Phyre2

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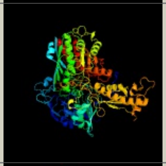
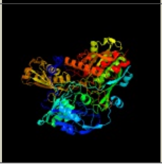
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0373c_(-)_449405_451804 |
| Date | Tue Jul 23 14:50:44 BST 2019 |
| Unique Job ID | 9ef1c4c7fb5e9e8b |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1ffvB_ | Alignment |  | 100.0 | 59 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**cutl, molybdoprotein of carbon monoxide<br>**PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava |
| 2 | c1n62E_ | Alignment |  | 100.0 | 57 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**carbon monoxide dehydrogenase large chain;<br>**PDBTitle:** crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state |
| 3 | c1t3qB_ | Alignment |  | 100.0 | 38 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**quinoline 2-oxidoreductase large subunit;<br>**PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86 |
| 4 | c1sb3D_ | Alignment |  | 100.0 | 28 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**4-hydroxybenzoyl-coa reductase alpha subunit;<br>**PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica |
| 5 | c1wygA_ | Alignment |  | 100.0 | 20 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**xanthine dehydrogenase/oxidase;<br>**PDBTitle:** crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s) |
| 6 | c2w54F_ | Alignment |  | 100.0 | 24 | **PDB header:**oxidoreductase<br>**Chain:** F: **PDB Molecule:**xanthine dehydrogenase;<br>**PDBTitle:** crystal structure of xanthine dehydrogenase from rhodobacter2 capsulatus in complex with bound inhibitor pterin-6-aldehyde |
| 7 | c4uhxA_ | Alignment |  | 100.0 | 22 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**aldehyde oxidase;<br>**PDBTitle:** human aldehyde oxidase in complex with phthalazine and thioridazine |
| 8 | c5y6qC_ | Alignment |  | 100.0 | 26 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**aldehyde oxidase large subunit;<br>**PDBTitle:** crystal structure of an aldehyde oxidase from methylobacillus sp.2 ky4400 |
| 9 | c3zyvA_ | Alignment |  | 100.0 | 22 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**aox3;<br>**PDBTitle:** crystal structure of the mouse liver aldehyde oxidase 3 (maox3) |
| 10 | c3eubL_ | Alignment |  | 100.0 | 21 | **PDB header:**oxidoreductase<br>**Chain:** L: **PDB Molecule:**xanthine dehydrogenase/oxidase;<br>**PDBTitle:** crystal structure of desulfo-xanthine oxidase with xanthine |
| 11 | c5g5hC_ | Alignment |  | 100.0 | 24 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**putative xanthine dehydrogenase yagr molybdenum-binding<br>**PDBTitle:** escherichia coli periplasmic aldehyde oxidase r440h mutant |

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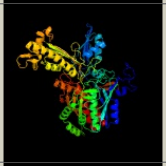
| 12 | c1vlbA_ | Alignment |  | 100.0 | 25 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**aldehyde oxidoreductase;<br>**PDBTitle:** structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a |
| 13 | c1dgjA_ | Alignment |  | 100.0 | 24 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**aldehyde oxidoreductase;<br>**PDBTitle:** crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774 |
| 14 | c4zohA_ | Alignment |  | 100.0 | 36 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative oxidoreductase molybdopterin-binding subunit;<br>**PDBTitle:** crystal structure of glyceraldehyde oxidoreductase |
| 15 | d1n62b2 | Alignment |  | 100.0 | 57 | **Fold:**Molybdenum cofactor-binding domain<br>**Superfamily:**Molybdenum cofactor-binding domain<br>**Family:**Molybdenum cofactor-binding domain |
| 16 | d1ffvb2 | Alignment |  | 100.0 | 61 | **Fold:**Molybdenum cofactor-binding domain<br>**Superfamily:**Molybdenum cofactor-binding domain<br>**Family:**Molybdenum cofactor-binding domain |
| 17 | d1rm6a2 | Alignment |  | 100.0 | 26 | **Fold:**Molybdenum cofactor-binding domain<br>**Superfamily:**Molybdenum cofactor-binding domain<br>**Family:**Molybdenum cofactor-binding domain |
| 18 | d1t3qb2 | Alignment |  | 100.0 | 37 | **Fold:**Molybdenum cofactor-binding domain<br>**Superfamily:**Molybdenum cofactor-binding domain<br>**Family:**Molybdenum cofactor-binding domain |
| 19 | d1jrob2 | Alignment |  | 100.0 | 22 | **Fold:**Molybdenum cofactor-binding domain<br>**Superfamily:**Molybdenum cofactor-binding domain<br>**Family:**Molybdenum cofactor-binding domain |
| 20 | d1v97a5 | Alignment |  | 100.0 | 20 | **Fold:**Molybdenum cofactor-binding domain<br>**Superfamily:**Molybdenum cofactor-binding domain<br>**Family:**Molybdenum cofactor-binding domain |
| 21 | d1vlba4 | Alignment | not modelled | 100.0 | 25 | **Fold:**Molybdenum cofactor-binding domain<br>**Superfamily:**Molybdenum cofactor-binding domain<br>**Family:**Molybdenum cofactor-binding domain |
| 22 | d1dgja4 | Alignment | not modelled | 100.0 | 24 | **Fold:**Molybdenum cofactor-binding domain<br>**Superfamily:**Molybdenum cofactor-binding domain<br>**Family:**Molybdenum cofactor-binding domain |
| 23 | c3hrdE_ | Alignment | not modelled | 100.0 | 26 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**nicotinate dehydrogenase large molybdopterin<br>**PDBTitle:** crystal structure of nicotinate dehydrogenase |
| 24 | c3hrdF_ | Alignment | not modelled | 100.0 | 31 | **PDB header:**oxidoreductase<br>**Chain:** F: **PDB Molecule:**nicotinate dehydrogenase medium molybdopterin<br>**PDBTitle:** crystal structure of nicotinate dehydrogenase |
| 25 | d1t3qb1 | Alignment | not modelled | 100.0 | 43 | **Fold:**alpha/beta-Hammerhead<br>**Superfamily:**CO dehydrogenase molybdoprotein N-domain-like<br>**Family:**CO dehydrogenase molybdoprotein N-domain-like |
| 26 | d1ffvb1 | Alignment | not modelled | 100.0 | 54 | **Fold:**alpha/beta-Hammerhead<br>**Superfamily:**CO dehydrogenase molybdoprotein N-domain-like<br>**Family:**CO dehydrogenase molybdoprotein N-domain-like |
| 27 | d1n62b1 | Alignment | not modelled | 100.0 | 58 | **Fold:**alpha/beta-Hammerhead<br>**Superfamily:**CO dehydrogenase molybdoprotein N-domain-like<br>**Family:**CO dehydrogenase molybdoprotein N-domain-like |
| 28 | d1v97a3 | Alignment | not modelled | 100.0 | 24 | **Fold:**alpha/beta-Hammerhead<br>**Superfamily:**CO dehydrogenase molybdoprotein N-domain-like<br>**Family:**CO dehydrogenase molybdoprotein N-domain-like |
| 29 | d3b9jc1 | Alignment | not modelled | 100.0 | 26 | **Fold:**alpha/beta-Hammerhead<br>**Superfamily:**CO dehydrogenase molybdoprotein N-domain-like |

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| | | | | | | **Family:**CO dehydrogenase molybdoprotein N-domain-like |
| 30 | d1rm6a1 | Alignment | not modelled | 100.0 | 37 | **Fold:**alpha/beta-Hammerhead<br>**Superfamily:**CO dehydrogenase molybdoprotein N-domain-like<br>**Family:**CO dehydrogenase molybdoprotein N-domain-like |
| 31 | d1jrob1 | Alignment | not modelled | 100.0 | 33 | **Fold:**alpha/beta-Hammerhead<br>**Superfamily:**CO dehydrogenase molybdoprotein N-domain-like<br>**Family:**CO dehydrogenase molybdoprotein N-domain-like |
| 32 | d1vlba3 | Alignment | not modelled | 100.0 | 33 | **Fold:**alpha/beta-Hammerhead<br>**Superfamily:**CO dehydrogenase molybdoprotein N-domain-like<br>**Family:**CO dehydrogenase molybdoprotein N-domain-like |
| 33 | d1dgja3 | Alignment | not modelled | 100.0 | 31 | **Fold:**alpha/beta-Hammerhead<br>**Superfamily:**CO dehydrogenase molybdoprotein N-domain-like<br>**Family:**CO dehydrogenase molybdoprotein N-domain-like |
| 34 | d1gd0a_ | Alignment | not modelled | 75.3 | 15 | **Fold:**Tautomerase/MIF<br>**Superfamily:**Tautomerase/MIF<br>**Family:**MIF-related |
| 35 | d2gdga1 | Alignment | not modelled | 74.4 | 14 | **Fold:**Tautomerase/MIF<br>**Superfamily:**Tautomerase/MIF<br>**Family:**MIF-related |
| 36 | d1hfoa_ | Alignment | not modelled | 74.2 | 13 | **Fold:**Tautomerase/MIF<br>**Superfamily:**Tautomerase/MIF<br>**Family:**MIF-related |
| 37 | d1uiza_ | Alignment | not modelled | 74.0 | 11 | **Fold:**Tautomerase/MIF<br>**Superfamily:**Tautomerase/MIF<br>**Family:**MIF-related |
| 38 | c5un4C_ | Alignment | not modelled | 72.8 | 12 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**4-oxalocrotonate tautomerase;<br>**PDBTitle:** crystal structure of native fused 4-ot |
| 39 | c4dh4A_ | Alignment | not modelled | 70.6 | 18 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**mif;<br>**PDBTitle:** macrophage migration inhibitory factor toxoplasma gondii |
| 40 | d1fima_ | Alignment | not modelled | 69.4 | 14 | **Fold:**Tautomerase/MIF<br>**Superfamily:**Tautomerase/MIF<br>**Family:**MIF-related |
| 41 | d1yh5a1 | Alignment | not modelled | 69.0 | 4 | **Fold:**YggU-like<br>**Superfamily:**YggU-like<br>**Family:**YggU-like |
| 42 | c6cuqB_ | Alignment | not modelled | 67.2 | 11 | **PDB header:**cytokine<br>**Chain:** B: **PDB Molecule:**macrophage migration inhibitory factor-like protein;<br>**PDBTitle:** crystal structure of macrophage migration inhibitory factor-like2 protein (ehmif) from entamoeba histolytica |
| 43 | d1dgja1 | Alignment | not modelled | 65.7 | 8 | **Fold:**CO dehydrogenase ISP C-domain like<br>**Superfamily:**CO dehydrogenase ISP C-domain like<br>**Family:**CO dehydrogenase ISP C-domain like |
| 44 | c2xczA_ | Alignment | not modelled | 65.6 | 10 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**possible atls1-like light-inducible protein;<br>**PDBTitle:** crystal structure of macrophage migration inhibitory factor homologue2 from prochlorococcus marinus |
| 45 | c2os5C_ | Alignment | not modelled | 64.7 | 10 | **PDB header:**cytokine<br>**Chain:** C: **PDB Molecule:**acemif;<br>**PDBTitle:** macrophage migration inhibitory factor from ancylostoma ceylanicum |
| 46 | c3gacD_ | Alignment | not modelled | 64.2 | 19 | **PDB header:**cytokine<br>**Chain:** D: **PDB Molecule:**macrophage migration inhibitory factor-like<br>**PDBTitle:** structure of mif with hpp |
| 47 | c3b64A_ | Alignment | not modelled | 62.4 | 13 | **PDB header:**cytokine<br>**Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like<br>**PDBTitle:** macrophage migration inhibitory factor (mif) from2 /leishmania major |
| 48 | c2rghA_ | Alignment | not modelled | 61.5 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**alpha-glycerophosphate oxidase;<br>**PDBTitle:** structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase |
| 49 | d2dt5a1 | Alignment | not modelled | 60.8 | 13 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Transcriptional repressor Rex, N-terminal domain |
| 50 | c5unqF_ | Alignment | not modelled | 60.8 | 5 | **PDB header:**hydrolase<br>**Chain:** F: **PDB Molecule:**putative tautomerase;<br>**PDBTitle:** crystal structure of pt0534 inactivated by 2-oxo-3-pentynoate |
| 51 | d1dpta_ | Alignment | not modelled | 59.0 | 12 | **Fold:**Tautomerase/MIF<br>**Superfamily:**Tautomerase/MIF<br>**Family:**MIF-related |
| 52 | c4lkbA_ | Alignment | not modelled | 58.3 | 16 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**hypothetical protein alr4568/putative 4-oxalocrotonate<br>**PDBTitle:** crystal structure of a putative 4-oxalocrotonate tautomerase from2 nostoc sp. pcc 7120 |
| 53 | c3fwtA_ | Alignment | not modelled | 57.0 | 14 | **PDB header:**cytokine<br>**Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like<br>**PDBTitle:** crystal structure of leishmania major mif2 |
| 54 | d1otfa_ | Alignment | not modelled | 52.6 | 14 | **Fold:**Tautomerase/MIF<br>**Superfamily:**Tautomerase/MIF<br>**Family:**4-oxalocrotonate tautomerase-like |
| 55 | c3abfB_ | Alignment | not modelled | 52.3 | 11 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; |

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| | | Alignment | not modelled | | | **PDBTitle:** crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242) |
| 56 | c3ry0A_ | Alignment | not modelled | 51.6 | 17 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**putative tautomerase;<br>**PDBTitle:** crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway |
| 57 | d1mwwa_ | Alignment | not modelled | 51.1 | 16 | **Fold:**Tautomerase/MIF<br>**Superfamily:**Tautomerase/MIF<br>**Family:**Hypothetical protein HI1388.1 |
| 58 | c2op8A_ | Alignment | not modelled | 51.0 | 14 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**probable tautomerase ywhb;<br>**PDBTitle:** crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase |
| 59 | c4fazB_ | Alignment | not modelled | 49.2 | 19 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**4-oxalocrotonate isomerase protein;<br>**PDBTitle:** kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozymes from methylibium petroleiphilum |
| 60 | c4fdxB_ | Alignment | not modelled | 49.0 | 14 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**4-oxalocrotonase tautomerase isozyme;<br>**PDBTitle:** kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozymes from methylibium petroleiphilum |
| 61 | d1vlba1 | Alignment | not modelled | 48.9 | 11 | **Fold:**CO dehydrogenase ISP C-domain like<br>**Superfamily:**CO dehydrogenase ISP C-domain like<br>**Family:**CO dehydrogenase ISP C-domain like |
| 62 | d1bjpa_ | Alignment | not modelled | 48.4 | 14 | **Fold:**Tautomerase/MIF<br>**Superfamily:**Tautomerase/MIF<br>**Family:**4-oxalocrotonate tautomerase-like |
| 63 | d2aala1 | Alignment | not modelled | 47.3 | 18 | **Fold:**Tautomerase/MIF<br>**Superfamily:**Tautomerase/MIF<br>**Family:**MSAD-like |
| 64 | c2dt5A_ | Alignment | not modelled | 46.8 | 12 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**at-rich dna-binding protein;<br>**PDBTitle:** crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8 |
| 65 | c2lfcA_ | Alignment | not modelled | 46.1 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**fumarate reductase, flavoprotein subunit;<br>**PDBTitle:** solution nmr structure of fumarate reductase flavoprotein subunit from2 lactobacillus plantarum, northeast structural genomics consortium3 target lpr145j |
| 66 | c3n2oA_ | Alignment | not modelled | 44.1 | 22 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**biosynthetic arginine decarboxylase;<br>**PDBTitle:** x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus |
| 67 | c3m20A_ | Alignment | not modelled | 43.7 | 17 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**4-oxalocrotonate tautomerase, putative;<br>**PDBTitle:** crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution |
| 68 | c2kwpA_ | Alignment | not modelled | 43.6 | 27 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcription elongation protein nusa;<br>**PDBTitle:** solution structure of the aminoterminal domain of e. coli nusa |
| 69 | d1knwa2 | Alignment | not modelled | 43.0 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**PLP-binding barrel<br>**Family:**Alanine racemase-like, N-terminal domain |
| 70 | c3mlcC_ | Alignment | not modelled | 42.1 | 12 | **PDB header:**isomerase<br>**Chain:** C: **PDB Molecule:**fg41 malonate semialdehyde decarboxylase;<br>**PDBTitle:** crystal structure of fg41msad inactivated by 3-chloropropiolate |
| 71 | d1hh2p4 | Alignment | not modelled | 42.0 | 36 | **Fold:**Transcription factor NusA, N-terminal domain<br>**Superfamily:**Transcription factor NusA, N-terminal domain<br>**Family:**Transcription factor NusA, N-terminal domain |
| 72 | c4aibC_ | Alignment | not modelled | 40.9 | 13 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**ornithine decarboxylase;<br>**PDBTitle:** crystal structure of ornithine decarboxylase from entamoeba2 histolytica. |
| 73 | c3mb2G_ | Alignment | not modelled | 39.1 | 9 | **PDB header:**isomerase<br>**Chain:** G: **PDB Molecule:**4-oxalocrotonate tautomerase family enzyme - alpha subunit;<br>**PDBTitle:** kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily |
| 74 | c2mt4A_ | Alignment | not modelled | 37.5 | 27 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcription termination/antitermination protein nusa;<br>**PDBTitle:** solution structure of the n-terminal domain of nusa from b. subtilis |
| 75 | c5wc3S_ | Alignment | not modelled | 37.2 | 20 | **PDB header:**protein transport<br>**Chain:** S: **PDB Molecule:**spoiiiag, stage iii sporulation engulfment assemblyprotein;<br>**PDBTitle:** spoiiiag |
| 76 | c2rgoA_ | Alignment | not modelled | 37.1 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**alpha-glycerophosphate oxidase;<br>**PDBTitle:** structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase |
| 77 | c2hlhA_ | Alignment | not modelled | 36.6 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**nodulation fucosyltransferase;<br>**PDBTitle:** crystal structure of fucosyltransferase nodz from bradyrhizobium |
| 78 | c2ormA_ | Alignment | not modelled | 36.6 | 20 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**probable tautomerase hp0924;<br>**PDBTitle:** crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori. |
| | | | | | | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; |

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| 79 | c2x4kB_ | Alignment | not modelled | 36.3 | 16 | **PDBTitle:** crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa) |
| 80 | c4gisB_ | Alignment | not modelled | 36.2 | 20 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**enolase;<br>**PDBTitle:** crystal structure of an enolase family member from vibrio harveyi2 (efi-target 501692) with homology to mannonate dehydratase, with mg,3 glycerol and dicarboxylates bound (mixed loops, space group i4122) |
| 81 | c3t5sA_ | Alignment | not modelled | 35.4 | 14 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor;<br>**PDBTitle:** structure of macrophage migration inhibitory factor from giardia2 lamblia |
| 82 | d1d4ca3 | Alignment | not modelled | 35.4 | 29 | **Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain<br>**Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain<br>**Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain |
| 83 | d1o6za2 | Alignment | not modelled | 34.3 | 17 | **Fold:**LDH C-terminal domain-like<br>**Superfamily:**LDH C-terminal domain-like<br>**Family:**Lactate & malate dehydrogenases, C-terminal domain |
| 84 | d1y0pa3 | Alignment | not modelled | 33.5 | 18 | **Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain<br>**Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain<br>**Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain |
| 85 | c3da1A_ | Alignment | not modelled | 33.2 | 22 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase;<br>**PDBTitle:** x-ray structure of the glycerol-3-phosphate dehydrogenase2 from bacillus halodurans complexed with fad. northeast3 structural genomics consortium target bhr167. |
| 86 | c5uifC_ | Alignment | not modelled | 33.1 | 10 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**ps01740;<br>**PDBTitle:** crystal structure of native ps01740 |
| 87 | c3ketA_ | Alignment | not modelled | 32.2 | 24 | **PDB header:**transcription/dna<br>**Chain:** A: **PDB Molecule:**redox-sensing transcriptional repressor rex;<br>**PDBTitle:** crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator |
| 88 | c3nzqB_ | Alignment | not modelled | 30.1 | 27 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**biosynthetic arginine decarboxylase;<br>**PDBTitle:** crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600 |
| 89 | d1nera_ | Alignment | not modelled | 29.8 | 32 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Phage repressors |
| 90 | c3nzpA_ | Alignment | not modelled | 29.4 | 15 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**arginine decarboxylase;<br>**PDBTitle:** crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast structural genomics consortium target3 br53 |
| 91 | c2lteA_ | Alignment | not modelled | 26.4 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**specialized acyl carrier protein;<br>**PDBTitle:** solution nmr structure of the specialized acyl carrier protein pa33342 (apo) from pseudomonas aeruginosa, northeast structural genomics3 consortium target pat415 |
| 92 | d1t0aa_ | Alignment | not modelled | 24.0 | 18 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**IpsF-like<br>**Family:**IpsF-like |
| 93 | c6aeoA_ | Alignment | not modelled | 23.9 | 24 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**maltose/maltodextrin-binding periplasmic protein,tssl;<br>**PDBTitle:** tssl periplasmic domain |
| 94 | c1l0oC_ | Alignment | not modelled | 23.4 | 29 | **PDB header:**protein binding<br>**Chain:** C: **PDB Molecule:**sigma factor;<br>**PDBTitle:** crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf |
| 95 | d1l0oc_ | Alignment | not modelled | 23.4 | 29 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**Sigma4 domain |
| 96 | c1w36E_ | Alignment | not modelled | 23.2 | 22 | **PDB header:**recombination<br>**Chain:** E: **PDB Molecule:**exodeoxyribonuclease v beta chain;<br>**PDBTitle:** recbcd:dna complex |
| 97 | c1vraA_ | Alignment | not modelled | 22.6 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**arginine biosynthesis bifunctional protein argj;<br>**PDBTitle:** crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution |
| 98 | d2fmra_ | Alignment | not modelled | 22.4 | 18 | **Fold:**Eukaryotic type KH-domain (KH-domain type I)<br>**Superfamily:**Eukaryotic type KH-domain (KH-domain type I)<br>**Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 99 | d2f2ab2 | Alignment | not modelled | 22.3 | 17 | **Fold:**Glutamine synthetase/guanido kinase<br>**Superfamily:**Glutamine synthetase/guanido kinase<br>**Family:**GatB/GatE catalytic domain-like |
| 100 | c3wg9D_ | Alignment | not modelled | 22.2 | 13 | **PDB header:**transcription<br>**Chain:** D: **PDB Molecule:**redox-sensing transcriptional repressor rex;<br>**PDBTitle:** crystal structure of rsp, a rex-family repressor |
| 101 | d7mdha2 | Alignment | not modelled | 21.7 | 11 | **Fold:**LDH C-terminal domain-like<br>**Superfamily:**LDH C-terminal domain-like<br>**Family:**Lactate & malate dehydrogenases, C-terminal domain |

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|---|---|---|---|---|---|---|
| 102 | c4w8jA_ | Alignment | not modelled | 21.3 | 15 | **PDB header:**toxin<br>**Chain:** A: **PDB Molecule:**pesticidal crystal protein cry1ac;<br>**PDBTitle:** structure of the full-length insecticidal protein cry1ac reveals2 intriguing details of toxin packaging into in vivo formed crystals |
| 103 | c5ijwA_ | Alignment | not modelled | 20.8 | 24 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**glutamate racemase;<br>**PDBTitle:** glutamate racemase (muri) from mycobacterium smegmatis with bound d-2 glutamate, 1.8 angstrom resolution, x-ray diffraction |
| 104 | c1af7A_ | Alignment | not modelled | 20.8 | 24 | **PDB header:**methyltransferase<br>**Chain:** A: **PDB Molecule:**chemotaxis receptor methyltransferase cher;<br>**PDBTitle:** cher from salmonella typhimurium |