Phyre^2

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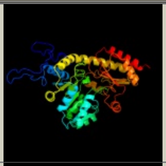
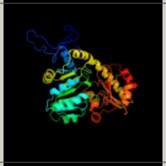
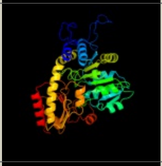
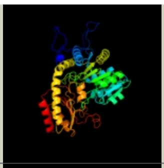
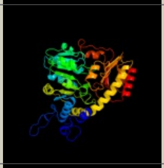
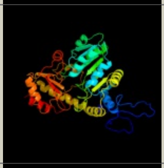
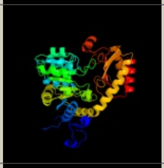
Description	P00935
Date	Wed Jan 25 15:20:10 GMT 2012
Unique Job ID	ccc038644b74c839

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1cs1a_	Alignment		100.0	100	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
2	c3ndnC_	Alignment		100.0	34	**PDB header:**lyase **Chain:** C: **PDB Molecule:**o-succinylhomoserine sulfhydrylase; **PDBTitle:** crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
3	d1qgna_	Alignment		100.0	34	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
4	c2nmpC_	Alignment		100.0	41	**PDB header:**lyase **Chain:** C: **PDB Molecule:**cystathionine gamma-lyase; **PDBTitle:** crystal structure of human cystathionine gamma lyase
5	d2ctza1	Alignment		100.0	33	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
6	d1y4ia1	Alignment		100.0	36	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
7	d1e5ea_	Alignment		100.0	37	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
8	c2cb1A_	Alignment		100.0	36	**PDB header:**lyase **Chain:** A: **PDB Molecule:**o-acetyl homoserine sulfhydrylase; **PDBTitle:** crystal structure of o-actetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
9	d1n8pa_	Alignment		100.0	38	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
10	c1i41J_	Alignment		100.0	34	**PDB header:**lyase **Chain:** J: **PDB Molecule:**cystathionine gamma-synthase; **PDBTitle:** cystathionine gamma-synthase in complex with the inhibitor2 appa
11	c1ibjC_	Alignment		100.0	39	**PDB header:**lyase **Chain:** C: **PDB Molecule:**cystathionine beta-lyase; **PDBTitle:** crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana

12	d1ibja_	Alignment		100.0	39	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
13	c2gqnB_	Alignment		100.0	31	**PDB header:**lyase **Chain:** B: **PDB Molecule:**cystathionine beta-lyase; **PDBTitle:** cystathionine beta-lyase (cbl) from escherichia coli in complex with2 n-hydrazinocarbonylmethyl-2-nitro-benzamide
14	d1cl1a_	Alignment		100.0	30	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
15	c3aemD_	Alignment		100.0	36	**PDB header:**lyase **Chain:** D: **PDB Molecule:**methionine gamma-lyase; **PDBTitle:** reaction intermediate structure of entamoeba histolytica methionine2 gamma-lyase 1 containing michaelis complex and methionine imine-3 pyridoxamine-5'-phosphate
16	c3qi6B_	Alignment		100.0	41	**PDB header:**lyase **Chain:** B: **PDB Molecule:**cystathionine gamma-synthase metb (cgs); **PDBTitle:** crystal structure of cystathionine gamma-synthase metb (cgs) from2 mycobacterium ulcerans agy99
17	c3e6gA_	Alignment		100.0	46	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cystathionine gamma-lyase-like protein; **PDBTitle:** crystal structure of xometc, a cystathionine c-lyase-like2 protein from xanthomonas oryzae pv.oryzae
18	d1gc0a_	Alignment		100.0	38	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
19	c3ri6A_	Alignment		100.0	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**o-acetylhomoserine sulfhydrylase; **PDBTitle:** a novel mechanism of sulfur transfer catalyzed by o-acetylhomoserine2 sulfhydrylase in methionine biosynthetic pathway of wolinella3 succinogenes
20	d1pffa_	Alignment		100.0	38	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
21	c3ht4B_	Alignment	not modelled	100.0	20	**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
22	c3hvyC_	Alignment	not modelled	100.0	20	**PDB header:**lyase **Chain:** C: **PDB Molecule:**cystathionine beta-lyase family protein, ynbb b.subtilis **PDBTitle:** crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_348457.1) from clostridium acetobutylicum at3 2.00 a resolution
23	c3fd0B_	Alignment	not modelled	100.0	17	**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
24	c3bcxA_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3- **PDBTitle:** e1 dehydrase
25	d1b9ha_	Alignment	not modelled	100.0	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
26	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
27	c2c7tA_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine-2-deoxy-scyllo-inosose **PDBTitle:** crystal structure of the plp-bound form of btrr,2 a dual functional aminotransferase involved in butirosin3 biosynthesis.

