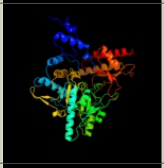
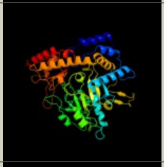
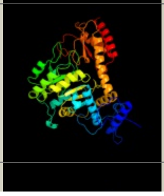
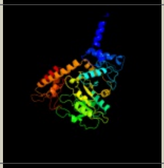
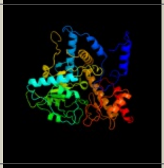
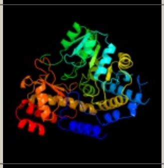
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P69910
Date	Thu Jan 5 12:12:18 GMT 2012
Unique Job ID	8c42f0d3e272b728

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pmma_	Alignment		100.0	100	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Pyridoxal-dependent decarboxylase
2	c3hbxB_	Alignment		100.0	45	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutamate decarboxylase 1; **PDBTitle:** crystal structure of gad1 from arabidopsis thaliana
3	c2qmaB_	Alignment		100.0	15	**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
4	d1js3a_	Alignment		100.0	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Pyridoxal-dependent decarboxylase
5	c2jisA_	Alignment		100.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cysteine sulfinic acid decarboxylase; **PDBTitle:** human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
6	c2okkA_	Alignment		100.0	16	**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)
7	c3k40B_	Alignment		100.0	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aromatic-l-amino-acid decarboxylase; **PDBTitle:** crystal structure of drosophila 3,4-dihydroxyphenylalanine2 decarboxylase
8	c3mafB_	Alignment		100.0	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**sphingosine-1-phosphate lyase; **PDBTitle:** crystal structure of stspl (asymmetric form)
9	c3mc6C_	Alignment		100.0	20	**PDB header:**lyase **Chain:** C: **PDB Molecule:**sphingosine-1-phosphate lyase; **PDBTitle:** crystal structure of scdpl1
10	c3hl2D_	Alignment		100.0	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**o-phosphoseryl-trna(sec) selenium transferase; **PDBTitle:** the crystal structure of the human sepsecs-trnasec complex
11	d3bc8a1	Alignment		100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SepSecS-like

12	c3f9tB_	Alignment		100.0	19	**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
13	d2z67a1	Alignment		100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SepSecS-like
14	d1wyub1	Alignment		100.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Glycine dehydrogenase subunits (GDC-P)
15	d1wyua1	Alignment		100.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Glycine dehydrogenase subunits (GDC-P)
16	c3bcxA_	Alignment		100.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3- **PDBTitle:** e1 dehydrase
17	d1kl1a_	Alignment		100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
18	d1jf9a_	Alignment		100.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
19	c3nnkC_	Alignment		100.0	14	**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
20	d1c4ka2	Alignment		100.0	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Ornithine decarboxylase major domain
21	c3e77A_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** human phosphoserine aminotransferase in complex with plp
22	d1qz9a_	Alignment	not modelled	100.0	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
23	c3caiA_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible aminotransferase; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv3778c2 protein
24	d1vjoa_	Alignment	not modelled	100.0	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
25	c2dr1A_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**386aa long hypothetical serine aminotransferase; **PDBTitle:** crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
26	c3e9kA_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**kynureninase; **PDBTitle:** crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
27	c2hzpA_	Alignment	not modelled	100.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**kynureninase; **PDBTitle:** crystal structure of homo sapiens kynureninase
28	c2hdyA_	Alignment	not modelled	100.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**selenocysteine lyase; **PDBTitle:** structure of human selenocysteine lyase
						PDB header:transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase serc;

29	c3ffrA_	Alignment	not modelled	100.0	14	**PDBTitle:** crystal structure of a phosphoserine aminotransferase serc (chu_0995)2 from cytophaga hutchinsonii atcc 33406 at 1.75 a resolution
30	c3islA_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine catabolism protein pucg; **PDBTitle:** crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
31	d2ch1a1	Alignment	not modelled	100.0	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
32	d1b9ha_	Alignment	not modelled	100.0	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
33	c2c7tA_	Alignment	not modelled	100.0	13	**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.
34	d2c0ra1	Alignment	not modelled	100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
35	c2fyfB_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
36	d1t3ia_	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
37	d1dfoa_	Alignment	not modelled	100.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
38	c3m5uA_	Alignment	not modelled	100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** crystal structure of phosphoserine aminotransferase from2 campylobacter jejuni
39	c2z9wA_	Alignment	not modelled	100.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
40	c3f0hA_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
41	d1h0ca_	Alignment	not modelled	100.0	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
42	d2bkwa1	Alignment	not modelled	100.0	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
43	c3lvmB_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cysteine desulfurase; **PDBTitle:** crystal structure of e.coli iscs
44	d1w23a_	Alignment	not modelled	100.0	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
45	c2r0tA_	Alignment	not modelled	100.0	14	**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
46	c2dkjB_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of t.th.hb8 serine hydroxymethyltransferase
47	c2po3B_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-dehydrase; **PDBTitle:** crystal structure analysis of desi in the presence of its2 tdp-sugar product
48	c2huuA_	Alignment	not modelled	100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alanine glyoxylate aminotransferase; **PDBTitle:** crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine
49	c3ecdC_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**serine hydroxymethyltransferase 2; **PDBTitle:** crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei
50	d1mdoa_	Alignment	not modelled	100.0	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
51	c3uwcA_	Alignment	not modelled	99.9	12	**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
52	c2ogeC_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**transaminase; **PDBTitle:** x-ray structure of s. venezuelae desv in its internal2 aldimine form
53	d1o69a_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
54	d1svva_	Alignment	not modelled	99.9	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
55	d1eg5a_	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases

						Family: Cystathionine synthase-like
56	d1p3wa_	Alignment	not modelled	99.9	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
57	c2w8wA_	Alignment	not modelled	99.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** n100y spt with plp-ser
58	d1v72a1	Alignment	not modelled	99.9	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
59	d2fnua1	Alignment	not modelled	99.9	9	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
60	c2yrrA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase, class v; **PDBTitle:** hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8
61	c3frkB_	Alignment	not modelled	99.9	13	**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
62	c3n0lA_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
63	d1m32a_	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
64	c3nysA_	Alignment	not modelled	99.9	13	**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
65	d1bjna_	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
66	d2bwna1	Alignment	not modelled	99.9	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
67	d1elua_	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
68	c3h7fB_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase 1; **PDBTitle:** crystal structure of serine hydroxymethyltransferase from2 mycobacterium tuberculosis
69	d1rv3a_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
70	c3dr4B_	Alignment	not modelled	99.9	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative perosamine synthetase; **PDBTitle:** gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
71	c3qm2A_	Alignment	not modelled	99.9	15	**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
72	d1bj4a_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
73	c3hqtB_	Alignment	not modelled	99.9	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cai-1 autoinducer synthase; **PDBTitle:** plp-dependent acyl-coa transferase cqsa
74	d1bs0a_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
75	c3ke3A_	Alignment	not modelled	99.9	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
76	c2a7vA_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** human mitochondrial serine hydroxymethyltransferase 2
77	d2a7va1	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
78	c3a2bA_	Alignment	not modelled	99.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
79	c3ju7B_	Alignment	not modelled	99.9	11	**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
80	c3tqxA_	Alignment	not modelled	99.9	10	**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
81	d1fc4a_	Alignment	not modelled	99.9	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
82	d2v1pa1	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
83	c1c4kA_	Alignment	not modelled	99.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**protein (ornithine decarboxylase); **PDBTitle:** ornithine decarboxylase mutant (gly121tyr)
84	d2e7ja1	Alignment	not modelled	99.9	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SepSecS-like
85	c2cb1A_	Alignment	not modelled	99.9	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**o-acetyl homoserine sulfhydrylase; **PDBTitle:** crystal structure of o-actetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
86	d1ejia_	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
87	c3pj0D_	Alignment	not modelled	99.9	10	**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
88	c3lwsF_	Alignment	not modelled	99.9	9	**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
89	d1ax4a_	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
90	d1c7ga_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
91	d1m6sa_	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
92	d1bw0a_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
93	c1ibjC_	Alignment	not modelled	99.9	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**cystathionine beta-lyase; **PDBTitle:** crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana
94	d1ibja_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
95	d1iuga_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
96	c2vycA_	Alignment	not modelled	99.9	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**biodegradative arginine decarboxylase; **PDBTitle:** crystal structure of acid induced arginine decarboxylase2 from e. coli
97	c3ndnC_	Alignment	not modelled	99.9	14	**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
98	c2nmpC_	Alignment	not modelled	99.9	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**cystathionine gamma-lyase; **PDBTitle:** crystal structure of human cystathionine gamma lyase
99	d1cs1a_	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
100	d2ctza1	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
101	c3jtxB_	Alignment	not modelled	99.9	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
102	d1n8pa_	Alignment	not modelled	99.9	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
103	c2x3lA_	Alignment	not modelled	99.9	13	**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
104	c3n75E_	Alignment	not modelled	99.9	15	**PDB header:**lyase **Chain:** E: **PDB Molecule:**lysine decarboxylase, inducible; **PDBTitle:** x-ray crystal structure of the escherichia coli inducible lysine2 decarboxylase ldci
105	c3aemD_	Alignment	not modelled	99.9	13	**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
106	c2gqnB_	Alignment	not modelled	99.9	12	**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
107	c3e6gA_	Alignment	not modelled	99.9	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cystathionine gamma-lyase-like protein; **PDBTitle:** crystal structure of xometc, a cystathionine c-lyase-like2 protein from xanthomonas oryzae pv.oryzae
108	d1lc5a_	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
109	c3dodA_	Alignment	not modelled	99.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenosylmethionine-8-amino-7-oxononanoate aminotransferase; **PDBTitle:** crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 bacillus subtilis
110	d1qgna_	Alignment	not modelled	99.9	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
111	d1y4ia1	Alignment	not modelled	99.9	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
112	d1tpla_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
113	d1xi9a_	Alignment	not modelled	99.8	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
114	d1x0ma1	Alignment	not modelled	99.8	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
115	c3ftbA_	Alignment	not modelled	99.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** the crystal structure of the histidinol-phosphate2 aminotransferase from clostridium acetobutylicum
116	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
117	c3l8aB_	Alignment	not modelled	99.8	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative aminotransferase, probable beta-cystathionase; **PDBTitle:** crystal structure of metc from streptococcus mutans
118	d1cl1a_	Alignment	not modelled	99.8	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
119	d1gc0a_	Alignment	not modelled	99.8	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
120	c3nx3A_	Alignment	not modelled	99.8	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylornithine aminotransferase; **PDBTitle:** crystal structure of acetylornithine aminotransferase (argd) from2 campylobacter jejuni