Phyre^2

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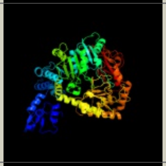
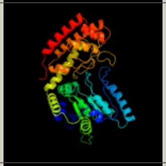
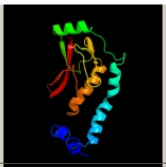
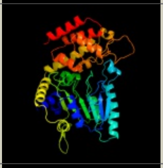
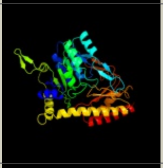
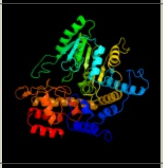
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1c4kA_	Alignment		100.0	54	**PDB header:**lyase **Chain:** A: **PDB Molecule:**protein (ornithine decarboxylase); **PDBTitle:** ornithine decarboxylase mutant (gly121tyr)
2	c2vycA_	Alignment		100.0	32	**PDB header:**lyase **Chain:** A: **PDB Molecule:**biodegradative arginine decarboxylase; **PDBTitle:** crystal structure of acid induced arginine decarboxylase2 from e. coli
3	c3n75E_	Alignment		100.0	34	**PDB header:**lyase **Chain:** E: **PDB Molecule:**lysine decarboxylase, inducible; **PDBTitle:** x-ray crystal structure of the escherichia coli inducible lysine2 decarboxylase ldci
4	d1c4ka2	Alignment		100.0	62	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Ornithine decarboxylase major domain
5	c2x3lA_	Alignment		100.0	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**orn/lys/arg decarboxylase family protein; **PDBTitle:** crystal structure of the orn_lys_arg decarboxylase family2 protein sar0482 from methicillin-resistant staphylococcus3 aureus
6	d1rv3a_	Alignment		100.0	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
7	d1bj4a_	Alignment		100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
8	d1ejia_	Alignment		100.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
9	d2z67a1	Alignment		100.0	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SepSecS-like
10	d2a7va1	Alignment		100.0	23	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
11	c2a7vA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** human mitochondrial serine hydroxymethyltransferase 2

12	d1c4ka3	Alignment		100.0	46	**Fold:**Ornithine decarboxylase C-terminal domain **Superfamily:**Ornithine decarboxylase C-terminal domain **Family:**Ornithine decarboxylase C-terminal domain
13	c3hl2D_	Alignment		100.0	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**o-phosphoseryl-trna(sec) selenium transferase; **PDBTitle:** the crystal structure of the human sepsecs-trnasec complex
14	c3h7fB_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase 1; **PDBTitle:** crystal structure of serine hydroxymethyltransferase from2 mycobacterium tuberculosis
15	d3bc8a1	Alignment		100.0	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SepSecS-like
16	c3ecdC_	Alignment		100.0	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**serine hydroxymethyltransferase 2; **PDBTitle:** crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei
17	c3n0lA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
18	d1dfoa_	Alignment		100.0	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
19	d1kl1a_	Alignment		100.0	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
20	c2dkjB_	Alignment		100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of t.th.hb8 serine hydroxymethyltransferase
21	d2e7ja1	Alignment	not modelled	100.0	19	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SepSecS-like
22	c3mc6C_	Alignment	not modelled	99.9	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**sphingosine-1-phosphate lyase; **PDBTitle:** crystal structure of scdpl1
23	c3mafB_	Alignment	not modelled	99.9	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**sphingosine-1-phosphate lyase; **PDBTitle:** crystal structure of stspl (asymmetric form)
24	d1wyub1	Alignment	not modelled	99.9	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Glycine dehydrogenase subunits (GDC-P)
25	c3f9tB_	Alignment	not modelled	99.9	16	**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
26	d1o69a_	Alignment	not modelled	99.9	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
27	d1vjoa_	Alignment	not modelled	99.9	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
28	c3bcxA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3- **PDBTitle:** e1 dehydrase
						PDB header:hydrolase

