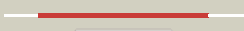
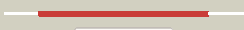


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dzzB_	 Alignment		100.0	30	PDB header: transferase Chain: B: PDB Molecule: putative pyridoxal 5'-phosphate-dependent c-s lyase; PDBTitle: crystal structure of a putative plp-dependent aminotransferase2 (lbul_1103) from lactobacillus delbrueckii subsp. at 1.61 a3 resolution
2	d1c7na_	 Alignment		100.0	27	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
3	c3l8aB_	 Alignment		100.0	29	PDB header: lyase Chain: B: PDB Molecule: putative aminotransferase, probable beta-cystathionase; PDBTitle: crystal structure of metc from streptococcus mutans
4	c1d2fB_	 Alignment		100.0	99	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
5	c3fdbA_	 Alignment		100.0	26	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
6	d1d2fa_	 Alignment		100.0	100	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
7	c3kaxB_	 Alignment		100.0	30	PDB header: lyase Chain: B: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative c-s lyase from bacillus anthracis
8	c3g0tA_	 Alignment		100.0	15	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
9	d2r5ea1	 Alignment		100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
10	c2o0rA_	 Alignment		100.0	19	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
11	d1xi9a_	 Alignment		100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like

12	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
13	c3e2yB_	Alignment		100.0	18	PDB header: transferase, lyase Chain: B: PDB Molecule: kynurenine-oxoglutarate transaminase 3; PDBTitle: crystal structure of mouse kynurenine aminotransferase iii in complex2 with glutamine
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	dlw7la_	Alignment		100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
16	dlu08a_	Alignment		100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
17	dlj32a_	Alignment		100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
18	clynuA_	Alignment		100.0	17	PDB header: lyase Chain: A: PDB Molecule: 1-aminocyclopropane-1-carboxylate synthase; PDBTitle: crystal structure of apple acc synthase in complex with l-vinylglycine
19	c3eibB_	Alignment		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
20	dliaya_	Alignment		100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
21	dlgdea_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
22	dlm7ya_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
23	c3if2B_	Alignment	not modelled	100.0	15	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
24	c3qguB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: l,l-diaminopimelate aminotransferase from chlamydomonas reinhardtii
25	c2o1bA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class i; PDBTitle: structure of aminotransferase from staphylococcus aureus
26	c3eleB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: amino transferase; PDBTitle: crystal structure of amino transferase (rer070207001803) from2 eubacterium rectale at 2.10 a resolution
27	dl04sa_	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
28	c3nraA_	Alignment	not modelled	100.0	16	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
29	d1bw0a_	Alignment	not modelled	100.0	15 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
30	d1b5pa_	Alignment	not modelled	100.0	18 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
31	c2zc0C_	Alignment	not modelled	100.0	15 PDB header: transferase Chain: C: PDB Molecule: alanine glyoxylate transaminase; PDBTitle: crystal structure of an archaeal alanine:glyoxylate aminotransferase
32	c3ihjA_	Alignment	not modelled	100.0	16 PDB header: transferase Chain: A: PDB Molecule: alanine aminotransferase 2; PDBTitle: human alanine aminotransferase 2 in complex with plp
33	c3pplB_	Alignment	not modelled	100.0	17 PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of an aspartate transaminase (ncgl0237, cgl0240)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.25 a3 resolution
34	c3jtxB_	Alignment	not modelled	100.0	18 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
35	c2x5dD_	Alignment	not modelled	100.0	19 PDB header: transferase Chain: D: PDB Molecule: probable aminotransferase; PDBTitle: crystal structure of a probable aminotransferase from2 pseudomonas aeruginosa
36	c3ezsB_	Alignment	not modelled	100.0	17 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
37	d1vp4a_	Alignment	not modelled	100.0	14 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
38	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
39	d2gb3a1	Alignment	not modelled	100.0	16 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
40	d1x0ma1	Alignment	not modelled	100.0	15 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
41	d1wsta1	Alignment	not modelled	100.0	16 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
42	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
43	c3tl8D_	Alignment	not modelled	100.0	14 PDB header: transferase Chain: D: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of aminotransferase from anaerococcus prevotii dsm2 20548.
44	c2z61A_	Alignment	not modelled	100.0	16 PDB header: transferase Chain: A: PDB Molecule: probable aspartate aminotransferase 2; PDBTitle: crystal structure of nj0684 from methanococcus jannaschii2 reveals its similarity in the active site to kynurenine3 aminotransferases
45	c2x5fB_	Alignment	not modelled	100.0	13 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
46	c3dydB_	Alignment	not modelled	100.0	16 PDB header: transferase Chain: B: PDB Molecule: tyrosine aminotransferase; PDBTitle: human tyrosine aminotransferase
47	c3pdxA_	Alignment	not modelled	100.0	16 PDB header: transferase Chain: A: PDB Molecule: tyrosine aminotransferase; PDBTitle: crystal structural of mouse tyrosine aminotransferase
48	c3dc1A_	Alignment	not modelled	100.0	13 PDB header: transferase Chain: A: PDB Molecule: kynurenine/alpha-aminoadipate aminotransferase PDBTitle: crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate
49	c3g7qA_	Alignment	not modelled	100.0	16 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
50	d2csta_	Alignment	not modelled	100.0	15 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
51	d1v2da_	Alignment	not modelled	100.0	20 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
52	c3ez1A_	Alignment	not modelled	100.0	13 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

53	d1ajsa_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
54	c3rq1A_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of aminotransferase class i and ii from veillonella2 parvula
55	c2zy3A_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: A: PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase
56	c3k7yA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: aspartate aminotransferase of plasmodium falciparum
57	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
58	d7aata_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
59	d2ay1a_	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
60	d2q7wa1	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
61	c3op7A_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of a plp-dependent aminotransferase (zp_03625122.1)2 from streptococcus suis 89-1591 at 1.70 a resolution
62	d1yaaa_	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
63	c3d6kB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: putative aminotransferase; PDBTitle: the crystal structure of a putative aminotransferase from2 corynebacterium diphtheriae
64	c3ly1C_	Alignment	not modelled	100.0	14	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
65	d1lc5a_	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
66	c3getA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: crystal structure of putative histidinol-phosphate aminotransferase2 (np_281508.1) from campylobacter jejuni at 2.01 a resolution
67	c3f6tA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of aspartate aminotransferase (e.c. 2.6.1.1)2 from lactobacillus acidophilus ncfm at 2.15 a3 resolution
68	c3cq6E_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: E: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound)
69	c3bwnF_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: F: PDB Molecule: l-tryptophan aminotransferase; PDBTitle: l-tryptophan aminotransferase
70	c3mebB_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase; PDBTitle: structure of cytoplasmic aspartate aminotransferase from giardia2 lamblia
71	d3tata_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
72	c3eucB_	Alignment	not modelled	100.0	13	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
73	d1fg7a_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
74	c3ftbA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of the histidinol-phosphate2 aminotransferase from clostridium acetobutylicum
75	c3hdoB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
76	d2f8ja1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
77	c3ffhA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of histidinol-phosphate aminotransferase from2 listeria innocua clip11262.
						Fold: PLP-dependent transferase-like

78	d2hoxa1	Alignment	not modelled	100.0	16	Superfamily: PLP-dependent transferases Family: AAT-like
79	c3fkdC	Alignment	not modelled	100.0	15	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
80	c3p1tB	Alignment	not modelled	100.0	14	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	9	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SelA-like
82	c3nnkC	Alignment	not modelled	100.0	10	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
83	c3f0hA	Alignment	not modelled	100.0	10	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
84	d1tpla	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
85	c3hqtB	Alignment	not modelled	100.0	13	PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cgsa
86	d1vjoa	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
87	c2dkjB	Alignment	not modelled	100.0	11	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of t.th.bh8 serine hydroxymethyltransferase
88	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
89	d1m6sa	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
90	d1v72a1	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
91	c2huuA	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: alanine glyoxylate aminotransferase; PDBTitle: crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine
92	c3islA	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: purine catabolism protein pucg; PDBTitle: crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
93	d1b9ha	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
94	c2ordA	Alignment	not modelled	100.0	12	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
95	c3a2bA	Alignment	not modelled	100.0	11	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
96	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
97	c2po3B	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: 4-dehydrase; PDBTitle: crystal structure analysis of desi in the presence of its2 tdp-sugar product
98	d1leg5a	Alignment	not modelled	100.0	7	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
99	d1svva	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
100	c2eh6A	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase from aquifex2 aeolicus vf5
101	d1kl1a	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
102	c3nx3A	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase (argd) from2 campylobacter jejuni
						PDB header: transferase

103	c3tqxA_	Alignment	not modelled	100.0	11	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
104	c2yrrA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class v; PDBTitle: hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8
105	d1bs0a_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
106	d1vefa1	Alignment	not modelled	100.0	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
107	c2w8wA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
108	d1h0ca_	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
109	d2ch1a1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
110	c3mc6C_	Alignment	not modelled	100.0	9	PDB header: lyase Chain: C: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of scdpl1
111	d2bwna1	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
112	d1fc4a_	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
113	d1dfoa_	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
114	c2dr1A_	Alignment	not modelled	100.0	10	PDB header: transferase Chain: A: PDB Molecule: 386aa long hypothetical serine aminotransferase; PDBTitle: crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
115	d1sffa_	Alignment	not modelled	100.0	10	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
116	d1jf9a_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
117	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
118	d1t3ia_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
119	d2cfba1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
120	d1c7ga_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases