







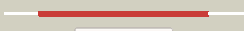















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jf9a_	 Alignment		100.0	100	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
2	d1t3ia_	 Alignment		100.0	48	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
3	c3caiA_	 Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: possible aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv3778c2 protein
4	c3e9kA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
5	d1qz9a_	 Alignment		100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
6	c2hzpA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase
7	d1elua_	 Alignment		100.0	25	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
8	d2c0ra1	 Alignment		100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
9	d1eg5a_	 Alignment		100.0	25	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
10	c3lvmB_	 Alignment		100.0	24	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of e.coli iscs
11	d1p3wa_	 Alignment		100.0	25	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like

12	c2hdyA_	Alignment		100.0	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: selenocysteine lyase; PDBTitle: structure of human selenocysteine lyase
13	d1w23a_	Alignment		100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
14	c3ffrA_	Alignment		100.0	15	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
15	c3nnkC_	Alignment		100.0	15	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
16	c3m5uA_	Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase; PDBTitle: crystal structure of phosphoserine aminotransferase from2 campylobacter jejuni
17	c3f0hA_	Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
18	d1bjna_	Alignment		100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
19	c3e77A_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase; PDBTitle: human phosphoserine aminotransferase in complex with plp
20	d2ch1a1	Alignment		100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
21	d1vjoa_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
22	d1h0ca_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
23	c3islA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: purine catabolism protein pucg; PDBTitle: crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
24	c2huuA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: alanine glyoxylate aminotransferase; PDBTitle: crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine
25	c2fyfB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: phosphoserine aminotransferase; PDBTitle: structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
26	c2dr1A_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: 386aa long hypothetical serine aminotransferase; PDBTitle: crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
27	c2z9wA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
28	c3qm2A_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase; PDBTitle: 2.25 angstrom crystal structure of phosphoserine aminotransferase2 (serc) from salmonella enterica subsp. enterica

					serovar typhimurium
29	d2bkwa1	Alignment	not modelled	100.0	15 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
30	c3mafB	Alignment	not modelled	100.0	18 PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (asymmetric form)
31	c2yrrA	Alignment	not modelled	100.0	15 PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class v; PDBTitle: hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8
32	d1wyua1	Alignment	not modelled	100.0	16 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
33	c3f9tB	Alignment	not modelled	100.0	17 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
34	d1js3a	Alignment	not modelled	100.0	15 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase
35	c2w8wA	Alignment	not modelled	100.0	18 PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
36	d1m32a	Alignment	not modelled	100.0	15 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
37	dliuga	Alignment	not modelled	100.0	15 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
38	c3hbxB	Alignment	not modelled	100.0	18 PDB header: lyase Chain: B: PDB Molecule: glutamate decarboxylase 1; PDBTitle: crystal structure of gad1 from arabidopsis thaliana
39	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)
40	c2jisA	Alignment	not modelled	100.0	16 PDB header: lyase Chain: A: PDB Molecule: cysteine sulfinic acid decarboxylase; PDBTitle: human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
41	c3bcxA	Alignment	not modelled	100.0	13 PDB header: transferase Chain: A: PDB Molecule: cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3- PDBTitle: e1 dehydrase
42	c3eucB	Alignment	not modelled	100.0	15 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
43	c3mc6C	Alignment	not modelled	100.0	15 PDB header: lyase Chain: C: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of scdpl1
44	c2ogeC	Alignment	not modelled	100.0	15 PDB header: transferase Chain: C: PDB Molecule: transaminase; PDBTitle: x-ray structure of s. venezuelae desv in its internal2 aldimine form
45	c3getA	Alignment	not modelled	100.0	14 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
46	c3cbfA	Alignment	not modelled	100.0	16 PDB header: transferase Chain: A: PDB Molecule: alpha-aminodipate aminotransferase; PDBTitle: crystal structure of lysn, alpha-aminoadipate2 aminotransferase, from thermus thermophilus hb27
47	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
48	c3ffhA	Alignment	not modelled	100.0	21 PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of histidinol-phosphate aminotransferase from2 listeria innocua clip11262.
49	c3uwCA	Alignment	not modelled	100.0	16 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
50	d1wyub1	Alignment	not modelled	100.0	17 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
51	c3k40B	Alignment	not modelled	100.0	11 PDB header: lyase Chain: B: PDB Molecule: aromatic-l-amino-acid decarboxylase; PDBTitle: crystal structure of drosophila 3,4-dihydroxyphenylalanine2 decarboxylase
52	c3ke3A	Alignment	not modelled	100.0	12 PDB header: transferase Chain: A: PDB Molecule: putative serine-pyruvate aminotransferase; PDBTitle: crystal structure of putative serine-pyruvate aminotransferase2 (yp_263484.1) from psychrobacter arcticum 273-4 at 2.20 a resolution
53	d1pmma	Alignment	not modelled	100.0	14 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase

54	c2c7tA_	Alignment	not modelled	100.0	14	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.
55	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
56	d1mdoa_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
57	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 burnetii
58	d1x0ma1	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
59	d1bs0a_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
60	d2bwna1	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
61	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
62	c2r0tA_	Alignment	not modelled	100.0	14	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
63	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
64	d1bw0a_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
65	c3ly1C_	Alignment	not modelled	100.0	13	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
66	c3dr4B_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: putative perosamine synthetase; PDBTitle: gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
67	c3ju7B_	Alignment	not modelled	100.0	15	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
68	d1kl1a_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
69	d1o69a_	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
70	d1b9ha_	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
71	c3cq6E_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: E: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound)
72	d1fg7a_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
73	c3hqtB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
74	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
75	d1fc4a_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
76	c3l8aB_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: B: PDB Molecule: putative aminotransferase, probable beta-cystathionase; PDBTitle: crystal structure of metc from streptococcus mutans
77	d1lc5a_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
78	c3frkB_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: B: PDB Molecule: qdtb; PDBTitle: x-ray structure of qdtb from t. thermosaccharolyticum in2 complex with a plp:tdp-3-aminoquinovose aldimine PDB header: transferase

79	c3h14A_	Alignment	not modelled	100.0	17	Chain: A: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
80	c2qmaB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: diaminobutyrate-pyruvate transaminase and l-2,4- PDBTitle: crystal structure of glutamate decarboxylase domain of2 diaminobutyrate-pyruvate transaminase and l-2,4-diaminobutyrate3 decarboxylase from vibrio parahaemolyticus
81	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
82	c3nysA_	Alignment	not modelled	100.0	16	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
83	c3g0tA_	Alignment	not modelled	100.0	14	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
84	c3eibB_	Alignment	not modelled	100.0	10	PDB header: transferase Chain: B: PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: crystal structure of k270n variant of ll-diaminopimelate2 aminotransferase from arabidopsis thaliana
85	d1xi9a_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
86	d2r5ea1	Alignment	not modelled	100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
87	d1v72a1	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
88	c2dkjB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of t.th.hb8 serine hydroxymethyltransferase
89	d1cs1a_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
90	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
91	c3b46B_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: aminotransferase bna3; PDBTitle: crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
92	d1j32a_	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
93	c3p1tB_	Alignment	not modelled	100.0	16	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
94	d2fnua1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
95	d1dfoa_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
96	d1o4sa_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
97	c2o1bA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class i; PDBTitle: structure of aminotransferase from staphylococcus aureus
98	c3pplB_	Alignment	not modelled	100.0	15	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
99	c3eleB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: amino transferase; PDBTitle: crystal structure of amino transferase (rer070207001803) from2 eubacterium rectale at 2.10 a resolution
100	c3dzzB_	Alignment	not modelled	100.0	13	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
101	d1c4ka2	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Ornithine decarboxylase major domain
102	d1v2da_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
103	d1vp4a_	Alignment	not modelled	100.0	9	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases

					Family: AAT-like
104	d1w7la_	Alignment	not modelled	100.0	14 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
105	c3fkdc_	Alignment	not modelled	100.0	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
106	d1wsta1	Alignment	not modelled	100.0	17 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
107	c3op7A_	Alignment	not modelled	100.0	16 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
108	d1qgna_	Alignment	not modelled	100.0	15 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
109	d1svva_	Alignment	not modelled	100.0	16 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
110	d1c7na_	Alignment	not modelled	100.0	14 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
111	c2douA_	Alignment	not modelled	100.0	17 PDB header: transferase Chain: A: PDB Molecule: probable n-succinyl diaminopimelate aminotransferase; PDBTitle: probable n-succinyl diaminopimelate aminotransferase (ttha0342) from2 thermus thermophilus hb8
112	c3dydB_	Alignment	not modelled	100.0	14 PDB header: transferase Chain: B: PDB Molecule: tyrosine aminotransferase; PDBTitle: human tyrosine aminotransferase
113	c2cb1A_	Alignment	not modelled	100.0	15 PDB header: lyase Chain: A: PDB Molecule: o-acetyl homoserine sulfhydrylase; PDBTitle: crystal structure of o-actetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
114	d1cl1a_	Alignment	not modelled	100.0	10 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
115	c3asaA_	Alignment	not modelled	100.0	16 PDB header: transferase Chain: A: PDB Molecule: II-di aminopimelate aminotransferase; PDBTitle: crystal structure of apo-II-di aminopimelate aminotransferase from2 chlamydia trachomatis
116	d1b5pa_	Alignment	not modelled	100.0	17 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
117	c3e2yB_	Alignment	not modelled	100.0	15 PDB header: transferase, lyase Chain: B: PDB Molecule: kynurenine-oxoglutarate transaminase 3; PDBTitle: crystal structure of mouse kynurenine aminotransferase iii in complex2 with glutamine
118	c3fdbA_	Alignment	not modelled	100.0	15 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
119	c3pdxA_	Alignment	not modelled	100.0	14 PDB header: transferase Chain: A: PDB Molecule: tyrosine aminotransferase; PDBTitle: crystal structural of mouse tyrosine aminotransferase
120	c1d2fB_	Alignment	not modelled	100.0	16 PDB header: transferase Chain: B: PDB Molecule: maly protein; PDBTitle: x-ray structure of maly from escherichia coli: a pyridoxal-5'-2 phosphate-dependent enzyme acting as a modulator in mal gene3 expression