28	d1mdoa_	Alignment	not modelled	100.0	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
29	d1o69a_	Alignment	not modelled	100.0	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
30	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
31	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
32	c3caiA_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible aminotransferase; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv3778c2 protein
33	c2r0tA_	Alignment	not modelled	100.0	15	**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
34	c3ju7B_	Alignment	not modelled	100.0	12	**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
35	c3gwpA_	Alignment	not modelled	100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbon-sulfur lyase involved in aluminum resistance; **PDBTitle:** crystal structure of carbon-sulfur lyase involved in aluminum2 resistance (yp_878183.1) from clostridium novyi nt at 2.90 a3 resolution
36	c3uwcA_	Alignment	not modelled	100.0	12	**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
37	c3nysA_	Alignment	not modelled	100.0	14	**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
38	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
39	c3hqtB_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cai-1 autoinducer synthase; **PDBTitle:** plp-dependent acyl-coa transferase cqsa
40	c2w8wA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** n100y spt with plp-ser
41	d1jf9a_	Alignment	not modelled	100.0	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
42	c3a2bA_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
43	d2fnua1	Alignment	not modelled	100.0	10	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
44	d1qz9a_	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
45	d2bwna1	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
46	d1bs0a_	Alignment	not modelled	100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
47	c3e9kA_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**kynureninase; **PDBTitle:** crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
48	c3nnkC_	Alignment	not modelled	100.0	16	**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
49	d1vjoa_	Alignment	not modelled	100.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
50	d1dfoa_	Alignment	not modelled	100.0	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
51	c2hdyA_	Alignment	not modelled	100.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**selenocysteine lyase; **PDBTitle:** structure of human selenocysteine lyase
52	c3ecdC_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**serine hydroxymethyltransferase 2; **PDBTitle:** crystal structure of serine hydroxymethyltransferase

						from burkholderia2 pseudomallei
53	d1kl1a_	Alignment	not modelled	100.0	19	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
54	d2hoxa1	Alignment	not modelled	100.0	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
55	c3b46B_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain: B: PDB Molecule:**aminotransferase bna3; **PDBTitle:** crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
56	d1x0ma1	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
57	c2hzpA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain: A: PDB Molecule:**kynureninase; **PDBTitle:** crystal structure of homo sapiens kynureninase
58	c3h14A_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain: A: PDB Molecule:**aminotransferase, classes i and ii; **PDBTitle:** crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
59	c2dkjB_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain: B: PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of t.th.hb8 serine hydroxymethyltransferase
60	c3lwsF_	Alignment	not modelled	100.0	16	**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
61	c3f0hA_	Alignment	not modelled	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
62	d1w7la_	Alignment	not modelled	100.0	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
63	c3tqxA_	Alignment	not modelled	100.0	15	**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
64	d1fc4a_	Alignment	not modelled	100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
65	c1ynuA_	Alignment	not modelled	99.9	20	**PDB header:**lyase **Chain: A: PDB Molecule:**1-aminocyclopropane-1-carboxylate synthase; **PDBTitle:** crystal structure of apple acc synthase in complex with l-vinylglycine
66	c3hdoB_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain: B: PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
67	c3pplB_	Alignment	not modelled	99.9	13	**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
68	c3pj0D_	Alignment	not modelled	99.9	16	**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
69	c3islA_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain: A: PDB Molecule:**purine catabolism protein pucg; **PDBTitle:** crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
70	d2r5ea1	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
71	c3jtxB_	Alignment	not modelled	99.9	13	**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
72	c3ihjA_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain: A: PDB Molecule:**alanine aminotransferase 2; **PDBTitle:** human alanine aminotransferase 2 in complex with plp
73	d1m6sa_	Alignment	not modelled	99.9	20	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
74	d1t3ia_	Alignment	not modelled	99.9	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
75	c3dc1A_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain: A: PDB Molecule:**kynurenine/alpha-aminoadipate aminotransferase **PDBTitle:** crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate
76	c3mafB_	Alignment	not modelled	99.9	16	**PDB header:**lyase **Chain: B: PDB Molecule:**sphingosine-1-phosphate lyase; **PDBTitle:** crystal structure of stspl (asymmetric form)
77	d1wsta1	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
						PDB header:lyase

78	c3kaxB_	Alignment	not modelled	99.9	13	**Chain:** B: **PDB Molecule:**aminotransferase, classes i and ii; **PDBTitle:** crystal structure of a putative c-s lyase from bacillus anthracis
79	c2z9wA_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
80	c2dr1A_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**386aa long hypothetical serine aminotransferase; **PDBTitle:** crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
81	d1bw0a_	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
82	d1h0ca_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
83	c3op7A_	Alignment	not modelled	99.9	17	**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
84	c3e2yB_	Alignment	not modelled	99.9	14	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**kynurenine-oxoglutarate transaminase 3; **PDBTitle:** crystal structure of mouse kynurenine aminotransferase iii in complex2 with glutamine
85	d1c4ka2	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Ornithine decarboxylase major domain
86	d1iaya_	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
87	c3n0lA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
88	c3lvmB_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cysteine desulfurase; **PDBTitle:** crystal structure of e.coli iscs
89	c2zc0C_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**alanine glyoxylate transaminase; **PDBTitle:** crystal structure of an archaeal alanine:glyoxylate aminotransferase
90	c3if2B_	Alignment	not modelled	99.9	17	**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
91	d1m7ya_	Alignment	not modelled	99.9	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
92	c3nraA_	Alignment	not modelled	99.9	17	**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
93	d2ch1a1	Alignment	not modelled	99.9	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
94	c3eucB_	Alignment	not modelled	99.9	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
95	c3g7qA_	Alignment	not modelled	99.9	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
96	c3dzzB_	Alignment	not modelled	99.9	15	**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
97	c3ftbA_	Alignment	not modelled	99.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** the crystal structure of the histidinol-phosphate2 aminotransferase from clostridium acetobutylicum
98	d1tpla_	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
99	c3cbfA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-aminodipate aminotransferase; **PDBTitle:** crystal structure of lysn, alpha-aminoadipate2 aminotransferase, from thermus thermophilus hb27
100	c1d2fB_	Alignment	not modelled	99.9	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
101	c3hbxB_	Alignment	not modelled	99.9	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutamate decarboxylase 1; **PDBTitle:** crystal structure of gad1 from arabidopsis thaliana
						Fold:PLP-dependent transferase-like

102	d1j32a_	Alignment	not modelled	99.9	17	**Superfamily:**PLP-dependent transferases **Family:**AAT-like
103	c2huuA_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alanine glyoxylate aminotransferase; **PDBTitle:** crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine
104	c3l8aB_	Alignment	not modelled	99.9	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative aminotransferase, probable beta-cystathionase; **PDBTitle:** crystal structure of metc from streptococcus mutans
105	d1vp4a_	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
106	d1b5pa_	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
107	d1c7na_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
108	c2zy3A_	Alignment	not modelled	99.9	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-aspartate beta-decarboxylase; **PDBTitle:** dodecameric l-aspartate beta-decarboxylase
109	d1xi9a_	Alignment	not modelled	99.9	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
110	d2c0ra1	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
111	d1o4sa_	Alignment	not modelled	99.9	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
112	d1svva_	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
113	d1wyua1	Alignment	not modelled	99.9	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Glycine dehydrogenase subunits (GDC-P)
114	d1p3wa_	Alignment	not modelled	99.9	19	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
115	d1fg7a_	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
116	c2o0rA_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rv0858c (n-succinyldiaminopimelate aminotransferase); **PDBTitle:** the three-dimensional structure of n-succinyldiaminopimelate2 aminotransferase from mycobacterium tuberculosis
117	c3fdbA_	Alignment	not modelled	99.9	11	**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
118	c2x5fB_	Alignment	not modelled	99.9	15	**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
119	c3ez1A_	Alignment	not modelled	99.9	16	**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
120	c3mc6C_	Alignment	not modelled	99.9	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**sphingosine-1-phosphate lyase; **PDBTitle:** crystal structure of scdpl1