Phyre2

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Description	P12995
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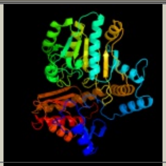
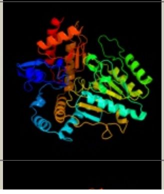
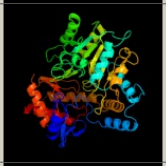
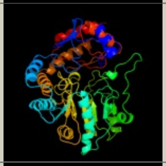
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1s0aa_	Alignment		100.0	98	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
2	c3fcrA_	Alignment		100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative aminotransferase; **PDBTitle:** crystal structure of putative aminotransferase (yp_614685.1) from2 silicibacter sp. tm1040 at 1.80 a resolution
3	c3lv2A_	Alignment		100.0	50	**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
4	c3hmuA_	Alignment		100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase, class iii; **PDBTitle:** crystal structure of a class iii aminotransferase from2 silicibacter pomeroyi
5	c3n5mD_	Alignment		100.0	31	**PDB header:**transferase **Chain:** D: **PDB Molecule:**adenosylmethionine-8-amino-7-oxononanoate aminotransferase; **PDBTitle:** crystals structure of a bacillus anthracis aminotransferase
6	c3i5tB_	Alignment		100.0	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase prk07036 from rhodobacter2 sphaeroides kd131
7	c3bv0A_	Alignment		100.0	50	**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
8	c3a8uX_	Alignment		100.0	29	**PDB header:**transferase **Chain:** X: **PDB Molecule:**omega-amino acid--pyruvate aminotransferase; **PDBTitle:** crystal structure of omega-amino acid:pyruvate aminotransferase
9	d1ohwa_	Alignment		100.0	20	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
10	c3oksB_	Alignment		100.0	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-aminobutyrate transaminase; **PDBTitle:** crystal structure of 4-aminobutyrate transaminase from mycobacterium2 smegmatis
11	c2cjdA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**l-lysine-epsilon aminotransferase; **PDBTitle:** lysine aminotransferase from m. tuberculosis in external2 aldimine form

12	c2eo5A_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**419aa long hypothetical aminotransferase; **PDBTitle:** crystal structure of 4-aminobutyrate aminotransferase from sulfolobus2 tokodaii strain7
13	d1zoda1	Alignment		100.0	23	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
14	c3dodA_	Alignment		100.0	33	**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
15	c2e7uA_	Alignment		100.0	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate-1-semialdehyde 2,1-aminomutase; **PDBTitle:** crystal structure of glutamate-1-semialdehyde 2,1-aminomutase from2 thermus thermophilus hb8
16	c3nuiA_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate transaminase; **PDBTitle:** crystal structure of omega-transferase from vibrio fluvialis js17
17	c3bs8A_	Alignment		100.0	23	**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
18	d1sffa_	Alignment		100.0	28	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
19	d2gsaa_	Alignment		100.0	23	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
20	c3dxvA_	Alignment		100.0	28	**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
21	d2byla1	Alignment	not modelled	100.0	27	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
22	c1oatB_	Alignment	not modelled	100.0	28	**PDB header:**aminotransferase **Chain:** B: **PDB Molecule:**ornithine aminotransferase; **PDBTitle:** ornithine aminotransferase
23	c3ruyB_	Alignment	not modelled	100.0	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ornithine aminotransferase; **PDBTitle:** crystal structure of the ornithine-oxo acid transaminase rocd from2 bacillus anthracis
24	c2zsmA_	Alignment	not modelled	100.0	22	**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
25	c2ordA_	Alignment	not modelled	100.0	28	**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
26	c3l44A_	Alignment	not modelled	100.0	21	**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
27	d1z7da1	Alignment	not modelled	100.0	27	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
28	d1vefa1	Alignment	not modelled	100.0	32	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like

29	c1z7dE_	Alignment	not modelled	100.0	27	**PDB header:**transferase **Chain:** E: **PDB Molecule:**ornithine aminotransferase; **PDBTitle:** ornithine aminotransferase py00104 from plasmodium yoelii
30	c2pb2B_	Alignment	not modelled	100.0	30	**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
31	c3nx3A_	Alignment	not modelled	100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylornithine aminotransferase; **PDBTitle:** crystal structure of acetylornithine aminotransferase (argd) from2 campylobacter jejuni
32	c3i4jC_	Alignment	not modelled	100.0	28	**PDB header:**transferase **Chain:** C: **PDB Molecule:**aminotransferase, class iii; **PDBTitle:** crystal structure of aminotransferase, class iii from2 deinococcus radiodurans
33	c2cy8A_	Alignment	not modelled	100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**d-phenylglycine aminotransferase; **PDBTitle:** crystal structure of d-phenylglycine aminotransferase (d-phgat) from2 pseudomonas strutzeri st-201
34	c2eh6A_	Alignment	not modelled	100.0	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylornithine aminotransferase; **PDBTitle:** crystal structure of acetylornithine aminotransferase from aquifex2 aeolicus vf5
35	d2cfba1	Alignment	not modelled	100.0	27	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
36	c2w8wA_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** n100y spt with plp-ser
37	c3a2bA_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
38	d1fc4a_	Alignment	not modelled	100.0	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
39	d2bwna1	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
40	d1bs0a_	Alignment	not modelled	100.0	19	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
41	c3tqxA_	Alignment	not modelled	100.0	14	**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
42	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
43	c3pj0D_	Alignment	not modelled	100.0	13	**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
44	c3ke3A_	Alignment	not modelled	100.0	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
45	d1m6sa_	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
46	d1c7ga_	Alignment	not modelled	100.0	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
47	d1qz9a_	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
48	d1svva_	Alignment	not modelled	100.0	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
49	d1wyub1	Alignment	not modelled	100.0	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Glycine dehydrogenase subunits (GDC-P)
50	d1tpla_	Alignment	not modelled	100.0	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
51	d1wsta1	Alignment	not modelled	100.0	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
52	c3lwsF_	Alignment	not modelled	100.0	15	**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
53	d1v72a1	Alignment	not modelled	100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
						Fold:PLP-dependent transferase-like

54	d1ax4a_	Alignment	not modelled	100.0	14	**Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
55	c3mafB_	Alignment	not modelled	100.0	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**sphingosine-1-phosphate lyase; **PDBTitle:** crystal structure of stspl (asymmetric form)
56	c3f9tB_	Alignment	not modelled	100.0	12	**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
57	d1x0ma1	Alignment	not modelled	100.0	8	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
58	c2hzpA_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**kynureninase; **PDBTitle:** crystal structure of homo sapiens kynureninase
59	d2v1pa1	Alignment	not modelled	100.0	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
60	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
61	d1lc5a_	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
62	d1wyua1	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Glycine dehydrogenase subunits (GDC-P)
63	c2ogeC_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**transaminase; **PDBTitle:** x-ray structure of s. venezuelae desv in its internal2 aldimine form
64	c2hdyA_	Alignment	not modelled	99.9	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**selenocysteine lyase; **PDBTitle:** structure of human selenocysteine lyase
65	d1js3a_	Alignment	not modelled	99.9	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Pyridoxal-dependent decarboxylase
66	d1jf9a_	Alignment	not modelled	99.9	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
67	d1c7na_	Alignment	not modelled	99.9	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
68	d1xi9a_	Alignment	not modelled	99.9	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
69	d1o4sa_	Alignment	not modelled	99.9	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
70	d1eg5a_	Alignment	not modelled	99.9	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
71	c2zc0C_	Alignment	not modelled	99.9	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**alanine glyoxylate transaminase; **PDBTitle:** crystal structure of an archaeal alanine:glyoxylate aminotransferase
72	c2x5dD_	Alignment	not modelled	99.9	9	**PDB header:**transferase **Chain:** D: **PDB Molecule:**probable aminotransferase; **PDBTitle:** crystal structure of a probable aminotransferase from2 pseudomonas aeruginosa
73	c2dkjB_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of t.th.hb8 serine hydroxymethyltransferase
74	c3ftbA_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** the crystal structure of the histidinol-phosphate2 aminotransferase from clostridium acetobutylicum
75	d1elua_	Alignment	not modelled	99.9	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
76	d1b5pa_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
77	d1kl1a_	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
78	c2dr1A_	Alignment	not modelled	99.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**386aa long hypothetical serine aminotransferase; **PDBTitle:** crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
79	c3cbfA_	Alignment	not modelled	99.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-aminodipate aminotransferase; **PDBTitle:** crystal structure of lysn, alpha-aminoadipate2 aminotransferase, from thermus thermophilus hb27
80	c2douA_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable n-succinyldiaminopimelate aminotransferase;

						PDBTitle: probable n-succinyldiaminopimelate aminotransferase (ttha0342) from2 thermus thermophilus hb8
81	c3kaxB_	Alignment	not modelled	99.9	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aminotransferase, classes i and ii; **PDBTitle:** crystal structure of a putative c-s lyase from bacillus anthracis
82	d1j32a_	Alignment	not modelled	99.9	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
83	c3l8aB_	Alignment	not modelled	99.9	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative aminotransferase, probable beta-cystathionase; **PDBTitle:** crystal structure of metc from streptococcus mutans
84	c3getA_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of putative histidinol-phosphate aminotransferase2 (np_281508.1) from campylobacter jejuni at 2.01 a resolution
85	c3qguB_	Alignment	not modelled	99.9	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ll-diaminopimelate aminotransferase; **PDBTitle:** l,l-diaminopimelate aminotransferase from chalmydomonas reinhardtii
86	c3caiA_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible aminotransferase; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv3778c2 protein
87	d1t3ia_	Alignment	not modelled	99.9	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
88	c3jtxB_	Alignment	not modelled	99.9	9	**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
89	d1vp4a_	Alignment	not modelled	99.9	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
90	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
91	c3op7A_	Alignment	not modelled	99.9	10	**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
92	c3lvmB_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cysteine desulfurase; **PDBTitle:** crystal structure of e.coli iscs
93	c3eibB_	Alignment	not modelled	99.9	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ll-diaminopimelate aminotransferase; **PDBTitle:** crystal structure of k270n variant of ll-diaminopimelate2 aminotransferase from arabidopsis thaliana
94	c3dc1A_	Alignment	not modelled	99.9	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**kynurenine/alpha-aminoadipate aminotransferase **PDBTitle:** crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate
95	c3k40B_	Alignment	not modelled	99.9	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aromatic-l-amino-acid decarboxylase; **PDBTitle:** crystal structure of drosophila 3,4-dihydroxyphenylalanine2 decarboxylase
96	c3nysA_	Alignment	not modelled	99.9	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
97	c3hdoB_	Alignment	not modelled	99.9	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
98	c2okkA_	Alignment	not modelled	99.9	11	**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)
99	c3fkdC_	Alignment	not modelled	99.9	12	**PDB header:**lyase **Chain:** C: **PDB Molecule:**l-threonine-o-3-phosphate decarboxylase; **PDBTitle:** the crystal structure of l-threonine-o-3-phosphate2 decarboxylase from porphyromonas gingivalis
100	d1d2fa_	Alignment	not modelled	99.9	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
101	c3pdxA_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine aminotransferase; **PDBTitle:** crystal structural of mouse tyrosine aminotransferase
102	c3dr4B_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative perosamine synthetase; **PDBTitle:** gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
103	c2jisA_	Alignment	not modelled	99.9	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cysteine sulfinic acid decarboxylase; **PDBTitle:** human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
104	c3uwcA_	Alignment	not modelled	99.9	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

105	d1v2da_	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
106	c1d2fB_	Alignment	not modelled	99.9	12	**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
107	d1o69a_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
108	d2fnua1	Alignment	not modelled	99.9	9	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
109	d1mdoa_	Alignment	not modelled	99.9	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
110	c3frkB_	Alignment	not modelled	99.9	12	**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
111	c3dzzB_	Alignment	not modelled	99.9	11	**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
112	d1b9ha_	Alignment	not modelled	99.9	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
113	d1p3wa_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
114	c3mc6C_	Alignment	not modelled	99.9	10	**PDB header:**lyase **Chain:** C: **PDB Molecule:**sphingosine-1-phosphate lyase; **PDBTitle:** crystal structure of scdpl1
115	d1vjoa_	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
116	c3nraA_	Alignment	not modelled	99.9	15	**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
117	d2f8ja1	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
118	c3ly1C_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**putative histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of putative histidinol-phosphate aminotransferase2 (yp_050345.1) from erwinia carotovora atroseptica scri1043 at 1.80 a3 resolution
119	c2r0tA_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxamine 5-phosphate-dependent dehydrase; **PDBTitle:** crystal srtucture of gdp-4-keto-6-deoxymannose-3-dehydratase2 with a trapped plp-glutamate geminal diamine
120	c3cq6E_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** E: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound)