--------------------------------|
| Email         | mdejesus@rockefeller.edu       |
| Description   | RVBD0761c_(adhB)_854702_855829 |
| Date          | Fri Jul 26 01:50:34 BST 2019   |
| Unique Job ID | e811e7555c01c173               |

Detailed template information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|--|---|------------|--------|---|
| 1  | <a href="#">c1ma0B_</a> | <br>Alignment   |    | 100.0      | 34     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glutathione-dependent formaldehyde dehydrogenase;<br><b>PDBTitle:</b> ternary complex of human glutathione-dependent formaldehyde2 dehydrogenase with nad+ and dodecanoic acid       |
| 2  | <a href="#">c1hf3A_</a> | <br>Alignment   |    | 100.0      | 34     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase e chain;<br><b>PDBTitle:</b> atomic x-ray structure of liver alcohol dehydrogenase containing2 cadmium and a hydroxide adduct to nadh                          |
| 3  | <a href="#">c3ukoA_</a> | <br>Alignment   |    | 100.0      | 30     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase class-3;<br><b>PDBTitle:</b> crystal structure of s-nitrosogluthatione reductase from arabidopsis2 thaliana, complex with nadh                                 |
| 4  | <a href="#">c1cdoB_</a> | <br>Alignment   |   | 100.0      | 35     | <b>PDB header:</b> oxidoreductase (ch-oh(d)-nad(a))<br><b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase;<br><b>PDBTitle:</b> alcohol dehydrogenase (e.c.1.1.1.1) (ee isozyme) complexed with2 nicotinamide adenine dinucleotide (nad), and zinc      |
| 5  | <a href="#">c4rquA_</a> | <br>Alignment |  | 100.0      | 31     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase;<br><b>PDBTitle:</b> alcohol dehydrogenase crystal structure in complex with nad   |
| 6  | <a href="#">c3cosD_</a> | <br>Alignment |  | 100.0      | 32     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> alcohol dehydrogenase 4;<br><b>PDBTitle:</b> crystal structure of human class ii alcohol dehydrogenase (adh4) in2 complex with nad and zn  |
| 7  | <a href="#">c5tnxA_</a> | <br>Alignment |  | 100.0      | 28     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase zinc-binding domain protein;<br><b>PDBTitle:</b> crystal structure of alcohol dehydrogenase zinc-binding domain protein2 from burkholderia ambifaria           |
| 8  | <a href="#">c3krtC_</a> | <br>Alignment |  | 100.0      | 19     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> crotonyl coa reductase;<br><b>PDBTitle:</b> crystal structure of putative crotonyl coa reductase from streptomyces2 coelicolor a3(2)   |
| 9  | <a href="#">c4gi2B_</a> | <br>Alignment |  | 100.0      | 21     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> crotonyl-coa carboxylase/reductase;<br><b>PDBTitle:</b> crotonyl-coa carboxylase/reductase   |
| 10 | <a href="#">c1f8fA_</a> | <br>Alignment |  | 100.0      | 27     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> benzyl alcohol dehydrogenase;<br><b>PDBTitle:</b> crystal structure of benzyl alcohol dehydrogenase from acinetobacter2 calcoaceticus  |
| 11 | <a href="#">c1p0fA_</a> | <br>Alignment |  | 100.0      | 27     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nadp-dependent alcohol dehydrogenase;<br><b>PDBTitle:</b> crystal structure of the binary complex: nadp(h)-dependent vertebrate2 alcohol dehydrogenase (adh8) with the cofactor nadp |

|    |                         |           |              |       |    |  |
|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | <a href="#">c4y0kA_</a> | Alignment |              | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ante;<br><b>PDBTitle:</b> structure of crotonyl-coa carboxylase/reductase ante in complex with2 nadp  |
| 13 | <a href="#">c1pl6A_</a> | Alignment |              | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sorbitol dehydrogenase;<br><b>PDBTitle:</b> human sdh/nadh/inhibitor complex  |
| 14 | <a href="#">c1vj0B_</a> | Alignment |              | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase, zinc-containing;<br><b>PDBTitle:</b> crystal structure of alcohol dehydrogenase (tm0436) from thermotoga2 maritima at 2.00 a resolution      |
| 15 | <a href="#">c2dphA_</a> | Alignment |              | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> formaldehyde dismutase;<br><b>PDBTitle:</b> crystal structure of formaldehyde dismutase   |
| 16 | <a href="#">c4a10A_</a> | Alignment |              | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> octenoyl-coa reductase/carboxylase;<br><b>PDBTitle:</b> apo-structure of 2-octenoyl-coa carboxylase reductase cinf from2 streptomyces sp.                           |
| 17 | <a href="#">c3uogB_</a> | Alignment |              | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase;<br><b>PDBTitle:</b> crystal structure of putative alcohol dehydrogenase from sinorhizobium2 meliloti 1021                                    |
| 18 | <a href="#">c5ylnB_</a> | Alignment |              | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase, zinc-containing;<br><b>PDBTitle:</b> zinc dependent alcohol dehydrogenase 2 from streptococcus pneumonia -2 apo form                         |
| 19 | <a href="#">c1kolA_</a> | Alignment |              | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> formaldehyde dehydrogenase;<br><b>PDBTitle:</b> crystal structure of formaldehyde dehydrogenase   |
| 20 | <a href="#">c2cf5A_</a> | Alignment |              | 100.0 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cinnamyl alcohol dehydrogenase;<br><b>PDBTitle:</b> crystal structures of the arabidopsis cinnamyl alcohol2 dehydrogenases, atcad5                                  |
| 21 | <a href="#">c2dfvB_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable l-threonine 3-dehydrogenase;<br><b>PDBTitle:</b> hyperthermophilic threonine dehydrogenase from pyrococcus horikoshii                                      |
| 22 | <a href="#">c1yqxB_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> sinapyl alcohol dehydrogenase;<br><b>PDBTitle:</b> sinapyl alcohol dehydrogenase at 2.5 angstrom resolution   |
| 23 | <a href="#">c2ouiB_</a> | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nadp-dependent alcohol dehydrogenase;<br><b>PDBTitle:</b> d275p mutant of alcohol dehydrogenase from protozoa entamoeba2 histolytica                                |
| 24 | <a href="#">c4a2cB_</a> | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> galactitol-1-phosphate 5-dehydrogenase;<br><b>PDBTitle:</b> crystal structure of galactitol-1-phosphate dehydrogenase from2 escherichia coli                        |
| 25 | <a href="#">c4cpdA_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase;<br><b>PDBTitle:</b> alcohol dehydrogenase tadh from thermus sp. atn1   |
| 26 | <a href="#">c1h2bA_</a> | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase;<br><b>PDBTitle:</b> crystal structure of the alcohol dehydrogenase from the2 hyperthermophilic archaeon aeropyrum pernix at 1.65a resolution |
| 27 | <a href="#">c1e3jA_</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nadp(h)-dependent ketose reductase;<br><b>PDBTitle:</b> ketose reductase (sorbitol dehydrogenase) from silverleaf2 whitefly   |
| 28 | <a href="#">c1kevB_</a> | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nadp-dependent alcohol dehydrogenase;<br><b>PDBTitle:</b> structure of nadp-dependent alcohol dehydrogenase   |
|    |                         |           |              |       |    | <b>PDB header:</b> oxidoreductase  |

|    |                        |           |              |       |    |   |
|----|------------------------|-----------|--------------|-------|----|---|
| 29 | <a href="#">c2eihA</a> | Alignment | not modelled | 100.0 | 24 | <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase;<br><b>PDBTitle:</b> crystal structure of nad-dependent alcohol dehydrogenase   |
| 30 | <a href="#">c5vktB</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cinnamyl alcohol dehydrogenases (sbcad4);<br><b>PDBTitle:</b> cinnamyl alcohol dehydrogenases (sbcad4) from sorghum bicolor (l.)2 moench   |
| 31 | <a href="#">c3ip1C</a> | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> alcohol dehydrogenase, zinc-containing;<br><b>PDBTitle:</b> structure of putative alcohol dehydrogenase (tm_042) from thermotoga2 maritima   |
| 32 | <a href="#">c2ejvA</a> | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-threonine 3-dehydrogenase;<br><b>PDBTitle:</b> crystal structure of threonine 3-dehydrogenase complexed with nad+  |
| 33 | <a href="#">c4oaqA</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> r-specific carbonyl reductase;<br><b>PDBTitle:</b> crystal structure of the r-specific carbonyl reductase from candida2 parapsilosis atcc 7330   |
| 34 | <a href="#">c4ilkB</a> | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> starvation sensing protein rspb;<br><b>PDBTitle:</b> crystal structure of short chain alcohol dehydrogenase (rspb) from e.2 coli cft073 (efi target efi-506413) complexed with cofactor nadh |
| 35 | <a href="#">c4ejmA</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative zinc-binding dehydrogenase;<br><b>PDBTitle:</b> crystal structure of a putative zinc-binding dehydrogenase (target2 psi-012003) from sinorhizobium meliloti 1021 bound to nadp      |
