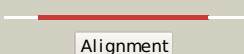
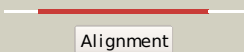
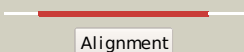
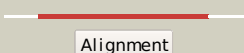
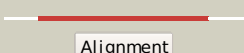
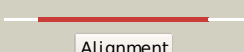
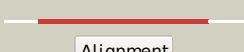
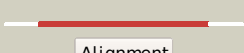
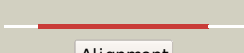


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1fg7a_	 Alignment		100.0	99	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
2	c3eucB_	 Alignment		100.0	26	PDB header: transferase Chain: B; PDB Molecule: histidinol-phosphate aminotransferase 2; PDBTitle: crystal structure of histidinol-phosphate aminotransferase2 (yp_297314.1) from ralstonia eutropha jmp134 at 2.05 a resolution
3	c3ly1C_	 Alignment		100.0	24	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 atrosepica scri1043 at 1.80 a3 resolution
4	c3ffhA_	 Alignment		100.0	26	PDB header: transferase Chain: A; PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of histidinol-phosphate aminotransferase from2 listeria innocua clip11262.
5	c3getA_	 Alignment		100.0	25	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
6	c3hdoB_	 Alignment		100.0	27	PDB header: transferase Chain: B; PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
7	c3h14A_	 Alignment		100.0	18	PDB header: transferase Chain: A; PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
8	c3cq6E_	 Alignment		100.0	31	PDB header: transferase Chain: E; PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound)
9	d1lc5a_	 Alignment		100.0	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
10	c3p1tB_	 Alignment		100.0	25	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
11	c3g0tA_	 Alignment		100.0	16	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

12	c3ftbA_	Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of the histidinol-phosphate2 aminotransferase from clostridium acetobutylicum
13	d2f8ja1	Alignment		100.0	29	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
14	c3pplB_	Alignment		100.0	18	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
15	d1b5pa_	Alignment		100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
16	c3e2yB_	Alignment		100.0	17	PDB header: transferase, lyase Chain: B: PDB Molecule: kynurenine-oxoglutarate transaminase 3; PDBTitle: crystal structure of mouse kynurenine aminotransferase iii in complex2 with glutamine
17	d1o4sa_	Alignment		100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
18	d2qb3a1	Alignment		100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
19	c3dzzB_	Alignment		100.0	16	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
20	c3b46B_	Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: aminotransferase bna3; PDBTitle: crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
21	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
22	c3ihjA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: alanine aminotransferase 2; PDBTitle: human alanine aminotransferase 2 in complex with plp
23	d1m7ya_	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
24	c1ynuA_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: A: PDB Molecule: 1-aminocyclopropane-1-carboxylate synthase; PDBTitle: crystal structure of apple acc synthase in complex with l-vinylglycine
25	c3fkdC_	Alignment	not modelled	100.0	21	PDB header: lyase Chain: C: PDB Molecule: l-threonine-o-3-phosphate decarboxylase; PDBTitle: the crystal structure of l-threonine-o-3-phosphate2 decarboxylase from porphyromonas gingivalis
26	d1iaya_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
27	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
28	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
29	dlw7la_	Alignment	not modelled	100.0	16 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
30	dlj32a_	Alignment	not modelled	100.0	19 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
31	c2o1bA_	Alignment	not modelled	100.0	18 PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class i; PDBTitle: structure of aminotransferase from staphylococcus aureus
32	c3l8aB_	Alignment	not modelled	100.0	19 PDB header: lyase Chain: B: PDB Molecule: putative aminotransferase, probable beta-cystathionase; PDBTitle: crystal structure of metc from streptococcus mutans
33	dlxi9a_	Alignment	not modelled	100.0	20 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
34	dlwsta1	Alignment	not modelled	100.0	18 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
35	c3qguB_	Alignment	not modelled	100.0	19 PDB header: transferase Chain: B: PDB Molecule: II-diaminopimelate aminotransferase; PDBTitle: I,I-diaminopimelate aminotransferase from chlamydomonas reinhardtii
36	c3eibB_	Alignment	not modelled	100.0	18 PDB header: transferase Chain: B: PDB Molecule: II-diaminopimelate aminotransferase; PDBTitle: crystal structure of k270n variant of II-diaminopimelate2 aminotransferase from arabidopsis thaliana
37	dlbw0a_	Alignment	not modelled	100.0	18 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
38	c2douA_	Alignment	not modelled	100.0	23 PDB header: transferase Chain: A: PDB Molecule: probable n-succinyl diaminopimelate aminotransferase; PDBTitle: probable n-succinyl diaminopimelate aminotransferase (ttha0342) from2 thermus thermophilus hb8
39	c3if2B_	Alignment	not modelled	100.0	16 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
40	c2zc0C_	Alignment	not modelled	100.0	17 PDB header: transferase Chain: C: PDB Molecule: alanine glyoxylate transaminase; PDBTitle: crystal structure of an archaeal alanine:glyoxylate aminotransferase
41	c3kaxB_	Alignment	not modelled	100.0	18 PDB header: lyase Chain: B: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative c-s lyase from bacillus anthracis
42	c3ez1A_	Alignment	not modelled	100.0	20 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
43	dlx0ma1	Alignment	not modelled	100.0	18 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
44	d2r5ea1	Alignment	not modelled	100.0	17 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
45	dlc7na_	Alignment	not modelled	100.0	15 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
46	c2o0rA_	Alignment	not modelled	100.0	21 PDB header: transferase Chain: A: PDB Molecule: rv0858c (n-succinyl diaminopimelate aminotransferase); PDBTitle: the three-dimensional structure of n-succinyl diaminopimelate2 aminotransferase from mycobacterium tuberculosis
47	dlu08a_	Alignment	not modelled	100.0	17 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
48	dlvp4a_	Alignment	not modelled	100.0	16 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
49	c3asaA_	Alignment	not modelled	100.0	21 PDB header: transferase Chain: A: PDB Molecule: II-diaminopimelate aminotransferase; PDBTitle: crystal structure of apo-II-diaminopimelate aminotransferase from2 chlamydia trachomatis
50	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
51	c3cbfA_	Alignment	not modelled	100.0	17 PDB header: transferase Chain: A: PDB Molecule: alpha-aminodipate aminotransferase; PDBTitle: crystal structure of lysn, alpha-aminodipate2 aminotransferase, from thermus thermophilus hb27
52	dlv2da_	Alignment	not modelled	100.0	18 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
53	c3dc1A_	Alignment	not modelled	100.0	16 PDB header: transferase Chain: A: PDB Molecule: kynurenine/alpha-aminodipate aminotransferase PDBTitle: crystal structure of kynurenine aminotransferase ii

						complex with2 alpha-ketoglutarate
54	c3fdbA	Alignment	not modelled	100.0	19	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
55	c1d2fB	Alignment	not modelled	100.0	16	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
56	c3d6kB	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: putative aminotransferase; PDBTitle: the crystal structure of a putative aminotransferase from2 corynebacterium diphtheriae
57	d1gdea	Alignment	not modelled	100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
58	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.
59	c2z61A	Alignment	not modelled	100.0	13	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
60	c3pdxA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: tyrosine aminotransferase; PDBTitle: crystal structural of mouse tyrosine aminotransferase
61	d1d2fa	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
62	c3nraA	Alignment	not modelled	100.0	18	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
63	c3rq1A	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of aminotransferase class i and ii from veillonella2 parvula
64	c3op7A	Alignment	not modelled	100.0	20	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
65	c3dydB	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: tyrosine aminotransferase; PDBTitle: human tyrosine aminotransferase
66	c3g7qA	Alignment	not modelled	100.0	17	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
67	c2zy3A	Alignment	not modelled	100.0	17	PDB header: lyase Chain: A: PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase
68	c3k7yA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: aspartate aminotransferase of plasmodium falciparum
69	c3bwnF	Alignment	not modelled	100.0	17	PDB header: transferase Chain: F: PDB Molecule: l-tryptophan aminotransferase; PDBTitle: l-tryptophan aminotransferase
70	c2x5fB	Alignment	not modelled	100.0	18	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
71	d2csta	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
72	d2q7wa1	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
73	d2ay1a	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
74	d1ajsa	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
75	d7aata	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
76	d1yaaa	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
77	c3f6tA	Alignment	not modelled	100.0	19	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
78	d2hoxa1	Alignment	not modelled	100.0	14 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
79	d3tata_	Alignment	not modelled	100.0	20 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
80	c3mebB_	Alignment	not modelled	100.0	17 PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase; PDBTitle: structure of cytoplasmic aspartate aminotransferase from giardia2 lamblia
81	d2aeua1	Alignment	not modelled	100.0	14 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SelA-like
82	d1svva_	Alignment	not modelled	100.0	12 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
83	d1vjoa_	Alignment	not modelled	100.0	16 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
84	d1v72a1	Alignment	not modelled	100.0	11 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
85	c3caiA_	Alignment	not modelled	100.0	16 PDB header: transferase Chain: A: PDB Molecule: possible aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv3778c2 protein
86	c3ffrA_	Alignment	not modelled	100.0	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
87	d2e7ja1	Alignment	not modelled	100.0	16 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-like
88	d1t3ia_	Alignment	not modelled	100.0	20 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
89	d1iuga_	Alignment	not modelled	100.0	12 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
90	c3hqtB_	Alignment	not modelled	100.0	14 PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
91	d1jf9a_	Alignment	not modelled	100.0	17 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
92	d1m6sa_	Alignment	not modelled	100.0	15 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
93	d1eg5a_	Alignment	not modelled	100.0	16 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
94	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
95	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
96	d2bkwa1	Alignment	not modelled	100.0	13 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
97	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
98	c3isiA_	Alignment	not modelled	100.0	16 PDB header: transferase Chain: A: PDB Molecule: purine catabolism protein pucg; PDBTitle: crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
99	c3nnkC_	Alignment	not modelled	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
100	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
101	c3e9kA_	Alignment	not modelled	100.0	15 PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
102	c2w8wA_	Alignment	not modelled	100.0	14 PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
103	d2bwna1	Alignment	not modelled	99.9	14 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like

104	d2ch1a1	Alignment	not modelled	99.9	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
105	c3lwsF	Alignment	not modelled	99.9	12	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
106	c3a2bA	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
107	c3nysA	Alignment	not modelled	99.9	12	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
108	c2dr1A	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A: PDB Molecule: 386aa long hypothetical serine aminotransferase; PDBTitle: crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
109	c2huuA	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: alanine glyoxylate aminotransferase; PDBTitle: crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine
110	d1gc0a	Alignment	not modelled	99.9	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
111	d1qz9a	Alignment	not modelled	99.9	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
112	d1h0ca	Alignment	not modelled	99.9	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
113	d1bs0a	Alignment	not modelled	99.9	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
114	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
115	d1m32a	Alignment	not modelled	99.9	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
116	d1kl1a	Alignment	not modelled	99.9	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
117	c3i4jC	Alignment	not modelled	99.9	15	PDB header: transferase Chain: C: PDB Molecule: aminotransferase, class iii; PDBTitle: crystal structure of aminotransferase, class iii from2 deinococcus radiodurans
118	c3ju7B	Alignment	not modelled	99.9	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
119	d1tp1a	Alignment	not modelled	99.9	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
120	d1dfoa	Alignment	not modelled	99.9	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like