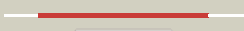


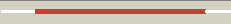
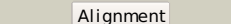
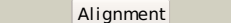
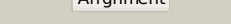
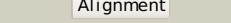
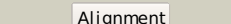
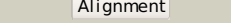
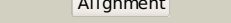
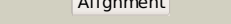
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bcxA_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3- PDBTitle: e1 dehydrase
2	c2r0tA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: pyridoxamine 5-phosphate-dependent dehydrase; PDBTitle: crystal sructure of gdp-4-keto-6-deoxymannose-3-dehydratase2 with a trapped plp-glutamate geminal diamine
3	c3dr4B_	 Alignment		100.0	31	PDB header: transferase Chain: B: PDB Molecule: putative perosamine synthetase; PDBTitle: gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
4	d1mdoa_	 Alignment		100.0	32	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
5	c2c7tA_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: glutamine-2-deoxy-scylllo-inosose PDBTitle: crystal structure of the plp-bound form of btrr,2 a dual functional aminotransferase involved in butirosin3 biosynthesis.
6	d2fnua1	 Alignment		100.0	24	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
7	c3uwcA_	 Alignment		100.0	25	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
8	c3nysA_	 Alignment		100.0	29	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
9	d1b9ha_	 Alignment		100.0	26	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
10	c2po3B_	 Alignment		100.0	25	PDB header: transferase Chain: B: PDB Molecule: 4-dehydrase; PDBTitle: crystal structure analysis of desi in the presence of its2 tdp-sugar product
11	c2ogeC_	 Alignment		100.0	29	PDB header: transferase Chain: C: PDB Molecule: transaminase; PDBTitle: x-ray structure of s. venezuelae desv in its internal2 aldimine form

12	dlo69a_	Alignment		100.0	23	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
13	c3frkB_	Alignment		100.0	30	PDB header: transferase Chain: B: PDB Molecule: qdtb; PDBTitle: x-ray structure of qdtb from t. thermosaccharolyticum in2 complex with a plp:tdp-3-aminoquinoxaline aldimine
14	c3ju7B_	Alignment		100.0	21	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
15	c2cb1A_	Alignment		100.0	16	PDB header: lyase Chain: A: PDB Molecule: o-acetyl homoserine sulfhydrylase; PDBTitle: crystal structure of o-acetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
16	dlqgna_	Alignment		100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
17	c3aemD_	Alignment		100.0	14	PDB header: lyase Chain: D: PDB Molecule: methionine gamma-lyase; PDBTitle: reaction intermediate structure of entamoeba histolytica methionine2 gamma-lyase 1 containing michaelis complex and methionine imine-3 pyridoxamine-5'-phosphate
18	clibjC_	Alignment		100.0	13	PDB header: lyase Chain: C: PDB Molecule: cystathionine beta-lyase; PDBTitle: crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana
19	dlibja_	Alignment		100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
20	cli41J_	Alignment		100.0	13	PDB header: lyase Chain: J: PDB Molecule: cystathionine gamma-synthase; PDBTitle: cystathionine gamma-synthase in complex with the inhibitor2 appa
21	d2cta1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
22	dlcs1a_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
23	c2nmpC_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: C: PDB Molecule: cystathionine gamma-lyase; PDBTitle: crystal structure of human cystathionine gamma lyase
24	c3caiA_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: possible aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv3778c2 protein
25	dly4ia1	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
26	c3ndnC_	Alignment	not modelled	100.0	17	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
27	dlc4ka2	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Ornithine decarboxylase major domain
28	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
						PDB header: transferase

29	c2w8wA_	Alignment	not modelled	100.0	16	Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
30	d1gc0a_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
31	d1cl1a_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
32	d1e5ea_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
33	c3a2bA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
34	c3ri6A_	Alignment	not modelled	100.0	13	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 wolfinella3 succinogenes
35	c3qi6B_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: B: PDB Molecule: cystathionine gamma-synthase meth (cgs); PDBTitle: crystal structure of cystathionine gamma-synthase meth (cgs) from2 mycobacterium ulcerans agy99
36	d1n8pa_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
37	d1bs0a_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
38	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
39	d1jf9a_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
40	c3ffrA_	Alignment	not modelled	100.0	10	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
41	c2gqnB_	Alignment	not modelled	100.0	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
42	c3jtxB_	Alignment	not modelled	100.0	16	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
43	d2bwna1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
44	c3e6ga_	Alignment	not modelled	100.0	15	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
45	d1vjoa_	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
46	c2hdyA_	Alignment	not modelled	100.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: selenocysteine lyase; PDBTitle: structure of human selenocysteine lyase
47	c3hdoB_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: B: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
48	d1qz9a_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
49	d1m6sa_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
50	d1t3ia_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
51	c3nnkC_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: C: PDB Molecule: ureidoglycine-glyoxylate aminotransferase; PDBTitle: biochemical and structural characterization of a ureidoglycine2 aminotransferase in the klebsiella pneumoniae uric acid catabolic3 pathway
52	c2fyfB_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: phosphoserine aminotransferase; PDBTitle: structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
53	c3kaxB_	Alignment	not modelled	100.0	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
						PDB header: lyase Chain: B: PDB Molecule: l-tyrosine decarboxylase mfna;

