Phyre^2

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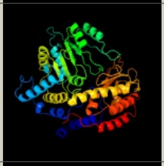
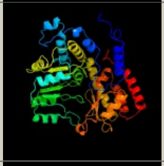
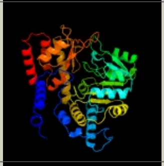
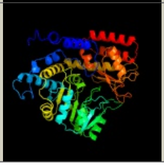
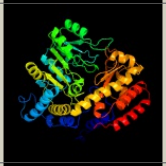
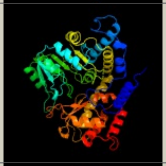
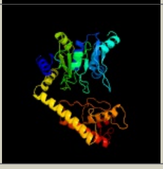
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h7fB_	Alignment		100.0	68	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase 1; **PDBTitle:** crystal structure of serine hydroxymethyltransferase from2 mycobacterium tuberculosis
2	d1ejia_	Alignment		100.0	47	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
3	d1bj4a_	Alignment		100.0	49	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
4	c3n0lA_	Alignment		100.0	51	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
5	c6cd1A_	Alignment		100.0	47	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of medicago truncatula serine2 hydroxymethyltransferase 3 (mtshmt3), complexes with reaction3 intermediates
6	d1rv3a_	Alignment		100.0	49	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
7	d2a7va1	Alignment		100.0	51	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
8	c2a7vA_	Alignment		100.0	51	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** human mitochondrial serine hydroxymethyltransferase 2
9	c4j5uB_	Alignment		100.0	54	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** x-ray crystal structure of a serine hydroxymethyltransferase with2 covalently bound plp from rickettsia rickettsii str. sheila smith
10	c4o6zC_	Alignment		100.0	39	**PDB header:**transferase **Chain:** C: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of serine hydroxymethyltransferase with covalently2 bound plp schiff-base from plasmodium falciparum
11	c4n0wA_	Alignment		100.0	56	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** x-ray crystal structure of a serine hydroxymethyltransferase from2 burkholderia cenocepacia with covalently attached pyridoxal phosphate

12	c5vc2A_	Alignment		100.0	47	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of a serine hydroxymethyltransferase from2 helicobacter pylori
13	c4wxfC_	Alignment		100.0	53	**PDB header:**transferase **Chain:** C: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of l-serine hydroxymethyltransferase in complex with2 glycine
14	c3ecdC_	Alignment		100.0	57	**PDB header:**transferase **Chain:** C: **PDB Molecule:**serine hydroxymethyltransferase 2; **PDBTitle:** crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei
15	d1dfoa_	Alignment		100.0	55	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
16	c2dkjB_	Alignment		100.0	60	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of t.th.hb8 serine hydroxymethyltransferase
17	c4bheI_	Alignment		100.0	30	**PDB header:**transferase **Chain:** I: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** methanococcus jannaschii serine hydroxymethyl-transferase2 in complex with plp
18	d1kl1a_	Alignment		100.0	58	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
19	c5z0yA_	Alignment		100.0	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystallization and structure determination of cytoplasm serine2 hydroxymethyltransferase (shmt) from pichia pastoris
20	c5fkzE_	Alignment		100.0	14	**PDB header:**lyase **Chain:** E: **PDB Molecule:**lysine decarboxylase, constitutive; **PDBTitle:** structure of e.coli constitutive lysine decarboxylase
21	c2vycA_	Alignment	not modelled	100.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**biodegradative arginine decarboxylase; **PDBTitle:** crystal structure of acid induced arginine decarboxylase2 from e. coli
22	c1c4kA_	Alignment	not modelled	100.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**protein (ornithine decarboxylase); **PDBTitle:** ornithine decarboxylase mutant (gly121tyr)
23	c5txtA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-aminolevulinate synthase, mitochondrial; **PDBTitle:** structure of asymmetric apo/holo alas dimer from s. cerevisiae
24	c3n75E_	Alignment	not modelled	100.0	15	**PDB header:**lyase **Chain:** E: **PDB Molecule:**lysine decarboxylase, inducible; **PDBTitle:** x-ray crystal structure of the escherichia coli inducible lysine2 decarboxylase ldci
25	d1c4ka2	Alignment	not modelled	100.0	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Ornithine decarboxylase major domain
26	c6hrhA_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5-aminolevulinate synthase, erythroid-specific, **PDBTitle:** structure of human erythroid-specific 5'-aminolevulinate synthase,2 alas2
27	c3bcxA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydrase; **PDBTitle:** e1 dehydrase
28	c5w70B_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l-glutamine:2-deoxy-scyllo-inosose aminotransferase;

						PDBTitle: x-ray structure of rbmb from streptomyces ribosidificus
29	c4k2bA_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ntd biosynthesis operon protein ntda; **PDBTitle:** crystal structure of ntda from bacillus subtilis in complex with the2 internal aldimine
30	c2w8wA_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** n100y spt with plp-ser
31	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
32	c2c7tA_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine-2-deoxy-scyllo-inosose aminotransferase; **PDBTitle:** crystal structure of the plp-bound form of btrr, a dual functional2 aminotransferase involved in butirosin biosynthesis.
33	c5k8bA_	Alignment	not modelled	100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**8-amino-3,8-dideoxy-alpha-d-manno-octulosonate **PDBTitle:** x-ray structure of kdna, 8-amino-3,8-dideoxy-alpha-d-manno-2 octulosonate transaminase, from shewanella oneidensis in the presence3 of the external aldimine with plp and glutamate
34	c4q6rB_	Alignment	not modelled	100.0	12	**PDB header:**lyase/lyase inhibitor **Chain:** B: **PDB Molecule:**sphingosine-1-phosphate lyase 1; **PDBTitle:** crystal structure of human sphingosine-1-phosphate lyase in complex2 with inhibitor 6-[(2r)-4-(4-benzyl-7-chlorophthalazin-1-yl)-2-3 methylpiperazin-1-yl]pyridine-3-carbonitrile
35	d1c7ga_	Alignment	not modelled	100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
36	c5k1rB_	Alignment	not modelled	100.0	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**burkholderia pseudomallei sphingosine-1-phosphate lyase **PDBTitle:** structure of burkholderia pseudomallei k96243 sphingosine-1-phosphate2 lyase bpss2021
37	d2v1pa1	Alignment	not modelled	100.0	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
38	c2ogeC_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**transaminase; **PDBTitle:** x-ray structure of s. venezuelae desv in its internal2 aldimine form
39	c2r0tA_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxamine 5-phosphate-dependent dehydrase; **PDBTitle:** crystal structure of gdp-4-keto-6-deoxymannose-3-dehydratase with a2 trapped plp-glutamate geminal diamine
40	d1bs0a_	Alignment	not modelled	100.0	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
41	d1tpla_	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
42	d1o69a_	Alignment	not modelled	100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
43	d1b9ha_	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
44	c2po3B_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-dehydrase; **PDBTitle:** crystal structure analysis of desi in the presence of its2 tdp-sugar product
45	d2bwna1	Alignment	not modelled	100.0	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
46	c3a2bA_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
47	c3nnkC_	Alignment	not modelled	100.0	18	**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
48	c3hbxB_	Alignment	not modelled	100.0	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutamate decarboxylase 1; **PDBTitle:** crystal structure of gad1 from arabidopsis thaliana
49	c3wy7D_	Alignment	not modelled	100.0	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**8-amino-7-oxononanoate synthase; **PDBTitle:** crystal structure of mycobacterium smegmatis 7-keto-8-aminopelargonic2 acid (kapa) synthase biof
50	d1mdoa_	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
51	c4qgrA_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**degt/dnrj/eryc1/strs aminotransferase; **PDBTitle:** crystal structure of a degt dnrj eryc1 strs aminotransferase from2 brucella abortus
52	d1vjoa_	Alignment	not modelled	100.0	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
						Fold:PLP-dependent transferase-like

53	d1wyub1	Alignment	not modelled	100.0	17	**Superfamily:**PLP-dependent transferases **Family:**Glycine dehydrogenase subunits (GDC-P)
54	c2x3lA_	Alignment	not modelled	100.0	12	**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
55	c3nysA_	Alignment	not modelled	100.0	17	**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
56	c2cb1A_	Alignment	not modelled	100.0	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**o-acetyl homoserine sulfhydrylase; **PDBTitle:** crystal structure of o-actetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
57	d2fnua1	Alignment	not modelled	100.0	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
58	c3mafB_	Alignment	not modelled	100.0	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**sphingosine-1-phosphate lyase; **PDBTitle:** crystal structure of stspl (asymmetric form)
59	d1qgna_	Alignment	not modelled	100.0	19	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
60	c3tqxA_	Alignment	not modelled	100.0	19	**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
61	c3madA_	Alignment	not modelled	100.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**sphingosine-1-phosphate lyase; **PDBTitle:** crystal structure of stspl (symmetric form)
62	c3aemD_	Alignment	not modelled	100.0	17	**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
63	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
64	d1m6sa_	Alignment	not modelled	100.0	19	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
65	d1jf9a_	Alignment	not modelled	100.0	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
66	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
67	c3frkB_	Alignment	not modelled	100.0	15	**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
68	c3wgcB_	Alignment	not modelled	100.0	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**l-allo-threonine aldolase; **PDBTitle:** aeromonas jandaei l-allo-threonine aldolase h128y/s292r double mutant
69	c3uwcA_	Alignment	not modelled	100.0	14	**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
70	d1h0ca_	Alignment	not modelled	100.0	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
71	c5dx5B_	Alignment	not modelled	100.0	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**methionine gamma-lyase; **PDBTitle:** crystal structure of methionine gamma-lyase from clostridium2 sporogenes
72	c3dr4B_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative perosamine synthetase; **PDBTitle:** gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
73	c5gp4C_	Alignment	not modelled	100.0	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**glutamate decarboxylase; **PDBTitle:** lactobacillus brevis cgmcc 1306 glutamate decarboxylase
74	d2ctza1	Alignment	not modelled	100.0	20	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
75	c4xauG_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** G: **PDB Molecule:**putative aminotransferase; **PDBTitle:** crystal structure of ats13 from actinomadura melliaura
76	c4oc9N_	Alignment	not modelled	100.0	15	**PDB header:**lyase **Chain:** N: **PDB Molecule:**putative o-acetylhomoserine (thiol)-lyase; **PDBTitle:** 2.35 angstrom resolution crystal structure of putative o-2 acetylhomoserine (thiol)-lyase (mety) from campylobacter jejuni3 subsp. jejuni nctc 11168 with n'-pyridoxyl-lysine-5'-monophosphate at4 position 205
77	c4j8lA_	Alignment	not modelled	100.0	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yhfs; **PDBTitle:** crystal structure of the pyridoxal-5'-phosphate dependent protein yhfs2 from escherichia coli
78	c3mc6C_	Alignment	not modelled	99.9	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**sphingosine-1-phosphate lyase;

						PDBTitle: crystal structure of scdpl1
79	c5u20C_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**putative aminotransferase; **PDBTitle:** x-ray structure of the wlarg aminotransferase from campylobacter2 jejuni, internal plp-aldimine
80	c3hvyC_	Alignment	not modelled	99.9	21	**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
81	c3ndnC_	Alignment	not modelled	99.9	21	**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
82	d1fc4a_	Alignment	not modelled	99.9	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
83	d2ch1a1	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
84	c4ritB_	Alignment	not modelled	99.9	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**pyridoxal-dependent decarboxylase; **PDBTitle:** the yellow crystal structure of pyridoxal-dependent decarboxylase from2 sphaerobacter thermophilus dsm 20745
85	d3bc8a1	Alignment	not modelled	99.9	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SepSecS-like
86	d1wyua1	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Glycine dehydrogenase subunits (GDC-P)
87	d1y4ia1	Alignment	not modelled	99.9	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
88	c6enzA_	Alignment	not modelled	99.9	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**acidic amino acid decarboxylase gadl1; **PDBTitle:** crystal structure of mouse gadl1
89	d1pmma_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Pyridoxal-dependent decarboxylase
90	c2jisA_	Alignment	not modelled	99.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cysteine sulfinic acid decarboxylase; **PDBTitle:** human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
91	c3zrrB_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine-pyruvate aminotransferase (agxt); **PDBTitle:** crystal structure and substrate specificity of a thermophilic2 archaeal serine : pyruvate aminotransferase from sulfolobus3 solfataricus
92	c3fd0B_	Alignment	not modelled	99.9	16	**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
93	c4obuG_	Alignment	not modelled	99.9	15	**PDB header:**lyase **Chain:** G: **PDB Molecule:**pyridoxal-dependent decarboxylase domain protein; **PDBTitle:** ruminococcus gnavus tryptophan decarboxylase rumgna_01526 (apo)
94	c3ju7B_	Alignment	not modelled	99.9	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
95	c1i41J_	Alignment	not modelled	99.9	19	**PDB header:**lyase **Chain:** J: **PDB Molecule:**cystathionine gamma-synthase; **PDBTitle:** cystathionine gamma-synthase in complex with the inhibitor2 appa
96	c2huuA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alanine glyoxylate aminotransferase; **PDBTitle:** crystal structure of aedes aegypti alanine glyoxylate aminotransferase2 in complex with alanine
97	c4e1oC_	Alignment	not modelled	99.9	12	**PDB header:**lyase **Chain:** C: **PDB Molecule:**histidine decarboxylase; **PDBTitle:** human histidine decarboxylase complex with histidine methyl ester2 (hme)
98	c4lc3B_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative udp-4-amino-4-deoxy-l-arabinose--oxoglutarate **PDBTitle:** x-ray crystal structure of a putative udp-4-amino-4-deoxy-l-arabinose-2 -oxoglutarate aminotransferase from burkholderia cenocepacia
99	c3f9tB_	Alignment	not modelled	99.9	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
100	d1cl1a_	Alignment	not modelled	99.9	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
101	c2dr1A_	Alignment	not modelled	99.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**386aa long hypothetical serine aminotransferase; **PDBTitle:** crystal structure of the ph1308 protein from pyrococcus horikoshii ot3

102	c2okkA_	Alignment	not modelled	99.9	14	**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)
103	d1js3a_	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Pyridoxal-dependent decarboxylase
104	c6ewqA_	Alignment	not modelled	99.9	13	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative capsular polysaccharide biosynthesis protein; **PDBTitle:** putative sugar aminotransferase spr1654 from streptococcus pneumoniae,2 plp-form
105	c6jrlA_	Alignment	not modelled	99.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3,4-dihydroxyphenylacetaldehyde synthase; **PDBTitle:** crystal structure of drosophila alpha methyldopa-resistant protein/3,2 4-dihydroxyphenylacetaldehyde synthase
106	c5ijgB_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cys/met metabolism pyridoxal-phosphate-dependent enzyme; **PDBTitle:** crystal structure of o-acetylhomoserine sulfhydrolase from brucella2 melitensis at 2.0 a resolution
107	c3f0hA_	Alignment	not modelled	99.9	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
108	d1cs1a_	Alignment	not modelled	99.9	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
109	c5x5hA_	Alignment	not modelled	99.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cystathionine beta-lyases/cystathionine gamma-synthases; **PDBTitle:** crystal strcuture of metb from corynebacterium glutamicum
110	c4lnjA_	Alignment	not modelled	99.9	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**low-specificity l-threonine aldolase; **PDBTitle:** structure of escherichia coli threonine aldolase in unliganded form
111	c5j8qA_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cysteine desulfurase sufs; **PDBTitle:** crystal structure of the cysteine desulfurase sufs of bacillus2 subtilis
112	c3qi6B_	Alignment	not modelled	99.9	20	**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
113	c3b1dD_	Alignment	not modelled	99.9	14	**PDB header:**lyase **Chain:** D: **PDB Molecule:**betac-s lyase; **PDBTitle:** crystal structure of betac-s lyase from streptococcus anginosus in2 complex with l-serine: external aldimine form
114	c2gqnB_	Alignment	not modelled	99.9	16	**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
115	c3l8aB_	Alignment	not modelled	99.9	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative aminotransferase, probable beta-cystathionase; **PDBTitle:** crystal structure of metc from streptococcus mutans
116	c4xk1A_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** crystal structure of a phosphoserine/phosphohydroxythreonine2 aminotransferase (psat) from pseudomonas aeruginosa with cofactor3 pyridoxal phosphate and bound glutamate
117	c4q31A_	Alignment	not modelled	99.9	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cystathione gamma lyase cale6; **PDBTitle:** the crystal structure of cystathione gamma lyase (cale6) from2 micromonospora echinospora
118	c3hl2D_	Alignment	not modelled	99.9	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**o-phosphoseryl-trna(sec) selenium transferase; **PDBTitle:** the crystal structure of the human sepsecs-trnasec complex
119	c2nmpC_	Alignment	not modelled	99.9	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**cystathionine gamma-lyase; **PDBTitle:** crystal structure of human cystathionine gamma lyase
120	d1c7na_	Alignment	not modelled	99.9	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like