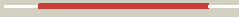























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pplB_	 Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of an aspartate transaminase (ncgl0237, cgl0240)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.25 a3 resolution
2	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
3	dlwsta1	 Alignment		100.0	25	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
4	dlvp4a_	 Alignment		100.0	22	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
5	dlx0ma1	 Alignment		100.0	27	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
6	c3dc1A_	 Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: kynurenine/alpha-aminoadipate aminotransferase PDBTitle: crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate
7	c3d6kB_	 Alignment		100.0	16	PDB header: transferase Chain: B: PDB Molecule: putative aminotransferase; PDBTitle: the crystal structure of a putative aminotransferase from2 corynebacterium diphtheriae
8	c3if2B_	 Alignment		100.0	19	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
9	c2zc0C_	 Alignment		100.0	23	PDB header: transferase Chain: C: PDB Molecule: alanine glyoxylate transaminase; PDBTitle: crystal structure of an archaeal alanine:glyoxylate aminotransferase
10	c2zy3A_	 Alignment		100.0	17	PDB header: lyase Chain: A: PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase
11	c2x5fB_	 Alignment		100.0	16	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

12	c1ynuA_	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
13	c3ihjA_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: alanine aminotransferase 2; PDBTitle: human alanine aminotransferase 2 in complex with plp
14	d1iaya_	Alignment		100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
15	d1m7ya_	Alignment		100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
16	d2r5ea1	Alignment		100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
17	c3qguB_	Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: l,l-diaminopimelate aminotransferase; PDBTitle: l,l-diaminopimelate aminotransferase from chlamydomonas reinhardtii
18	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
19	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
20	c3cbfA_	Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: alpha-aminodipate aminotransferase; PDBTitle: crystal structure of lysn, alpha-amino dipeptide2 aminotransferase, from thermus thermophilus hb27
21	c3f6tA_	Alignment	not modelled	100.0	14	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
22	d1w7la_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
23	c3eibB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: l,l-diaminopimelate aminotransferase; PDBTitle: crystal structure of k270n variant of l,l-diaminopimelate2 aminotransferase from arabidopsis thaliana
24	c3g7gA_	Alignment	not modelled	100.0	18	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
25	d1u08a_	Alignment	not modelled	100.0	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
26	c3h14A_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
27	d2gb3a1	Alignment	not modelled	100.0	22	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
28	c3dzzB_	Alignment	not modelled	100.0	16	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
29	c3b46B_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: aminotransferase bna3; PDBTitle: crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
30	c3jtxB_	Alignment	not modelled	100.0	19	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
31	c3l8aB_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: B: PDB Molecule: putative aminotransferase, probable beta-cystathionase; PDBTitle: crystal structure of metc from streptococcus mutans
32	c2o1bA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class i; PDBTitle: structure of aminotransferase from staphylococcus aureus
33	c3t18D_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: D: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of aminotransferase from anaerococcus prevotii dsm2 20548.
34	c3rq1A_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of aminotransferase class i and ii from veillonella2 parvula
35	c3eleB_	Alignment	not modelled	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
36	c2o0rA_	Alignment	not modelled	100.0	17	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
37	d2csta_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
38	d1xi9a_	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
39	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
40	d1bw0a_	Alignment	not modelled	100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
41	c3ezsB_	Alignment	not modelled	100.0	19	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
42	d1o4sa_	Alignment	not modelled	100.0	22	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
43	d1c7na_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
44	d1gdea_	Alignment	not modelled	100.0	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
45	c3nraA_	Alignment	not modelled	100.0	20	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
46	c3k7yA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: aspartate aminotransferase of plasmodium falciparum
47	d1j32a_	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
48	c3asaA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: II-diaminopimelate aminotransferase; PDBTitle: crystal structure of apo-II-diaminopimelate aminotransferase from2 chlamydia trachomatis
49	d1b5pa_	Alignment	not modelled	100.0	23	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
50	d2ay1a_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
51	d1yaaa_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
52	c2x5dD_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: D: PDB Molecule: probable aminotransferase; PDBTitle: crystal structure of a probable aminotransferase from2 pseudomonas aeruginosa
53	c3fdbA_	Alignment	not modelled	100.0	17	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 PDB header: lyase Chain: B: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative c-s lyase from bacillus anthracis
54	c3kaxB_	Alignment	not modelled	100.0	17
55	d1ajsa_	Alignment	not modelled	100.0	16
56	d7aata_	Alignment	not modelled	100.0	14
57	d2q7wa1	Alignment	not modelled	100.0	16
58	c3pdxA_	Alignment	not modelled	100.0	19
59	c3dydB_	Alignment	not modelled	100.0	20
60	d1v2da_	Alignment	not modelled	100.0	21
61	c1d2fB_	Alignment	not modelled	100.0	17
62	c3op7A_	Alignment	not modelled	100.0	21
63	c3mebB_	Alignment	not modelled	100.0	14
64	d3tata_	Alignment	not modelled	100.0	18
65	d1d2fa_	Alignment	not modelled	100.0	17
66	c3ly1C_	Alignment	not modelled	100.0	17
67	c2z61A_	Alignment	not modelled	100.0	23
68	c3eucB_	Alignment	not modelled	100.0	16
69	c3bwnF_	Alignment	not modelled	100.0	16
70	d1fg7a_	Alignment	not modelled	100.0	17
71	d2hoxa1	Alignment	not modelled	100.0	14
72	c3getA_	Alignment	not modelled	100.0	14
73	c3cq6E_	Alignment	not modelled	100.0	15
74	d1lc5a_	Alignment	not modelled	100.0	14
75	c3hdoB_	Alignment	not modelled	100.0	18
76	d2f8ja1	Alignment	not modelled	100.0	16
77	c3fkdC_	Alignment	not modelled	100.0	18
78	c3fthA_	Alignment	not modelled	100.0	15

