





















# Phyre2

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|---------------|----------------------------------|
| Email         | mdejesus@rockefeller.edu         |
| Description   | RVBD3085 (-)<br>_3450917_3451747 |
| Date          | Thu Aug 8 16:20:26 BST<br>2019   |
| Unique Job ID | 7d8ebc41d83d677a                 |

Detailed template information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|--|---|------------|--------|---|
| 1  | <a href="#">d1xsea_</a> | <br>Alignment   |    | 100.0      | 24     | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases  |
| 2  | <a href="#">c5ig2B_</a> | <br>Alignment   |    | 100.0      | 33     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr;<br><b>PDBTitle:</b> crystal structure of a short chain dehydrogenase/reductase sdr from2 burkholderia phymatum in complex with nad                              |
| 3  | <a href="#">d1y5ma1</a> | <br>Alignment   |    | 100.0      | 24     | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases  |
| 4  | <a href="#">d1xu9a_</a> | <br>Alignment   |    | 100.0      | 25     | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases  |
| 5  | <a href="#">c3tjrA_</a> | <br>Alignment |  | 100.0      | 28     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> short chain dehydrogenase;<br><b>PDBTitle:</b> crystal structure of a rv0851c ortholog short chain dehydrogenase from2 mycobacterium paratuberculosis  |
| 6  | <a href="#">c5epoD_</a> | <br>Alignment |  | 100.0      | 24     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> 7-alpha-hydroxysteroid dehydrogenase;<br><b>PDBTitle:</b> the three-dimensional structure of clostridium absonum 7alpha-2 hydroxysteroid dehydrogenase   |
| 7  | <a href="#">c5jy1C_</a> | <br>Alignment |  | 100.0      | 21     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative short-chain dehydrogenase/reductase;<br><b>PDBTitle:</b> crystal structure of putative short-chain dehydrogenase/reductase from2 burkholderia xenovorans lb400 bound to nad                     |
| 8  | <a href="#">d1ybl_a</a> | <br>Alignment |  | 100.0      | 31     | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases  |
| 9  | <a href="#">c4yacA_</a> | <br>Alignment |  | 100.0      | 28     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> c alpha-dehydrogenase;<br><b>PDBTitle:</b> crystal structure of ligo in complex with nadh from sphingobium sp.2 strain syk-6   |
| 10 | <a href="#">c4fn4A_</a> | <br>Alignment |  | 100.0      | 26     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> short chain dehydrogenase;<br><b>PDBTitle:</b> short-chain nad(h)-dependent dehydrogenase/reductase from sulfobolus2 acidocaldarius  |
| 11 | <a href="#">c4imrA_</a> | <br>Alignment |  | 100.0      | 21     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier-protein) reductase;<br><b>PDBTitle:</b> crystal structure of 3-oxoacyl (acyl-carrier-protein) reductase2 (target efi-506442) from agrobacterium tumefaciens c58 with nadp3 bound |

|    |                         |           |              |       |    |  |
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| 12 | <a href="#">c5fydB_</a> | Alignment |              | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase<br><b>PDBTitle:</b> structural and biochemical insights into 7beta-2 hydroxysteroid dehydrogenase stereoselectivity                                 |
| 13 | <a href="#">c1yb1B_</a> | Alignment |              | 100.0 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 17-beta-hydroxysteroid dehydrogenase type xi;<br><b>PDBTitle:</b> crystal structure of human 17-beta-hydroxysteroid dehydrogenase type2 xi  |
| 14 | <a href="#">c4j2hA_</a> | Alignment |              | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> short chain alcohol dehydrogenase-related dehydrogenase;<br><b>PDBTitle:</b> crystal structure of a putative short-chain alcohol dehydrogenase from2 sinorhizobium meliloti 1021 (target nysgrc-011708) |
| 15 | <a href="#">d2ae2a_</a> | Alignment |              | 100.0 | 24 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases   |
| 16 | <a href="#">c4iboA_</a> | Alignment |              | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> gluconate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of a putative gluconate dehydrogenase from2 agrobacterium tumefaciens (target efi-506446)  |
| 17 | <a href="#">c5u9pB_</a> | Alignment |              | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> gluconate 5-dehydrogenase;<br><b>PDBTitle:</b> crystal structure of a gluconate 5-dehydrogenase from burkholderia2 cenocepacia j2315 in complex with nadp and tartrate                                  |
