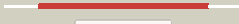



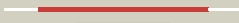



















# Phyre2

|               |                                  |
|---------------|----------------------------------|
| Email         | mdejesus@rockefeller.edu         |
| Description   | RVBD2298 (-)<br>_2569092_2570063 |
| Date          | Mon Aug 5 13:25:44 BST<br>2019   |
| Unique Job ID | f312160b65dca4f7                 |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|---|---|------------|--------|---|
| 1  | <a href="#">d1lqaa_</a> |  Alignment   |    | 100.0      | 28     | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)  |
| 2  | <a href="#">c3n2tA_</a> |  Alignment   |    | 100.0      | 27     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase;<br><b>PDBTitle:</b> structure of the glycerol dehydrogenase akr11b4 from gluconobacter2 oxydans                         |
| 3  | <a href="#">c4xk2A_</a> |  Alignment   |    | 100.0      | 30     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aldo/keto reductase;<br><b>PDBTitle:</b> crystal structure of aldo-keto reductase from polaromonas sp. js666                                     |
| 4  | <a href="#">d1pyfa_</a> |  Alignment   |   | 100.0      | 31     | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)  |
| 5  | <a href="#">c3erpA_</a> |  Alignment |  | 100.0      | 29     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase;<br><b>PDBTitle:</b> structure of idp01002, a putative oxidoreductase from and essential2 gene of salmonella typhimurium |
| 6  | <a href="#">d3eaau1</a> |  Alignment |  | 100.0      | 29     | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)  |
| 7  | <a href="#">d1pz1a_</a> |  Alignment |  | 100.0      | 28     | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)  |
| 8  | <a href="#">c3lutA_</a> |  Alignment |  | 100.0      | 29     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> voltage-gated potassium channel subunit beta-2;<br><b>PDBTitle:</b> a structural model for the full-length shaker potassium channel kv1.2      |
| 9  | <a href="#">c6hg6A_</a> |  Alignment |  | 100.0      | 27     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-glyceraldehyde 3-phosphate reductase;<br><b>PDBTitle:</b> clostridium beijerinckii aldo-keto reductase cbei_3974 with nadph                    |
| 10 | <a href="#">c3n6qF_</a> |  Alignment |  | 100.0      | 28     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> F: <b>PDB Molecule:</b> yghz aldo-keto reductase;<br><b>PDBTitle:</b> crystal structure of yghz from e. coli   |
| 11 | <a href="#">d1ur3m_</a> |  Alignment |  | 100.0      | 23     | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)  |

|    |                         |           |              |       |    |  |
|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | <a href="#">c5danA_</a> | Alignment |              | 100.0 | 34 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> 2,5-diketo-d-gluconic acid reductase;<br><b>PDBTitle:</b> crystal structure of a novel aldo keto reductase tm1743 from <i>Thermotoga maritima</i> in complex with nadp+           |
| 13 | <a href="#">d1gvea_</a> | Alignment |              | 100.0 | 25 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)   |
| 14 | <a href="#">c1ynpA_</a> | Alignment |              | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> oxidoreductase;<br><b>PDBTitle:</b> aldo-keto reductase akr11c1 from <i>Bacillus halodurans</i> (apo form)  |
| 15 | <a href="#">c2bp1C_</a> | Alignment |              | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C; <b>PDB Molecule:</b> afatoxin b1 aldehyde reductase member 2;<br><b>PDBTitle:</b> structure of the aflatoxin aldehyde reductase in complex with nadph  |
| 16 | <a href="#">d1j96a_</a> | Alignment |              | 100.0 | 25 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)   |
| 17 | <a href="#">d1q5ma_</a> | Alignment |              | 100.0 | 23 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)   |
| 18 | <a href="#">c4pmjA_</a> | Alignment |              | 100.0 | 34 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> putative oxidoreductase;<br><b>PDBTitle:</b> crystal structure of a putative oxidoreductase from <i>Sinorhizobium meliloti</i> 1021 in complex with nadp                          |
| 19 | <a href="#">c3h7uA_</a> | Alignment |              | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> aldo-keto reductase;<br><b>PDBTitle:</b> crystal structure of the plant stress-response enzyme akr4c9   |
