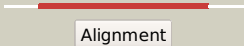

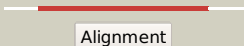

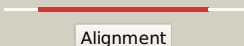







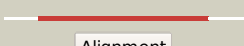











Phyre2

| | |
|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3468c_(-)_3885154_3886248 |
| Date | Fri Aug 9 18:20:14 BST 2019 |
| Unique Job ID | 53d48971e9617224 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c1z7eC_ |  Alignment |  | 100.0 | 15 | PDB header: hydrolase Chain: C: PDB Molecule: protein arna; PDBTitle: crystal structure of full length arna |
| 2 | c1z45A_ |  Alignment |  | 100.0 | 23 | PDB header: isomerase Chain: A: PDB Molecule: gal10 bifunctional protein; PDBTitle: crystal structure of the gal10 fusion protein galactose2 mutarotase/udp-galactose 4-epimerase from saccharomyces cerevisiae3 complexed with nad, udp-glucose, and galactose |
| 3 | d1i24a_ |  Alignment |  | 100.0 | 16 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 4 | d2c5aa1 |  Alignment |  | 100.0 | 13 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 5 | d1kewa_ |  Alignment |  | 100.0 | 21 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 6 | c5msuC_ |  Alignment |  | 100.0 | 19 | PDB header: oxidoreductase Chain: C: PDB Molecule: carboxylic acid reductase; PDBTitle: structure of the r domain of carboxylic acid reductase (car) from2 mycobacterium marinum in complex with nadp, p21 form |
| 7 | c5df1A_ |  Alignment |  | 100.0 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: iridoid synthase; PDBTitle: iridoid synthase from catharanthus roseus - ternary complex with nadp+2 and geranic acid |
| 8 | d1oc2a_ |  Alignment |  | 100.0 | 17 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 9 | c3oh8A_ |  Alignment |  | 100.0 | 14 | PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate sugar epimerase (sula family); PDBTitle: crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91 |
| 10 | c2b69A_ |  Alignment |  | 100.0 | 20 | PDB header: lyase Chain: A: PDB Molecule: udp-glucuronate decarboxylase 1; PDBTitle: crystal structure of human udp-glucuronic acid decarboxylase |
| 11 | d2b69a1 |  Alignment |  | 100.0 | 20 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 12 | c4pvcB_ | Alignment | | 100.0 | 19 | PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-dependent methylglyoxal reductase gre2; PDBTitle: crystal structure of yeast methylglyoxal/ isovaleraldehyde reductase2 gre2 |
| 13 | d1db3a_ | Alignment | | 100.0 | 14 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 14 | c3m2pD_ | Alignment | | 100.0 | 19 | PDB header: isomerase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4-epimerase; PDBTitle: the crystal structure of udp-n-acetylglucosamine 4-epimerase2 from bacillus cereus |
| 15 | c6bwlA_ | Alignment | | 100.0 | 19 | PDB header: lyase Chain: A: PDB Molecule: pal; PDBTitle: x-ray structure of pal from bacillus thuringiensis |
| 16 | d1e6ua_ | Alignment | | 100.0 | 18 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 17 | c4b8wB_ | Alignment | | 100.0 | 19 | PDB header: oxidoreductase Chain: B: PDB Molecule: gdp-l-fucose synthase; PDBTitle: crystal structure of human gdp-l-fucose synthase with bound nadp and2 gdp, tetragonal crystal form |
| 18 | c2v6gA_ | Alignment | | 100.0 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: progesterone 5-beta-reductase; PDBTitle: structure of progesterone 5beta-reductase from digitalis2 lanata in complex with nadp |
| 19 | c6aqyD_ | Alignment | | 100.0 | 15 | PDB header: oxidoreductase Chain: D: PDB Molecule: gdp-l-fucose synthetase; PDBTitle: crystal structure of a gdp-l-fucose synthetase from naegleria fowleri |
| 20 | c4lisA_ | Alignment | | 100.0 | 23 | PDB header: isomerase Chain: A: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of udp-galactose-4-epimerase from aspergillus2 nidulans |
| 21 | d1gy8a_ | Alignment | not modelled | 100.0 | 23 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 22 | d2blla1 | Alignment | not modelled | 100.0 | 14 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 23 | c2hrzA_ | Alignment | not modelled | 100.0 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: the crystal structure of the nucleoside-diphosphate-sugar epimerase2 from agrobacterium tumefaciens |
| 24 | c5l9aB_ | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: l-threonine 3-dehydrogenase; PDBTitle: l-threonine dehydrogenase from trypanosoma brucei. |
| 25 | c1n7gB_ | Alignment | not modelled | 100.0 | 13 | PDB header: lyase Chain: B: PDB Molecule: gdp-d-mannose-4,6-dehydratase; PDBTitle: crystal structure of the gdp-mannose 4,6-dehydratase2 ternary complex with nadph and gdp-rhamnose. |
| 26 | c2z1mC_ | Alignment | not modelled | 100.0 | 16 | PDB header: lyase Chain: C: PDB Molecule: gdp-d-mannose dehydratase; PDBTitle: crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5 |
| 27 | c2pk3B_ | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: B: PDB Molecule: gdp-6-deoxy-d-lyxo-4-hexulose reductase; PDBTitle: crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase |
| 28 | d1r6da_ | Alignment | not modelled | 100.0 | 26 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 29 | c3w1vA_ | Alignment | not modelled | 100.0 | 22 | PDB header: lyase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap8e; |

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|----|-------------------------|-----------|--------------|-------|----|---|
| | | | | | | PDBTitle: crystal structure of capsular polysaccharide synthesizing enzyme cape2 from staphylococcus aureus in complex with inhibitor |
| 30 | c4idgB_ | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase; PDBTitle: crystal structure of a short-chain dehydrogenase/reductase superfamily2 protein from agrobacterium tumefaciens (target efi-506441) with bound3 nad, monoclinic form 2 |
| 31 | c3lu1C_ | Alignment | not modelled | 100.0 | 23 | PDB header: isomerase Chain: C: PDB Molecule: wbgu; PDBTitle: crystal structure analysis of wbgu: a udp-galnac 4-epimerase |
| 32 | c5zedA_ | Alignment | not modelled | 100.0 | 15 | PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein adh; PDBTitle: crystal structure of kluyveromyces polyspora adh (kpadh) mutant2 (e214v/t215s) |
| 33 | d1rkxa_ | Alignment | not modelled | 100.0 | 20 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 34 | c5gmoA_ | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: protein induced by osmotic stress; PDBTitle: x-ray structure of carbonyl reductase sscr |
| 35 | c4zrmB_ | Alignment | not modelled | 100.0 | 22 | PDB header: isomerase Chain: B: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of udp-glucose 4-epimerase (tm0509) from2 hyperthermophilic eubacterium thermotoga maritima |
| 36 | c5b6kA_ | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein cgkr1; PDBTitle: crystal structure of ketoreductase 1 from candida glabrata |
| 37 | c2hunB_ | Alignment | not modelled | 100.0 | 22 | PDB header: lyase Chain: B: PDB Molecule: 336aa long hypothetical dtdp-glucose 4,6-dehydratase; PDBTitle: crystal structure of hypothetical protein ph0414 from pyrococcus2 horikoshii ot3 |
| 38 | c3pvzD_ | Alignment | not modelled | 100.0 | 13 | PDB header: lyase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase; PDBTitle: udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri |
| 39 | c6nbrC_ | Alignment | not modelled | 100.0 | 17 | PDB header: transferase Chain: C: PDB Molecule: kavalactone reductase 1; PDBTitle: crystal structure of piper methysticum kavalactone reductase 1 in2 complex with nadp |
| 40 | c6el3A_ | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxo-delta(4,5)-steroid 5-beta-reductase; PDBTitle: structure of progesterone 5beta-reductase from arabidopsis thaliana in2 complex with nadp |
| 41 | c4egbC_ | Alignment | not modelled | 100.0 | 16 | PDB header: lyase Chain: C: PDB Molecule: dtdp-glucose 4,6-dehydratase; PDBTitle: 3.0 angstrom resolution crystal structure of dtdp-glucose 4,6-2 dehydratase (rfbb) from bacillus anthracis str. ames in complex with3 nad |
| 42 | d1orra_ | Alignment | not modelled | 100.0 | 16 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 43 | d1wvga1 | Alignment | not modelled | 100.0 | 19 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 44 | c4dqvA_ | Alignment | not modelled | 100.0 | 18 | PDB header: ligase Chain: A: PDB Molecule: probable peptide synthetase nrp (peptide synthase); PDBTitle: crystal structure of reductase (r) domain of non-ribosomal peptide2 synthetase from mycobacterium tuberculosis |
| 45 | c5uzhA_ | Alignment | not modelled | 100.0 | 14 | PDB header: transferase Chain: A: PDB Molecule: nafoa.00085.b; PDBTitle: crystal structure of a gdp-mannose dehydratase from naegleria fowleri |
| 46 | d1bxka_ | Alignment | not modelled | 100.0 | 21 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 47 | d1n7ha_ | Alignment | not modelled | 100.0 | 13 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 48 | c3slgF_ | Alignment | not modelled | 100.0 | 14 | PDB header: transferase Chain: F: PDB Molecule: pbgp3 protein; PDBTitle: crystal structure of pbgp3 protein from burkholderia pseudomallei |
| 49 | d1sb8a_ | Alignment | not modelled | 100.0 | 24 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 50 | c2x4gA_ | Alignment | not modelled | 100.0 | 19 | PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of pa4631, a nucleoside-diphosphate-sugar epimerase2 from pseudomonas aeruginosa |
| 51 | c2p5uC_ | Alignment | not modelled | 100.0 | 21 | PDB header: isomerase Chain: C: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of thermus thermophilus hb8 udp-glucose 4-epimerase2 complex with nad |
| 52 | c3enkB_ | Alignment | not modelled | 100.0 | 17 | PDB header: isomerase Chain: B: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: 1.9a crystal structure of udp-glucose 4-epimerase from burkholderia2 pseudomallei |
| 53 | c2iodD_ | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: D: PDB Molecule: dihydroflavonol 4-reductase; PDBTitle: binding of two substrate analogue molecules to2 dihydroflavonol-4-reductase alters the functional geometry3 of the catalytic site |
| 54 | c4r1eB_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: B: PDB Molecule: cinnamoyl coa reductase; |

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|----|--------------------------|-----------|--------------|-------|----|---|
| 54 | c413b_ | Alignment | not modelled | 100.0 | 10 | PDBTitle: crystal structure of petunia hybrida cinnamoyl-coa reductase |
| 55 | d1vl0a_ | Alignment | not modelled | 100.0 | 16 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 56 | c4w4tA_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: mxaa; PDBTitle: the crystal structure of the terminal r domain from the myxalamid pks-2 nrps biosynthetic pathway |
| 57 | d1t2aa_ | Alignment | not modelled | 100.0 | 13 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 58 | c4j2oD_ | Alignment | not modelled | 100.0 | 23 | PDB header: isomerase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase/5-epimerase; PDBTitle: crystal structure of nadp-bound wbjb from a. baumannii community2 strain d1279779 |
| 59 | c3wmxC_ | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: C: PDB Molecule: nad dependent epimerase/dehydratase; PDBTitle: gale-like l-threonine dehydrogenase from cupriavidus necator (holo2 form) |
| 60 | d1n2sa_ | Alignment | not modelled | 100.0 | 18 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 61 | c6dntA_ | Alignment | not modelled | 100.0 | 19 | PDB header: sugar binding protein Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: udp-n-acetylglucosamine 4-epimerase from methanobrevibacter2 ruminantium m1 in complex with udp-n-acetylmuramic acid |
| 62 | c4b4oA_ | Alignment | not modelled | 100.0 | 18 | PDB header: isomerase Chain: A: PDB Molecule: epimerase family protein sdr39u1; PDBTitle: crystal structure of human epimerase family protein sdr39u1 (isoform2)2 with nadph |
| 63 | d1y1pa1 | Alignment | not modelled | 100.0 | 17 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 64 | c1t2aC_ | Alignment | not modelled | 100.0 | 13 | PDB header: structural genomics,lyase Chain: C: PDB Molecule: gdp-mannose 4,6 dehydratase; PDBTitle: crystal structure of human gdp-d-mannose 4,6-dehydratase |
| 65 | c4twrA_ | Alignment | not modelled | 100.0 | 21 | PDB header: isomerase Chain: A: PDB Molecule: nad binding site:nad-dependent epimerase/dehydratase:udp- PDBTitle: structure of udp-glucose 4-epimerase from brucella abortus |
| 66 | c4f6cA_ | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: ausa reductase domain protein; PDBTitle: crystal structure of aureusimine biosynthetic cluster reductase domain |
| 67 | d1z45a2 | Alignment | not modelled | 100.0 | 23 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 68 | c2c20D_ | Alignment | not modelled | 100.0 | 20 | PDB header: isomerase Chain: D: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of udp-glucose 4-epimerase |
| 69 | c6d2vA_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: terb oxidoreductase; PDBTitle: apo structure of terb, an nadp dependent oxidoreductase in the2 terfestatin biosynthesis pathway |
| 70 | d1rpna_ | Alignment | not modelled | 100.0 | 18 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 71 | c3iusB_ | Alignment | not modelled | 100.0 | 19 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: the structure of a functionally unknown conserved protein2 from silicibacter pomeroyi dss |
| 72 | c4ej0D_ | Alignment | not modelled | 100.0 | 15 | PDB header: isomerase Chain: D: PDB Molecule: adp-l-glycero-d-manno-heptose-6-epimerase; PDBTitle: crystal structure of adp-l-glycero-d-manno-heptose-6-epimerase from2 burkholderia thailandensis |
| 73 | c2yy7B_ | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: B: PDB Molecule: l-threonine dehydrogenase; PDBTitle: crystal structure of thermolabile l-threonine dehydrogenase from2 flavobacterium frigidimaris kuc-1 |
| 74 | c3icpA_ | Alignment | not modelled | 100.0 | 26 | PDB header: isomerase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of udp-galactose 4-epimerase |
| 75 | c5u4qB_ | Alignment | not modelled | 100.0 | 17 | PDB header: lipid-binding protein Chain: B: PDB Molecule: dtdp-glucose 4,6-dehydratase; PDBTitle: 1.5 angstrom resolution crystal structure of nad-dependent epimerase2 from klebsiella pneumoniae in complex with nad. |
| 76 | c3slgB_ | Alignment | not modelled | 100.0 | 13 | PDB header: transferase Chain: B: PDB Molecule: pbgp3 protein; PDBTitle: crystal structure of pbgp3 protein from burkholderia pseudomallei |
| 77 | c4lw8B_ | Alignment | not modelled | 100.0 | 17 | PDB header: isomerase Chain: B: PDB Molecule: putative epimerase; PDBTitle: crystal structure of a putative epimerase from burkholderia2 cenocepacia j2315 |
| 78 | d1ludca_ | Alignment | not modelled | 100.0 | 25 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 79 | c2q1uA_ | Alignment | not modelled | 100.0 | 18 | PDB header: sugar binding protein Chain: A: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; |

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|-----|-------------------------|-----------|--------------|-------|----|---|
| | | | | | | PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmf in2 complex with nad+ and udp |
| 80 | d1ek6a_ | Alignment | not modelled | 100.0 | 20 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 81 | c2q1wC_ | Alignment | not modelled | 100.0 | 20 | PDB header: sugar binding protein Chain: C: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+ |
| 82 | c2p4hX_ | Alignment | not modelled | 100.0 | 14 | PDB header: plant protein Chain: X: PDB Molecule: vestitone reductase; PDBTitle: crystal structure of vestitone reductase from alfalfa2 (medicago sativa l.) |
| 83 | c2zkA_ | Alignment | not modelled | 100.0 | 19 | PDB header: isomerase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap5f; PDBTitle: crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus |
| 84 | c3wj7B_ | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of gox2253 |
| 85 | c3a1nB_ | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: B: PDB Molecule: ndp-sugar epimerase; PDBTitle: crystal structure of l-threonine dehydrogenase from hyperthermophilic2 archaeon thermoplasma volcanium |
| 86 | c2pzB_ | Alignment | not modelled | 100.0 | 20 | PDB header: sugar binding protein Chain: B: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad and udp |
| 87 | c4wpgA_ | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: ddtp-4-dehydrorhamnose reductase; PDBTitle: group a streptococcus gaca is an essential dtdp-4-dehydrorhamnose2 reductase (rmlf) |
| 88 | c4qukA_ | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroflavonol-4-reductase; PDBTitle: crystal structure of cinnamyl-alcohol dehydrogenase 2 mutant k169a |
| 89 | c3ehB_ | Alignment | not modelled | 100.0 | 19 | PDB header: isomerase Chain: B: PDB Molecule: udp-glucose 4-epimerase (gale-1); PDBTitle: crystal structure of udp-glucose 4 epimerase (gale-1) from2 archaeoglobus fulgidus |
| 90 | c3sc6F_ | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: F: PDB Molecule: ddtp-4-dehydrorhamnose reductase; PDBTitle: 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp |
| 91 | c2ggsB_ | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: B: PDB Molecule: 273aa long hypothetical dtdp-4-dehydrorhamnose PDBTitle: crystal structure of hypothetical dtdp-4-dehydrorhamnose2 reductase from sulfobolus tokodaii |
| 92 | c3vpsB_ | Alignment | not modelled | 100.0 | 16 | PDB header: transferase Chain: B: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: structure of a novel nad dependent-ndp-hexosamine 5,6-dehydratase,2 tuna, involved in tunicamycin biosynthesis |
| 93 | c3gpiA_ | Alignment | not modelled | 100.0 | 20 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: structure of putative nad-dependent epimerase/dehydratase from2 methylobacillus flagellatus |
| 94 | c2rh8A_ | Alignment | not modelled | 100.0 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: anthocyanidin reductase; PDBTitle: structure of apo anthocyanidin reductase from vitis vinifera |
| 95 | c4qqrB_ | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: 3,5-epimerase/4-reductase; PDBTitle: structural insight into nucleotide rhamnose synthase/epimerase-2 reductase from arabidopsis thaliana |
| 96 | c5u9cC_ | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase,oxidoreductase Chain: C: PDB Molecule: ddtp-4-dehydrorhamnose reductase; PDBTitle: 1.9 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase from yersinia enterocolitica |
| 97 | c5lnkd_ | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: D: PDB Molecule: PDBTitle: entire ovine respiratory complex i |
| 98 | c2ydyA_ | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: methionine adenosyltransferase 2 subunit beta; PDBTitle: crystal structure of human s-adenosylmethionine synthetase 2, beta2 subunit in orthorhombic crystal form |
| 99 | c4yraD_ | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: D: PDB Molecule: l-threonine 3-dehydrogenase, mitochondrial; PDBTitle: mouse tdh in the apo form |
| 100 | d1eq2a_ | Alignment | not modelled | 100.0 | 16 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 101 | c6bwcA_ | Alignment | not modelled | 100.0 | 22 | PDB header: biosynthetic protein Chain: A: PDB Molecule: polysaccharide biosynthesis protein capd; PDBTitle: x-ray structure of pen from bacillus thuringiensis |
| 102 | c5y1dB_ | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: nad dependent epimerase/dehydratase family; PDBTitle: monomeric l-threonine 3-dehydrogenase from metagenome database (apo2 form) |
| 103 | c3sxpD_ | Alignment | not modelled | 100.0 | 18 | PDB header: isomerase Chain: D: PDB Molecule: adp-l-glycero-d-mannoheptose-6-epimerase; |

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|-----|-------------------------|-----------|--------------|-------|----|---|
| | | | | | | PDBTitle: crystal structure of helicobacter pylori adp-l-glycero-d-manno-2 heptose-6-epimerase (rfad, hp0859) |
| 104 | c5z76D_ | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: D: PDB Molecule: artificial l-threonine 3-dehydrogenase; PDBTitle: artificial l-threonine 3-dehydrogenase designed by full consensus2 design |
| 105 | c6gcsE_ | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase Chain: E: PDB Molecule: nuem subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica |
| 106 | c2gn9B_ | Alignment | not modelled | 100.0 | 19 | PDB header: lyase Chain: B: PDB Molecule: udp-glcnac c6 dehydratase; PDBTitle: crystal structure of udp-glcnac inverting 4,6-dehydratase in complex2 with nadp and udp-glc |
| 107 | c2x86K_ | Alignment | not modelled | 100.0 | 13 | PDB header: isomerase Chain: K: PDB Molecule: adp-l-glycero-d-manno-heptose-6-epimerase; PDBTitle: agme bound to adp-b-mannose |
| 108 | c3wmwB_ | Alignment | not modelled | 100.0 | 24 | PDB header: oxidoreductase Chain: B: PDB Molecule: nad dependent epimerase/dehydratase; PDBTitle: gale-like l-threonine dehydrogenase from cupriavidus necator (apo2 form) |
| 109 | c5bjua_ | Alignment | not modelled | 100.0 | 16 | PDB header: membrane protein Chain: A: PDB Molecule: wlal protein; PDBTitle: x-ray structure of the pglf dehydratase from campylobacter jejuni in2 complex with udp and nad(h) |
| 110 | c2qx7A_ | Alignment | not modelled | 100.0 | 14 | PDB header: plant protein Chain: A: PDB Molecule: eugenol synthase 1; PDBTitle: structure of eugenol synthase from ocimum basilicum |
| 111 | c3e48B_ | Alignment | not modelled | 100.0 | 12 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of a nucleoside-diphosphate-sugar epimerase2 (sav0421) from staphylococcus aureus, northeast structural genomics3 consortium target zr319 |
| 112 | c5l3za_ | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide ketoreductase simc7; PDBTitle: polyketide ketoreductase simc7 - binary complex with nadp+ |
| 113 | c3nzoB_ | Alignment | not modelled | 100.0 | 16 | PDB header: lyase Chain: B: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase; PDBTitle: udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri. |
| 114 | c3rfxB_ | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: uronate dehydrogenase; PDBTitle: crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad |
| 115 | c4lk3A_ | Alignment | not modelled | 100.0 | 19 | PDB header: lyase Chain: A: PDB Molecule: udp-glucuronic acid decarboxylase 1; PDBTitle: crystal structure of human udp-xylose synthase r236a substitution |
| 116 | c3ay3C_ | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: C: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of glucuronic acid dehydrogeanse from2 chromohalobacter salexigens |
| 117 | d1qyda_ | Alignment | not modelled | 100.0 | 14 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 118 | d1qyca_ | Alignment | not modelled | 100.0 | 17 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases |
| 119 | c3i5mA_ | Alignment | not modelled | 100.0 | 11 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative leucoanthocyanidin reductase 1; PDBTitle: structure of the apo form of leucoanthocyanidin reductase from vitis2 vinifera |
| 120 | c3c1oA_ | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: eugenol synthase; PDBTitle: the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages |