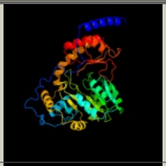
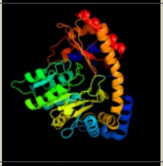
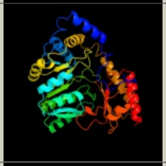
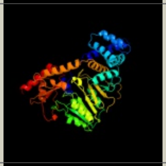
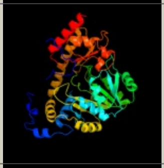
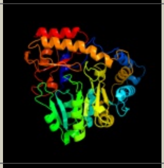
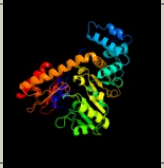
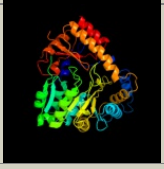
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P77730
Date	Thu Jan 5 12:32:10 GMT 2012
Unique Job ID	bef595b5eaccc362

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pplB_	Alignment		100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of an aspartate transaminase (ncgl0237, cgl0240)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.25 a3 resolution
2	d1vp4a_	Alignment		100.0	25	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
3	c3ez1A_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase mocr family; **PDBTitle:** crystal structure of putative aminotransferase (mocr family)2 (yp_604413.1) from deinococcus geothermalis dsm 11300 at 2.60 a3 resolution
4	d1wsta1	Alignment		100.0	28	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
5	d1x0ma1	Alignment		100.0	26	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
6	c3dc1A_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**kynurenine/alpha-aminoadipate aminotransferase **PDBTitle:** crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate
7	c2zc0C_	Alignment		100.0	27	**PDB header:**transferase **Chain:** C: **PDB Molecule:**alanine glyoxylate transaminase; **PDBTitle:** crystal structure of an archaeal alanine:glyoxylate aminotransferase
8	c3if2B_	Alignment		100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of putative amino-acid aminotransferase2 (yp_265399.1) from psychrobacter arcticum 273-4 at 2.50 a resolution
9	c3d6kB_	Alignment		100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative aminotransferase; **PDBTitle:** the crystal structure of a putative aminotransferase from2 corynebacterium diphtheriae
10	c2zy3A_	Alignment		100.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-aspartate beta-decarboxylase; **PDBTitle:** dodecameric l-aspartate beta-decarboxylase
11	c1ynuA_	Alignment		100.0	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**1-aminocyclopropane-1-carboxylate synthase; **PDBTitle:** crystal structure of apple acc synthase in complex with l-vinylglycine

12	c3ihjA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alanine aminotransferase 2; **PDBTitle:** human alanine aminotransferase 2 in complex with plp
13	c3g0tA_	Alignment		100.0	17	**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
14	d1m7ya_	Alignment		100.0	23	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
15	d2r5ea1	Alignment		100.0	19	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
16	c3cbfA_	Alignment		100.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-aminodipate aminotransferase; **PDBTitle:** crystal structure of lysn, alpha-aminoadipate2 aminotransferase, from thermus thermophilus hb27
17	d1iaya_	Alignment		100.0	23	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
18	c3f6tA_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of aspartate aminotransferase (e.c. 2.6.1.1)2 (yp_194538.1) from lactobacillus acidophilus ncfm at 2.15 a3 resolution
19	c2x5fB_	Alignment		100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartate_tyrosine_phenylalanine pyridoxal-5' **PDBTitle:** crystal structure of the methicillin-resistant2 staphylococcus aureus sar2028, an3 aspartate_tyrosine_phenylalanine pyridoxal-5'-phosphate4 dependent aminotransferase
20	c3e2yB_	Alignment		100.0	20	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**kynurenine-oxoglutarate transaminase 3; **PDBTitle:** crystal structure of mouse kynurenine aminotransferase iii in complex2 with glutamine
21	c3qguB_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ll-diaminopimelate aminotransferase; **PDBTitle:** l,l-diaminopimelate aminotransferase from chalmydomonas reinhardtii
22	d1w7la_	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
23	c3eibB_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ll-diaminopimelate aminotransferase; **PDBTitle:** crystal structure of k270n variant of ll-diaminopimelate2 aminotransferase from arabidopsis thaliana
24	d1u08a_	Alignment	not modelled	100.0	22	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
25	c3g7qA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**valine-pyruvate aminotransferase; **PDBTitle:** crystal structure of valine-pyruvate aminotransferase avta2 (np_462565.1) from salmonella typhimurium lt2 at 1.80 a resolution
26	c3b46B_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminotransferase bna3; **PDBTitle:** crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
27	c3h14A_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase, classes i and ii; **PDBTitle:** crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
28	c3l8aB_	Alignment	not modelled	100.0	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative aminotransferase, probable beta-cystathionase; **PDBTitle:** crystal structure of metc from streptococcus mutans

29	c3dzzB_	Alignment	not modelled	100.0	19	**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
30	c3eleB_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**amino transferase; **PDBTitle:** crystal structure of amino transferase (rer070207001803) from2 eubacterium rectale at 2.10 a resolution
31	d1xi9a_	Alignment	not modelled	100.0	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
32	d1bw0a_	Alignment	not modelled	100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
33	d2gb3a1	Alignment	not modelled	100.0	20	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
34	c2o1bA_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase, class i; **PDBTitle:** structure of aminotransferase from staphylococcus aureus
35	c3jtxB_	Alignment	not modelled	100.0	20	**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
36	c2o0rA_	Alignment	not modelled	100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rv0858c (n-succinyldiaminopimelate aminotransferase); **PDBTitle:** the three-dimensional structure of n-succinyldiaminopimelate2 aminotransferase from mycobacterium tuberculosis
37	d1gdea_	Alignment	not modelled	100.0	21	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
38	d1c7na_	Alignment	not modelled	100.0	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
39	d1j32a_	Alignment	not modelled	100.0	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
40	d1o4sa_	Alignment	not modelled	100.0	22	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
41	c2douA_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable n-succinyldiaminopimelate aminotransferase; **PDBTitle:** probable n-succinyldiaminopimelate aminotransferase (ttha0342) from2 thermus thermophilus hb8
42	c3t18D_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**aminotransferase class i and ii; **PDBTitle:** crystal structure of aminotransferase from anaerococcus prevotii dsm2 20548.
43	c3nraA_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of an aspartate aminotransferase (yp_354942.1) from2 rhodobacter sphaeroides 2.4.1 at 2.15 a resolution
44	c3ezsB_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminotransferase aspb; **PDBTitle:** crystal structure of aminotransferase aspb (np_207418.1) from2 helicobacter pylori 26695 at 2.19 a resolution
45	d1b5pa_	Alignment	not modelled	100.0	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
46	d2csta_	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
47	c3rq1A_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase class i and ii; **PDBTitle:** crystal structure of aminotransferase class i and ii from veillonella2 parvula
48	c3k7yA_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** aspartate aminotransferase of plasmodium falciparum
49	c3kaxB_	Alignment	not modelled	100.0	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aminotransferase, classes i and ii; **PDBTitle:** crystal structure of a putative c-s lyase from bacillus anthracis
50	c3asaA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ll-diaminopimelate aminotransferase; **PDBTitle:** crystal structure of apo-ll-diaminopimelate aminotransferase from2 chlamydia trachomatis
51	c3fdbA_	Alignment	not modelled	100.0	17	**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
52	d2ay1a_	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
53	c3pdxA_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine aminotransferase;

						PDBTitle: crystal structural of mouse tyrosine aminotransferase
54	d2q7wa1	Alignment	not modelled	100.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
55	c2x5dD_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**probable aminotransferase; **PDBTitle:** crystal structure of a probable aminotransferase from2 pseudomonas aeruginosa
56	c3dydB_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**tyrosine aminotransferase; **PDBTitle:** human tyrosine aminotransferase
57	d7aata_	Alignment	not modelled	100.0	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
58	d1ajsa_	Alignment	not modelled	100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
59	d1yaaa_	Alignment	not modelled	100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
60	d1v2da_	Alignment	not modelled	100.0	22	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
61	c3op7A_	Alignment	not modelled	100.0	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
62	c1d2fB_	Alignment	not modelled	100.0	19	**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
63	d1d2fa_	Alignment	not modelled	100.0	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
64	d3tata_	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
65	c3mebB_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** structure of cytoplasmic aspartate aminotransferase from giardia2 lamblia
66	c2z61A_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable aspartate aminotransferase 2; **PDBTitle:** crystal structure of mj0684 from methanococcus jannaschii2 reveals its similarity in the active site to kynurenine3 aminotransferases
67	c3eucB_	Alignment	not modelled	100.0	17	**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
68	c3ly1C_	Alignment	not modelled	100.0	13	**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
69	c3cq6E_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** E: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound)
70	c3getA_	Alignment	not modelled	100.0	16	**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
71	d2hoxa1	Alignment	not modelled	100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
72	d1lc5a_	Alignment	not modelled	100.0	19	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
73	c3bwnF_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** F: **PDB Molecule:**l-tryptophan aminotransferase; **PDBTitle:** l-tryptophan aminotransferase
74	d1fg7a_	Alignment	not modelled	100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
75	c3hdoB_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
76	c3ftbA_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** the crystal structure of the histidinol-phosphate2 aminotransferase from clostridium acetobutylicum
77	d2f8ja1	Alignment	not modelled	100.0	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
						PDB header:lyase **Chain:** C: **PDB Molecule:**l-threonine-o-3-phosphate

78	c3fkdC_	Alignment	not modelled	100.0	19	decarboxylase; **PDBTitle:** the crystal structure of l-threonine-o-3-phosphate2 decarboxylase from porphyromonas gingivalis
79	c3ffhA_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** the crystal structure of histidinol-phosphate aminotransferase from2 listeria innocua clip11262.
80	c3p1tB_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of a putative aminotransferase (bpsl1724) from2 burkholderia pseudomallei k96243 at 2.60 a resolution
81	d2aeua1	Alignment	not modelled	100.0	10	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SelA-like
82	c3e9kA_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**kynureninase; **PDBTitle:** crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
83	d1vjoa_	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
84	c2z9wA_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
85	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
86	c3hqtB_	Alignment	not modelled	100.0	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cai-1 autoinducer synthase; **PDBTitle:** plp-dependent acyl-coa transferase cqsa
87	c2dr1A_	Alignment	not modelled	100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**386aa long hypothetical serine aminotransferase; **PDBTitle:** crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
88	c3nnkC_	Alignment	not modelled	100.0	13	**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
89	d1v72a1	Alignment	not modelled	100.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
90	c2huuA_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alanine glyoxylate aminotransferase; **PDBTitle:** crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine
91	d1m6sa_	Alignment	not modelled	100.0	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
92	c3f0hA_	Alignment	not modelled	100.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
93	c3mc6C_	Alignment	not modelled	100.0	11	**PDB header:**lyase **Chain:** C: **PDB Molecule:**sphingosine-1-phosphate lyase; **PDBTitle:** crystal structure of scdpl1
94	c3tqxA_	Alignment	not modelled	100.0	12	**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
95	d1tpla_	Alignment	not modelled	100.0	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
96	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
97	d2ch1a1	Alignment	not modelled	100.0	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
98	c2w8wA_	Alignment	not modelled	100.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** n100y spt with plp-ser
99	d1fc4a_	Alignment	not modelled	100.0	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
100	c2hzpA_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**kynureninase; **PDBTitle:** crystal structure of homo sapiens kynureninase
101	c3ffrA_	Alignment	not modelled	100.0	14	**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	d1bs0a_	Alignment	not modelled	100.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like

103	d1h0ca_	Alignment	not modelled	100.0	19	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
104	c2yrrA_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase, class v; **PDBTitle:** hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8
105	d1iuga_	Alignment	not modelled	100.0	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
106	d1svva_	Alignment	not modelled	99.9	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
107	d1t3ia_	Alignment	not modelled	99.9	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
108	d2bwna1	Alignment	not modelled	99.9	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
109	c2po3B_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-dehydrase; **PDBTitle:** crystal structure analysis of desi in the presence of its2 tdp-sugar product
110	d2e7ja1	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SepSecS-like
111	c3mafB_	Alignment	not modelled	99.9	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**sphingosine-1-phosphate lyase; **PDBTitle:** crystal structure of stspl (asymmetric form)
112	c2ordA_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylornithine aminotransferase; **PDBTitle:** crystal structure of acetylornithine aminotransferase (ec 2.6.1.11)2 (acoat) (tm1785) from thermotoga maritima at 1.40 a resolution
113	d1dfoa_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
114	d1kl1a_	Alignment	not modelled	99.9	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
115	c2dkjB_	Alignment	not modelled	99.9	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of t.th.hb8 serine hydroxymethyltransferase
116	d1m32a_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
117	d1gc0a_	Alignment	not modelled	99.9	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
118	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
119	d1b9ha_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
120	d1jf9a_	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like