| 20 | <a href="#">c4wghA_</a> | Alignment |              | 100.0 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> aldehyde reductase;<br><b>PDBTitle:</b> crystal structure of aldo/keto reductase from <i>Klebsiella pneumoniae</i> in2 complex with nadp and acetate at 1.8 Å resolution          |
| 21 | <a href="#">c3v0tA_</a> | Alignment | not modelled | 100.0 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> perakine reductase;<br><b>PDBTitle:</b> crystal structure of perakine reductase, founder member of a novel akr2 subfamily with unique conformational changes during nadph binding |
| 22 | <a href="#">d1afsa_</a> | Alignment | not modelled | 100.0 | 23 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)   |
| 23 | <a href="#">c5az0A_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of aldo-keto reductase (akr2e5) of the silkworm, <i>Bombyx mori</i>  |
| 24 | <a href="#">c6gtmA_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> aldo-keto reductase family protein;<br><b>PDBTitle:</b> crystal structure of smba in complex with pppgpp.  |
| 25 | <a href="#">c3up8B_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B; <b>PDB Molecule:</b> putative 2,5-diketo-d-gluconic acid reductase b;<br><b>PDBTitle:</b> crystal structure of a putative 2,5-diketo-d-gluconic acid reductase b                                       |
| 26 | <a href="#">d1us0a_</a> | Alignment | not modelled | 100.0 | 25 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)   |
| 27 | <a href="#">c5ketA_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> aldo-keto reductase 1;<br><b>PDBTitle:</b> structure of the aldo-keto reductase from <i>Coptotermes gestroi</i>   |
| 28 | <a href="#">c3wczA_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> aldo-keto reductase 2e;<br><b>PDBTitle:</b> crystal structure of <i>Bombyx mori</i> aldo-keto reductase (akr2e4) in2 complex with nadp  |
| 29 | <a href="#">d1qwka_</a> | Alignment | not modelled | 100.0 | 25 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)   |

|    |                         |           |              |       |    |  |
|----|-------------------------|-----------|--------------|-------|----|--|
| 30 | <a href="#">d1frba_</a> | Alignment | not modelled | 100.0 | 24 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)   |
| 31 | <a href="#">d1hqta_</a> | Alignment | not modelled | 100.0 | 27 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)   |
| 32 | <a href="#">d1s1pa_</a> | Alignment | not modelled | 100.0 | 23 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)   |
| 33 | <a href="#">d1mi3a_</a> | Alignment | not modelled | 100.0 | 24 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)   |
| 34 | <a href="#">c3h7rA_</a> | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aldo-keto reductase;<br><b>PDBTitle:</b> crystal structure of the plant stress-response enzyme akr4c8   |
| 35 | <a href="#">c3f7jB_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> yvgn protein;<br><b>PDBTitle:</b> b.subtilis yvgn   |
| 36 | <a href="#">c3wg6C_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> conjugated polyketone reductase c1;<br><b>PDBTitle:</b> crystal structure of conjugated polyketone reductase c1 from candida2 parapsilosis complexed with nadph                   |
| 37 | <a href="#">c4otkA_</a> | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> mycobacterial enzyme rv2971;<br><b>PDBTitle:</b> a structural characterization of the isoniazid mycobacterium2 tuberculosis drug target, rv2971, in its unliganded form           |
| 38 | <a href="#">c3buvb_</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxo-5-beta-steroid 4-dehydrogenase;<br><b>PDBTitle:</b> crystal structure of human delta(4)-3-ketosteroid 5-beta-reductase in2 complex with nadp and hepes. resolution: 1.35 a. |
| 39 | <a href="#">c2wztA_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aldo-keto reductase;<br><b>PDBTitle:</b> crystal structure of a mycobacterium aldo-keto reductase in its apo2 and liganded form   |
| 40 | <a href="#">c4mhbf_</a> | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> F: <b>PDB Molecule:</b> putative aldo/keto reductase;<br><b>PDBTitle:</b> structure of a putative reductase from yersinia pestis  |
| 41 | <a href="#">c1zgdB_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> plant protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> chalcone reductase;<br><b>PDBTitle:</b> chalcone reductase complexed with nadp+ at 1.7 angstrom2 resolution  |
