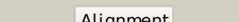
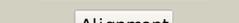
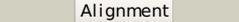
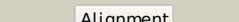
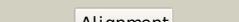
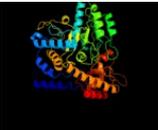
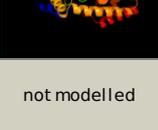


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P69908
Date	Thu Jan 5 12:12:17 GMT 2012
Unique Job ID	b3826c17add934fa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1pmma_</a>	 Alignment		100.0	99	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Pyri doxal-dependent decarboxylase
2	<a href="#">c3hbxB_</a>	 Alignment		100.0	45	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate decarboxylase 1; <b>PDBTitle:</b> crystal structure of gad1 from arabidopsis thaliana
3	<a href="#">c2qmaB_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> diaminobutyrate-pyruvate transaminase and l-2,4- <b>PDBTitle:</b> crystal structure of glutamate decarboxylase domain of 2 diaminobutyrate-pyruvate transaminase and l-2,4-diaminobutyrate3 decarboxylase from vibrio parahaemolyticus
4	<a href="#">d1js3a_</a>	 Alignment		100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Pyri doxal-dependent decarboxylase
5	<a href="#">c2jisA_</a>	 Alignment		100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine sulfinic acid decarboxylase; <b>PDBTitle:</b> human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
6	<a href="#">c2okkA_</a>	 Alignment		100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate decarboxylase 2; <b>PDBTitle:</b> the x-ray crystal structure of the 65kda isoform of glutamic acid2 decarboxylase (gad65)
7	<a href="#">c3k40B_</a>	 Alignment		100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> aromatic l-amino-acid decarboxylase; <b>PDBTitle:</b> crystal structure of drosophila 3,4-dihydroxyphenylalanine2 decarboxylase
8	<a href="#">c3mafB_</a>	 Alignment		100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> sphingosine-1-phosphate lyase; <b>PDBTitle:</b> crystal structure of stspl (asymmetric form)
9	<a href="#">c3mc6C_</a>	 Alignment		100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> sphingosine-1-phosphate lyase; <b>PDBTitle:</b> crystal structure of scdpl1
10	<a href="#">c3hl2D_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> o-phosphoseryl-trna(sec) selenium transferase; <b>PDBTitle:</b> the crystal structure of the human sepsecs-trnasec complex
11	<a href="#">d3bc8a1</a>	 Alignment		100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> SepSecS-like

12	<a href="#">c3f9tB</a>	Alignment		100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> l-tyrosine decarboxylase mfnA; <b>PDBTitle:</b> crystal structure of l-tyrosine decarboxylase mfnA (ec 4.1.1.25)2 (np_247014.1) from methanococcus jannaschii at 2.11 Å resolution
13	<a href="#">d2z67a1</a>	Alignment		100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> SepSecS-like
14	<a href="#">d1wyub1</a>	Alignment		100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Glycine dehydrogenase subunits (GDC-P)
15	<a href="#">d1wyua1</a>	Alignment		100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Glycine dehydrogenase subunits (GDC-P)
16	<a href="#">c3bcxA</a>	Alignment		100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3- <b>PDBTitle:</b> e1 dehydrase
17	<a href="#">d1c4ka2</a>	Alignment		100.0	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Ornithine decarboxylase major domain
18	<a href="#">c3e77A</a>	Alignment		100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> human phosphoserine aminotransferase in complex with plp
19	<a href="#">c3nnkC</a>	Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> ureidoglycine-glyoxylate aminotransferase; <b>PDBTitle:</b> biochemical and structural characterization of a ureidoglycine2 aminotransferase in the klebsiella pneumoniae uric acid catabolic3 pathway
20	<a href="#">d1jf9a</a>	Alignment		100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
21	<a href="#">d1kl1a</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
22	<a href="#">d1vjoa</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
23	<a href="#">d1qz9a</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
24	<a href="#">c2hzpA</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> kynureninase; <b>PDBTitle:</b> crystal structure of homo sapiens kynureninase
25	<a href="#">c3e9kA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> kynureninase; <b>PDBTitle:</b> crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
26	<a href="#">c3caiA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> possible aminotransferase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis rv3778c2 protein
27	<a href="#">c2dr1A</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 386aa long hypothetical serine aminotransferase; <b>PDBTitle:</b> crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
28	<a href="#">c2hdyA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine lyase; <b>PDBTitle:</b> structure of human selenocysteine lyase
						<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine aminotransferase serc;

