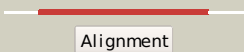

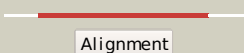

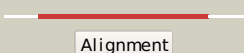

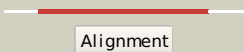

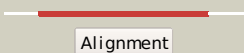

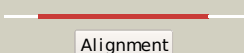

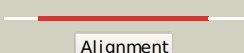

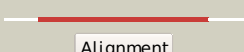

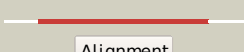

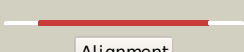

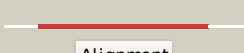












Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P77690
Date	Thu Jan 5 12:31:41 GMT 2012
Unique Job ID	e2da7f9ddcdf764

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1mdoa_	 Alignment		100.0	79	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
2	c3bcxA_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3- PDBTitle: e1 dehydrase
3	c2r0tA_	 Alignment		100.0	24	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
4	d2fnua1	 Alignment		100.0	28	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-scyllo-inosose PDBTitle: crystal structure of the plp-bound form of btrr,2 a dual functional aminotransferase involved in butirosin3 biosynthesis.
6	c2po3B_	 Alignment		100.0	32	PDB header: transferase Chain: B: PDB Molecule: 4-dehydrase; PDBTitle: crystal structure analysis of desi in the presence of its2 tdp-sugar product
7	c3dr4B_	 Alignment		100.0	34	PDB header: transferase Chain: B: PDB Molecule: putative perosamine synthetase; PDBTitle: gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
8	d1b9ha_	 Alignment		100.0	28	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
9	c2ogeC_	 Alignment		100.0	37	PDB header: transferase Chain: C: PDB Molecule: transaminase; PDBTitle: x-ray structure of s. venezuelae desv in its internal2 aldimine form
10	c3nysA_	 Alignment		100.0	33	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
11	c3uwCA_	 Alignment		100.0	29	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

12	d1o69a_	Alignment		100.0	25	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
13	c3frkB_	Alignment		100.0	31	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	22	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	d1qgna_	Alignment		100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
16	d1jf9a_	Alignment		100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
17	c2w8wA_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
18	c3hqtB_	Alignment		100.0	12	PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
19	d1cl1a_	Alignment		100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
20	c2gqnB_	Alignment		100.0	15	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
21	c3aemD_	Alignment	not modelled	100.0	15	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
22	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
23	d2ctza1	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
24	d1gc0a_	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
25	c1i41j_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: J: PDB Molecule: cystathionine gamma-synthase; PDBTitle: cystathionine gamma-synthase in complex with the inhibitor2 appa
26	c3caiA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: possible aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv3778c2 protein
27	c3a2bA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
28	d1cs1a_	Alignment	not modelled	100.0	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like

29	d1t3ia_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
30	c2cb1A_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: A: PDB Molecule: o-acetyl homoserine sulfhydrylase; PDBTitle: crystal structure of o-acetyl homoserine sulfhydrylase2 from thermus thermophilus hb8.oah2.
31	d1c4ka2	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Ornithine decarboxylase major domain
32	c3ndnC_	Alignment	not modelled	100.0	18	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
33	d1m6sa_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
34	d1qz9a_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
35	c3tqxA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: 2-amino-3-ketobutyrate coenzyme a ligase; PDBTitle: structure of the 2-amino-3-ketobutyrate coenzyme a ligase (kbl) from2 coxiella burnetii
36	d1y4ia1	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
37	c3l8aB_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: B: PDB Molecule: putative aminotransferase, probable beta-cystathionase; PDBTitle: crystal structure of metc from streptococcus mutans
38	c1ibjC_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: C: PDB Molecule: cystathionine beta-lyase; PDBTitle: crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana
39	d1libja_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
40	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
41	c3qi6B_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: B: PDB Molecule: cystathionine gamma-synthase metb (cgs); PDBTitle: crystal structure of cystathionine gamma-synthase metb (cgs) from2 mycobacterium ulcerans agy99
42	d1bs0a_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
43	c3e9kA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
44	d1kl1a_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
45	c2dkjB_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of t.th.hb8 serine hydroxymethyltransferase
46	d1n8pa_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
47	d1e5ea_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
48	c3ri6A_	Alignment	not modelled	100.0	17	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
49	c2fyfB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: phosphoserine aminotransferase; PDBTitle: structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
50	c2hzpA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase
51	c3hbxB_	Alignment	not modelled	100.0	11	PDB header: lyase Chain: B: PDB Molecule: glutamate decarboxylase 1; PDBTitle: crystal structure of gad1 from arabidopsis thaliana
52	d2bwna1	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
53	c3ftbA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of the histidinol-phosphate2 aminotransferase from clostridium acetobutylicum
54	d1vjoa_	Alianment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases

					Family: Cystathionine synthase-like
55	d1fc4a_	Alignment	not modelled	100.0	17 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
56	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
57	d1tpla_	Alignment	not modelled	100.0	16 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
58	c3e6gA_	Alignment	not modelled	100.0	19 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
59	c3ecdC_	Alignment	not modelled	100.0	19 PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase 2; PDBTitle: crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei
60	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
61	d1dfoa_	Alignment	not modelled	100.0	14 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
62	c3n0lA_	Alignment	not modelled	100.0	18 PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
63	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
64	c3hdoB_	Alignment	not modelled	100.0	14 PDB header: transferase Chain: B: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
65	c3h14A_	Alignment	not modelled	100.0	16 PDB header: transferase Chain: A: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
66	d1c7ga_	Alignment	not modelled	100.0	16 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
67	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
68	c2dr1A_	Alignment	not modelled	100.0	14 PDB header: transferase Chain: A: PDB Molecule: 386aa long hypothetical serine aminotransferase; PDBTitle: crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
69	c3dzzB_	Alignment	not modelled	100.0	14 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
70	d1c7na_	Alignment	not modelled	100.0	12 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
71	d2e7ja1	Alignment	not modelled	100.0	14 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-like
72	d2r5ea1	Alignment	not modelled	100.0	14 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
73	d1x0ma1	Alignment	not modelled	100.0	14 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
74	c3f9tB_	Alignment	not modelled	100.0	16 PDB header: lyase Chain: B: PDB Molecule: l-tyrosine decarboxylase mfna; PDBTitle: crystal structure of l-tyrosine decarboxylase mfna (ec 4.1.1.25)2 (np_247014.1) from methanococcus jannaschii at 2.11 a resolution
75	c3getA_	Alignment	not modelled	100.0	12 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
76	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
77	d1lc5a_	Alignment	not modelled	100.0	16 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
78	c3islA_	Alignment	not modelled	100.0	15 PDB header: transferase Chain: A: PDB Molecule: purine catabolism protein pucg; PDBTitle: crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis

79	c3jtxB_	Alignment	not modelled	100.0	12	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
80	d1h0ca	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
81	c3cbfA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: alpha-aminodipate aminotransferase; PDBTitle: crystal structure of lysn, alpha-aminodipate2 aminotransferase, from thermus thermophilus hb27
82	d2c0ra1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
83	d1m32a_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
84	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)
85	c3ly1C_	Alignment	not modelled	100.0	12	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
86	d1vp4a_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
87	c2okkA_	Alignment	not modelled	100.0	14	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)
88	d1pmma_	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase
89	c3eucB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: histidinol-phosphate aminotransferase 2; PDBTitle: crystal structure of histidinol-phosphate aminotransferase2 (yp_297314.1) from ralstonia eutropha jmp134 at 2.05 a resolution
90	d1xi9a_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
91	d1bw0a_	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
92	d1j32a_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
93	c3h7fB_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase 1; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 mycobacterium tuberculosis
94	c3cq6E_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: E: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound)
95	d1p3wa_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
96	c2z9wA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
97	d1iuga_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
98	c2jisA_	Alignment	not modelled	99.9	16	PDB header: lyase Chain: A: PDB Molecule: cysteine sulfinic acid decarboxylase; PDBTitle: human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
99	d1js3a_	Alignment	not modelled	99.9	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase
100	d1wsta1	Alignment	not modelled	99.9	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
101	d1wyua1	Alignment	not modelled	99.9	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
102	c3b46B_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: B: PDB Molecule: aminotransferase bna3; PDBTitle: crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
103	c2o0rA_	Alignment	not modelled	99.9	18	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
						PDB header: lyase Chain: F: PDB Molecule: aromatic amino acid beta-eliminating

104	c3lwsF_	Alignment	not modelled	99.9	14	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
105	c3p1tB_	Alignment	not modelled	99.9	11	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
106	c3q0tA_	Alignment	not modelled	99.9	11	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
107	d1w7la_	Alignment	not modelled	99.9	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
108	c2huuA_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A: PDB Molecule: alanine glyoxylate aminotransferase; PDBTitle: crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine
109	d1b5pa_	Alignment	not modelled	99.9	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
110	d1elua_	Alignment	not modelled	99.9	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
111	c3pj0D_	Alignment	not modelled	99.9	14	PDB header: lyase Chain: D: PDB Molecule: lmo0305 protein; PDBTitle: crystal structure of a putative l-allo-threonine aldolase (lmo0305)2 from listeria monocytogenes egd-e at 1.80 a resolution
112	c3e77A_	Alignment	not modelled	99.9	10	PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase; PDBTitle: human phosphoserine aminotransferase in complex with plp
113	c3lvmB_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of e.coli iscs
114	d1v72a1	Alignment	not modelled	99.9	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
115	d2ch1a1	Alignment	not modelled	99.9	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
116	c1d2fB_	Alignment	not modelled	99.9	15	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
117	d1d2fa_	Alignment	not modelled	99.9	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
118	c3fkdC_	Alignment	not modelled	99.9	11	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
119	c3op7A_	Alignment	not modelled	99.9	15	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
120	d1pffa_	Alignment	not modelled	99.9	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like