| 42 | <a href="#">d1vp5a_</a> | Alignment | not modelled | 100.0 | 28 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)   |
| 43 | <a href="#">c4fziA_</a> | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> prostaglandin f synthase;<br><b>PDBTitle:</b> crystal structure of prostaglandin f synthase from trypanosoma cruzi  |
| 44 | <a href="#">d1ah4a_</a> | Alignment | not modelled | 100.0 | 26 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)   |
| 45 | <a href="#">d1c9wa_</a> | Alignment | not modelled | 100.0 | 26 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)   |
| 46 | <a href="#">c4q3mF_</a> | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> F: <b>PDB Molecule:</b> mgs-m4;<br><b>PDBTitle:</b> crystal structure of mgs-m4, an aldo-keto reductase enzyme from a2 medee basin deep-sea metagenome library   |
| 47 | <a href="#">d2alra_</a> | Alignment | not modelled | 100.0 | 29 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)   |
| 48 | <a href="#">c2bgsA_</a> | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aldose reductase;<br><b>PDBTitle:</b> holo aldose reductase from barley   |
| 49 | <a href="#">c4hbka_</a> | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aldo-keto reductase family 1, member b4 (aldose reductase);<br><b>PDBTitle:</b> structure of the aldose reductase from schistosoma japonicum                                      |
| 50 | <a href="#">c3o0kB_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> aldo/keto reductase;<br><b>PDBTitle:</b> crystal structure of aldo/keto reductase from brucella melitensis  |
| 51 | <a href="#">c1vbjB_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> prostaglandin f synthase;<br><b>PDBTitle:</b> the crystal structure of prostaglandin f synthase from trypanosoma2 brucei  |
| 52 | <a href="#">d1hw6a_</a> | Alignment | not modelled | 100.0 | 24 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)   |
| 53 | <a href="#">d1mzra_</a> | Alignment | not modelled | 100.0 | 27 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> NAD(P)-linked oxidoreductase<br><b>Family:</b> Aldo-keto reductases (NADP)   |
| 54 | <a href="#">c3wbwA_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative 2,5-diketo-d-gluconic acid reductase;<br><b>PDBTitle:</b> crystal structure of gox0644 in complex with nadph   |
| 55 | <a href="#">c3b3dA_</a> | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative morphine dehydrogenase;<br><b>PDBTitle:</b> b.subtilis ytbe  |
|    |                         |           |              |       |    | <b>PDB header:</b> oxidoreductase  |

|    |                         |           |              |       |    |  |
|----|-------------------------|-----------|--------------|-------|----|--|
| 56 | <a href="#">c4f40B_</a> | Alignment | not modelled | 100.0 | 27 | <b>Chain:</b> B: <b>PDB Molecule:</b> prostaglandin f2-alpha synthase/d-arabinose dehydrogenase;<br><b>PDBTitle:</b> x-ray crystal structure of apo prostaglandin f synthase from2 leishmania major friedlin   |
| 57 | <a href="#">c3vxgA_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> conjugated polyketone reductase c2;<br><b>PDBTitle:</b> crystal structure of conjugated polyketone reductase c2 from candida2 parapsilosis  |
| 58 | <a href="#">c4exaD_</a> | Alignment | not modelled | 100.0 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of the pa4992, the putative aldo-keto reductase from2 pseudomona aeruginosa   |
| 59 | <a href="#">c3krbB_</a> | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> aldose reductase;<br><b>PDBTitle:</b> structure of aldose reductase from giardia lamblia at 1.75a resolution  |
| 60 | <a href="#">c4ijrA_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> d-arabinose dehydrogenase [nad(p)+] heavy chain;<br><b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae arabinose dehydrogenase2 ara1 complexed with nadph   |
| 61 | <a href="#">c3ln3A_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodiol dehydrogenase;<br><b>PDBTitle:</b> crystal structure of putative reductase (np_038806.2) from mus2 musculus at 1.18 a resolution  |
| 62 | <a href="#">c3pueA_</a> | Alignment | not modelled | 82.1  | 15 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> crystal structure of the complex of dihydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution  |
| 63 | <a href="#">c6mqhA_</a> | Alignment | not modelled | 82.0  | 14 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate synthase;<br><b>PDBTitle:</b> crystal structure of 4-hydroxy-tetrahydrodipicolinate synthase (htpa2 synthase) from burkholderia mallei  |
| 64 | <a href="#">c3noeA_</a> | Alignment | not modelled | 77.7  | 14 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa   |
| 65 | <a href="#">d1jpmA1</a> | Alignment | not modelled | 74.0  | 11 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Enolase C-terminal domain-like<br><b>Family:</b> D-glucarate dehydratase-like  |
| 66 | <a href="#">d1vp8a_</a> | Alignment | not modelled | 70.3  | 19 | <b>Fold:</b> Pyruvate kinase C-terminal domain-like<br><b>Superfamily:</b> PK C-terminal domain-like<br><b>Family:</b> MTH1675-like  |
| 67 | <a href="#">d1xkya1</a> | Alignment | not modelled | 69.3  | 12 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase  |
| 68 | <a href="#">c3fluD_</a> | Alignment | not modelled | 69.2  | 18 | <b>PDB header:</b> lyase<br><b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis  |
| 69 | <a href="#">d1uwka_</a> | Alignment | not modelled | 67.1  | 12 | <b>Fold:</b> Urocanase<br><b>Superfamily:</b> Urocanase<br><b>Family:</b> Urocanase  |
| 70 | <a href="#">c3hf3A_</a> | Alignment | not modelled | 60.1  | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> chromate reductase;<br><b>PDBTitle:</b> old yellow enzyme from thermus scotoductus sa-01  |
| 71 | <a href="#">c2vwtA_</a> | Alignment | not modelled | 57.6  | 11 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> yfau, 2-keto-3-deoxy sugar aldolase;<br><b>PDBTitle:</b> crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex  |
| 72 | <a href="#">c3si9B_</a> | Alignment | not modelled | 57.2  | 18 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from bartonella2 henselae  |
| 73 | <a href="#">c3onoA_</a> | Alignment | not modelled | 56.5  | 12 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ribose/galactose isomerase;<br><b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase lacab_rpiB from2 vibrio parahaemolyticus   |
| 74 | <a href="#">c2fknC_</a> | Alignment | not modelled | 54.9  | 12 | <b>PDB header:</b> lyase<br><b>Chain:</b> C: <b>PDB Molecule:</b> urocanate hydratase;<br><b>PDBTitle:</b> crystal structure of urocanase from bacillus subtilis   |
| 75 | <a href="#">d1x87a_</a> | Alignment | not modelled | 54.3  | 10 | <b>Fold:</b> Urocanase<br><b>Superfamily:</b> Urocanase<br><b>Family:</b> Urocanase  |
| 76 | <a href="#">c3g8rA_</a> | Alignment | not modelled | 52.4  | 14 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable spore coat polysaccharide biosynthesis protein e;<br><b>PDBTitle:</b> crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472                        |
| 77 | <a href="#">c4icnB_</a> | Alignment | not modelled | 50.8  | 13 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> dihydrodipicolinate synthase from shewanella benthica  |
| 78 | <a href="#">d1t57a_</a> | Alignment | not modelled | 50.5  | 17 | <b>Fold:</b> Pyruvate kinase C-terminal domain-like<br><b>Superfamily:</b> PK C-terminal domain-like<br><b>Family:</b> MTH1675-like  |
| 79 | <a href="#">c1xuzA_</a> | Alignment | not modelled | 50.1  | 20 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> polysialic acid capsule biosynthesis protein siaC;<br><b>PDBTitle:</b> crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol |
| 80 | <a href="#">c3g0sA_</a> | Alignment | not modelled | 49.2  | 13 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> dihydrodipicolinate synthase from salmonella typhimurium lt2   |

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| 81  | <a href="#">c4qiwF</a>  | Alignment | not modelled | 48.4 | 8  | <b>PDB header:</b> transcription<br><b>Chain:</b> F; <b>PDB Molecule:</b> dna-directed rna polymerase, subunit f;<br><b>PDBTitle:</b> crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis  |
| 82  | <a href="#">d1hl2a</a>  | Alignment | not modelled | 47.0 | 12 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase   |
| 83  | <a href="#">c3lciA</a>  | Alignment | not modelled | 47.0 | 14 | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> n-acetylneuraminate lyase;<br><b>PDBTitle:</b> the d-sialic acid aldolase mutant v251w  |
| 84  | <a href="#">c4i7vD</a>  | Alignment | not modelled | 44.7 | 15 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> D; <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> agrobacterium tumefaciens dhds with pyruvate   |
| 85  | <a href="#">c3bi8A</a>  | Alignment | not modelled | 44.6 | 11 | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> structure of dihydrodipicolinate synthase from clostridium2 botulinum   |
| 86  | <a href="#">c2ehhE</a>  | Alignment | not modelled | 41.5 | 18 | <b>PDB header:</b> lyase<br><b>Chain:</b> E; <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus  |
| 87  | <a href="#">c2v5jB</a>  | Alignment | not modelled | 40.7 | 11 | <b>PDB header:</b> lyase<br><b>Chain:</b> B; <b>PDB Molecule:</b> 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase;<br><b>PDBTitle:</b> apo class ii aldolase hpch   |
| 88  | <a href="#">c2h90A</a>  | Alignment | not modelled | 36.4 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> xenobiotic reductase a;<br><b>PDBTitle:</b> xenobiotic reductase a in complex with coumarin  |
| 89  | <a href="#">c6ewvA</a>  | Alignment | not modelled | 36.1 | 47 | <b>PDB header:</b> peptide binding protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> nrps kj12c-ndd, nrps kj12b-cdd;<br><b>PDBTitle:</b> solution structure of docking domain complex of rxp nrps: kj12c ndd -2 kj12b cdd  |
| 90  | <a href="#">d2a6na1</a> | Alignment | not modelled | 35.5 | 13 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase   |
| 91  | <a href="#">c2ph5A</a>  | Alignment | not modelled | 35.1 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> A; <b>PDB Molecule:</b> homospermidine synthase;<br><b>PDBTitle:</b> crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54   |
| 92  | <a href="#">c6r62A</a>  | Alignment | not modelled | 34.7 | 15 | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> hpch/hpai aldolase;<br><b>PDBTitle:</b> crystal structure of a class ii pyruvate aldolase from sphingomonas2 wittichii rw1 in complex with hydroxypyruvate  |
| 93  | <a href="#">c5b46B</a>  | Alignment | not modelled | 34.6 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B; <b>PDB Molecule:</b> 2-oxoacid--ferredoxin oxidoreductase beta subunit;<br><b>PDBTitle:</b> 2-oxoacid:ferredoxin oxidoreductase 2 from sulfolobus tokodai - ligand2 free form   |
| 94  | <a href="#">c3c5yD</a>  | Alignment | not modelled | 33.9 | 15 | <b>PDB header:</b> isomerase<br><b>Chain:</b> D; <b>PDB Molecule:</b> ribose/galactose isomerase;<br><b>PDBTitle:</b> crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution  |
| 95  | <a href="#">d1vlia2</a> | Alignment | not modelled | 33.0 | 15 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> NeuB-like  |
| 96  | <a href="#">c6ei9A</a>  | Alignment | not modelled | 31.6 | 10 | <b>PDB header:</b> flavoprotein<br><b>Chain:</b> A; <b>PDB Molecule:</b> trna-dihydrouridine synthase b;<br><b>PDBTitle:</b> crystal structure of e. coli trna-dihydrouridine synthase b (dusb)   |
| 97  | <a href="#">d1xxxa1</a> | Alignment | not modelled | 31.1 | 17 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase   |
| 98  | <a href="#">c3ju2A</a>  | Alignment | not modelled | 30.5 | 10 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein smc04130;<br><b>PDBTitle:</b> crystal structure of protein smc04130 from sinorhizobium meliloti 1021  |
| 99  | <a href="#">d2vvpa1</a> | Alignment | not modelled | 30.4 | 6  | <b>Fold:</b> Ribose/Galactose isomerase RpiB/AlsB<br><b>Superfamily:</b> Ribose/Galactose isomerase RpiB/AlsB<br><b>Family:</b> Ribose/Galactose isomerase RpiB/AlsB  |
| 100 | <a href="#">c2aamA</a>  | Alignment | not modelled | 29.4 | 12 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein tm1410;<br><b>PDBTitle:</b> crystal structure of a putative glycosidase (tm1410) from thermotoga2 maritima at 2.20 a resolution  |
| 101 | <a href="#">d2aama1</a> | Alignment | not modelled | 29.4 | 12 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> (Trans)glycosidases<br><b>Family:</b> TM1410-like   |
| 102 | <a href="#">c4nq1B</a>  | Alignment | not modelled | 29.1 | 15 | <b>PDB header:</b> lyase<br><b>Chain:</b> B; <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate synthase;<br><b>PDBTitle:</b> legionella pneumophila dihydrodipicolinate synthase with first2 substrate pyruvate bound in the active site  |
| 103 | <a href="#">c3ng3A</a>  | Alignment | not modelled | 27.7 | 17 | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> deoxyribose-phosphate aldolase;<br><b>PDBTitle:</b> crystal structure of deoxyribose phosphate aldolase from mycobacterium2 avium 104 in a schiff base with an unknown aldehyde   |