78	c3fwa_	Alignment	not modelled	100.0	13	PDBTitle: the crystal structure of the histidinol-phosphate2 aminotransferase from clostridium acetobutylicum PDB header: transferase
79	c3ffhA_	Alignment	not modelled	100.0	15	Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of histidinol-phosphate aminotransferase from2 listeria innocua clip11262.
80	c3p1tB_	Alignment	not modelled	100.0	15	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	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
83	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
84	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
85	d1tpla_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
86	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
87	c3nnkC_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: C: PDB Molecule: ureidoglycine-glyoxylate aminotransferase; PDBTitle: biochemical and structural characterization of a ureidoglycine2 aminotransferase in the klebsiella pneumoniae uric acid catabolic3 pathway
88	d1v72a1	Alignment	not modelled	100.0	10	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
89	c3hqtB_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
90	c2huuA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: alanine glyoxylate aminotransferase; PDBTitle: crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine
91	d1m6sa_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
92	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
93	c3isiA_	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
94	c3a2bA_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
95	d2ch1a1	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
96	c3tqxA_	Alignment	not modelled	100.0	13	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
97	c2yrrA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class v; PDBTitle: hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8
98	c3mc6C_	Alignment	not modelled	100.0	12	PDB header: lyase Chain: C: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of scdpl1
99	c2hzpA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase
100	c3ffrA_	Alignment	not modelled	99.9	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
101	c2w8wA_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
102	d1dfoa_	Alignment	not modelled	99.9	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
						Fold: PLP-dependent transferase-like

103	d1svva_	Alignment	not modelled	99.9	12	Superfamily: PLP-dependent transferases Family: AAT-like
104	c2po3B_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: B: PDB Molecule: 4-dehydrase; PDBTitle: crystal structure analysis of desi in the presence of its2 tdp-sugar product
105	d1gc0a_	Alignment	not modelled	99.9	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
106	d1h0ca_	Alignment	not modelled	99.9	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
107	c2dkjB_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of t.th.hb8 serine hydroxymethyltransferase
108	d1iuga_	Alignment	not modelled	99.9	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
109	d1kl1a_	Alignment	not modelled	99.9	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
110	d1bs0a_	Alignment	not modelled	99.9	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
111	d1fc4a_	Alignment	not modelled	99.9	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
112	d1b9ha_	Alignment	not modelled	99.9	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
113	d2e7ja1	Alignment	not modelled	99.9	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-like
114	d1t3ia_	Alignment	not modelled	99.9	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
115	c3pj0D_	Alignment	not modelled	99.9	8	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
116	c3mafB_	Alignment	not modelled	99.9	14	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (asymmetric form)
117	d1jf9a_	Alignment	not modelled	99.9	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
118	d1m32a_	Alignment	not modelled	99.9	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
119	d2bwna1	Alignment	not modelled	99.9	10	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
120	c3lwsF_	Alignment	not modelled	99.9	9	PDB header: lyase Chain: F: PDB Molecule: aromatic amino acid beta-eliminating PDBTitle: crystal structure of putative aromatic amino acid beta-2 eliminating lyase/threonine aldolase. (yp_001813866.1) from3 exiguobacterium sp. 255-15 at 2.00 a resolution