29	c3e9kA_	Alignment	not modelled	99.9	15	**Chain:** A: **PDB Molecule:**kynureninase; **PDBTitle:** crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
30	d1wyua1	Alignment	not modelled	99.9	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Glycine dehydrogenase subunits (GDC-P)
31	c2w8wA_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** n100y spt with plp-ser
32	d1m6sa_	Alignment	not modelled	99.9	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
33	d1mdoa_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
34	c2hzpA_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**kynureninase; **PDBTitle:** crystal structure of homo sapiens kynureninase
35	c2po3B_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-dehydrase; **PDBTitle:** crystal structure analysis of desi in the presence of its2 tdp-sugar product
36	c2z9wA_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
37	c3nysA_	Alignment	not modelled	99.9	14	**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
38	c3hbxB_	Alignment	not modelled	99.9	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutamate decarboxylase 1; **PDBTitle:** crystal structure of gad1 from arabidopsis thaliana
39	c3nnkC_	Alignment	not modelled	99.9	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
40	d1h0ca_	Alignment	not modelled	99.9	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
41	d1fc4a_	Alignment	not modelled	99.9	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
42	c3a2bA_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
43	c2r0tA_	Alignment	not modelled	99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxamine 5-phosphate-dependent dehydrase; **PDBTitle:** crystal sructure of gdp-4-keto-6-deoxymannose-3-dehydratase2 with a trapped plp-glutamate geminal diamine
44	d1js3a_	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Pyridoxal-dependent decarboxylase
45	c2c7tA_	Alignment	not modelled	99.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine-2-deoxy-scyllo-inosose **PDBTitle:** crystal structure of the plp-bound form of btrr,2 a dual functional aminotransferase involved in butirosin3 biosynthesis.
46	c2jisA_	Alignment	not modelled	99.9	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cysteine sulfinic acid decarboxylase; **PDBTitle:** human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
47	c3uwcA_	Alignment	not modelled	99.9	15	**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
48	d2bwna1	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
49	d1bs0a_	Alignment	not modelled	99.9	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
50	c2ogeC_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**transaminase; **PDBTitle:** x-ray structure of s. venezuelae desv in its internal2 aldimine form
51	d1svva_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
52	c3hqtB_	Alignment	not modelled	99.9	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cai-1 autoinducer synthase; **PDBTitle:** plp-dependent acyl-coa transferase cqsa
53	c3frkB_	Alignment	not modelled	99.9	12	**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
54	c3pj0D_	Alignment	not modelled	99.9	14	**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

55	c3islA_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine catabolism protein pucg; **PDBTitle:** crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
56	c2dr1A_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**386aa long hypothetical serine aminotransferase; **PDBTitle:** crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
57	c3dr4B_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative perosamine synthetase; **PDBTitle:** gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
58	c3tqxA_	Alignment	not modelled	99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-amino-3-ketobutyrate coenzyme a ligase; **PDBTitle:** structure of the 2-amino-3-ketobutyrate coenzyme a ligase (kbl) from2 coxiella burnetii
59	c3k40B_	Alignment	not modelled	99.9	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aromatic-l-amino-acid decarboxylase; **PDBTitle:** crystal structure of drosophila 3,4-dihydroxyphenylalanine2 decarboxylase
60	d2ch1a1	Alignment	not modelled	99.8	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
61	d1pmma_	Alignment	not modelled	99.8	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Pyridoxal-dependent decarboxylase
62	c3lwsF_	Alignment	not modelled	99.8	15	**PDB header:**lyase **Chain:** F: **PDB Molecule:**aromatic amino acid beta-eliminating **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
63	c2okkA_	Alignment	not modelled	99.8	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glutamate decarboxylase 2; **PDBTitle:** the x-ray crystal structure of the 65kda isoform of glutamic acid2 decarboxylase (gad65)
64	c3l8aB_	Alignment	not modelled	99.8	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative aminotransferase, probable beta-cystathionase; **PDBTitle:** crystal structure of metc from streptococcus mutans
65	d1v72a1	Alignment	not modelled	99.8	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
66	d1b9ha_	Alignment	not modelled	99.8	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
67	d1tpla_	Alignment	not modelled	99.8	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
68	d1m32a_	Alignment	not modelled	99.8	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
69	d2v1pa1	Alignment	not modelled	99.8	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
70	c2huuA_	Alignment	not modelled	99.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alanine glyoxylate aminotransferase; **PDBTitle:** crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine
71	c2cb1A_	Alignment	not modelled	99.8	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**o-acetyl homoserine sulfhydrylase; **PDBTitle:** crystal structure of o-actetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
72	c3ffrA_	Alignment	not modelled	99.8	13	**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
73	d2aeua1	Alignment	not modelled	99.8	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SelA-like
74	c3kaxB_	Alignment	not modelled	99.8	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aminotransferase, classes i and ii; **PDBTitle:** crystal structure of a putative c-s lyase from bacillus anthracis
75	c3ju7B_	Alignment	not modelled	99.8	14	**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
76	d2fnua1	Alignment	not modelled	99.8	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
77	d1c7ga_	Alignment	not modelled	99.8	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
78	d1cl1a_	Alignment	not modelled	99.8	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
79	d1qgna_	Alignment	not modelled	99.8	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like

80	d1jf9a_	Alignment	not modelled	99.8	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
81	c3f0hA_	Alignment	not modelled	99.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
82	d1cs1a_	Alignment	not modelled	99.8	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
83	c3ly1C_	Alignment	not modelled	99.8	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
84	c1i41J_	Alignment	not modelled	99.8	14	**PDB header:**lyase **Chain:** J: **PDB Molecule:**cystathionine gamma-synthase; **PDBTitle:** cystathionine gamma-synthase in complex with the inhibitor2 appa
85	c3ke3A_	Alignment	not modelled	99.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative serine-pyruvate aminotransferase; **PDBTitle:** crystal structure of putative serine-pyruvate aminotransferase2 (yp_263484.1) from psychrobacter arcticum 273-4 at 2.20 a resolution
86	d1qz9a_	Alignment	not modelled	99.8	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
87	c3aemD_	Alignment	not modelled	99.8	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
88	c3b46B_	Alignment	not modelled	99.8	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminotransferase bna3; **PDBTitle:** crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
89	d1elua_	Alignment	not modelled	99.8	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
90	c3dc1A_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**kynurenine/alpha-aminoadipate aminotransferase **PDBTitle:** crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate
91	c3qm2A_	Alignment	not modelled	99.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** 2.25 angstrom crystal structure of phosphoserine aminotransferase2 (serc) from salmonella enterica subsp. enterica serovar typhimurium
92	c1d2fB_	Alignment	not modelled	99.8	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**maly protein; **PDBTitle:** x-ray structure of maly from escherichia coli: a pyridoxal-5'-2 phosphate-dependent enzyme acting as a modulator in mal gene3 expression
93	d1c7na_	Alignment	not modelled	99.8	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
94	d1lc5a_	Alignment	not modelled	99.8	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
95	c3ri6A_	Alignment	not modelled	99.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**o-acetylhomoserine sulfhydrylase; **PDBTitle:** a novel mechanism of sulfur transfer catalyzed by o-acetylhomoserine2 sulfhydrylase in methionine biosynthetic pathway of wolinella3 succinogenes
96	c2qmaB_	Alignment	not modelled	99.8	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**diaminobutyrate-pyruvate transaminase and l-2,4- **PDBTitle:** crystal structure of glutamate decarboxylase domain of2 diaminobutyrate-pyruvate transaminase and l-2,4-diaminobutyrate3 decarboxylase from vibrio parahaemolyticus
97	c2gqnB_	Alignment	not modelled	99.8	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**cystathionine beta-lyase; **PDBTitle:** cystathionine beta-lyase (cbl) from escherichia coli in complex with2 n-hydrazinocarbonylmethyl-2-nitro-benzamide
98	c3caiA_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible aminotransferase; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv3778c2 protein
99	c3hdoB_	Alignment	not modelled	99.8	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
100	d1gc0a_	Alignment	not modelled	99.8	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
101	c3op7A_	Alignment	not modelled	99.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase class i and ii; **PDBTitle:** crystal structure of a plp-dependent aminotransferase (zp_03625122.1)2 from streptococcus suis 89-1591 at 1.70 a resolution
102	c2fyfB_	Alignment	not modelled	99.7	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
						PDB header:transferase

103	c3getA_	Alignment	not modelled	99.7	14	**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
104	c3eibB_	Alignment	not modelled	99.7	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ll-diaminopimelate aminotransferase; **PDBTitle:** crystal structure of k270n variant of ll-diaminopimelate2 aminotransferase from arabidopsis thaliana
105	d1x0ma1	Alignment	not modelled	99.7	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
106	c3qguB_	Alignment	not modelled	99.7	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ll-diaminopimelate aminotransferase; **PDBTitle:** l,l-diaminopimelate aminotransferase from chalmydomonas reinhardtii
107	c3dzzB_	Alignment	not modelled	99.7	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
108	c1ibjC_	Alignment	not modelled	99.7	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**cystathionine beta-lyase; **PDBTitle:** crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana
109	c3eucB_	Alignment	not modelled	99.7	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
110	c3asaA_	Alignment	not modelled	99.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ll-diaminopimelate aminotransferase; **PDBTitle:** crystal structure of apo-ll-diaminopimelate aminotransferase from2 chlamydia trachomatis
111	d1iaya_	Alignment	not modelled	99.7	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
112	d1ibja_	Alignment	not modelled	99.7	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
113	d1c4ka1	Alignment	not modelled	99.7	30	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Ornithine decarboxylase N-terminal "wing" domain
114	d1v2da_	Alignment	not modelled	99.7	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
115	c3ndnC_	Alignment	not modelled	99.7	13	**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
116	d1y4ia1	Alignment	not modelled	99.7	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
117	d1d2fa_	Alignment	not modelled	99.7	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
118	d1vp4a_	Alignment	not modelled	99.7	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
119	c2nmpC_	Alignment	not modelled	99.7	18	**PDB header:**lyase **Chain:** C: **PDB Molecule:**cystathionine gamma-lyase; **PDBTitle:** crystal structure of human cystathionine gamma lyase
120	d2c0ra1	Alignment	not modelled	99.7	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like