| 104 | <a href="#">c2rfgB</a>  | Alignment | not modelled | 27.6 | 17 | <b>PDB header:</b> lyase<br><b>Chain:</b> B; <b>PDB Molecule:</b> dihydrodipicolinate synthase;<br><b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution   |
| 105 | <a href="#">c5ggoB</a>  | Alignment | not modelled | 27.2 | 22 | <b>PDB header:</b> sugar binding protein<br><b>Chain:</b> B; <b>PDB Molecule:</b> protein o-linked-mannose beta-1,2-n-<br><b>PDBTitle:</b> crystal structure of n-terminal domain of human protein o-mannose2 beta-1,2-n-acetylglucosaminyltransferase in complex with galnac-3 beta1,3-glcnac-beta-pnp<br><b>PDB header:</b> isomerase |

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| 106 | <a href="#">c3k7pA_</a> | Alignment | not modelled | 27.1 | 8  | <b>Chain:</b> A: <b>PDB Molecule:</b> ribose 5-phosphate isomerase;<br><b>PDBTitle:</b> structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.  |
| 107 | <a href="#">c6mywA_</a> | Alignment | not modelled | 26.5 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> n-ethylmaleimide reductase;<br><b>PDBTitle:</b> gluconobacter ene-reductase (gluer) mutant - t36a   |
| 108 | <a href="#">c4w8aA_</a> | Alignment | not modelled | 26.1 | 17 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> exo-xyloglucanase;<br><b>PDBTitle:</b> crystal structure of xeg5b, a gh5 xyloglucan-specific beta-1,4-2 glucanase from ruminal metagenomic library, in the native form       |
| 109 | <a href="#">c3ktcB_</a> | Alignment | not modelled | 25.5 | 15 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> xylose isomerase;<br><b>PDBTitle:</b> crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution         |
| 110 | <a href="#">c5ktIA_</a> | Alignment | not modelled | 25.4 | 12 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate synthase;<br><b>PDBTitle:</b> dihydrodipicolinate synthase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis. |
| 111 | <a href="#">c3bdkB_</a> | Alignment | not modelled | 24.9 | 10 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> d-mannonate dehydratase;<br><b>PDBTitle:</b> crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue                                    |
| 112 | <a href="#">d1qbaa3</a> | Alignment | not modelled | 24.9 | 27 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> (Trans)glycosidases<br><b>Family:</b> beta-N-acetylhexosaminidase catalytic domain   |
| 113 | <a href="#">c3cprB_</a> | Alignment | not modelled | 24.9 | 16 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthetase;<br><b>PDBTitle:</b> the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution                        |
| 114 | <a href="#">c3ddmD_</a> | Alignment | not modelled | 24.6 | 12 | <b>PDB header:</b> lyase<br><b>Chain:</b> D: <b>PDB Molecule:</b> putative mandelate racemase/muconate lactonizing<br><b>PDBTitle:</b> crystal structure of mandelate racemase/muconate2 lactonizing enzyme from bordetella bronchiseptica rb50    |
| 115 | <a href="#">c3lmyA_</a> | Alignment | not modelled | 24.6 | 24 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> beta-hexosaminidase subunit beta;<br><b>PDBTitle:</b> the crystal structure of beta-hexosaminidase b in complex with2 pyrimethamine  |
| 116 | <a href="#">c3oqbF_</a> | Alignment | not modelled | 24.1 | 11 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> F: <b>PDB Molecule:</b> oxidoreductase;<br><b>PDBTitle:</b> crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110  |
| 117 | <a href="#">c1qbaA_</a> | Alignment | not modelled | 23.9 | 27 | <b>PDB header:</b> glycosyl hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> chitobiase;<br><b>PDBTitle:</b> bacterial chitobiase, glycosyl hydrolase family 20  |
| 118 | <a href="#">c2gg8A_</a> | Alignment | not modelled | 23.8 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, frn-binding;<br><b>PDBTitle:</b> structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone                        |
| 119 | <a href="#">c4a1dG_</a> | Alignment | not modelled | 23.7 | 16 | <b>PDB header:</b> ribosome<br><b>Chain:</b> G: <b>PDB Molecule:</b> rpl30;<br><b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.                 |
| 120 | <a href="#">d1rioa_</a> | Alignment | not modelled | 23.6 | 17 | <b>Fold:</b> lambda repressor-like DNA-binding domains<br><b>Superfamily:</b> lambda repressor-like DNA-binding domains<br><b>Family:</b> Phage repressors   |