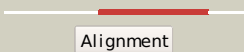

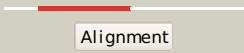



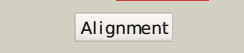



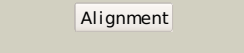

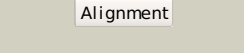

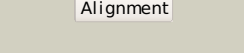



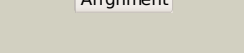

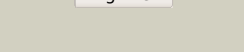












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wyub1	 Alignment		100.0	42	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
2	d1wyua1	 Alignment		100.0	31	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
3	d1ax4a_	 Alignment		100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
4	d3bc8a1	 Alignment		100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-like
5	c3hl2D_	 Alignment		100.0	17	PDB header: transferase Chain: D: PDB Molecule: o-phosphoseryl-trna(sec) selenium transferase; PDBTitle: the crystal structure of the human sepsecs-trnasec complex
6	c3mafB_	 Alignment		100.0	16	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (asymmetric form)
7	d1pmma_	 Alignment		100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase
8	c3hbxB_	 Alignment		100.0	14	PDB header: lyase Chain: B: PDB Molecule: glutamate decarboxylase 1; PDBTitle: crystal structure of gad1 from arabidopsis thaliana
9	c3f9tb_	 Alignment		100.0	18	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
10	c3mc6C_	 Alignment		100.0	14	PDB header: lyase Chain: C: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of scdpl1
11	d1c7ga_	 Alignment		100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases

12	d1ejia_	Alignment		100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
13	c2hzaA_	Alignment		100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase
14	c2jisA_	Alignment		100.0	15	PDB header: lyase Chain: A: PDB Molecule: cysteine sulfinic acid decarboxylase; PDBTitle: human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
15	d1bj4a_	Alignment		99.9	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
16	d2z67a1	Alignment		99.9	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-like
17	d1js3a_	Alignment		99.9	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase
18	c3e9kA_	Alignment		99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
19	d2v1pa1	Alignment		99.9	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
20	c2okkA_	Alignment		99.9	15	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)
21	d1rv3a_	Alignment	not modelled	99.9	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
22	d1jf9a_	Alignment	not modelled	99.9	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
23	c3ecdC_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase 2; PDBTitle: crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei
24	d1dfoa_	Alignment	not modelled	99.9	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
25	c2qmaB_	Alignment	not modelled	99.9	15	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
26	c2dkjB_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of t.th.hb8 serine hydroxymethyltransferase
27	d1c4ka2	Alignment	not modelled	99.9	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Ornithine decarboxylase major domain
28	c3k40B_	Alignment	not modelled	99.9	16	PDB header: lyase Chain: B: PDB Molecule: aromatic-l-amino-acid decarboxylase; PDBTitle: crystal structure of drosophila 3,4-dihydroxyphenylalanine2 decarboxylase

29	d1kl1a_	Alignment	not modelled	99.9	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
30	d1t3ia_	Alignment	not modelled	99.9	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
31	d1tpla_	Alignment	not modelled	99.8	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
32	d1qz9a_	Alignment	not modelled	99.8	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
33	d1vjoa_	Alignment	not modelled	99.8	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
34	c3h7fB_	Alignment	not modelled	99.8	22	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase 1; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 mycobacterium tuberculosis
35	c3caiA_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: possible aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv3778c2 protein
36	c3n0IA_	Alignment	not modelled	99.8	19	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
37	c3isIA_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: purine catabolism protein pucg; PDBTitle: crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
38	c3hmuA_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class iii; PDBTitle: crystal structure of a class iii aminotransferase from2 silicibacter pomeroyi
39	d1o69a_	Alignment	not modelled	99.8	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
40	d1bs0a_	Alignment	not modelled	99.8	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
41	d2ch1a1	Alignment	not modelled	99.8	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
42	d2bwna1	Alignment	not modelled	99.8	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
43	d1h0ca_	Alignment	not modelled	99.8	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
44	d1s0aa_	Alignment	not modelled	99.8	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
45	c3dodA_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 bacillus subtilis
46	c3bcxA_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3- PDBTitle: e1 dehydrase
47	c2w8wA_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
48	c3lv2A_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis 7,8-diaminopelargonic2 acid synthase in complex with substrate analog sinefungin
49	c3i4jC_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: C: PDB Molecule: aminotransferase, class iii; PDBTitle: crystal structure of aminotransferase, class iii from2 deinococcus radiodurans
50	c2dr1A_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: 386aa long hypothetical serine aminotransferase; PDBTitle: crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
51	d2e7ja1	Alignment	not modelled	99.8	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-like
52	c2z9wA_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
53	c2yrrA_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class v; PDBTitle: hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8
54	d1fc4a_	Alignment	not modelled	99.8	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases

						Family: GABA-aminotransferase-like
55	c2c7tA_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: glutamine-2-deoxy-scylo-inosose PDBTitle: crystal structure of the plp-bound form of btrr,2 a dual functional aminotransferase involved in butirosin3 biosynthesis.
56	c3nnkC_	Alignment	not modelled	99.8	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
57	d1mdoa_	Alignment	not modelled	99.8	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
58	c2po3B_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: B: PDB Molecule: 4-dehydrase; PDBTitle: crystal structure analysis of desi in the presence of its2 tdp-sugar product
59	c3f0hA_	Alignment	not modelled	99.8	12	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
60	c3a2bA_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
61	c2a7vA_	Alignment	not modelled	99.8	21	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: human mitochondrial serine hydroxymethyltransferase 2
62	d2a7va1	Alignment	not modelled	99.8	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
63	c2huuA_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: alanine glyoxylate aminotransferase; PDBTitle: crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine
64	c3dr4B_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: B: PDB Molecule: putative perosamine synthetase; PDBTitle: gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
65	c3tqxA_	Alignment	not modelled	99.8	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
66	c3lvmB_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of e.coli iscs
67	c2r0tA_	Alignment	not modelled	99.8	16	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
68	d1elua_	Alignment	not modelled	99.7	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
69	c3ffrA_	Alignment	not modelled	99.7	9	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
70	c3uwcA_	Alignment	not modelled	99.7	10	PDB header: transferase Chain: A: PDB Molecule: nucleotide-sugar aminotransferase; PDBTitle: strcture of an aminotransferase (degt-dnrj-eryc1-strs family) from2 coxiella burnetii in complex with pmp
71	c3hqtB_	Alignment	not modelled	99.7	14	PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
72	d2fnua1	Alignment	not modelled	99.7	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
73	d1b9ha_	Alignment	not modelled	99.7	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
74	c3n5mD_	Alignment	not modelled	99.7	15	PDB header: transferase Chain: D: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystals structure of a bacillus anthracis aminotransferase
75	d1p3wa_	Alignment	not modelled	99.7	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
76	c3a8uX_	Alignment	not modelled	99.7	17	PDB header: transferase Chain: X: PDB Molecule: omega-amino acid--pyruvate aminotransferase; PDBTitle: crystal structure of omega-amino acid:pyruvate aminotransferase
77	c3pj0D_	Alignment	not modelled	99.7	12	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
78	c3nx3A_	Alignment	not modelled	99.7	9	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase (argd) from2 campylobacter jejuni
						PDB header: transferase

79	c2ogeC	Alignment	not modelled	99.7	12	Chain: C: PDB Molecule: transaminase; PDBTitle: x-ray structure of s. venezuelae desv in its internal2 aldimine form
80	d2bkwa1	Alignment	not modelled	99.7	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
81	d1svva	Alignment	not modelled	99.7	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
82	c3bv0A	Alignment	not modelled	99.7	14	PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 mycobacterium tuberculosis
83	c3ke3A	Alignment	not modelled	99.7	15	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
84	d1m32a	Alignment	not modelled	99.7	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
85	d2cfba1	Alignment	not modelled	99.7	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
86	c2hdyA	Alignment	not modelled	99.7	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: selenocysteine lyase; PDBTitle: structure of human selenocysteine lyase
87	c2ordA	Alignment	not modelled	99.7	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
88	c3bs8A	Alignment	not modelled	99.6	18	PDB header: isomerase Chain: A: PDB Molecule: glutamate-1-semialdehyde 2,1-aminomutase; PDBTitle: crystal structure of glutamate 1-semialdehyde aminotransferase2 complexed with pyridoxamine-5'-phosphate from bacillus subtilis
89	c3frkB	Alignment	not modelled	99.6	14	PDB header: transferase Chain: B: PDB Molecule: qdtb; PDBTitle: x-ray structure of qdtb from t. thermosaccharolyticum in2 complex with a plp:tdp-3-aminoquinoxose aldimine
90	c3i5tB	Alignment	not modelled	99.6	15	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase prk07036 from rhodobacter2 sphaeroides kd131
91	c3ht4B	Alignment	not modelled	99.6	21	PDB header: lyase Chain: B: PDB Molecule: aluminum resistance protein; PDBTitle: crystal structure of the q81a77_baccr protein from bacillus2 cereus. northeast structural genomics consortium target3 bcr213
92	d1eg5a	Alignment	not modelled	99.6	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
93	c2x3lA	Alignment	not modelled	99.6	14	PDB header: lyase Chain: A: PDB Molecule: orn/lys/arg decarboxylase family protein; PDBTitle: crystal structure of the orn_lys_arg decarboxylase family2 protein sar0482 from methicillin-resistant staphylococcus3 aureus
94	c3ruyB	Alignment	not modelled	99.6	16	PDB header: transferase Chain: B: PDB Molecule: ornithine aminotransferase; PDBTitle: crystal structure of the ornithine-oxo acid transaminase rocd from2 bacillus anthracis
95	d2byla1	Alignment	not modelled	99.6	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
96	d1v72a1	Alignment	not modelled	99.6	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
97	c2cb1A	Alignment	not modelled	99.6	18	PDB header: lyase Chain: A: PDB Molecule: o-acetyl homoserine sulfhydrylase; PDBTitle: crystal structure of o-acetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
98	d1m6sa	Alignment	not modelled	99.6	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
99	c3fd0B	Alignment	not modelled	99.6	20	PDB header: lyase Chain: B: PDB Molecule: putative cystathionine beta-lyase involved in aluminum PDBTitle: crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_470671.1) from listeria innocua at 2.12 a3 resolution
100	c1oatB	Alignment	not modelled	99.6	16	PDB header: aminotransferase Chain: B: PDB Molecule: ornithine aminotransferase; PDBTitle: ornithine aminotransferase
101	c3nysA	Alignment	not modelled	99.6	13	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
102	c3nuiA	Alignment	not modelled	99.6	16	PDB header: transferase Chain: A: PDB Molecule: pyruvate transaminase; PDBTitle: crystal structure of omega-transferase from vibrio fluvialis js17

103	d2c0ra1	Alignment	not modelled	99.6	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
104	c2eh6A_	Alignment	not modelled	99.6	17	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase from aquifex2 aeolicus v5
105	c2pb2B_	Alignment	not modelled	99.6	13	PDB header: transferase Chain: B: PDB Molecule: acetylornithine/succinyldiaminopimelate aminotransferase; PDBTitle: structure of biosynthetic n-acetylornithine aminotransferase from2 salmonella typhimurium: studies on substrate specificity and3 inhibitor binding
106	c3l44A_	Alignment	not modelled	99.6	19	PDB header: isomerase Chain: A: PDB Molecule: glutamate-1-semialdehyde 2,1-aminomutase 1; PDBTitle: crystal structure of bacillus anthracis heml-1, glutamate semialdehyde2 aminotransferase
107	d1z7da1	Alignment	not modelled	99.6	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
108	d2gsaa_	Alignment	not modelled	99.6	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
109	c1c4kA_	Alignment	not modelled	99.6	16	PDB header: lyase Chain: A: PDB Molecule: protein (ornithine decarboxylase); PDBTitle: ornithine decarboxylase mutant (gly121tyr)
110	c2zsmA_	Alignment	not modelled	99.6	16	PDB header: isomerase Chain: A: PDB Molecule: glutamate-1-semialdehyde 2,1-aminomutase; PDBTitle: crystal structure of glutamate-1-semialdehyde 2,1-2 aminomutase from aeropyrum pernix, hexagonal form
111	d1w23a_	Alignment	not modelled	99.6	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
112	d1lc5a_	Alignment	not modelled	99.6	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
113	c3dxvA_	Alignment	not modelled	99.6	14	PDB header: isomerase Chain: A: PDB Molecule: alpha-amino-epsilon-caprolactam racemase; PDBTitle: the crystal structure of alpha-amino-epsilon-caprolactam racemase from2 achromobacter obae
114	d1qgna_	Alignment	not modelled	99.6	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
115	c2fyfB_	Alignment	not modelled	99.6	11	PDB header: transferase Chain: B: PDB Molecule: phosphoserine aminotransferase; PDBTitle: structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
116	d1zoda1	Alignment	not modelled	99.5	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
117	dliuga_	Alignment	not modelled	99.5	10	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
118	d1sffa_	Alignment	not modelled	99.5	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
119	dlibja_	Alignment	not modelled	99.5	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
120	c1ibjC_	Alignment	not modelled	99.5	18	PDB header: lyase Chain: C: PDB Molecule: cystathionine beta-lyase; PDBTitle: crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana