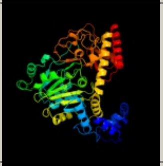
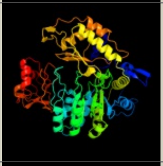
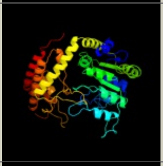
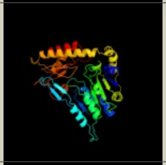
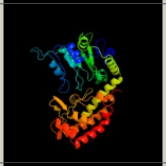
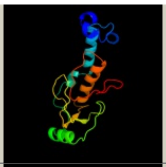
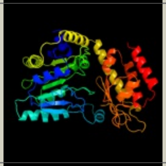
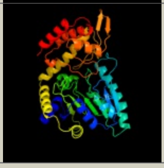
# Phyre$^2$

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P28629 |
| Date | Wed Jan 25 15:20:47 GMT 2012 |
| Unique Job ID | 37e0a61e85fc00e8 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2vycA_ | Alignment |  | 100.0 | 100 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**biodegradative arginine decarboxylase;<br>**PDBTitle:** crystal structure of acid induced arginine decarboxylase2 from e. coli |
| 2 | c3n75E_ | Alignment |  | 100.0 | 36 | **PDB header:**lyase<br>**Chain:** E: **PDB Molecule:**lysine decarboxylase, inducible;<br>**PDBTitle:** x-ray crystal structure of the escherichia coli inducible lysine2 decarboxylase ldci |
| 3 | c1c4kA_ | Alignment |  | 100.0 | 29 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**protein (ornithine decarboxylase);<br>**PDBTitle:** ornithine decarboxylase mutant (gly121tyr) |
| 4 | d1c4ka2 | Alignment |  | 100.0 | 32 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Ornithine decarboxylase major domain |
| 5 | c2x3lA_ | Alignment |  | 100.0 | 20 | **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 |
| 6 | d1rv3a_ | Alignment |  | 100.0 | 16 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 7 | d1bj4a_ | Alignment |  | 100.0 | 14 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 8 | d1ejia_ | Alignment |  | 100.0 | 15 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 9 | d2z67a1 | Alignment |  | 100.0 | 14 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**SepSecS-like |
| 10 | d2a7va1 | Alignment |  | 100.0 | 20 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 11 | c2a7vA_ | Alignment |  | 100.0 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase;<br>**PDBTitle:** human mitochondrial serine hydroxymethyltransferase 2 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 12 | d1c4ka3 | Alignment |  | 100.0 | 29 | **Fold:**Ornithine decarboxylase C-terminal domain<br>**Superfamily:**Ornithine decarboxylase C-terminal domain<br>**Family:**Ornithine decarboxylase C-terminal domain |
| 13 | c3h7fB_ | Alignment |  | 100.0 | 15 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase 1;<br>**PDBTitle:** crystal structure of serine hydroxymethyltransferase from2 mycobacterium tuberculosis |
| 14 | c3hl2D_ | Alignment |  | 100.0 | 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 |
| 15 | d3bc8a1 | Alignment |  | 100.0 | 11 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**SepSecS-like |
| 16 | c3ecdC_ | Alignment |  | 100.0 | 18 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**serine hydroxymethyltransferase 2;<br>**PDBTitle:** crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei |
| 17 | c3n0lA_ | Alignment |  | 100.0 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase;<br>**PDBTitle:** crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni |
| 18 | d1dfoa_ | Alignment |  | 100.0 | 19 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 19 | d1kl1a_ | Alignment |  | 100.0 | 16 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 20 | c2dkjB_ | Alignment |  | 100.0 | 17 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase;<br>**PDBTitle:** crystal structure of t.th.hb8 serine hydroxymethyltransferase |
| 21 | d2e7ja1 | Alignment | not modelled | 100.0 | 17 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**SepSecS-like |
| 22 | c3mafB_ | Alignment | not modelled | 99.9 | 18 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**sphingosine-1-phosphate lyase;<br>**PDBTitle:** crystal structure of stspl (asymmetric form) |
| 23 | c3mc6C_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**sphingosine-1-phosphate lyase;<br>**PDBTitle:** crystal structure of scdpl1 |
| 24 | d1vjoa_ | Alignment | not modelled | 99.9 | 14 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 25 | d1wyub1 | Alignment | not modelled | 99.9 | 14 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Glycine dehydrogenase subunits (GDC-P) |
| 26 | c3f9tB_ | Alignment | not modelled | 99.9 | 12 | **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 |
| 27 | d1wyua1 | Alignment | not modelled | 99.9 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Glycine dehydrogenase subunits (GDC-P) |
| 28 | d1js3a_ | Alignment | not modelled | 99.9 | 17 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Pyridoxal-dependent decarboxylase |
| | | | | | | **PDB header:**lyase |

| | | | | | | |
|---|---|---|---|---|---|---|
| 29 | c2jisA_ | Alignment | not modelled | 99.9 | 16 | **Chain:** A: **PDB Molecule:**cysteine sulfinic acid decarboxylase;<br>**PDBTitle:** human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp. |
| 30 | d1o69a_ | Alignment | not modelled | 99.9 | 12 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 31 | c2z9wA_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**aspartate aminotransferase;<br>**PDBTitle:** crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal |
| 32 | c3nnkC_ | Alignment | not modelled | 99.9 | 13 | **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 |
| 33 | 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 |
| 34 | c3hbxB_ | Alignment | not modelled | 99.9 | 17 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**glutamate decarboxylase 1;<br>**PDBTitle:** crystal structure of gad1 from arabidopsis thaliana |
| 35 | c3bcxA_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-<br>**PDBTitle:** e1 dehydrase |
| 36 | d1m6sa_ | Alignment | not modelled | 99.9 | 19 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| 37 | c2hzpA_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**kynureninase;<br>**PDBTitle:** crystal structure of homo sapiens kynureninase |
| 38 | c2w8wA_ | Alignment | not modelled | 99.9 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**serine palmitoyltransferase;<br>**PDBTitle:** n100y spt with plp-ser |
| 39 | d1h0ca_ | Alignment | not modelled | 99.9 | 14 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 40 | d1mdoa_ | Alignment | not modelled | 99.9 | 16 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 41 | d1bs0a_ | Alignment | not modelled | 99.9 | 15 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 42 | c3k40B_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**aromatic-l-amino-acid decarboxylase;<br>**PDBTitle:** crystal structure of drosophila 3,4-dihydroxyphenylalanine2 decarboxylase |
| 43 | c2po3B_ | Alignment | not modelled | 99.9 | 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 |
| 44 | c3l8aB_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**putative aminotransferase, probable beta-cystathionase;<br>**PDBTitle:** crystal structure of metc from streptococcus mutans |
| 45 | c3islA_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**purine catabolism protein pucg;<br>**PDBTitle:** crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis |
| 46 | c3nysA_ | Alignment | not modelled | 99.9 | 14 | **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 |
| 47 | 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 |
| 48 | d2bwna1 | Alignment | not modelled | 99.9 | 16 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 49 | c2ogeC_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**transaminase;<br>**PDBTitle:** x-ray structure of s. venezuelae desv in its internal2 aldimine form |
| 50 | c2c7tA_ | Alignment | not modelled | 99.9 | 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. |
| 51 | d2ch1a1 | Alignment | not modelled | 99.9 | 11 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 52 | d1tpla_ | Alignment | not modelled | 99.9 | 12 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Beta-eliminating lyases |
| 53 | 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 |
| 54 | d1svva_ | Alignment | not modelled | 99.9 | 11 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |

| | | | | | | |
|---|---|---|---|---|---|---|
| 55 | c3hqtB_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**cai-1 autoinducer synthase;<br>**PDBTitle:** plp-dependent acyl-coa transferase cqsa |
| 56 | d1fc4a_ | Alignment | not modelled | 99.9 | 18 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 57 | c3frkB_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**qdtb;<br>**PDBTitle:** x-ray structure of qdtb from t. thermosaccharolyticum in2 complex with a plp:tdp-3-aminoquinovose aldimine |
| 58 | c3pj0D_ | Alignment | not modelled | 99.9 | 12 | **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 |
| 59 | c2dr1A_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**386aa long hypothetical serine aminotransferase;<br>**PDBTitle:** crystal structure of the ph1308 protein from pyrococcus horikoshii ot3 |
| 60 | c2okkA_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**glutamate decarboxylase 2;<br>**PDBTitle:** the x-ray crystal structure of the 65kda isoform of glutamic acid2 decarboxylase (gad65) |
| 61 | c3tqxA_ | Alignment | not modelled | 99.9 | 17 | **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 |
| 62 | d2v1pa1 | Alignment | not modelled | 99.9 | 14 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Beta-eliminating lyases |
| 63 | c2r0tA_ | Alignment | not modelled | 99.9 | 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 |