| 36 | <a href="#">c1r37B</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nad-dependent alcohol dehydrogenase;<br><b>PDBTitle:</b> alcohol dehydrogenase from sulfolobus solfataricus2 complexed with nad(h) and 2-ethoxyethanol                                       |
| 37 | <a href="#">c5k1sD</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, zinc-binding dehydrogenase family;<br><b>PDBTitle:</b> crystal structure of aibc   |
| 38 | <a href="#">c5fi5A</a> | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tetrahydroalstonine synthase;<br><b>PDBTitle:</b> heteroyohimbine synthase thas1 from catharanthus roseus - apo form   |
| 39 | <a href="#">c5kiaA</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-threonine 3-dehydrogenase;<br><b>PDBTitle:</b> crystal structure of l-threonine 3-dehydrogenase from burkholderia2 thailandensis   |
| 40 | <a href="#">c6c49A</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase;<br><b>PDBTitle:</b> crystal structure of alcohol dehydrogenase from acinetobacter2 baumannii  |
| 41 | <a href="#">c5vm2A</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase;<br><b>PDBTitle:</b> crystal structure of eck1772, an oxidoreductase/dehydrogenase of 2 unknown specificity involved in membrane biogenesis from escherichia3 coli     |
| 42 | <a href="#">c1piwA</a> | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical zinc-type alcohol dehydrogenase-<br><b>PDBTitle:</b> apo and holo structures of an nadp(h)-dependent cinnamyl2 alcohol dehydrogenase from saccharomyces cerevisiae              |
| 43 | <a href="#">c2xaaC</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> secondary alcohol dehydrogenase;<br><b>PDBTitle:</b> alcohol dehydrogenase adh-'a' from rhodococcus ruber dsm2 44541 at ph 8.5 in complex with nad and butane-1,4-diol                       |
| 44 | <a href="#">c2cdaA</a> | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glucose dehydrogenase;<br><b>PDBTitle:</b> sulfolobus solfataricus glucose dehydrogenase 1 in complex with nadp  |
| 45 | <a href="#">c2hcyD</a> | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> alcohol dehydrogenase 1;<br><b>PDBTitle:</b> yeast alcohol dehydrogenase i, saccharomyces cerevisiae fermentative2 enzyme  |
| 46 | <a href="#">c4j6fB</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative alcohol dehydrogenase;<br><b>PDBTitle:</b> crystal structure of putative alcohol dehydrogenase from sinorhizobium2 meliloti 1021, nysgrc-target 012230                              |
| 47 | <a href="#">c6dkhC</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> l-idonate 5-dehydrogenase (nad(p)(+));<br><b>PDBTitle:</b> the crystal structure of l-idonate 5-dehydrogenase from escherichia2 coli str. k-12 substr. mg1655                                |
| 48 | <a href="#">c1rjwA</a> | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase;<br><b>PDBTitle:</b> crystal structure of nad(+)-dependent alcohol dehydrogenase2 from bacillus stearothermophilus strain lld-r  |
| 49 | <a href="#">c3b70A</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enoyl reductase;<br><b>PDBTitle:</b> crystal structure of aspergillus terreus trans-acting lovastatin2 polyketide enoyl reductase (lov) with bound nadp                                      |
| 50 | <a href="#">c5h81A</a> | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> heteroyohimbine synthase thas2;<br><b>PDBTitle:</b> heteroyohimbine synthase thas2 from catharanthus roseus - complex with2 nadp+  |
| 51 | <a href="#">c4gkvC</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> alcohol dehydrogenase, propanol-preferring;<br><b>PDBTitle:</b> structure of escherichia coli adh(p) (ethanol-inducible dehydrogenase)2 with bound nad                                       |
| 52 | <a href="#">c1uufA</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc-type alcohol dehydrogenase-like protein<br><b>PDBTitle:</b> crystal structure of a zinc-type alcohol dehydrogenase-like2 protein yahk   |
| 53 | <a href="#">c1z6kD</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> alcohol dehydrogenase;   |

|    |                         |           |              |       |    |   |
|----|-------------------------|-----------|--------------|-------|----|---|
| 53 | <a href="#">c4z0kD_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDBTitle:</b> alcohol dehydrogenase from the antarctic psychrophile moraxella sp.2 tae 123<br><b>PDB header:</b> oxidoreductase  |
| 54 | <a href="#">c4eezB_</a> | Alignment | not modelled | 100.0 | 23 | <b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase 1;<br><b>PDBTitle:</b> crystal structure of lactococcus lactis alcohol dehydrogenase variant2 re1   |
| 55 | <a href="#">c4jbiB_</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase (zinc);<br><b>PDBTitle:</b> 2.35a resolution structure of nadph bound thermostable alcohol2 dehydrogenase from pyrobaculum aerophilum                              |
| 56 | <a href="#">c3m6iA_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-arabinitol 4-dehydrogenase;<br><b>PDBTitle:</b> l-arabinitol 4-dehydrogenase   |
| 57 | <a href="#">c3widC_</a> | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> glucose 1-dehydrogenase;<br><b>PDBTitle:</b> structure of a glucose dehydrogenase t277f mutant in complex with nadp  |
| 58 | <a href="#">c2j8zA_</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> quinone oxidoreductase;<br><b>PDBTitle:</b> crystal structure of human p53 inducible oxidoreductase (2 tp53i3.pig3)  |
| 59 | <a href="#">c1lluD_</a> | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> alcohol dehydrogenase;<br><b>PDBTitle:</b> the ternary complex of pseudomonas aeruginosa alcohol2 dehydrogenase with its coenzyme and weak substrate                                     |
| 60 | <a href="#">c2vvpA_</a> | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glucose dehydrogenase;<br><b>PDBTitle:</b> haloferax mediterranei glucose dehydrogenase in complex with nadph and2 zn.   |
| 61 | <a href="#">c6n7lB_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase;<br><b>PDBTitle:</b> crystal structure of an alcohol dehydrogenase from elizabethkingia2 anophelis nuhp1   |
| 62 | <a href="#">c3qwbC_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> probable quinone oxidoreductase;<br><b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae zeta-crystallin-like2 quinone oxidoreductase zta1 complexed with nadph                |
| 63 | <a href="#">c1n9gF_</a> | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> F: <b>PDB Molecule:</b> 2,4-dienoyl-coa reductase;<br><b>PDBTitle:</b> mitochondrial 2-enoyl thioester reductase etr1p/etr2p heterodimer from2 candida tropicalis   |
| 64 | <a href="#">c3iupB_</a> | Alignment | not modelled | 100.0 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative nadph:quinone oxidoreductase;<br><b>PDBTitle:</b> crystal structure of putative nadph:quinone oxidoreductase2 (yp_296108.1) from ralstonia eutropha jmp134 at 1.70 a resolution |
| 65 | <a href="#">c2h6eA_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> d-arabinose 1-dehydrogenase;<br><b>PDBTitle:</b> crystal structure of the d-arabinose dehydrogenase from sulfolobus2 solfataricus  |
| 66 | <a href="#">c3gazA_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase superfamily protein;<br><b>PDBTitle:</b> crystal structure of an alcohol dehydrogenase superfamily protein from2 novosphingobium aromaticivorans                   |
| 67 | <a href="#">c1qorA_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> quinone oxidoreductase;<br><b>PDBTitle:</b> crystal structure of escherichia coli quinone oxidoreductase complexed2 with nadph   |
| 68 | <a href="#">c3pi7A_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nadh oxidoreductase;<br><b>PDBTitle:</b> crystal structure of a putative nadph:quinone reductase (ml13093) from2 mesorhizobium loti at 1.71 a resolution                                 |
| 69 | <a href="#">c1xa0B_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative nadph dependent oxidoreductases;<br><b>PDBTitle:</b> crystal structure of mcsg target apc35536 from bacillus2 stearothermophilus                         |
| 70 | <a href="#">c2c0cB_</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> zinc binding alcohol dehydrogenase, domain containing 2;<br><b>PDBTitle:</b> structure of the mgc45594 gene product  |
| 71 | <a href="#">c3fbgA_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative arginate lyase;<br><b>PDBTitle:</b> crystal structure of a putative arginate lyase from staphylococcus2 haemolyticus                                     |
| 72 | <a href="#">c5gxeA_</a> | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acrylyl-coa reductase acui;<br><b>PDBTitle:</b> crystal structure of acryloyl-coa reductase acui in complex with nadph   |
| 73 | <a href="#">c2vcyA_</a> | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> trans-2-enoyl-coa reductase;<br><b>PDBTitle:</b> crystal structure of 2-enoyl thioester reductase of human fas ii  |
| 74 | <a href="#">c4rvsA_</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> electron transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable quinone reductase qor (nadph:quinone reductase)<br><b>PDBTitle:</b> the native structure of mycobacterial quinone oxidoreductase rv154c.                                    |
| 75 | <a href="#">c5zxnA_</a> | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nadp-dependent oxidoreductase;<br><b>PDBTitle:</b> crystal structure of cura from vibrio vulnificus  |
| 76 | <a href="#">c3gmsA_</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative nadph:quinone reductase;<br><b>PDBTitle:</b> crystal structure of putative nadph:quinone reductase from bacillus2 thuringiensis                          |
| 77 | <a href="#">c1y9eB_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein yhfp;<br><b>PDBTitle:</b> crystal structure of bacillus subtilis protein yhfp with nad bound   |
|    |                         |           |              |       |    | <b>PDB header:</b> structural genomics, unknown function  |

|     |                         |           |              |       |    |  |
|-----|-------------------------|-----------|--------------|-------|----|--|
| 78  | <a href="#">c1o89A_</a> | Alignment | not modelled | 100.0 | 15 | <b>Chain:</b> A: <b>PDB Molecule:</b> yhdh;<br><b>PDBTitle:</b> crystal structure of e. coli k-12 yhdh   |
| 79  | <a href="#">c4jxkA_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase;<br><b>PDBTitle:</b> crystal structure of oxidoreductase rop_24000 (target efi-506400) from <i>rhodococcus opacus</i> b4   |
| 80  | <a href="#">c2j3iB_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nadp-dependent oxidoreductase p1;<br><b>PDBTitle:</b> crystal structure of arabidopsis thaliana double bond2 reductase (at5g16970)-binary complex   |
| 81  | <a href="#">c4dviA_</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative zinc-dependent alcohol dehydrogenase protein;<br><b>PDBTitle:</b> crystal structure of a putative zinc-dependent alcohol dehydrogenase2 protein from <i>rhizobium etli</i> cfn 42  |
| 82  | <a href="#">c1wlyA_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 2-haloacrylate reductase;<br><b>PDBTitle:</b> crystal structure of 2-haloacrylate reductase   |
| 83  | <a href="#">c3jynA_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> quinone oxidoreductase;<br><b>PDBTitle:</b> crystal structures of <i>pseudomonas syringae</i> pv. tomato dc30002 quinone oxidoreductase complexed with nadph  |
| 84  | <a href="#">c5a3jF_</a> | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> F: <b>PDB Molecule:</b> putative quinone-oxidoreductase homolog, chloroplastic;<br><b>PDBTitle:</b> crystal structure of the chloroplastic gamma-ketol reductase from <i>arabidopsis thaliana</i> bound to 13-oxo-9(z),11(e),15(z)-3 octadecatrienoic acid. |
| 85  | <a href="#">c4a27A_</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> synaptic vesicle membrane protein vat-1 homolog-like;<br><b>PDBTitle:</b> crystal structure of human synaptic vesicle membrane protein vat-12 homolog-like protein  |
| 86  | <a href="#">c2w4qA_</a> | Alignment | not modelled | 100.0 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> prostaglandin reductase 2;<br><b>PDBTitle:</b> crystal structure of human zinc-binding alcohol2 dehydrogenase 1 (zadh1) in ternary complex with nadp and 3 18beta-glycyrhethinic acid   |
| 87  | <a href="#">c1yb5A_</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> quinone oxidoreductase;<br><b>PDBTitle:</b> crystal structure of human zeta-crystallin with bound nadp  |
| 88  | <a href="#">c3gohA_</a> | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase, zinc-containing;<br><b>PDBTitle:</b> crystal structure of alcohol dehydrogenase superfamily protein2 (np_718042.1) from <i>shewanella oneidensis</i> at 1.55 a resolution                                    |
| 89  | <a href="#">c6eowC_</a> | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> ketone/zingerone synthase 1;<br><b>PDBTitle:</b> structure of raspberry ketone synthase with hydroxybenzalacetone  |
| 90  | <a href="#">c4b7cB_</a> | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable oxidoreductase;<br><b>PDBTitle:</b> crystal structure of hypothetical protein pa1648 from <i>pseudomonas aeruginosa</i> .  |
| 91  | <a href="#">c3tqhA_</a> | Alignment | not modelled | 100.0 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> quinone oxidoreductase;<br><b>PDBTitle:</b> structure of the quinone oxidoreductase from <i>coxiella burnetii</i>   |
| 92  | <a href="#">c4eyeA_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable oxidoreductase;<br><b>PDBTitle:</b> crystal structure of a probable oxidoreductase from <i>mycobacterium2 abscessus</i> solved by iodide ion sad   |
| 93  | <a href="#">c5dp1A_</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> curk;<br><b>PDBTitle:</b> crystal structure of curk enoyl reductase   |
| 94  | <a href="#">c4mkrC_</a> | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> plant protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> zingiber officinale double bond reductase;<br><b>PDBTitle:</b> structure of the apo form of a zingiber officinale double bond2 reductase   |
| 95  | <a href="#">c4dupB_</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> quinone oxidoreductase;<br><b>PDBTitle:</b> crystal structure of a quinone oxidoreductase from <i>rhizobium etli</i> cfn2 42  |
| 96  | <a href="#">c5dp2A_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> curf;<br><b>PDBTitle:</b> curf er cyclopropanase from curacin a biosynthetic pathway  |
| 97  | <a href="#">c4idbA_</a> | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ripening-induced protein;<br><b>PDBTitle:</b> structure of the fragaria x ananassa enone oxidoreductase in complex2 with nadp+  |
| 98  | <a href="#">c1zsvB_</a> | Alignment | not modelled | 100.0 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nadp-dependent leukotriene b4 12-<br><b>PDBTitle:</b> crystal structure of human nadp-dependent leukotriene b4 12-2 hydroxydehydrogenase  |
| 99  | <a href="#">c3slkB_</a> | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> polyketide synthase extender module 2;<br><b>PDBTitle:</b> structure of ketoreductase and enoylreductase didomain from modular2 polyketide synthase   |
| 100 | <a href="#">c2vn8B_</a> | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> receptor inhibitor<br><b>Chain:</b> B: <b>PDB Molecule:</b> reticulon-4-interacting protein 1;<br><b>PDBTitle:</b> crystal structure of human reticulon 4 interacting protein 1 in2 complex with nadph  |
| 101 | <a href="#">c5dovB_</a> | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> jamj;<br><b>PDBTitle:</b> crystal structure of jamj enoyl reductase (apo form)  |
| 102 | <a href="#">c1iz0A_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> quinone oxidoreductase;<br><b>PDBTitle:</b> crystal structures of the quinone oxidoreductase from2  |

|     |                         |           |              |       |    | thermus thermophilus hb8 and its complex with nadph   |
|-----|-------------------------|-----------|--------------|-------|----|---|
| 103 | <a href="#">d1cdoal</a> | Alignment | not modelled | 100.0 | 34 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain |
| 104 | <a href="#">d1p0fa1</a> | Alignment | not modelled | 100.0 | 30 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain |
| 105 | <a href="#">d2fzwa1</a> | Alignment | not modelled | 100.0 | 33 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain |
| 106 | <a href="#">d1uufa1</a> | Alignment | not modelled | 100.0 | 33 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain |
| 107 | <a href="#">d1u3ta1</a> | Alignment | not modelled | 100.0 | 32 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain |
| 108 | <a href="#">d1u3wa1</a> | Alignment | not modelled | 100.0 | 35 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain |
| 109 | <a href="#">d1d1ta1</a> | Alignment | not modelled | 100.0 | 32 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain |
| 110 | <a href="#">d2jhfa1</a> | Alignment | not modelled | 100.0 | 34 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain |
| 111 | <a href="#">d1u3ua1</a> | Alignment | not modelled | 100.0 | 34 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain |
| 112 | <a href="#">d1piwa1</a> | Alignment | not modelled | 100.0 | 23 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain |
| 113 | <a href="#">d1pl8a1</a> | Alignment | not modelled | 100.0 | 18 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain |
| 114 | <a href="#">d1e3ia1</a> | Alignment | not modelled | 100.0 | 30 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain |
| 115 | <a href="#">d1kola1</a> | Alignment | not modelled | 100.0 | 23 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain |
| 116 | <a href="#">d1jqba1</a> | Alignment | not modelled | 100.0 | 22 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain |
| 117 | <a href="#">d1vj0a1</a> | Alignment | not modelled | 99.9  | 25 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain |
| 118 | <a href="#">d1jvba1</a> | Alignment | not modelled | 99.9  | 26 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain |
| 119 | <a href="#">d1f8fa1</a> | Alignment | not modelled | 99.9  | 22 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain |
| 120 | <a href="#">d1ykfa1</a> | Alignment | not modelled | 99.9  | 23 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain |