Phyre²

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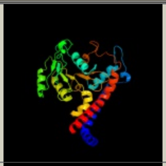
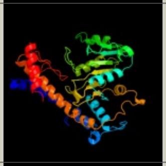
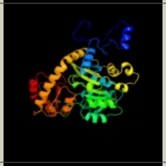
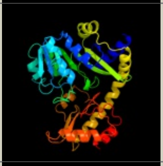
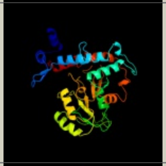
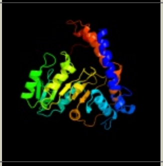
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0A821 |
| Date | Thu Jan 5 11:06:39 GMT 2012 |
| Unique Job ID | e33a0b0ca5a128c7 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3fd0B_ | Alignment |  | 100.0 | 15 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**putative cystathionine beta-lyase involved in aluminum<br>**PDBTitle:** crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_470671.1) from listeria innocua at 2.12 a3 resolution |
| 2 | c3ht4B_ | Alignment |  | 100.0 | 20 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**aluminum resistance protein;<br>**PDBTitle:** crystal structure of the q81a77_baccr protein from bacillus2 cereus. northeast structural genomics consortium target3 bcr213 |
| 3 | c2cb1A_ | Alignment |  | 100.0 | 21 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**o-acetyl homoserine sulfhydrylase;<br>**PDBTitle:** crystal structure of o-actetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2. |
| 4 | c3ndnC_ | Alignment |  | 100.0 | 20 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**o-succinylhomoserine sulfhydrylase;<br>**PDBTitle:** crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate |
| 5 | c3hvyC_ | Alignment |  | 100.0 | 17 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**cystathionine beta-lyase family protein, ynbb b.subtilis<br>**PDBTitle:** crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_348457.1) from clostridium acetobutylicum at3 2.00 a resolution |
| 6 | d1qgna_ | Alignment |  | 100.0 | 20 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 7 | c1ibjC_ | Alignment |  | 100.0 | 18 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**cystathionine beta-lyase;<br>**PDBTitle:** crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana |
| 8 | d1ibja_ | Alignment |  | 100.0 | 18 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 9 | c3gwpA_ | Alignment |  | 100.0 | 17 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**carbon-sulfur lyase involved in aluminum resistance;<br>**PDBTitle:** crystal structure of carbon-sulfur lyase involved in aluminum2 resistance (yp_878183.1) from clostridium novyi nt at 2.90 a3 resolution |
| 10 | c2gqnB_ | Alignment |  | 100.0 | 17 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**cystathionine beta-lyase;<br>**PDBTitle:** cystathionine beta-lyase (cbl) from escherichia coli in complex with2 n-hydrazinocarbonylmethyl-2-nitro-benzamide |
| 11 | c3bcxA_ | Alignment |  | 100.0 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-<br>**PDBTitle:** e1 dehydrase |

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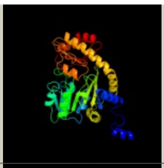
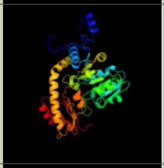
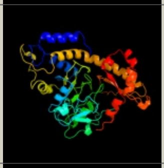
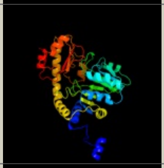
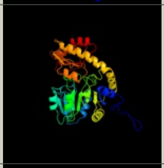
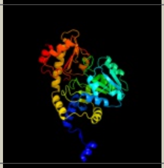
|---|---|---|---|---|---|---|
| 12 | d1y4ia1 | Alignment |  | 100.0 | 19 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 13 | d1cl1a_ | Alignment |  | 100.0 | 18 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 14 | d2ctza1 | Alignment |  | 100.0 | 17 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 15 | c2c7tA_ | Alignment |  | 100.0 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**glutamine-2-deoxy-scyllo-inosose<br>**PDBTitle:** crystal structure of the plp-bound form of btrr,2 a dual functional aminotransferase involved in butirosin3 biosynthesis. |
| 16 | c3aemD_ | Alignment |  | 100.0 | 14 | **PDB header:**lyase<br>**Chain:** D: **PDB Molecule:**methionine gamma-lyase;<br>**PDBTitle:** reaction intermediate structure of entamoeba histolytica methionine2 gamma-lyase 1 containing michaelis complex and methionine imine-3 pyridoxamine-5'-phosphate |
| 17 | c2nmpC_ | Alignment |  | 100.0 | 18 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**cystathionine gamma-lyase;<br>**PDBTitle:** crystal structure of human cystathionine gamma lyase |
| 18 | c1i41J_ | Alignment |  | 100.0 | 20 | **PDB header:**lyase<br>**Chain:** J: **PDB Molecule:**cystathionine gamma-synthase;<br>**PDBTitle:** cystathionine gamma-synthase in complex with the inhibitor2 appa |
| 19 | c3e6gA_ | Alignment |  | 100.0 | 20 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**cystathionine gamma-lyase-like protein;<br>**PDBTitle:** crystal structure of xometc, a cystathionine c-lyase-like2 protein from xanthomonas oryzae pv.oryzae |
| 20 | d1n8pa_ | Alignment |  | 100.0 | 19 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 21 | d1e5ea_ | Alignment | not modelled | 100.0 | 15 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 22 | d1cs1a_ | Alignment | not modelled | 100.0 | 19 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 23 | c2r0tA_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyridoxamine 5-phosphate-dependent dehydrase;<br>**PDBTitle:** crystal sructure of gdp-4-keto-6-deoxymannose-3-dehydratase2 with a trapped plp-glutamate geminal diamine |
| 24 | d1wyub1 | Alignment | not modelled | 100.0 | 18 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Glycine dehydrogenase subunits (GDC-P) |
| 25 | c3qi6B_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**cystathionine gamma-synthase metb (cgs);<br>**PDBTitle:** crystal structure of cystathionine gamma-synthase metb (cgs) from2 mycobacterium ulcerans agy99 |
| 26 | d1gc0a_ | Alignment | not modelled | 100.0 | 21 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 27 | d1mdoa_ | Alignment | not modelled | 100.0 | 17 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 28 | c2po3B_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**4-dehydrase;<br>**PDBTitle:** crystal structure analysis of desi in the presence of its2 tdp-sugar product |

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| 29 | d1b9ha_ | Alignment | not modelled | 100.0 | 17 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 30 | d1wyua1 | Alignment | not modelled | 100.0 | 15 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Glycine dehydrogenase subunits (GDC-P) |
| 31 | c3ju7B_ | Alignment | not modelled | 100.0 | 13 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**putative plp-dependent aminotransferase;<br>**PDBTitle:** crystal structure of putative plp-dependent aminotransferase2 (np_978343.1) from bacillus cereus atcc 10987 at 2.19 a resolution |
| 32 | c3pj0D_ | Alignment | not modelled | 100.0 | 13 | **PDB header:**lyase<br>**Chain:** D: **PDB Molecule:**lmo0305 protein;<br>**PDBTitle:** crystal structure of a putative l-allo-threonine aldolase (lmo0305)2 from listeria monocytogenes egd-e at 1.80 a resolution |
| 33 | d2fnua1 | Alignment | not modelled | 100.0 | 14 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 34 | d1o69a_ | Alignment | not modelled | 100.0 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 35 | c2ogeC_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**transaminase;<br>**PDBTitle:** x-ray structure of s. venezuelae desv in its internal2 aldimine form |
| 36 | c3nx3A_ | Alignment | not modelled | 99.9 | 10 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**acetylornithine aminotransferase;<br>**PDBTitle:** crystal structure of acetylornithine aminotransferase (argd) from2 campylobacter jejuni |
| 37 | c3mafB_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**sphingosine-1-phosphate lyase;<br>**PDBTitle:** crystal structure of stspl (asymmetric form) |
| 38 | c2w8wA_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**serine palmitoyltransferase;<br>**PDBTitle:** n100y spt with plp-ser |
| 39 | c3dr4B_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**putative perosamine synthetase;<br>**PDBTitle:** gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand |
| 40 | c3nysA_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**aminotransferase wbpe;<br>**PDBTitle:** x-ray structure of the k185a mutant of wbpe (wlbe) from pseudomonas2 aeruginosa in complex with plp at 1.45 angstrom resolution |
| 41 | d2byla1 | Alignment | not modelled | 99.9 | 9 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 42 | c3hbxB_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**glutamate decarboxylase 1;<br>**PDBTitle:** crystal structure of gad1 from arabidopsis thaliana |
| 43 | c3ruyB_ | Alignment | not modelled | 99.9 | 12 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**ornithine aminotransferase;<br>**PDBTitle:** crystal structure of the ornithine-oxo acid transaminase rocd from2 bacillus anthracis |
| 44 | c1oatB_ | Alignment | not modelled | 99.9 | 10 | **PDB header:**aminotransferase<br>**Chain:** B: **PDB Molecule:**ornithine aminotransferase;<br>**PDBTitle:** ornithine aminotransferase |
| 45 | c3caiA_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**possible aminotransferase;<br>**PDBTitle:** crystal structure of mycobacterium tuberculosis rv3778c2 protein |
| 46 | d1z7da1 | Alignment | not modelled | 99.9 | 11 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 47 | c3mc6C_ | Alignment | not modelled | 99.9 | 12 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**sphingosine-1-phosphate lyase;<br>**PDBTitle:** crystal structure of scdpl1 |
| 48 | d1bs0a_ | Alignment | not modelled | 99.9 | 19 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 49 | c3ri6A_ | Alignment | not modelled | 99.9 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**o-acetylhomoserine sulfhydrylase;<br>**PDBTitle:** a novel mechanism of sulfur transfer catalyzed by o-acetylhomoserine2 sulfhydrylase in methionine biosynthetic pathway of wolinella3 succinogenes |
| 50 | c3uwcA_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**nucleotide-sugar aminotransferase;<br>**PDBTitle:** structure of an aminotransferase (degt-dnrj-eryc1-strs family) from2 coxiella burnetii in complex with pmp |
| 51 | c3l44A_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**glutamate-1-semialdehyde 2,1-aminomutase 1;<br>**PDBTitle:** crystal structure of bacillus anthracis heml-1, glutamate semialdehyde2 aminotransferase |
| 52 | d1jf9a_ | Alignment | not modelled | 99.9 | 16 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 53 | d1c4ka2 | Alignment | not modelled | 99.9 | 16 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Ornithine decarboxylase major domain |
| 54 | c3frkB_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**qdtb; |

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|---|---|---|---|---|---|---|
| 54 | [illegible] | Alignment | not modelled | 99.9 | [illegible] | **PDBTitle:** x-ray structure of qdtb from t. thermosaccharolyticum in2 complex with a plp:tdp-3-aminoquinovose aldimine |
| 55 | c3h7fB_ | Alignment | not modelled | 99.9 | 19 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase 1;<br>**PDBTitle:** crystal structure of serine hydroxymethyltransferase from2 mycobacterium tuberculosis |
| 56 | d1vefa1 | Alignment | not modelled | 99.9 | 15 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 57 | c3b46B_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**aminotransferase bna3;<br>**PDBTitle:** crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae |
| 58 | d2bwna1 | Alignment | not modelled | 99.9 | 12 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 59 | c3e9kA_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**kynureninase;<br>**PDBTitle:** crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex |
| 60 | c3dodA_ | Alignment | not modelled | 99.9 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**adenosylmethionine-8-amino-7-oxononanoate aminotransferase;<br>**PDBTitle:** crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 bacillus subtilis |
| 61 | d1s0aa_ | Alignment | not modelled | 99.9 | 10 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 62 | c3n0lA_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase;<br>**PDBTitle:** crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni |
| 63 | c2pb2B_ | Alignment | not modelled | 99.9 | 12 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**acetylornithine/succinyldiaminopimelate aminotransferase;<br>**PDBTitle:** structure of biosynthetic n-acetylornithine aminotransferase from2 salmonella typhimurium: studies on substrate specificity and3 inhibitor binding |
| 64 | d1pffa_ | Alignment | not modelled | 99.9 | 16 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 65 | c3a8uX_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**transferase<br>**Chain:** X: **PDB Molecule:**omega-amino acid--pyruvate aminotransferase;<br>**PDBTitle:** crystal structure of omega-amino acid:pyruvate aminotransferase |
| 66 | d1fc4a_ | Alignment | not modelled | 99.9 | 15 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 67 | c3tqxA_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**2-amino-3-ketobutyrate coenzyme a ligase;<br>**PDBTitle:** structure of the 2-amino-3-ketobutyrate coenzyme a ligase (kbl) from2 coxiella burnetii |
| 68 | d1c7ga_ | Alignment | not modelled | 99.9 | 11 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Beta-eliminating lyases |
| 69 | c2ordA_ | Alignment | not modelled | 99.9 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**acetylornithine aminotransferase;<br>**PDBTitle:** crystal structure of acetylornithine aminotransferase (ec 2.6.1.11)2 (acoat) (tm1785) from thermotoga maritima at 1.40 a resolution |
| 70 | c3hmuA_ | Alignment | not modelled | 99.9 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**aminotransferase, class iii;<br>**PDBTitle:** crystal structure of a class iii aminotransferase from2 silicibacter pomeroyi |
| 71 | d2gsaa_ | Alignment | not modelled | 99.9 | 15 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 72 | c3i4jC_ | Alignment | not modelled | 99.9 | 9 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**aminotransferase, class iii;<br>**PDBTitle:** crystal structure of aminotransferase, class iii from2 deinococcus radiodurans |
| 73 | c2eh6A_ | Alignment | not modelled | 99.9 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**acetylornithine aminotransferase;<br>**PDBTitle:** crystal structure of acetylornithine aminotransferase from aquifex2 aeolicus vf5 |
| 74 | c3a2bA_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**serine palmitoyltransferase;<br>**PDBTitle:** crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine |
| 75 | c1z7dE_ | Alignment | not modelled | 99.9 | 11 | **PDB header:**transferase<br>**Chain:** E: **PDB Molecule:**ornithine aminotransferase;<br>**PDBTitle:** ornithine aminotransferase py00104 from plasmodium yoelii |
| 76 | d1zoda1 | Alignment | not modelled | 99.9 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 77 | d2aeua1 | Alignment | not modelled | 99.9 | 17 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**SelA-like |
| 78 | d3bc8a1 | Alignment | not modelled | 99.9 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**SepSecS-like |
| 79 | d1kl1a_ | Alignment | not modelled | 99.9 | 17 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases |

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|---|---|---|---|---|---|---|
| | | | | | | **Family:**GABA-aminotransferase-like |
| 80 | c3lwsF_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**lyase<br>**Chain:** F: **PDB Molecule:**aromatic amino acid beta-eliminating<br>**PDBTitle:** crystal structure of putative aromatic amino acid beta-2 eliminating lyase/threonine aldolase. (yp_001813866.1) from3 exiguobacterium sp. 255-15 at 2.00 a resolution |
| 81 | c2x3lA_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**orn/lys/arg decarboxylase family protein;<br>**PDBTitle:** crystal structure of the orn_lys_arg decarboxylase family2 protein sar0482 from methicillin-resistant staphylococcus3 aureus |
| 82 | c3e2yB_ | Alignment | not modelled | 99.9 | 11 | **PDB header:**transferase, lyase<br>**Chain:** B: **PDB Molecule:**kynurenine-oxoglutarate transaminase 3;<br>**PDBTitle:** crystal structure of mouse kynurenine aminotransferase iii in complex2 with glutamine |
| 83 | c3jtxB_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**aminotransferase;<br>**PDBTitle:** crystal structure of aminotransferase (np_283882.1) from neisseria2 meningitidis z2491 at 1.91 a resolution |
| 84 | c3bs8A_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**glutamate-1-semialdehyde 2,1-aminomutase;<br>**PDBTitle:** crystal structure of glutamate 1-semialdehyde aminotransferase2 complexed with pyridoxamine-5'-phosphate from bacillus subtilis |
| 85 | c3nuiA_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyruvate transaminase;<br>**PDBTitle:** crystal structure of omega-transferase from vibrio fluvialis js17 |
| 86 | c2cy8A_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**d-phenylglycine aminotransferase;<br>**PDBTitle:** crystal structure of d-phenylglycine aminotransferase (d-phgat) from2 pseudomonas strutzeri st-201 |
| 87 | d1qz9a_ | Alignment | not modelled | 99.9 | 17 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 88 | c2dkjB_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase;<br>**PDBTitle:** crystal structure of t.th.hb8 serine hydroxymethyltransferase |
| 89 | d2r5ea1 | Alignment | not modelled | 99.9 | 16 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| 90 | c2e7uA_ | Alignment | not modelled | 99.9 | 18 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**glutamate-1-semialdehyde 2,1-aminomutase;<br>**PDBTitle:** crystal structure of glutamate-1-semialdehyde 2,1-aminomutase from2 thermus thermophilus hb8 |
| 91 | c2zsmA_ | Alignment | not modelled | 99.9 | 17 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**glutamate-1-semialdehyde 2,1-aminomutase;<br>**PDBTitle:** crystal structure of glutamate-1-semialdehyde 2,1-2 aminomutase from aeropyrum pernix, hexagonal form |
| 92 | d1m6sa_ | Alignment | not modelled | 99.9 | 19 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| 93 | c3dxvA_ | Alignment | not modelled | 99.9 | 12 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**alpha-amino-epsilon-caprolactam racemase;<br>**PDBTitle:** the crystal structure of alpha-amino-epsilon-caprolactam racemase from2 achromobacter obae |
| 94 | c3ecdC_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**serine hydroxymethyltransferase 2;<br>**PDBTitle:** crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei |
| 95 | c2hzpA_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**kynureninase;<br>**PDBTitle:** crystal structure of homo sapiens kynureninase |
| 96 | d1dfoa_ | Alignment | not modelled | 99.9 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 97 | c3h14A_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**aminotransferase, classes i and ii;<br>**PDBTitle:** crystal structure of a putative aminotransferase from silicibacter2 pomeroyi |
| 98 | c3oksB_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**4-aminobutyrate transaminase;<br>**PDBTitle:** crystal structure of 4-aminobutyrate transaminase from mycobacterium2 smegmatis |
| 99 | d1bw0a_ | Alignment | not modelled | 99.9 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| 100 | c3hqtB_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**cai-1 autoinducer synthase;<br>**PDBTitle:** plp-dependent acyl-coa transferase cqsa |
| 101 | c1c4kA_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**protein (ornithine decarboxylase);<br>**PDBTitle:** ornithine decarboxylase mutant (gly121tyr) |
| 102 | d1sffa_ | Alignment | not modelled | 99.9 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 103 | d1w7la_ | Alignment | not modelled | 99.9 | 15 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| | | | | | | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**aspartate aminotransferase; |

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|---|---|---|---|---|---|---|
| 104 | c3nraA_ | Alignment | not modelled | 99.9 | 18 | **PDBTitle:** crystal structure of an aspartate aminotransferase (yp_354942.1) from2 rhodobacter sphaeroides 2.4.1 at 2.15 a resolution |
| 105 | d2cfba1 | Alignment | not modelled | 99.9 | 14 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 106 | d1tpla_ | Alignment | not modelled | 99.9 | 10 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Beta-eliminating lyases |
| 107 | c3hl2D_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**o-phosphoseryl-trna(sec) selenium transferase;<br>**PDBTitle:** the crystal structure of the human sepsecs-trnasec complex |
| 108 | c3dc1A_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**kynurenine/alpha-aminoadipate aminotransferase<br>**PDBTitle:** crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate |
| 109 | d1vjoa_ | Alignment | not modelled | 99.9 | 16 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 110 | c3nnkC_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**ureidoglycine-glyoxylate aminotransferase;<br>**PDBTitle:** biochemical and structural characterization of a ureidoglycine2 aminotransferase in the klebsiella pneumoniae uric acid catabolic3 pathway |
| 111 | c3f9tB_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**l-tyrosine decarboxylase mfna;<br>**PDBTitle:** crystal structure of l-tyrosine decarboxylase mfna (ec 4.1.1.25)2 (np_247014.1) from methanococcus jannaschii at 2.11 a resolution |
| 112 | c3f0hA_ | Alignment | not modelled | 99.9 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**aminotransferase;<br>**PDBTitle:** crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution |
| 113 | d1js3a_ | Alignment | not modelled | 99.9 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Pyridoxal-dependent decarboxylase |
| 114 | c3fcrA_ | Alignment | not modelled | 99.9 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative aminotransferase;<br>**PDBTitle:** crystal structure of putative aminotransferase (yp_614685.1) from2 silicibacter sp. tm1040 at 1.80 a resolution |
| 115 | c3i5tB_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**aminotransferase;<br>**PDBTitle:** crystal structure of aminotransferase prk07036 from rhodobacter2 sphaeroides kd131 |
| 116 | d2v1pa1 | Alignment | not modelled | 99.9 | 16 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Beta-eliminating lyases |
| 117 | c3ffrA_ | Alignment | not modelled | 99.9 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**phosphoserine aminotransferase serc;<br>**PDBTitle:** crystal structure of a phosphoserine aminotransferase serc (chu_0995)2 from cytophaga hutchinsonii atcc 33406 at 1.75 a resolution |
| 118 | d1j32a_ | Alignment | not modelled | 99.9 | 16 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| 119 | c2o0rA_ | Alignment | not modelled | 99.9 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**rv0858c (n-succinyldiaminopimelate aminotransferase);<br>**PDBTitle:** the three-dimensional structure of n-succinyldiaminopimelate2 aminotransferase from mycobacterium tuberculosis |
| 120 | c2jisA_ | Alignment | not modelled | 99.9 | 12 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**cysteine sulfinic acid decarboxylase;<br>**PDBTitle:** human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp. |