| 64 | c3dr4B_ | Alignment | not modelled | 99.8 | 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 |
| 65 | d1pmma_ | Alignment | not modelled | 99.8 | 14 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Pyridoxal-dependent decarboxylase |
| 66 | d1v72a1 | Alignment | not modelled | 99.8 | 16 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| 67 | c3lwsF_ | Alignment | not modelled | 99.8 | 15 | **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 |
| 68 | c3kaxB_ | Alignment | not modelled | 99.8 | 11 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**aminotransferase, classes i and ii;<br>**PDBTitle:** crystal structure of a putative c-s lyase from bacillus anthracis |
| 69 | c2cb1A_ | Alignment | not modelled | 99.8 | 16 | **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. |
| 70 | c2huuA_ | Alignment | not modelled | 99.8 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**alanine glyoxylate aminotransferase;<br>**PDBTitle:** crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine |
| 71 | c3ffrA_ | Alignment | not modelled | 99.8 | 13 | **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 |
| 72 | d1c7ga_ | Alignment | not modelled | 99.8 | 12 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Beta-eliminating lyases |
| 73 | d2aeua1 | Alignment | not modelled | 99.8 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**SelA-like |
| 74 | d1m32a_ | Alignment | not modelled | 99.8 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 75 | d1b9ha_ | Alignment | not modelled | 99.8 | 14 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 76 | d1qgna_ | Alignment | not modelled | 99.8 | 16 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 77 | c3ke3A_ | Alignment | not modelled | 99.8 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative serine-pyruvate aminotransferase;<br>**PDBTitle:** crystal structure of putative serine-pyruvate aminotransferase2 (yp_263484.1) from psychrobacter arcticum 273-4 at 2.20 a resolution |
| 78 | c2qmaB_ | Alignment | not modelled | 99.8 | 13 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**diaminobutyrate-pyruvate transaminase and l-2,4-<br>**PDBTitle:** crystal structure of glutamate decarboxylase domain of2 diaminobutyrate-pyruvate transaminase and l-2,4-diaminobutyrate3 decarboxylase from vibrio parahaemolyticus |
| | | | | | | **PDB header:**transferase |

| | | | | | | |
|---|---|---|---|---|---|---|
| 79 | c3ju7B_ | Alignment | not modelled | 99.8 | 16 | **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 |
| 80 | d1cs1a_ | Alignment | not modelled | 99.8 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 81 | d2fnua1 | Alignment | not modelled | 99.8 | 12 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 82 | d1c7na_ | Alignment | not modelled | 99.8 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 83 | d1cl1a_ | Alignment | not modelled | 99.8 | 9 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 84 | c3f0hA_ | Alignment | not modelled | 99.8 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**aminotransferase;<br>**PDBTitle:** crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution |
| 85 | d1qz9a_ | Alignment | not modelled | 99.8 | 15 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 86 | c1d2fB_ | Alignment | not modelled | 99.8 | 12 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**maly protein;<br>**PDBTitle:** x-ray structure of maly from escherichia coli: a pyridoxal-5'-2 phosphate-dependent enzyme acting as a modulator in mal gene3 expression |
| 87 | d1bw0a_ | Alignment | not modelled | 99.8 | 11 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| 88 | d1jf9a_ | Alignment | not modelled | 99.8 | 16 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 89 | c3eucB_ | Alignment | not modelled | 99.8 | 11 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**histidinol-phosphate aminotransferase 2;<br>**PDBTitle:** crystal structure of histidinol-phosphate aminotransferase2 (yp_297314.1) from ralstonia eutropha jmp134 at 2.05 a resolution |
| 90 | c1i41J_ | Alignment | not modelled | 99.8 | 16 | **PDB header:**lyase<br>**Chain:** J: **PDB Molecule:**cystathionine gamma-synthase;<br>**PDBTitle:** cystathionine gamma-synthase in complex with the inhibitor2 appa |
| 91 | c3aemD_ | Alignment | not modelled | 99.8 | 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 |
| 92 | d1d2fa_ | Alignment | not modelled | 99.8 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 93 | c3b46B_ | Alignment | not modelled | 99.8 | 15 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**aminotransferase bna3;<br>**PDBTitle:** crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae |
| 94 | d1lc5a_ | Alignment | not modelled | 99.8 | 12 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| 95 | d1iaya_ | Alignment | not modelled | 99.8 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 96 | c3asaA_ | Alignment | not modelled | 99.8 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**ll-diaminopimelate aminotransferase;<br>**PDBTitle:** crystal structure of apo-ll-diaminopimelate aminotransferase from2 chlamydia trachomatis |
| 97 | c3op7A_ | Alignment | not modelled | 99.8 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**aminotransferase class i and ii;<br>**PDBTitle:** crystal structure of a plp-dependent aminotransferase (zp_03625122.1)2 from streptococcus suis 89-1591 at 1.70 a resolution |
| 98 | c3pdxA_ | Alignment | not modelled | 99.8 | 10 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**tyrosine aminotransferase;<br>**PDBTitle:** crystal structural of mouse tyrosine aminotransferase |
| 99 | c3dc1A_ | Alignment | not modelled | 99.8 | 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 |
| 100 | d1gc0a_ | Alignment | not modelled | 99.8 | 14 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 101 | c2fyfB_ | Alignment | not modelled | 99.8 | 13 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**phosphoserine aminotransferase;<br>**PDBTitle:** structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis |
| 102 | c3jtxB_ | Alignment | not modelled | 99.8 | 13 | **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 |
| 103 | d1v2da_ | Alignment | not modelled | 99.8 | 14 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| | | | | | | **PDB header:**transferase |

| | | | | | | |
|---|---|---|---|---|---|---|
| 104 | c3ri6A_ | Alignment | not modelled | 99.8 | 12 | **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 |
| 105 | c3dzzB_ | Alignment | not modelled | 99.8 | 12 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**putative pyridoxal 5'-phosphate-dependent c-s lyase;<br>**PDBTitle:** crystal structure of a putative plp-dependent aminotransferase2 (lbul_1103) from lactobacillus delbrueckii subsp. at 1.61 a3 resolution |
| 106 | d2csta_ | Alignment | not modelled | 99.7 | 15 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| 107 | c3fkdC_ | Alignment | not modelled | 99.7 | 13 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**l-threonine-o-3-phosphate decarboxylase;<br>**PDBTitle:** the crystal structure of l-threonine-o-3-phosphate2 decarboxylase from porphyromonas gingivalis |
| 108 | d1elua_ | Alignment | not modelled | 99.7 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 109 | c3qm2A_ | Alignment | not modelled | 99.7 | 10 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**phosphoserine aminotransferase;<br>**PDBTitle:** 2.25 angstrom crystal structure of phosphoserine aminotransferase2 (serc) from salmonella enterica subsp. enterica serovar typhimurium |
| 110 | c3caiA_ | Alignment | not modelled | 99.7 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**possible aminotransferase;<br>**PDBTitle:** crystal structure of mycobacterium tuberculosis rv3778c2 protein |
| 111 | c3h14A_ | Alignment | not modelled | 99.7 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**aminotransferase, classes i and ii;<br>**PDBTitle:** crystal structure of a putative aminotransferase from silicibacter2 pomeroyi |
| 112 | c3qguB_ | Alignment | not modelled | 99.7 | 12 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**ll-diaminopimelate aminotransferase;<br>**PDBTitle:** l,l-diaminopimelate aminotransferase from chalmydomonas reinhardtii |
| 113 | c1ibjC_ | Alignment | not modelled | 99.7 | 12 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**cystathionine beta-lyase;<br>**PDBTitle:** crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana |
| 114 | d2r5ea1 | Alignment | not modelled | 99.7 | 12 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| 115 | d1ibja_ | Alignment | not modelled | 99.7 | 12 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 116 | c3hdoB_ | Alignment | not modelled | 99.7 | 14 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**histidinol-phosphate aminotransferase;<br>**PDBTitle:** crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens |
| 117 | c2gqnB_ | Alignment | not modelled | 99.7 | 10 | **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 |
| 118 | d1xi9a_ | Alignment | not modelled | 99.7 | 12 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| 119 | d1x0ma1 | Alignment | not modelled | 99.7 | 16 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| 120 | c3cbfA_ | Alignment | not modelled | 99.7 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**alpha-aminodipate aminotransferase;<br>**PDBTitle:** crystal structure of lysn, alpha-aminoadipate2 aminotransferase, from thermus thermophilus hb27 |