29	<a href="#">c3ffrA_</a>	Alignment	not modelled	100.0	13	<b>PDBTitle:</b> crystal structure of a phosphoserine aminotransferase serc (chu_0995)2 from cytophaga hutchinsonii atcc 33406 at 1.75 a resolution
30	<a href="#">d2c0ra1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
31	<a href="#">d1b9ha_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
32	<a href="#">d2ch1a1</a>	Alignment	not modelled	100.0	11	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
33	<a href="#">c3islA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine catabolism protein pucg; <b>PDBTitle:</b> crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
34	<a href="#">c2c7ta_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-2-deoxy-scyllo-inosose <b>PDBTitle:</b> crystal structure of the plp-bound form of btr, 2 a dual functional aminotransferase involved in butirosin3 biosynthesis.
35	<a href="#">c2fyfB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
36	<a href="#">c3m5uA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> crystal structure of phosphoserine aminotransferase from2 campylobacter jejuni
37	<a href="#">d1t3ia_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
38	<a href="#">d1h0ca_</a>	Alignment	not modelled	100.0	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
39	<a href="#">c3f0hA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
40	<a href="#">c2z9wA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
41	<a href="#">d1w23a_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
42	<a href="#">d1dfoa_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
43	<a href="#">c2huuA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine glyoxylate aminotransferase; <b>PDBTitle:</b> crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine
44	<a href="#">c3lvmB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine desulfurase; <b>PDBTitle:</b> crystal structure of e.coli iscs
45	<a href="#">d2bkwa1</a>	Alignment	not modelled	100.0	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
46	<a href="#">c2r0ta_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxamine 5-phosphate-dependent dehydrase; <b>PDBTitle:</b> crystal sructure of gdp-4-keto-6-deoxymannose-3-dehydratase2 with a trapped plp-glutamate geminal diamine
47	<a href="#">c2po3B_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-dehydrase; <b>PDBTitle:</b> crystal structure analysis of desi in the presence of its2 tdp-sugar product
48	<a href="#">d1o69a_</a>	Alignment	not modelled	100.0	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
49	<a href="#">c2dkjB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of t.th.hb8 serine hydroxymethyltransferase
50	<a href="#">d1p3wa_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
51	<a href="#">c3uwcA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotide-sugar aminotransferase; <b>PDBTitle:</b> structure of an aminotransferase (degt-dnrj-eryc1-strs family) from2 coxiella burnetii in complex with pmp
52	<a href="#">c2ogeC_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> transaminase; <b>PDBTitle:</b> x-ray structure of s. venezuelae desv in its internal2 aldimine form
53	<a href="#">d1mdoa_</a>	Alignment	not modelled	100.0	11	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
54	<a href="#">d1v72a1</a>	Alignment	not modelled	100.0	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
55	<a href="#">d1svva_</a>	Alignment	not modelled	100.0	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like

56	<a href="#">c3ecdC</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> serine hydroxymethyltransferase 2; <b>PDBTitle:</b> crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei
57	<a href="#">d1eg5a</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
58	<a href="#">d2fnua1</a>	Alignment	not modelled	100.0	9	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
59	<a href="#">c2yrrA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase, class v; <b>PDBTitle:</b> hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8
60	<a href="#">c2w8wA</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine palmitoyltransferase; <b>PDBTitle:</b> n100y spt with plp-ser
61	<a href="#">d1m32a</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
62	<a href="#">c3frkB</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> qdtb; <b>PDBTitle:</b> x-ray structure of qdtb from t. thermosaccharolyticum in 2 complex with a plp:tdp-3-aminoquinovose aldimine
63	<a href="#">d1bjna</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
64	<a href="#">c3nysA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase wbpe; <b>PDBTitle:</b> x-ray structure of the k185a mutant of wbpe (wlbe) from pseudomonas2 aeruginosa in complex with plp at 1.45 angstrom resolution
65	<a href="#">d1elua</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
66	<a href="#">c3qm2A</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> 2.25 angstrom crystal structure of phosphoserine aminotransferase2 (serc) from salmonella enterica subsp. enterica serovar typhimurium
67	<a href="#">c3n0lA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
68	<a href="#">d2bwna1</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
69	<a href="#">c3dr4B</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative perosamine synthetase; <b>PDBTitle:</b> gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
70	<a href="#">d1rv3a</a>	Alignment	not modelled	100.0	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
71	<a href="#">c3h7fB</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine hydroxymethyltransferase 1; <b>PDBTitle:</b> crystal structure of serine hydroxymethyltransferase from2 mycobacterium tuberculosis
72	<a href="#">c3ke3A</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative serine-pyruvate aminotransferase; <b>PDBTitle:</b> crystal structure of putative serine-pyruvate aminotransferase2 (yp_263484.1) from psychrobacter arcticum 273-4 at 2.20 a resolution
73	<a href="#">c3hqtB</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cai-1 autoinducer synthase; <b>PDBTitle:</b> plp-dependent acyl-coa transferase cgsa
74	<a href="#">d1bs0a</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
75	<a href="#">c3ju7B</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative plp-dependent aminotransferase; <b>PDBTitle:</b> crystal structure of putative plp-dependent aminotransferase2 (np_978343.1) from bacillus cereus atcc 10987 at 2.19 a resolution
76	<a href="#">c3a2bA</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine palmitoyltransferase; <b>PDBTitle:</b> crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
77	<a href="#">d2v1pa1</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Beta-eliminating lyases
78	<a href="#">c3tqxA</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-amino-3-ketobutyrate coenzyme a ligase; <b>PDBTitle:</b> structure of the 2-amino-3-ketobutyrate coenzyme a ligase (kbl) from2 coxiella burnetii
79	<a href="#">d1fc4a</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
80	<a href="#">c1c4kA</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (ornithine decarboxylase); <b>PDBTitle:</b> ornithine decarboxylase mutant (gly121tyr)

81	<a href="#">d2a7va1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
82	<a href="#">c2a7vA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> human mitochondrial serine hydroxymethyltransferase 2
83	<a href="#">d1bj4a</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
84	<a href="#">d2e7ja1</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> SepSecS-like
85	<a href="#">c2cb1A</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> o-acetyl homoserine sulfhydrylase; <b>PDBTitle:</b> crystal structure of o-acetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
86	<a href="#">d1c7ga</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Beta-eliminating lyases
87	<a href="#">c3lwsF</a>	Alignment	not modelled	99.9	9	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> aromatic amino acid beta-eliminating <b>PDBTitle:</b> 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
88	<a href="#">c3pj0D</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> lmo0305 protein; <b>PDBTitle:</b> crystal structure of a putative l-allo-threonine aldolase (lmo0305)2 from listeria monocytogenes egd-e at 1.80 a resolution
89	<a href="#">d1ax4a</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Beta-eliminating lyases
90	<a href="#">d1ejja</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
91	<a href="#">d2ctza1</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
92	<a href="#">d1m6sa</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
93	<a href="#">d1libja</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
94	<a href="#">c1libjC</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> cystathionine beta-lyase; <b>PDBTitle:</b> crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana
95	<a href="#">c2nmpC</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> cystathionine gamma-lyase; <b>PDBTitle:</b> crystal structure of human cystathionine gamma lyase
96	<a href="#">d1bw0a</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
97	<a href="#">c2vycA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> biodegradative arginine decarboxylase; <b>PDBTitle:</b> crystal structure of acid induced arginine decarboxylase2 from e. coli
98	<a href="#">d1iuga</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
99	<a href="#">c3ndnC</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> o-succinylhomoserine sulfhydrylase; <b>PDBTitle:</b> crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5- phosphate
100	<a href="#">c3aemD</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> methionine gamma-lyase; <b>PDBTitle:</b> reaction intermediate structure of entamoeba histolytica methionine2 gamma-lyase 1 containing michaelis complex and methionine imine-3 pyridoxamine-5'-phosphate
101	<a href="#">d1cs1a</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
102	<a href="#">c2x3lA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> orn/lys/arg decarboxylase family protein; <b>PDBTitle:</b> crystal structure of the orn_lys_arg decarboxylase family2 protein sar0482 from methicillin-resistant staphylococcus3 aureus
103	<a href="#">c3dodA</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7- oxononoate aminotransferase; <b>PDBTitle:</b> crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 bacillus subtilis
104	<a href="#">c3n75E</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> lysine decarboxylase, inducible; <b>PDBTitle:</b> x-ray crystal structure of the escherichia coli inducible lysine2 decarboxylase ldcI
105	<a href="#">d1n8pa</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
106	<a href="#">d1cl1a</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases

					<b>Family:</b> Cystathionine synthase-like
107	<a href="#">d1x0ma1</a>	Alignment	not modelled	99.9	13 <b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
108	<a href="#">d1tpla_</a>	Alignment	not modelled	99.9	12 <b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Beta-eliminating lyases
109	<a href="#">d1y4ia1</a>	Alignment	not modelled	99.9	14 <b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
110	<a href="#">c3e6gA_</a>	Alignment	not modelled	99.9	15 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cystathionine gamma-lyase-like protein; <b>PDBTitle:</b> crystal structure of xometc, a cystathionine c-lyase-like2 protein from xanthomonas oryzae pv.oryzae
111	<a href="#">c2gqnB_</a>	Alignment	not modelled	99.9	12 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cystathionine beta-lyase; <b>PDBTitle:</b> cystathionine beta-lyase (cbl) from escherichia coli in complex with2 n-hydrazinocarbonylmethyl-2-nitro-benzamide
112	<a href="#">d1xi9a_</a>	Alignment	not modelled	99.9	11 <b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
113	<a href="#">c3jtxB_</a>	Alignment	not modelled	99.9	12 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of aminotransferase (np_283882.1) from neisseria2 meningitidis z2491 at 1.91 a resolution
114	<a href="#">d1wsta1</a>	Alignment	not modelled	99.9	14 <b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
115	<a href="#">c3ftbA_</a>	Alignment	not modelled	99.9	13 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidinol-phosphate aminotransferase; <b>PDBTitle:</b> the crystal structure of the histidinol-phosphate2 aminotransferase from clostridium acetobutylicum
116	<a href="#">c3b46B_</a>	Alignment	not modelled	99.9	13 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase bna3; <b>PDBTitle:</b> crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
117	<a href="#">d1lc5a_</a>	Alignment	not modelled	99.9	14 <b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
118	<a href="#">d1qgna_</a>	Alignment	not modelled	99.9	11 <b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
119	<a href="#">c3a8uX_</a>	Alignment	not modelled	99.9	10 <b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> omega-amino acid--pyruvate aminotransferase; <b>PDBTitle:</b> crystal structure of omega-amino acid:pyruvate aminotransferase
120	<a href="#">d1gc0a_</a>	Alignment	not modelled	99.9	15 <b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like