| 18 | <a href="#">c4urfB_</a> | Alignment |              | 100.0 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cyclohexanol dehydrogenase;<br><b>PDBTitle:</b> molecular genetic and crystal structural analysis of 1-(4-2 hydroxyphenyl)-ethanol dehydrogenase from aromatoleum aromaticum ebn1                       |
| 19 | <a href="#">c4trrH_</a> | Alignment |              | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> H: <b>PDB Molecule:</b> putative d-beta-hydroxybutyrate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of a putative putative d-beta-hydroxybutyrate2 dehydrogenase from burkholderia cenocepacia j2315                   |
| 20 | <a href="#">c4lvuB_</a> | Alignment |              | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family;<br><b>PDBTitle:</b> crystal structure of a putative short chain dehydrogenase from2 burkholderia thailandensis                              |
| 21 | <a href="#">c6ci9D_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase;<br><b>PDBTitle:</b> rmm microcompartment-associated aminopropanol dehydrogenase nadp +2 aminoacetone holo-structure   |
| 22 | <a href="#">c4fc6B_</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal 2,4-dienoyl-coa reductase;<br><b>PDBTitle:</b> studies on dcr shed new light on peroxisomal beta-oxidation: crystal2 structure of the ternary complex of pdcr                               |
| 23 | <a href="#">c3cxtA_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dehydrogenase with different specificities;<br><b>PDBTitle:</b> quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2   |
| 24 | <a href="#">c3lf2B_</a> | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> short chain oxidoreductase q9hya2;<br><b>PDBTitle:</b> nadph bound structure of the short chain oxidoreductase q9hya2 from2 pseudomonas aeruginosa pao1 containing an atypical catalytic center         |
| 25 | <a href="#">c4afnB_</a> | Alignment | not modelled | 100.0 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase fabg;<br><b>PDBTitle:</b> crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase2 (fabg) from pseudomonas aeruginosa at 2.3a resolution            |
| 26 | <a href="#">c4nbvA_</a> | Alignment | not modelled | 100.0 | 33 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase putative short-<br><b>PDBTitle:</b> crystal structure of fabg from cupriavidus taiwanensis   |
| 27 | <a href="#">c2zatC_</a> | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> dehydrogenase/reductase sdr family member 4;<br><b>PDBTitle:</b> crystal structure of a mammalian reductase   |
| 28 | <a href="#">c3wtcB_</a> | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase;<br><b>PDBTitle:</b> crystal structure of gox2036   |

|    |                         |           |              |       |    |  |
|----|-------------------------|-----------|--------------|-------|----|--|
| 29 | <a href="#">d1yxma1</a> | Alignment | not modelled | 100.0 | 22 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases   |
| 30 | <a href="#">d1zema1</a> | Alignment | not modelled | 100.0 | 27 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases   |
| 31 | <a href="#">c4g81A</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative hexonate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of a hexonate dehydrogenase ortholog (target efi-2 506402 from salmonella enterica, unliganded structure)                        |
| 32 | <a href="#">d1geea</a>  | Alignment | not modelled | 100.0 | 25 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases   |
| 33 | <a href="#">c5itvC</a>  | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> dihydroantcapsin 7-dehydrogenase;<br><b>PDBTitle:</b> crystal structure of bacillus subtilis bacc dihydroantcapsin 7-2 dehydrogenase in complex with nadh   |
| 34 | <a href="#">d2c07a1</a> | Alignment | not modelled | 100.0 | 24 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases   |
| 35 | <a href="#">c2c07A</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier protein) reductase;<br><b>PDBTitle:</b> oxoacyl-acyl reductase of plasmodium falciparum   |
| 36 | <a href="#">c4gh5B</a>  | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr;<br><b>PDBTitle:</b> crystal structure of s-2-hydroxypropyl coenzyme m dehydrogenase (s-2 hpcdh)  |
| 37 | <a href="#">c3svtA</a>  | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> short-chain type dehydrogenase/reductase;<br><b>PDBTitle:</b> structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans  |
| 38 | <a href="#">c4yaiB</a>  | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> c alpha-dehydrogenase;<br><b>PDBTitle:</b> crystal structure of ligl in complex with nadh and gge from2 sphingobium sp. strain syk-6  |
| 39 | <a href="#">c4dqxB</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable oxidoreductase protein;<br><b>PDBTitle:</b> crystal structure of a short chain dehydrogenase from rhizobium etli2 cfn 42   |
| 40 | <a href="#">d1ae1a</a>  | Alignment | not modelled | 100.0 | 24 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases   |
| 41 | <a href="#">c4wuvB</a>  | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 2-hydroxycyclohexanecarboxyl-coa dehydrogenase;<br><b>PDBTitle:</b> crystal structure of a putative d-mannonate oxidoreductase from2 haemophilus influenza (avi_5165, target efi-513796) with bound nad |
| 42 | <a href="#">c3toxG</a>  | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> G: <b>PDB Molecule:</b> short chain dehydrogenase;<br><b>PDBTitle:</b> crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021  |
| 43 | <a href="#">c5un1A</a>  | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketoacyl-acyl reductase;<br><b>PDBTitle:</b> crystal structure of a d-beta-hydroxybutyrate dehydrogenase from2 burkholderia multivorans   |
| 44 | <a href="#">c4egfA</a>  | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-xylulose reductase;<br><b>PDBTitle:</b> crystal structure of a l-xylulose reductase from mycobacterium2 smegmatis   |
| 45 | <a href="#">c3awdD</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> putative polyol dehydrogenase;<br><b>PDBTitle:</b> crystal structure of gox2181   |
| 46 | <a href="#">c2p68A</a>  | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase;<br><b>PDBTitle:</b> crystal structure of aq_1716 from aquifex aeolicus vf5  |
| 47 | <a href="#">d1fmca</a>  | Alignment | not modelled | 100.0 | 23 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases   |
| 48 | <a href="#">c3ai3A</a>  | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nadph-sorbose reductase;<br><b>PDBTitle:</b> the crystal structure of l-sorbose reductase from gluconobacter2 frateurii complexed with nadph and l-sorbose  |
| 49 | <a href="#">c5h5xH</a>  | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> H: <b>PDB Molecule:</b> putative oxidoreductase;<br><b>PDBTitle:</b> crystal structure of nadh bound carbonyl reductase from streptomyces2 coelicolor   |
| 50 | <a href="#">d1xhla</a>  | Alignment | not modelled | 100.0 | 23 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases   |
| 51 | <a href="#">c5er6C</a>  | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family;<br><b>PDBTitle:</b> crystal structure of an oxidoreductase from brucella ovis   |
| 52 | <a href="#">d2bela</a>  | Alignment | not modelled | 100.0 | 24 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases   |
| 53 | <a href="#">c3ioyB</a>  | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr;<br><b>PDBTitle:</b> structure of putative short-chain dehydrogenase (saro_0793) from2 novosphingobium aromaticivorans  |
| 54 | <a href="#">c5ojgB</a>  | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dehydrogenase/reductase sdr family member 4;<br><b>PDBTitle:</b> crystal structure of the dehydrogenase/reductase sdr   |

|    |                         |           |              |       |    |  |
|----|-------------------------|-----------|--------------|-------|----|--|
|    |                         |           |              |       |    | family member 42 (dhrs4) from caenorhabditis elegans   |
| 55 | <a href="#">d1hdca</a>  | Alignment | not modelled | 100.0 | 28 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases   |
| 56 | <a href="#">d1iy8a</a>  | Alignment | not modelled | 100.0 | 27 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases   |
| 57 | <a href="#">c3t7cC</a>  | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> carveol dehydrogenase;<br><b>PDBTitle:</b> crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad  |
| 58 | <a href="#">c3imfA</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> short chain dehydrogenase;<br><b>PDBTitle:</b> 1.99 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor'                            |
| 59 | <a href="#">c6ds1C</a>  | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative oxidoreductase;<br><b>PDBTitle:</b> crystal structure of cj0485 dehydrogenase in complex with nadp+  |
| 60 | <a href="#">c3tzqD</a>  | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> short-chain type dehydrogenase/reductase;<br><b>PDBTitle:</b> crystal structure of a short-chain type dehydrogenase/reductase from2 mycobacterium marinum   |
| 61 | <a href="#">c3gvcB</a>  | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable short-chain type dehydrogenase/reductase;<br><b>PDBTitle:</b> crystal structure of probable short-chain dehydrogenase-reductase from2 mycobacterium tuberculosis                         |
| 62 | <a href="#">c6d9yB</a>  | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr;<br><b>PDBTitle:</b> crystal structure of a short chain dehydrogenase/reductase sdr from2 burkholderia phymatum with partially occupied nad               |
| 63 | <a href="#">c3rihB</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> short chain dehydrogenase or reductase;<br><b>PDBTitle:</b> crystal structure of a putative short chain dehydrogenase or reductase2 from mycobacterium abscessus                                  |
| 64 | <a href="#">c2q2qG</a>  | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> G: <b>PDB Molecule:</b> beta-d-hydroxybutyrate dehydrogenase;<br><b>PDBTitle:</b> structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida  |
| 65 | <a href="#">c3lylB</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier-protein) reductase;<br><b>PDBTitle:</b> structure of 3-oxoacyl-acylcarrier protein reductase, fabg2 from francisella tularensis   |
| 66 | <a href="#">c5ff9C</a>  | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> noroxomaritidine/norcraugsodine reductase;<br><b>PDBTitle:</b> noroxomaritidine/norcraugsodine reductase in complex with nadp+ and2 tyramine  |
| 67 | <a href="#">c4bmvH</a>  | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> H: <b>PDB Molecule:</b> short-chain dehydrogenase;<br><b>PDBTitle:</b> short-chain dehydrogenase from sphingobium yanoikuyae in2 complex with nadph   |
| 68 | <a href="#">c1w4zA</a>  | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> antibiotic biosynthesis<br><b>Chain:</b> A: <b>PDB Molecule:</b> ketoacyl reductase;<br><b>PDBTitle:</b> structure of actinorhodin polyketide (actiii) reductase  |
| 69 | <a href="#">c5k9zB</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative short-chain dehydrogenase/reductase;<br><b>PDBTitle:</b> crystal structure of putative short-chain dehydrogenase/reductase from2 burkholderia xenovorans lb400                           |
| 70 | <a href="#">c4weoD</a>  | Alignment | not modelled | 100.0 | 32 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> putative acetoin(diacetyl) reductase;<br><b>PDBTitle:</b> crystal structure of a putative acetoin(diacetyl) reductase2 burkholderia cenocepacia   |
| 71 | <a href="#">c2jahB</a>  | Alignment | not modelled | 100.0 | 33 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> clavulanic acid dehydrogenase;<br><b>PDBTitle:</b> biochemical and structural analysis of the clavulanic acid2 dehydrogenase (cad) from streptomyces clavuligerus                                 |
| 72 | <a href="#">c5idxB</a>  | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr;<br><b>PDBTitle:</b> crystal structure of an oxidoreductase from burkholderia vietnamiensis   |
| 73 | <a href="#">c3iccA</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative 3-oxoacyl-(acyl carrier protein) reductase;<br><b>PDBTitle:</b> crystal structure of a putative 3-oxoacyl-(acyl carrier protein)2 reductase from bacillus anthracis at 1.87 a resolution |
| 74 | <a href="#">c5x8hA</a>  | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> short-chain dehydrogenase reductase;<br><b>PDBTitle:</b> crystal structure of the ketone reductase chkred20 from the genome of2 chryseobacterium sp. ca49   |
| 75 | <a href="#">d2rhca1</a> | Alignment | not modelled | 100.0 | 28 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases   |
| 76 | <a href="#">c4npcA</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sorbitol dehydrogenase;<br><b>PDBTitle:</b> crystal structure of an oxidoreductase, short-chain2 dehydrogenase/reductase family protein from brucella suis  |
| 77 | <a href="#">c3rkrC</a>  | Alignment | not modelled | 100.0 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> short chain oxidoreductase;<br><b>PDBTitle:</b> crystal structure of a metagenomic short-chain oxidoreductase (sdr) in2 complex with nadp   |
| 78 | <a href="#">c3rkuC</a>  | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> oxidoreductase ymr226c;<br><b>PDBTitle:</b> substrate fingerprint and the structure of nadp+ dependent serine2 dehydrogenase from saccharomyces cerevisiae complexed with nadp+                   |

