

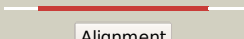

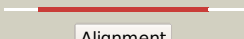
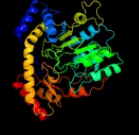





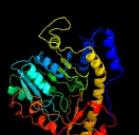


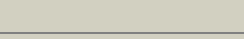


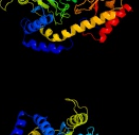
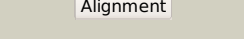

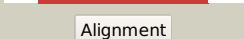



Phyre2

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|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3402c_(-)_3820833_3822071 |
| Date | Fri Aug 9 18:20:07 BST 2019 |
| Unique Job ID | f1f116d3cd55a0df |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c4k2bA_ |  Alignment |  | 100.0 | 19 | PDB header: transferase Chain: A; PDB Molecule: ntd biosynthesis operon protein ntda; PDBTitle: crystal structure of ntda from bacillus subtilis in complex with the2 internal aldimine |
| 2 | c3bcxA_ |  Alignment |  | 100.0 | 22 | PDB header: transferase Chain: A; PDB Molecule: cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydrase; PDBTitle: e1 dehydrase |
| 3 | c2po3B_ |  Alignment |  | 100.0 | 28 | PDB header: transferase Chain: B; PDB Molecule: 4-dehydrase; PDBTitle: crystal structure analysis of desi in the presence of its2 tdp-sugar product |
| 4 | c3ju7B_ |  Alignment |  | 100.0 | 31 | PDB header: transferase Chain: B; PDB Molecule: putative plp-dependent aminotransferase; PDBTitle: crystal structure of putative plp-dependent aminotransferase2 (np_978343.1) from bacillus cereus atcc 10987 at 2.19 a resolution |
| 5 | c5w70B_ |  Alignment |  | 100.0 | 24 | PDB header: transferase Chain: B; PDB Molecule: l-glutamine:2-deoxy-scylo-inosose aminotransferase; PDBTitle: x-ray structure of rbmb from streptomyces ribosidificus |
| 6 | c2c7tA_ |  Alignment |  | 100.0 | 24 | PDB header: transferase Chain: A; PDB Molecule: glutamine-2-deoxy-scylo-inosose aminotransferase; PDBTitle: crystal structure of the plp-bound form of btrr, a dual functional2 aminotransferase involved in butirosin biosynthesis. |
| 7 | c2r0tA_ |  Alignment |  | 100.0 | 18 | PDB header: transferase Chain: A; PDB Molecule: pyridoxamine 5-phosphate-dependent dehydrase; PDBTitle: crystal structure of gdp-4-keto-6-deoxymannose-3-dehydratase with a2 trapped plp-glutamate geminal diamine |
| 8 | c3uwcA_ |  Alignment |  | 100.0 | 17 | PDB header: transferase Chain: A; PDB Molecule: nucleotide-sugar aminotransferase; PDBTitle: structure of an aminotransferase (degt-dnrj-eryc1-strs family) from2 coxiella burnetii in complex with pmp |
| 9 | c3nysA_ |  Alignment |  | 100.0 | 23 | PDB header: transferase Chain: A; PDB Molecule: aminotransferase wbpe; PDBTitle: x-ray structure of the k185a mutant of wbpe (wlbe) from pseudomonas2 aeruginosa in complex with plp at 1.45 angstrom resolution |
| 10 | c2ogeC_ |  Alignment |  | 100.0 | 23 | PDB header: transferase Chain: C; PDB Molecule: transaminase; PDBTitle: x-ray structure of s. venezuelae desv in its internal2 aldimine form |
| 11 | d1b9ha_ |  Alignment |  | 100.0 | 23 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | d1o69a_ | Alignment | | 100.0 | 22 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like |
| 13 | c5u20C_ | Alignment | | 100.0 | 22 | PDB header: transferase Chain: C: PDB Molecule: putative aminotransferase; PDBTitle: x-ray structure of the wlarg aminotransferase from campylobacter2 jejuni, internal plp-aldimine |
| 14 | c3frkB_ | Alignment | | 100.0 | 23 | PDB header: transferase Chain: B: PDB Molecule: qdtb; PDBTitle: x-ray structure of qdtb from t. thermosaccharolyticum in2 complex with a plp:tdp-3-aminoquinovose aldimine |
| 15 | d2fnua1 | Alignment | | 100.0 | 24 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like |
| 16 | d1mdoa_ | Alignment | | 100.0 | 24 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like |
| 17 | c5k8bA_ | Alignment | | 100.0 | 24 | PDB header: transferase Chain: A: PDB Molecule: 8-amino-3,8-dideoxy-alpha-d-manno-octulosonate PDBTitle: x-ray structure of kdna, 8-amino-3,8-dideoxy-alpha-d-manno-2 octulosonate transaminase, from shewanella oneidensis in the presence3 of the external aldimine with plp and glutamate |
| 18 | c3dr4B_ | Alignment | | 100.0 | 26 | PDB header: transferase Chain: B: PDB Molecule: putative perosamine synthetase; PDBTitle: gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand |
| 19 | c6ewqA_ | Alignment | | 100.0 | 21 | PDB header: sugar binding protein Chain: A: PDB Molecule: putative capsular polysaccharide biosynthesis protein; PDBTitle: putative sugar aminotransferase spr1654 from streptococcus pneumoniae,2 plp-form |
| 20 | c4lc3B_ | Alignment | | 100.0 | 25 | PDB header: transferase Chain: B: PDB Molecule: putative udp-4-amino-4-deoxy-l-arabinose-oxoglutarate PDBTitle: x-ray crystal structure of a putative udp-4-amino-4-deoxy-l-arabinose-2 -oxoglutarate aminotransferase from burkholderia cenocepacia |
| 21 | c5uidC_ | Alignment | not modelled | 100.0 | 24 | PDB header: transferase Chain: C: PDB Molecule: aminotransferase tlmj; PDBTitle: the crystal structure of an aminotransferase tlmj from2 streptoaloteichus hindustanus |
| 22 | c4qgrA_ | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: A: PDB Molecule: degt/dnrj/eryc1/strs aminotransferase; PDBTitle: crystal structure of a degt dnrj eryc1 strs aminotransferase from2 brucella abortus |
| 23 | c4xauG_ | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: G: PDB Molecule: putative aminotransferase; PDBTitle: crystal structure of ats13 from actinomadura melliura |
| 24 | c4ytjC_ | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: C: PDB Molecule: cals13; PDBTitle: crystal structure of sugar aminotransferase cal13 from micromonospora2 echinospora |
| 25 | c3hqtB_ | Alignment | not modelled | 100.0 | 11 | PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa |
| 26 | c3caiA_ | Alignment | not modelled | 100.0 | 14 | PDB header: transferase Chain: A: PDB Molecule: possible aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv3778c2 protein |
| 27 | c3jtxB_ | Alignment | not modelled | 100.0 | 11 | PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase (np_283882.1) from neisseria2 meningitidis z2491 at 1.91 a resolution |
| 28 | c3wy7D_ | Alignment | not modelled | 100.0 | 14 | PDB header: transferase Chain: D: PDB Molecule: 8-amino-7-oxononanoate synthase; PDBTitle: crystal structure of mycobacterium smegmatis 7-keto-8-aminopelargonic2 acid (kapa) synthase biof PDB header: oxidoreductase |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 29 | c6hrhA_ | Alignment | not modelled | 100.0 | 11 | Chain: A: PDB Molecule: 5-aminolevulinate synthase, erythroid-specific, PDBTitle: structure of human erythroid-specific 5'-aminolevulinate synthase,2 alas2 |
| 30 | c4wbtA_ | Alignment | not modelled | 100.0 | 15 | PDB header: transferase Chain: A: PDB Molecule: probable histidinol-phosphate aminotransferase; PDBTitle: crystal structure of histidinol-phosphate aminotransferase from2 sinorhizobium meliloti in complex with pyridoxal-5'-phosphate |
| 31 | c3b46B_ | Alignment | not modelled | 100.0 | 10 | PDB header: transferase Chain: B: PDB Molecule: aminotransferase bna3; PDBTitle: crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae |
| 32 | c2w8wA_ | Alignment | not modelled | 100.0 | 13 | PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser |
| 33 | c2dkjB_ | Alignment | not modelled | 100.0 | 13 | PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of t.th.hb8 serine hydroxymethyltransferase |
| 34 | c3getA_ | Alignment | not modelled | 100.0 | 12 | PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: crystal structure of putative histidinol-phosphate aminotransferase2 (np_281508.1) from campylobacter jejuni at 2.01 a resolution |
| 35 | d1vjoa_ | Alignment | not modelled | 100.0 | 17 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like |
| 36 | c3nnkC_ | Alignment | not modelled | 100.0 | 12 | PDB header: transferase Chain: C: PDB Molecule: ureidoglycine-glyoxylate aminotransferase; PDBTitle: biochemical and structural characterization of a ureidoglycine2 aminotransferase in the klebsiella pneumoniae uric acid catabolic3 pathway |
| 37 | c3g0tA_ | Alignment | not modelled | 100.0 | 11 | PDB header: transferase Chain: A: PDB Molecule: putative aminotransferase; PDBTitle: crystal structure of putative aspartate aminotransferase (np_905498.1)2 from porphyromonas gingivalis w83 at 1.75 a resolution |
| 38 | d1lc5a_ | Alignment | not modelled | 100.0 | 12 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like |
| 39 | d1c7ga_ | Alignment | not modelled | 100.0 | 13 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases |
| 40 | c3hbxB_ | Alignment | not modelled | 100.0 | 13 | PDB header: lyase Chain: B: PDB Molecule: glutamate decarboxylase 1; PDBTitle: crystal structure of gad1 from arabidopsis thaliana |
| 41 | d1tpla_ | Alignment | not modelled | 100.0 | 14 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases |
| 42 | c3h14A_ | Alignment | not modelled | 100.0 | 13 | PDB header: transferase Chain: A: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative aminotransferase from silicibacter2 pomeroyi |
| 43 | c5zsqA_ | Alignment | not modelled | 100.0 | 13 | PDB header: biosynthetic protein Chain: A: PDB Molecule: cysteine desulfurase; PDBTitle: nifs from hydrogenimonas thermophila, soaked with l-cysteine for 4 min |
| 44 | d1jf9a_ | Alignment | not modelled | 100.0 | 13 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like |
| 45 | c5vc2A_ | Alignment | not modelled | 100.0 | 10 | PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of a serine hydroxymethyltransferase from2 helicobacter pylori |
| 46 | c5yhvA_ | Alignment | not modelled | 100.0 | 13 | PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aminotransferase from mycobacterium2 tuberculosis |
| 47 | c3ftbA_ | Alignment | not modelled | 100.0 | 13 | PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of the histidinol-phosphate aminotransferase2 from clostridium acetobutylicum |
| 48 | c4lnjA_ | Alignment | not modelled | 100.0 | 19 | PDB header: lyase Chain: A: PDB Molecule: low-specificity l-threonine aldolase; PDBTitle: structure of escherichia coli threonine aldolase in unliganded form |
| 49 | d1c7na_ | Alignment | not modelled | 100.0 | 8 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like |
| 50 | c4my5C_ | Alignment | not modelled | 100.0 | 13 | PDB header: transferase Chain: C: PDB Molecule: putative amino acid aminotransferase; PDBTitle: crystal structure of the aromatic amino acid aminotransferase from2 streptococcus mutants |
| 51 | c5kz5M_ | Alignment | not modelled | 100.0 | 11 | PDB header: transferase/oxidoreductase Chain: M: PDB Molecule: cysteine desulfurase, mitochondrial; PDBTitle: architecture of the human mitochondrial iron-sulfur cluster assembly2 machinery: the complex formed by the iron donor, the sulfur donor,3 and the scaffold |
| 52 | d1kl1a_ | Alignment | not modelled | 100.0 | 11 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like |
| 53 | c3kaxB_ | Alignment | not modelled | 100.0 | 7 | PDB header: lyase Chain: B: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative c-s lyase from bacillus anthracis |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 54 | c3dzzB_ | Alignment | not modelled | 100.0 | 11 | PDB header: transferase Chain: B: PDB Molecule: putative pyridoxal 5'-phosphate-dependent c-s lyase; PDBTitle: crystal structure of a putative plp-dependent aminotransferase2 (lbul_1103) from lactobacillus delbrueckii subsp. at 1.61 a3 resolution |
| 55 | c5txtA_ | Alignment | not modelled | 100.0 | 12 | PDB header: transferase Chain: A: PDB Molecule: 5-aminolevulinatase synthase, mitochondrial; PDBTitle: structure of asymmetric apo/holo alas dimer from s. cerevisiae |
| 56 | c5vprA_ | Alignment | not modelled | 100.0 | 13 | PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of cysteine desulfurase from elizabethkingia2 anophelis with covalently bound pyridoxal phosphate |
| 57 | c2o1bA_ | Alignment | not modelled | 100.0 | 14 | PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class i; PDBTitle: structure of aminotransferase from staphylococcus aureus |
| 58 | c4r8dB_ | Alignment | not modelled | 100.0 | 15 | PDB header: transferase Chain: B: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: crystal structure of rv1600 encoded aminotransferase in complex with2 plp-mes from mycobacterium tuberculosis |
| 59 | c3a2bA_ | Alignment | not modelled | 100.0 | 12 | PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine |
| 60 | c3zrrB_ | Alignment | not modelled | 100.0 | 12 | PDB header: transferase Chain: B: PDB Molecule: serine-pyruvate aminotransferase (agxt); PDBTitle: crystal structure and substrate specificity of a thermophilic2 archaeal serine : pyruvate aminotransferase from sulfobolus3 solfataricus |
| 61 | c3pj0D_ | Alignment | not modelled | 100.0 | 12 | PDB header: lyase Chain: D: PDB Molecule: lmo0305 protein; PDBTitle: crystal structure of a putative l-allo-threonine aldolase (lmo0305)2 from listeria monocytogenes egd-e at 1.80 a resolution |
| 62 | d1o4sa_ | Alignment | not modelled | 100.0 | 13 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like |
| 63 | c4wxfC_ | Alignment | not modelled | 100.0 | 10 | PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of l-serine hydroxymethyltransferase in complex with2 glycine |
| 64 | c3cq6E_ | Alignment | not modelled | 100.0 | 12 | PDB header: transferase Chain: E: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound) |
| 65 | c3ly1C_ | Alignment | not modelled | 100.0 | 11 | PDB header: transferase Chain: C: PDB Molecule: putative histidinol-phosphate aminotransferase; PDBTitle: crystal structure of putative histidinol-phosphate aminotransferase2 (yp_050345.1) from erwinia carotovora atroseptica scri1043 at 1.80 a3 resolution |
| 66 | c3wgcB_ | Alignment | not modelled | 100.0 | 19 | PDB header: lyase Chain: B: PDB Molecule: l-allo-threonine aldolase; PDBTitle: aeromonas jandaei l-allo-threonine aldolase h128y/s292r double mutant |
| 67 | c2hdyA_ | Alignment | not modelled | 100.0 | 13 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: selenocysteine lyase; PDBTitle: structure of human selenocysteine lyase |
| 68 | d1j32a_ | Alignment | not modelled | 100.0 | 13 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like |
| 69 | c6c9eB_ | Alignment | not modelled | 100.0 | 12 | PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of cysteine desulfurase from legionella pneumophila2 philadelphia 1 |
| 70 | c39ftB_ | Alignment | not modelled | 100.0 | 10 | PDB header: lyase Chain: B: PDB Molecule: l-tyrosine decarboxylase mfna; 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 |
| 71 | d1bs0a_ | Alignment | not modelled | 100.0 | 12 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like |
| 72 | c3aemD_ | Alignment | not modelled | 100.0 | 14 | PDB header: lyase Chain: D: PDB Molecule: methionine gamma-lyase; PDBTitle: reaction intermediate structure of entamoeba histolytica methionine2 gamma-lyase 1 containing michaelis complex and methionine imine-3 pyridoxamine-5'-phosphate |
| 73 | c4q76B_ | Alignment | not modelled | 100.0 | 14 | PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase 2, chloroplastic; PDBTitle: crystal structure of nfs2 c384s mutant, the plastidial cysteine2 desulfurase from arabidopsis thaliana |
| 74 | d1qgna_ | Alignment | not modelled | 100.0 | 13 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like |
| 75 | d1m6sa_ | Alignment | not modelled | 100.0 | 15 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like |
| 76 | c3b1dD_ | Alignment | not modelled | 100.0 | 10 | PDB header: lyase Chain: D: PDB Molecule: betac-s lyase; PDBTitle: crystal structure of betac-s lyase from streptococcus anginosus in2 complex with l-serine: external aldimine form |
| 77 | c3hdoB_ | Alignment | not modelled | 100.0 | 13 | PDB header: transferase Chain: B: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens |

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|-----|-------------------------|-----------|--------------|-------|----|--|
| 78 | d1w7la_ | Alignment | not modelled | 100.0 | 11 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like |
| 79 | d2r5ea1 | Alignment | not modelled | 100.0 | 13 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like |
| 80 | c3fdbA_ | Alignment | not modelled | 100.0 | 11 | PDB header: transferase Chain: A: PDB Molecule: putative plp-dependent beta-cystathionase; PDBTitle: crystal structure of a putative plp-dependent beta-cystathionase2 (aecd, dip1736) from corynebacterium diphtheriae at 1.99 a resolution |
| 81 | c3e9kA_ | Alignment | not modelled | 100.0 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex |
| 82 | c1ibjC_ | Alignment | not modelled | 100.0 | 16 | PDB header: lyase Chain: C: PDB Molecule: cystathionine beta-lyase; PDBTitle: crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana |
| 83 | c4ixoB_ | Alignment | not modelled | 100.0 | 11 | PDB header: protein binding Chain: B: PDB Molecule: nifs-like protein; PDBTitle: x-ray structure of nifs-like protein from rickettsia africae esf-5 |
| 84 | c3l8aB_ | Alignment | not modelled | 100.0 | 10 | PDB header: lyase Chain: B: PDB Molecule: putative aminotransferase, probable beta-cystathionase; PDBTitle: crystal structure of metc from streptococcus mutans |
| 85 | c3ffhA_ | Alignment | not modelled | 100.0 | 12 | PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of histidinol-phosphate aminotransferase from2 listeria innocua clip11262. |
| 86 | c5z0qG_ | Alignment | not modelled | 100.0 | 11 | PDB header: transferase Chain: G: PDB Molecule: aminotransferase, class i and ii; PDBTitle: crystal structure of ovob |
| 87 | c4dgtA_ | Alignment | not modelled | 100.0 | 7 | PDB header: transferase Chain: A: PDB Molecule: putative pyridoxal phosphate-dependent transferase; PDBTitle: crystal structure of plp-bound putative aminotransferase from2 clostridium difficile 630 crystallized with magnesium formate |
| 88 | c2huuA_ | Alignment | not modelled | 100.0 | 14 | PDB header: transferase Chain: A: PDB Molecule: alanine glyoxylate aminotransferase; PDBTitle: crystal structure of aedes aegypti alanine glyoxylate aminotransferase2 in complex with alanine |
| 89 | c4bhel_ | Alignment | not modelled | 100.0 | 12 | PDB header: transferase Chain: I: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: methanococcus jannaschii serine hydroxymethyltransferase2 in complex with plp |
| 90 | d1xi9a_ | Alignment | not modelled | 100.0 | 13 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like |
| 91 | c4j5uB_ | Alignment | not modelled | 100.0 | 12 | PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: x-ray crystal structure of a serine hydroxymethyltransferase with2 covalently bound plp from rickettsia rickettsii str. sheila smith |
| 92 | c5dx5B_ | Alignment | not modelled | 100.0 | 13 | PDB header: lyase Chain: B: PDB Molecule: methionine gamma-lyase; PDBTitle: crystal structure of methionine gamma-lyase from clostridium2 sporogenes |
| 93 | d2v1pa1 | Alignment | not modelled | 100.0 | 13 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases |
| 94 | d1t3ia_ | Alignment | not modelled | 100.0 | 13 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like |
| 95 | c4w91C_ | Alignment | not modelled | 100.0 | 16 | PDB header: transferase Chain: C: PDB Molecule: aminotransferase; PDBTitle: crystal structure of a cysteine desulfurase sufs from brucella suis2 bound to plp |
| 96 | c4j8lA_ | Alignment | not modelled | 100.0 | 12 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein yhfs; PDBTitle: crystal structure of the pyridoxal-5'-phosphate dependent protein yhfs2 from escherichia coli |
| 97 | c3ecdC_ | Alignment | not modelled | 100.0 | 11 | PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase 2; PDBTitle: crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei |
| 98 | c3ndnC_ | Alignment | not modelled | 100.0 | 16 | PDB header: lyase Chain: C: PDB Molecule: o-succinylhomoserine sulfhydrylase; PDBTitle: crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate |
| 99 | d1u08a_ | Alignment | not modelled | 100.0 | 11 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like |
| 100 | d1b5pa_ | Alignment | not modelled | 100.0 | 14 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like |
| 101 | c3ffrA_ | Alignment | not modelled | 100.0 | 9 | PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase serc; PDBTitle: crystal structure of a phosphoserine aminotransferase serc (chu_0995)2 from cytophaga hutchinsonii atcc 33406 at 1.75 a resolution |
| 102 | d1lba_ | Alignment | not modelled | 100.0 | 15 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like |

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|-----|-------------------------|-----------|--------------|-------|----|---|
| 103 | c3islA_ | Alignment | not modelled | 100.0 | 13 | PDB header: transferase Chain: A: PDB Molecule: purine catabolism protein pucg; PDBTitle: crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis |
| 104 | c5utsC_ | Alignment | not modelled | 100.0 | 12 | PDB header: lyase Chain: C: PDB Molecule: c-s lyase egt2; PDBTitle: carbon sulfoxide lyase, egt2 in the ergothioneine biosynthesis pathway |
| 105 | c2yrrA_ | Alignment | not modelled | 100.0 | 15 | PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class v; PDBTitle: hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8 |
| 106 | c5j8qA_ | Alignment | not modelled | 100.0 | 14 | PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase sufs; PDBTitle: crystal structure of the cysteine desulfurase sufs of bacillus2 subtilis |
| 107 | d1bw0a_ | Alignment | not modelled | 100.0 | 14 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like |
| 108 | d1cs1a_ | Alignment | not modelled | 100.0 | 17 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like |
| 109 | c2o0rA_ | Alignment | not modelled | 100.0 | 13 | PDB header: transferase Chain: A: PDB Molecule: rv0858c (n-succinylidiaminopimelate aminotransferase); PDBTitle: the three-dimensional structure of n-succinylidiaminopimelate2 aminotransferase from mycobacterium tuberculosis |
| 110 | d2bkwa1 | Alignment | not modelled | 100.0 | 10 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like |
| 111 | c3eucB_ | Alignment | not modelled | 100.0 | 14 | PDB header: transferase Chain: B: PDB Molecule: histidinol-phosphate aminotransferase 2; PDBTitle: crystal structure of histidinol-phosphate aminotransferase2 (yp_297314.1) from ralstonia eutropha jmp134 at 2.05 a resolution |
| 112 | c3f0hA_ | Alignment | not modelled | 100.0 | 12 | PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution |
| 113 | c4lw2C_ | Alignment | not modelled | 100.0 | 16 | PDB header: lyase Chain: C: PDB Molecule: cysteine sulfinatase desulfinase; PDBTitle: structural changes during cysteine desulfurase csda and sulfur-2 acceptor csde interactions provide insight into the trans-3 persulfuration |
| 114 | c5x5hA_ | Alignment | not modelled | 100.0 | 16 | PDB header: transferase Chain: A: PDB Molecule: cystathionine beta-lyases/cystathionine gamma-synthases; PDBTitle: crystal structure of metb from corynebacterium glutamicum |
| 115 | d2gb3a1 | Alignment | not modelled | 100.0 | 14 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like |
| 116 | c5jayB_ | Alignment | not modelled | 100.0 | 16 | PDB header: transferase Chain: B: PDB Molecule: 8-amino-7-oxononanoate synthase; PDBTitle: crystal structure of an 8-amino-7-oxononanoate synthase from2 burkholderia xenovorans |
| 117 | c4eb5B_ | Alignment | not modelled | 100.0 | 13 | PDB header: transferase/metal binding protein Chain: B: PDB Molecule: probable cysteine desulfurase 2; PDBTitle: a. fulgidus iscs-iscu complex structure |
| 118 | c3e2yB_ | Alignment | not modelled | 100.0 | 12 | PDB header: transferase, lyase Chain: B: PDB Molecule: kynurenine-oxoglutarate transaminase 3; PDBTitle: crystal structure of mouse kynurenine aminotransferase iii in complex2 with glutamine |
| 119 | d1qz9a_ | Alignment | not modelled | 100.0 | 13 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like |
| 120 | d1dfoa_ | Alignment | not modelled | 100.0 | 10 | Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like |