



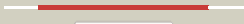

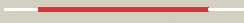


























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1dfoa_</a>	 Alignment		100.0	100	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
2	<a href="#">d1ejia_</a>	 Alignment		100.0	48	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
3	<a href="#">c3h7fB_</a>	 Alignment		100.0	55	<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
4	<a href="#">c3n0lA_</a>	 Alignment		100.0	54	<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
5	<a href="#">d1bj4a_</a>	 Alignment		100.0	49	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
6	<a href="#">d1rv3a_</a>	 Alignment		100.0	49	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
7	<a href="#">c2a7vA_</a>	 Alignment		100.0	49	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> human mitochondrial serine hydroxymethyltransferase 2
8	<a href="#">d2a7va1</a>	 Alignment		100.0	49	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
9	<a href="#">d1kl1a_</a>	 Alignment		100.0	61	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
10	<a href="#">c2dkjB_</a>	 Alignment		100.0	60	<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
11	<a href="#">c3ecdC_</a>	 Alignment		100.0	54	<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

12	<a href="#">c3hqtB_</a>	Alignment		100.0	14	<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
13	<a href="#">c2w8wA_</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine palmitoyltransferase; <b>PDBTitle:</b> n100y spt with plp-ser
14	<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
15	<a href="#">d1wyub1</a>	Alignment		100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Glycine dehydrogenase subunits (GDC-P)
16	<a href="#">d2bwna1</a>	Alignment		100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
17	<a href="#">d1vjoa_</a>	Alignment		100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
18	<a href="#">d1c4ka2</a>	Alignment		100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Ornithine decarboxylase major domain
19	<a href="#">c2vycA_</a>	Alignment		100.0	18	<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
20	<a href="#">c3a2bA_</a>	Alignment		100.0	19	<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
21	<a href="#">c1c4kA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (ornithine decarboxylase); <b>PDBTitle:</b> ornithine decarboxylase mutant (gly121tyr)
22	<a href="#">d1bs0a_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
23	<a href="#">c2z9wA_</a>	Alignment	not modelled	100.0	18	<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
24	<a href="#">c3bcxA_</a>	Alignment	not modelled	100.0	15	<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
25	<a href="#">c3islA_</a>	Alignment	not modelled	100.0	15	<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
26	<a href="#">c3b46B_</a>	Alignment	not modelled	100.0	14	<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
27	<a href="#">c3tqxA_</a>	Alignment	not modelled	100.0	18	<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
28	<a href="#">c2ogeC_</a>	Alignment	not modelled	100.0	14	<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

29	<a href="#">d1fc4a_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
30	<a href="#">c3mafB_</a>	Alignment	not modelled	100.0	12	<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)
31	<a href="#">c3g0tA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative aminotransferase; <b>PDBTitle:</b> crystal structure of putative aspartate aminotransferase (np_905498.1)2 from porphyromonas gingivalis w83 at 1.75 a resolution
32	<a href="#">c2po3B_</a>	Alignment	not modelled	100.0	14	<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
33	<a href="#">d1jf9a_</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
34	<a href="#">c2c7tA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-2-deoxy-scylo-inosose <b>PDBTitle:</b> crystal structure of the plp-bound form of btrr,2 a dual functional aminotransferase involved in butirosin3 biosynthesis.
35	<a href="#">d1c7na_</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
36	<a href="#">d1xi9a_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
37	<a href="#">d1b5pa_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
38	<a href="#">c3h14A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase, classes i and ii; <b>PDBTitle:</b> crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
39	<a href="#">c3l8aB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative aminotransferase, probable beta-cystathionase; <b>PDBTitle:</b> crystal structure of metc from streptococcus mutans
40	<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
41	<a href="#">d2ch1a1</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
42	<a href="#">c3n75E_</a>	Alignment	not modelled	100.0	18	<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
43	<a href="#">d1wyua1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Glycine dehydrogenase subunits (GDC-P)
44	<a href="#">d1h0ca_</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
45	<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
46	<a href="#">d1o4sa_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
47	<a href="#">c2huuA_</a>	Alignment	not modelled	100.0	13	<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
48	<a href="#">c3hbxB_</a>	Alignment	not modelled	100.0	12	<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
49	<a href="#">d1w7la_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
50	<a href="#">d1c7ga_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Beta-eliminating lyases
51	<a href="#">d1tpla_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Beta-eliminating lyases
52	<a href="#">c3f9tB_</a>	Alignment	not modelled	100.0	16	<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 a resolution
53	<a href="#">d1m6sa_</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
54	<a href="#">c2r0tA_</a>	Alignment	not modelled	100.0	20	<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 <b>PDB header:</b> hydrolase

55	<a href="#">c3e9kA</a>	Alignment	not modelled	100.0	12	<b>Chain:</b> A: <b>PDB Molecule:</b> kynureninase; <b>PDBTitle:</b> crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
56	<a href="#">d2c0ra1</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
57	<a href="#">c2hzpA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> kynureninase; <b>PDBTitle:</b> crystal structure of homo sapiens kynureninase
58	<a href="#">c2dr1A</a>	Alignment	not modelled	100.0	17	<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
59	<a href="#">d2r5ea1</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
60	<a href="#">d1js3a</a>	Alignment	not modelled	100.0	11	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Pyridoxal-dependent decarboxylase
61	<a href="#">c3kaxB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase, classes i and ii; <b>PDBTitle:</b> crystal structure of a putative c-s lyase from bacillus anthracis
62	<a href="#">c3f0hA</a>	Alignment	not modelled	100.0	11	<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
63	<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
64	<a href="#">c3dzzB</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative pyridoxal 5'-phosphate-dependent c-s lyase; <b>PDBTitle:</b> crystal structure of a putative plp-dependent aminotransferase2 (lbul_1103) from lactobacillus delbrueckii subsp. at 1.61 a3 resolution
65	<a href="#">c3nysA</a>	Alignment	not modelled	100.0	16	<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
66	<a href="#">c3frkB</a>	Alignment	not modelled	100.0	12	<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 in2 complex with a plp:tdp-3-aminoquinovose aldimine
67	<a href="#">d1o69a</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
68	<a href="#">c3mc6C</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> sphingosine-1-phosphate lyase; <b>PDBTitle:</b> crystal structure of scdpl1
69	<a href="#">c3qguB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ll-diaminopimelate aminotransferase; <b>PDBTitle:</b> l,l-diaminopimelate aminotransferase from chlamydomonas reinhardtii
70	<a href="#">c3pplB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> crystal structure of an aspartate transaminase (ncgl0237, cgl0240)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.25 a3 resolution
71	<a href="#">c3e2yB</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase, lyase <b>Chain:</b> B: <b>PDB Molecule:</b> kynurenine-oxoglutarate transaminase 3; <b>PDBTitle:</b> crystal structure of mouse kynurenine aminotransferase iii in complex2 with glutamine
72	<a href="#">c2o0rA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rv0858c (n-succinyl-diaminopimelate aminotransferase); <b>PDBTitle:</b> the three-dimensional structure of n-succinyl-diaminopimelate2 aminotransferase from mycobacterium tuberculosis
73	<a href="#">d1j32a</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
74	<a href="#">d1mdoa</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
75	<a href="#">c1ynuA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-aminocyclopropane-1-carboxylate synthase; <b>PDBTitle:</b> crystal structure of apple acc synthase in complex with l-vinylglycine
76	<a href="#">d1iaya</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
77	<a href="#">c3lvmB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine desulfurase; <b>PDBTitle:</b> crystal structure of e.coli iscs
78	<a href="#">c3ftbA</a>	Alignment	not modelled	100.0	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
79	<a href="#">d1bw0a</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like

80	<a href="#">c2jisA_</a>	Alignment	not modelled	100.0	13	<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.
81	<a href="#">c3ffrA_</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine aminotransferase serc; <b>PDBTitle:</b> crystal structure of a phosphoserine aminotransferase serc (chu_0995)2 from cytophaga hutchinsonii atcc 33406 at 1.75 a resolution
82	<a href="#">d1p3wa_</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
83	<a href="#">c3jtbB_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of apo-II-di-aminopimelate aminotransferase (np_283882.1) from neisseria2 meningitidis z2491 at 1.91 a resolution
84	<a href="#">c3asaA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> II-di-aminopimelate aminotransferase; <b>PDBTitle:</b> crystal structure of a histidinol-phosphate aminotransferase from2 chlamydia trachomatis
85	<a href="#">c3hdoB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> histidinol-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
86	<a href="#">d1t3ia_</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
87	<a href="#">c2x3lA_</a>	Alignment	not modelled	100.0	12	<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
88	<a href="#">c3if2B_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of putative amino-acid aminotransferase2 (yp_265399.1) from psychrobacter arcticum 273-4 at 2.50 a resolution
89	<a href="#">d1m7ya_</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
90	<a href="#">d1qz9a_</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
91	<a href="#">d1gdea_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
92	<a href="#">d1u08a_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
93	<a href="#">c3eibB_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> II-di-aminopimelate aminotransferase; <b>PDBTitle:</b> crystal structure of k270n variant of II-di-aminopimelate2 aminotransferase from arabidopsis thaliana
94	<a href="#">d1x0ma1</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
95	<a href="#">c3getA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidinol-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of putative histidinol-phosphate aminotransferase2 (np_281508.1) from campylobacter jejuni at 2.01 a resolution
96	<a href="#">d2fnua1</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
97	<a href="#">c2x5dD_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> probable aminotransferase; <b>PDBTitle:</b> crystal structure of a probable aminotransferase from2 pseudomonas aeruginosa
98	<a href="#">c3nraA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> crystal structure of an aspartate aminotransferase (yp_354942.1) from2 rhodobacter sphaeroides 2.4.1 at 2.15 a resolution
99	<a href="#">d2v1pa1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Beta-eliminating lyases
100	<a href="#">c2hdyA_</a>	Alignment	not modelled	100.0	14	<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
101	<a href="#">d1svva_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
102	<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
103	<a href="#">d1eg5a_</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
104	<a href="#">c3pj0D_</a>	Alignment	not modelled	100.0	13	<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
						<b>PDB header:</b> transferase



105	<a href="#">c3dr4B_</a>	Alignment	not modelled	100.0	15	<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
106	<a href="#">c3pdxA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine aminotransferase; <b>PDBTitle:</b> crystal structural of mouse tyrosine aminotransferase
107	<a href="#">d1lc5a_</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
108	<a href="#">c3rq1A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase class i and ii; <b>PDBTitle:</b> crystal structure of aminotransferase class i and ii from veillonella2 parvula
109	<a href="#">c3ly1C_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> putative histidinol-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of putative histidinol-phosphate aminotransferase2 (yp_050345.1) from erwinia carotovora atroseptica scri1043 at 1.80 a3 resolution
110	<a href="#">d1pmma_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Pyridoxal-dependent decarboxylase
111	<a href="#">d1d2fa_</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
112	<a href="#">c2douA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable n-succinyldiaminopimelate aminotransferase; <b>PDBTitle:</b> probable n-succinyldiaminopimelate aminotransferase (ttha0342) from2 thermus thermophilus hb8
113	<a href="#">c3eucB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> histidinol-phosphate aminotransferase 2; <b>PDBTitle:</b> crystal structure of histidinol-phosphate aminotransferase2 (yp_297314.1) from ralstonia eutropha jmp134 at 2.05 a resolution
114	<a href="#">c3op7A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase class i and ii; <b>PDBTitle:</b> crystal structure of a plp-dependent aminotransferase (zp_03625122.1)2 from streptococcus suis 89-1591 at 1.70 a resolution
115	<a href="#">d1m32a_</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
116	<a href="#">c2o1bA_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase, class i; <b>PDBTitle:</b> structure of aminotransferase from staphylococcus aureus
117	<a href="#">c3cq6E_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> histidinol-phosphate aminotransferase; <b>PDBTitle:</b> histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound )
118	<a href="#">c2zc0C_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> alanine glyoxylate transaminase; <b>PDBTitle:</b> crystal structure of an archaeal alanine:glyoxylate aminotransferase
119	<a href="#">c1d2fB_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> maly protein; <b>PDBTitle:</b> x-ray structure of maly from escherichia coli: a pyridoxal-5'-2 phosphate-dependent enzyme acting as a modulator in mal gene3 expression
120	<a href="#">c2okkA_</a>	Alignment	not modelled	100.0	14	<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)