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| 79  | <a href="#">d1xkqa_</a> | Alignment | not modelled | 100.0 | 24 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases  |
| 80  | <a href="#">d2bgka1</a> | Alignment | not modelled | 100.0 | 21 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases  |
| 81  | <a href="#">d1w6ua_</a> | Alignment | not modelled | 100.0 | 21 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases  |
| 82  | <a href="#">c1fdvA_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> dehydrogenase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 17-beta-hydroxysteroid dehydrogenase;<br><b>PDBTitle:</b> human 17-beta-hydroxysteroid-dehydrogenase type 1 mutant h221l2 complexed with nad+   |
| 83  | <a href="#">c4jroC_</a> | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> fabg protein;<br><b>PDBTitle:</b> crystal structure of 3-oxoacyl-[acyl-carrier protein]reductase (fabg)2 from listeria monocytogenes in complex with nadp+   |
| 84  | <a href="#">c2uvdE_</a> | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> E: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier-protein) reductase;<br><b>PDBTitle:</b> the crystal structure of a 3-oxoacyl-(acyl carrier protein) reductase2 from bacillus anthracis (ba3989)  |
| 85  | <a href="#">c3emkA_</a> | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glucose/ribitol dehydrogenase;<br><b>PDBTitle:</b> 2.5a crystal structure of glucose/ribitol dehydrogenase from brucella2 melitensis   |
| 86  | <a href="#">c3pk0B_</a> | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr;<br><b>PDBTitle:</b> crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis  |
| 87  | <a href="#">d1jtva_</a> | Alignment | not modelled | 100.0 | 26 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases  |
| 88  | <a href="#">d1ja9a_</a> | Alignment | not modelled | 100.0 | 25 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases  |
| 89  | <a href="#">c4nqzF_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh] fabi;<br><b>PDBTitle:</b> crystal structure of the pseudomonas aeruginosa enoyl-acyl carrier2 protein reductase (fabi) in apo form   |
| 90  | <a href="#">c5jc8C_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative short-chain dehydrogenase/reductase;<br><b>PDBTitle:</b> crystal structure of a putative short-chain dehydrogenase/reductase2 from burkholderia xenovorans  |
| 91  | <a href="#">d1xg5a_</a> | Alignment | not modelled | 100.0 | 26 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases  |
| 92  | <a href="#">c3o38D_</a> | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> short chain dehydrogenase;<br><b>PDBTitle:</b> crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis  |
| 93  | <a href="#">c5g4kB_</a> | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase<br><b>PDBTitle:</b> phloroglucinol reductase from clostridium sp. apo-form   |
| 94  | <a href="#">c6ixjK_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> cytosolic protein<br><b>Chain:</b> K: <b>PDB Molecule:</b> sulfoacetaldehyde reductase;<br><b>PDBTitle:</b> the crystal structure of sulfoacetaldehyde reductase from klebsiella2 oxytoca  |
| 95  | <a href="#">c3itdA_</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 17beta-hydroxysteroid dehydrogenase;<br><b>PDBTitle:</b> crystal structure of an inactive 17beta-hydroxysteroid dehydrogenase2 (y167f mutated form) from fungus cochliobolus lunatus   |
| 96  | <a href="#">d2ew8a1</a> | Alignment | not modelled | 100.0 | 27 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases  |
| 97  | <a href="#">d1k2wa_</a> | Alignment | not modelled | 100.0 | 21 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases  |
| 98  | <a href="#">c2cfcB_</a> | Alignment | not modelled | 100.0 | 30 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 2-(r)-hydroxypropyl-com dehydrogenase;<br><b>PDBTitle:</b> structural basis for stereo selectivity in the (r)- and2 (s)-hydroxypropylethane thiosulfonate dehydrogenases   |
| 99  | <a href="#">c3uf0A_</a> | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr;<br><b>PDBTitle:</b> crystal structure of a putative nad(p) dependent gluconate 5-2 dehydrogenase from beutenbergia cavernae(efi target efi-502044) with3 bound nadp (low occupancy) |
| 100 | <a href="#">c3k31B_</a> | Alignment | not modelled | 100.0 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase;<br><b>PDBTitle:</b> crystal structure of enoyl-(acyl-carrier-protein) reductase from2 anaplasma phagocytophilum in complex with nad at 1.9a resolution                               |
| 101 | <a href="#">c5jydA_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> short chain dehydrogenase;<br><b>PDBTitle:</b> crystal structure of a putative short chain dehydrogenase from2 burkholderia cenocepacia  |
| 102 | <a href="#">c4z9yA_</a> | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 2-deoxy-d-gluconate 3-dehydrogenase;<br><b>PDBTitle:</b> crystal structure of 2-keto-3-deoxy-d-gluconate dehydrogenase from2 pectobacterium carotovorum  |
| 103 | <a href="#">c3ftpD_</a> | Alignment | not modelled | 100.0 | 32 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier protein] reductase;<br><b>PDBTitle:</b> crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase from2 burkholderia pseudomallei at 2.05 a resolution  |

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| 104 | <a href="#">c3oecA_</a>  | Alignment | not modelled | 100.0 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> carveol dehydrogenase (mytha.01326.c, a0r518 homolog);<br><b>PDBTitle:</b> crystal structure of carveol dehydrogenase from mycobacterium2 thermoresistibile            |
| 105 | <a href="#">c4mowB_</a>  | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glucose 1-dehydrogenase;<br><b>PDBTitle:</b> crystal structure of a putative glucose 1-dehydrogenase from2 burkholderia cenocepacia j2315                              |
| 106 | <a href="#">c2et6A_</a>  | Alignment | not modelled | 100.0 | 30 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> (3r)-hydroxyacyl-coa dehydrogenase;<br><b>PDBTitle:</b> (3r)-hydroxyacyl-coa dehydrogenase domain of candida tropicalis2 peroxisomal multifunctional enzyme type 2     |
| 107 | <a href="#">c3i1jB_</a>  | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family;<br><b>PDBTitle:</b> structure of a putative short chain dehydrogenase from pseudomonas2 syringae           |
| 108 | <a href="#">d1nffa_</a>  | Alignment | not modelled | 100.0 | 28 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases  |
| 109 | <a href="#">c2yz7B_</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> d-3-hydroxybutyrate dehydrogenase;<br><b>PDBTitle:</b> x-ray analyses of 3-hydroxybutyrate dehydrogenase from2 alcaligenes faecalis                                    |
| 110 | <a href="#">c2z1nA_</a>  | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dehydrogenase;<br><b>PDBTitle:</b> crystal structure of ape0912 from aeropyrum pernix k1   |
| 111 | <a href="#">c4kzpC_</a>  | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family<br><b>PDBTitle:</b> crystal structure of a putative short chain dehydrogenase from2 mycobacterium smegmatis |
| 112 | <a href="#">d1q7ba_</a>  | Alignment | not modelled | 100.0 | 29 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases  |
| 113 | <a href="#">d1ledoa_</a> | Alignment | not modelled | 100.0 | 29 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases  |
| 114 | <a href="#">c3sjuA_</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> keto reductase;<br><b>PDBTitle:</b> hedamycin polyketide ketoreductase bound to nadph  |
| 115 | <a href="#">c3tscB_</a>  | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase;<br><b>PDBTitle:</b> crystal structure of short chain dehydrogenase map_2410 from2 mycobacterium paratuberculosis bound to nad                 |
| 116 | <a href="#">c5o30A_</a>  | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase;<br><b>PDBTitle:</b> crystal structure of the novel halohydrin dehalogenase hheg  |
| 117 | <a href="#">c3ak4C_</a>  | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> nadh-dependent quinuclidinone reductase;<br><b>PDBTitle:</b> crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens              |
| 118 | <a href="#">c4wecA_</a>  | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> short chain dehydrogenase;<br><b>PDBTitle:</b> crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis  |
| 119 | <a href="#">c3sc4A_</a>  | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> short chain dehydrogenase (a0qtm2 homolog);<br><b>PDBTitle:</b> crystal structure of a short chain dehydrogenase (a0qtm2 homolog)2 mycobacterium thermoresistibile     |
| 120 | <a href="#">c6f9qC_</a>  | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> 7s-cis-cis-nepetalactol cyclase;<br><b>PDBTitle:</b> binary complex of a 7s-cis-cis-nepetalactol cyclase from nepeta2 mussinii with nad+                         |