54	c3f9tB_	Alignment	not modelled	100.0	15	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
55	c3hbxB_	Alignment	not modelled	100.0	12	PDB header: lyase Chain: B: PDB Molecule: glutamate decarboxylase 1; PDBTitle: crystal structure of gad1 from arabidopsis thaliana
56	c3tqxA_	Alignment	not modelled	100.0	16	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 burneti
57	c2dkjB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of t.th.hb8 serine hydroxymethyltransferase
58	d2c0ra1	Alignment	not modelled	100.0	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
59	d2r5ea1	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
60	d1h0ca_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
61	c3f0hA_	Alignment	not modelled	100.0	8	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
62	c3lwsF_	Alignment	not modelled	100.0	14	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	c3h14A_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
64	d1fc4a_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
65	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
66	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
67	c2hzpA_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase
68	d1kl1a_	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
69	d1elua_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
70	c3ecdC_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase 2; PDBTitle: crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei
71	c3ftbA_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of the histidinol-phosphate2 aminotransferase from clostridium acetobutylicum
72	c3l8aB_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: B: PDB Molecule: putative aminotransferase, probable beta-cystathionase; PDBTitle: crystal structure of metc from streptococcus mutans
73	c3fdbA_	Alignment	not modelled	100.0	14	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
74	c3ly1C_	Alignment	not modelled	100.0	15	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
75	d1pffa_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
76	c3mafB_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (asymmetric form)
77	d1b5pa_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
78	d1iuga_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
						Fold: PLP-dependent transferase-like

79	d1m32a_	Alignment	not modelled	100.0	13	Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
80	c2o1bA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class i; PDBTitle: structure of aminotransferase from staphylococcus aureus
81	d1dfoa_	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
82	c2douA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: probable n-succinyldiaminopimelate aminotransferase; PDBTitle: probable n-succinyldiaminopimelate aminotransferase (ttha0342) from2 thermus thermophilus hb8
83	c3b46B_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: aminotransferase bna3; PDBTitle: crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
84	d1tpla_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
85	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
86	d1lc5a_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
87	c2z9wA_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
88	d1j32a_	Alignment	not modelled	100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
89	c3g0tA_	Alignment	not modelled	100.0	13	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
90	d1x0ma1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
91	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
92	d2ch1a1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
93	d1c7ga_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
94	c3cbfA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: alpha-aminodipate aminotransferase; PDBTitle: crystal structure of lysn, alpha-aminoadipate2 aminotransferase, from thermus thermophilus hb27
95	c3dzzB_	Alignment	not modelled	100.0	15	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
96	d1js3a_	Alignment	not modelled	100.0	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase
97	d1o4sa_	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
98	d1w23a_	Alignment	not modelled	100.0	10	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
99	d2e7ja1	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-like
100	c2jisA_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: A: PDB Molecule: cysteine sulfinic acid decarboxylase; PDBTitle: human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
101	d1c7na_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
102	d1bw0a_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
103	c3mc6C_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: C: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of scdpl1
104	c2zc0C_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: C: PDB Molecule: alanine glyoxylate transaminase; PDBTitle: crystal structure of an archaeal alanine:glyoxylate aminotransferase

105	c2okkA	 Alignment	not modelled	100.0	12	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)
106	c3op7A	 Alignment	not modelled	100.0	14	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
107	d1pmma	 Alignment	not modelled	99.9	10	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase
108	c2yrrA	 Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class v; PDBTitle: hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8
109	d1u08a	 Alignment	not modelled	99.9	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
110	c3hl2D	 Alignment	not modelled	99.9	14	PDB header: transferase Chain: D: PDB Molecule: o-phosphoseryl-trna(sec) selenium transferase; PDBTitle: the crystal structure of the human sepsecs-trnasec complex
111	d1w7la	 Alignment	not modelled	99.9	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
112	d1wsta1	 Alignment	not modelled	99.9	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
113	c3p1tB	 Alignment	not modelled	99.9	13	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
114	c3e2yB	 Alignment	not modelled	99.9	16	PDB header: transferase, lyase Chain: B: PDB Molecule: kynurenine-oxoglutarate transaminase 3; PDBTitle: crystal structure of mouse kynurenine aminotransferase iii in complex2 with glutamine
115	d1vp4a	 Alignment	not modelled	99.9	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
116	c3fkdc	 Alignment	not modelled	99.9	14	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
117	d2gb3a1	 Alignment	not modelled	99.9	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
118	c3ffhA	 Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of histidinol-phosphate aminotransferase from2 listeria innocua clip11262.
119	c3n0lA	 Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
120	d1wyua1	 Alignment	not modelled	99.9	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)