







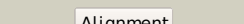



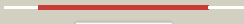



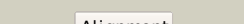

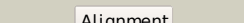

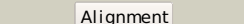
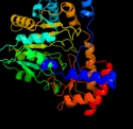


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3if2B_	 Alignment		100.0	43	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of putative amino-acid aminotransferase2 (yp_265399.1) from psychrobacter arcticum 273-4 at 2.50 a resolution
2	c3g7qA_	 Alignment		100.0	86	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
3	d1vp4a_	 Alignment		100.0	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
4	c3pplB_	 Alignment		100.0	16	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
5	d1wsta1	 Alignment		100.0	24	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
6	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
7	c2zc0C_	 Alignment		100.0	19	PDB header: transferase Chain: C: PDB Molecule: alanine glyoxylate transaminase; PDBTitle: crystal structure of an archaeal alanine:glyoxylate aminotransferase
8	d1x0ma1	 Alignment		100.0	22	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
9	c3e2yB_	 Alignment		100.0	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
10	c3ez1A_	 Alignment		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
11	c3eleB_	 Alignment		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

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	d2r5ea1	Alignment		100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
14	c3b46B_	Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: aminotransferase bna3; PDBTitle: crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
15	d1w7la_	Alignment		100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
16	c1ynuA_	Alignment		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
17	d1iaya_	Alignment		100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
18	c3d6kB_	Alignment		100.0	15	PDB header: transferase Chain: B: PDB Molecule: putative aminotransferase; PDBTitle: the crystal structure of a putative aminotransferase from2 corynebacterium diphtheriae
19	d2gb3a1	Alignment		100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
20	d1b5pa_	Alignment		100.0	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
21	c3h14A_	Alignment	not modelled	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
22	d1j32a_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
23	c3dc1A_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: kynurenine/alpha-aminoadipate aminotransferase PDBTitle: crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate
24	d1m7ya_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
25	c3jtxB_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aspartate aminotransferase (np_283882.1) from neisseria2 meningitidis z2491 at 1.91 a resolution
26	d1o4sa_	Alignment	not modelled	100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
27	c3nraA_	Alignment	not modelled	100.0	19	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
28	d1bw0a_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like

29	c3l8aB_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: B: PDB Molecule: putative aminotransferase, probable beta-cystathionase; PDBTitle: crystal structure of metc from streptococcus mutans
30	c3dzzB_	Alignment	not modelled	100.0	12	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
31	c3qguB_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: l,l-diaminopimelate aminotransferase from chlamydomonas reinhardtii
32	c2x5fB_	Alignment	not modelled	100.0	14	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
33	d1c7na_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
34	c3eibB_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: crystal structure of k270n variant of ll-diaminopimelate2 aminotransferase from arabidopsis thaliana
35	d1u08a_	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
36	d1xi9a_	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
37	c2o0rA_	Alignment	not modelled	100.0	16	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
38	d1gdea_	Alignment	not modelled	100.0	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
39	c3kaxB_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: B: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative c-s lyase from bacillus anthracis
40	d2csta_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
41	c3cbfA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: alpha-aminodipate aminotransferase; PDBTitle: crystal structure of lysn, alpha-aminodipate2 aminotransferase, from thermus thermophilus hb27
42	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
43	c1d2fB_	Alignment	not modelled	100.0	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
44	c2o1bA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class i; PDBTitle: structure of aminotransferase from staphylococcus aureus
45	d1ajsa_	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
46	c3asaA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: crystal structure of apo-ll-diaminopimelate aminotransferase from2 chlamydia trachomatis
47	c2douA_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: probable n-succinyl diaminopimelate aminotransferase; PDBTitle: probable n-succinyl diaminopimelate aminotransferase (ttha0342) from2 thermus thermophilus hb8
48	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
49	c2x5dD_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: D: PDB Molecule: probable aminotransferase; PDBTitle: crystal structure of a probable aminotransferase from2 pseudomonas aeruginosa
50	c3k7yA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: aspartate aminotransferase of plasmodium falciparum
51	d1d2fa_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
52	d2q7wa1	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases

					Family: AAT-like
53	d1v2da_	Alignment	not modelled	100.0	19 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
54	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.
55	d7aata_	Alignment	not modelled	100.0	13 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
56	d1yaaa_	Alignment	not modelled	100.0	15 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
57	d2ay1a_	Alignment	not modelled	100.0	18 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
58	c3rq1A_	Alignment	not modelled	100.0	12 PDB header: transferase Chain: A: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of aminotransferase class i and ii from veillonella2 parvula
59	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
60	c3mebB_	Alignment	not modelled	100.0	14 PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase; PDBTitle: structure of cytoplasmic aspartate aminotransferase from giardia2 lamblia
61	c2zy3A_	Alignment	not modelled	100.0	15 PDB header: lyase Chain: A: PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase
62	c3f6tA_	Alignment	not modelled	100.0	16 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
63	c3pdxA_	Alignment	not modelled	100.0	19 PDB header: transferase Chain: A: PDB Molecule: tyrosine aminotransferase; PDBTitle: crystal structural of mouse tyrosine aminotransferase
64	c3dydB_	Alignment	not modelled	100.0	19 PDB header: transferase Chain: B: PDB Molecule: tyrosine aminotransferase; PDBTitle: human tyrosine aminotransferase
65	c2z61A_	Alignment	not modelled	100.0	19 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
66	d3tata_	Alignment	not modelled	100.0	16 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
67	c3bwnF_	Alignment	not modelled	100.0	12 PDB header: transferase Chain: F: PDB Molecule: l-tryptophan aminotransferase; PDBTitle: l-tryptophan aminotransferase
68	d2hoxa1	Alignment	not modelled	100.0	14 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
69	c3eucB_	Alignment	not modelled	100.0	19 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
70	c3ly1C_	Alignment	not modelled	100.0	19 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
71	c3getA_	Alignment	not modelled	100.0	15 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
72	d1fg7a_	Alignment	not modelled	100.0	17 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
73	c3cq6E_	Alignment	not modelled	100.0	19 PDB header: transferase Chain: E: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: histidinol-phosphate aminotransferase from corynebacterium2 glutamicum hol o-form (plp covalently bound)
74	d1lc5a_	Alignment	not modelled	100.0	16 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
75	c3ffhA_	Alignment	not modelled	100.0	18 PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of histidinol-phosphate aminotransferase from2 listeria innocua clip11262.
76	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
					PDB header: transferase

77	c3hdoB_	Alignment	not modelled	100.0	20	Chain: B: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
78	d2f8ja1	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
79	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
80	c3p1tB_	Alignment	not modelled	100.0	20	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	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SelA-like
82	d1vjoa_	Alignment	not modelled	100.0	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
83	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
84	c2hdyA_	Alignment	not modelled	100.0	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: selenocysteine lyase; PDBTitle: structure of human selenocysteine lyase
85	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
86	c3mc6C_	Alignment	not modelled	100.0	12	PDB header: lyase Chain: C: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of scdpl1
87	d1m6sa_	Alignment	not modelled	100.0	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
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	c3caiA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: possible aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv3778c2 protein
90	c3isiA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: purine catabolism protein pucg; PDBTitle: crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
91	d1qz9a_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
92	d1tpla_	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
93	c2eh6A_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase from aquifex2 aeolicus vf5
94	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
95	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
96	d1v72a1	Alignment	not modelled	100.0	8	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
97	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
98	d1gc0a_	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
99	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)
100	d1kl1a_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
101	c2dkjB_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of t.th.hb8 serine hydroxymethyltransferase
102	c2ordA_	Alignment	not modelled	100.0	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
103	c3a2bA_	Alignment	not modelled	100.0	13 PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
104	d1eg5a_	Alignment	not modelled	100.0	11 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
105	c2w8wA_	Alignment	not modelled	100.0	12 PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
106	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
107	d1vefa1	Alignment	not modelled	100.0	17 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
108	c2hzpA_	Alignment	not modelled	100.0	15 PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase
109	c2yrrA_	Alignment	not modelled	100.0	12 PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class v; PDBTitle: hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8
110	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
111	d1t3ia_	Alignment	not modelled	100.0	13 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
112	c2po3B_	Alignment	not modelled	100.0	13 PDB header: transferase Chain: B: PDB Molecule: 4-dehydrase; PDBTitle: crystal structure analysis of desi in the presence of its2 tdp-sugar product
113	c3nx3A_	Alignment	not modelled	100.0	13 PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase (argd) from2 campylobacter jejuni
114	d1jf9a_	Alignment	not modelled	100.0	13 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
115	d2ch1a1	Alignment	not modelled	100.0	10 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
116	c3lvmB_	Alignment	not modelled	100.0	14 PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of e.coli iscs
117	d1h0ca_	Alignment	not modelled	100.0	9 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
118	c3pj0D_	Alignment	not modelled	100.0	11 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	c3i4jC_	Alignment	not modelled	100.0	12 PDB header: transferase Chain: C: PDB Molecule: aminotransferase, class iii; PDBTitle: crystal structure of aminotransferase, class iii from2 deinococcus radiodurans
120	d1b9ha_	Alignment	not modelled	100.0	14 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like