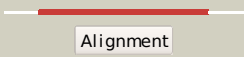

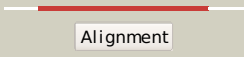

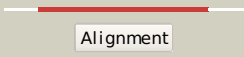



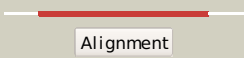

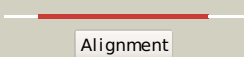

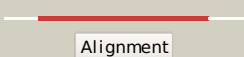

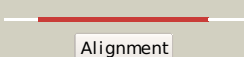

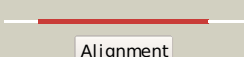

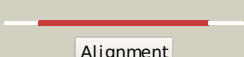

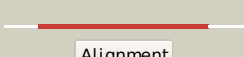











# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P00509
Date	Thu Jan 5 10:56:40 GMT 2012
Unique Job ID	ef26111aac21be1a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2ay1a_</a>	 Alignment		100.0	45	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
2	<a href="#">d7aata_</a>	 Alignment		100.0	40	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
3	<a href="#">d1ajsa_</a>	 Alignment		100.0	40	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
4	<a href="#">c3k7yA_</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> aspartate aminotransferase of plasmodium falciparum
5	<a href="#">d1yaaa_</a>	 Alignment		100.0	37	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
6	<a href="#">d3tata_</a>	 Alignment		100.0	43	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
7	<a href="#">d2csta_</a>	 Alignment		100.0	39	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
8	<a href="#">c3mebB_</a>	 Alignment		100.0	36	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> structure of cytoplasmic aspartate aminotransferase from giardia2 lamblia
9	<a href="#">d2q7wa1</a>	 Alignment		100.0	98	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
10	<a href="#">c3rq1A_</a>	 Alignment		100.0	24	<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
11	<a href="#">c2x5fB_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate_tyrosine_phenylalanine pyridoxal-5' <b>PDBTitle:</b> crystal structure of the methicillin-resistant2 staphylococcus aureus sar2028, an3 aspartate_tyrosine_phenylalanine pyridoxal-5'-phosphate4 dependent aminotransferase

12	<a href="#">c3t18D_</a>	Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> aminotransferase class i and ii; <b>PDBTitle:</b> crystal structure of aminotransferase from anaerococcus prevotii dsm2 20548.
13	<a href="#">c3g0tA_</a>	Alignment		100.0	15	<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
14	<a href="#">c3ihjA_</a>	Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine aminotransferase 2; <b>PDBTitle:</b> human alanine aminotransferase 2 in complex with plp
15	<a href="#">c3e2yB_</a>	Alignment		100.0	18	<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
16	<a href="#">c3pplB_</a>	Alignment		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
17	<a href="#">c3if2B_</a>	Alignment		100.0	20	<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
18	<a href="#">c1ynuA_</a>	Alignment		100.0	17	<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
19	<a href="#">d1m7ya_</a>	Alignment		100.0	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
20	<a href="#">d1iaya_</a>	Alignment		100.0	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
21	<a href="#">d1w7la_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
22	<a href="#">c2zc0C_</a>	Alignment	not modelled	100.0	17	<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
23	<a href="#">d2r5ea1</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
24	<a href="#">c3b46B_</a>	Alignment	not modelled	100.0	18	<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
25	<a href="#">c3ez1A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase mocr family; <b>PDBTitle:</b> crystal structure of putative aminotransferase (mocr family)2 (yp_604413.1) from deinococcus geothermalis dsm 11300 at 2.60 a3 resolution
26	<a href="#">c3qguB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> l,l-diaminopimelate aminotransferase; <b>PDBTitle:</b> l,l-diaminopimelate aminotransferase from chlamydomonas reinhardtii
27	<a href="#">d1vp4a_</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
28	<a href="#">c3h14A_</a>	Alignment	not modelled	100.0	20	<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

29	<a href="#">d1u08a_</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
30	<a href="#">d1bw0a_</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
31	<a href="#">c3jtbB_</a>	Alignment	not modelled	100.0	17	<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
32	<a href="#">d1wsta1</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
33	<a href="#">d1o4sa_</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
34	<a href="#">c3l8aB_</a>	Alignment	not modelled	100.0	14	<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
35	<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
36	<a href="#">c3ezsB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase aspb; <b>PDBTitle:</b> crystal structure of aminotransferase aspb (np_207418.1) from2 helicobacter pylori 26695 at 2.19 a resolution
37	<a href="#">c3eibB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> II-diaminopimelate aminotransferase; <b>PDBTitle:</b> crystal structure of k270n variant of II-diaminopimelate2 aminotransferase from arabidopsis thaliana
38	<a href="#">d1xi9a_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
39	<a href="#">c3d6kB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative aminotransferase; <b>PDBTitle:</b> the crystal structure of a putative aminotransferase from2 corynebacterium diphtheriae
40	<a href="#">c2o0rA_</a>	Alignment	not modelled	100.0	17	<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
41	<a href="#">d1x0ma1</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
42	<a href="#">c2zy3A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-aspartate beta-decarboxylase; <b>PDBTitle:</b> dodecameric l-aspartate beta-decarboxylase
43	<a href="#">c2o1bA_</a>	Alignment	not modelled	100.0	14	<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
44	<a href="#">c3eleB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> amino transferase; <b>PDBTitle:</b> crystal structure of amino transferase (rer070207001803) from2 eubacterium rectale at 2.10 a resolution
45	<a href="#">d1c7na_</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
46	<a href="#">d1j32a_</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
47	<a href="#">d1gdea_</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
48	<a href="#">d1b5pa_</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
49	<a href="#">c3nraA_</a>	Alignment	not modelled	100.0	20	<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
50	<a href="#">c2x5dD_</a>	Alignment	not modelled	100.0	18	<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
51	<a href="#">d2gb3a1</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
52	<a href="#">c3kaxB_</a>	Alignment	not modelled	100.0	13	<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
53	<a href="#">c3asaA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> II-diaminopimelate aminotransferase; <b>PDBTitle:</b> crystal structure of apo-II-diaminopimelate aminotransferase from2 chlamydia trachomatis
						<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> kynurenine/alpha-aminoadipate

54	<a href="#">c3dc1A_</a>	Alignment	not modelled	100.0	14	aminotransferase <b>PDBTitle:</b> crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate
55	<a href="#">c3f6tA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> crystal structure of aspartate aminotransferase (e.c. 2.6.1.1)2 (yp_194538.1) from lactobacillus acidophilus ncfm at 2.15 a3 resolution
56	<a href="#">c2douA_</a>	Alignment	not modelled	100.0	19	<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
57	<a href="#">c3fdbA_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative plp-dependent beta-cystathionase; <b>PDBTitle:</b> crystal structure of a putative plp-dependent beta-cystathionase2 (aecd, dip1736) from corynebacterium diphtheriae at 1.99 a resolution
58	<a href="#">c3dydB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine aminotransferase; <b>PDBTitle:</b> human tyrosine aminotransferase
59	<a href="#">c3g7qA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> valine-pyruvate aminotransferase; <b>PDBTitle:</b> crystal structure of valine-pyruvate aminotransferase avta2 (np_462565.1) from salmonella typhimurium lt2 at 1.80 a resolution
60	<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
61	<a href="#">d1v2da_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
62	<a href="#">c1d2fB_</a>	Alignment	not modelled	100.0	14	<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
63	<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
64	<a href="#">c2z61A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable aspartate aminotransferase 2; <b>PDBTitle:</b> crystal structure of mj0684 from methanococcus jannaschii2 reveals its similarity in the active site to kynurenine3 aminotransferases
65	<a href="#">c3ly1C_</a>	Alignment	not modelled	100.0	15	<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
66	<a href="#">c3cbfA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-aminodipate aminotransferase; <b>PDBTitle:</b> crystal structure of lysn, alpha-aminoadipate2 aminotransferase, from thermus thermophilus hb27
67	<a href="#">c3op7A_</a>	Alignment	not modelled	100.0	20	<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
68	<a href="#">c3bwnF_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> l-tryptophan aminotransferase; <b>PDBTitle:</b> l-tryptophan aminotransferase
69	<a href="#">d2f8ja1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
70	<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
71	<a href="#">c3cq6E_</a>	Alignment	not modelled	100.0	15	<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 )
72	<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
73	<a href="#">d1fg7a_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
74	<a href="#">d2hoxa1</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
75	<a href="#">d1lc5a_</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
76	<a href="#">c3hdoB_</a>	Alignment	not modelled	100.0	19	<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
77	<a href="#">c3ffhA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidinol-phosphate aminotransferase; <b>PDBTitle:</b> the crystal structure of histidinol-phosphate

						aminotransferase from2 listeria innocua clip11262.
78	<a href="#">c3p1tB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative histidinol-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of a putative aminotransferase (bpsl1724) from2 burkholderia pseudomallei k96243 at 2.60 a resolution
79	<a href="#">c3fkdC_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> l-threonine-o-3-phosphate decarboxylase; <b>PDBTitle:</b> the crystal structure of l-threonine-o-3-phosphate2 decarboxylase from porphyromonas gingivalis
80	<a href="#">c3ftbA_</a>	Alignment	not modelled	100.0	14	<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
81	<a href="#">d2aeua1</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> SelA-like
82	<a href="#">d1tpla_</a>	Alignment	not modelled	100.0	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Beta-eliminating lyases
83	<a href="#">d1svva_</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
84	<a href="#">c2dkjB_</a>	Alignment	not modelled	100.0	17	<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
85	<a href="#">d2e7ja1</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> SepSecS-like
86	<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
87	<a href="#">d1vjoa_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
88	<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
89	<a href="#">c3ffrA_</a>	Alignment	not modelled	100.0	13	<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
90	<a href="#">c3nnkC_</a>	Alignment	not modelled	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
91	<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 stsp1 (asymmetric form)
92	<a href="#">c3i4jC_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> aminotransferase, class iii; <b>PDBTitle:</b> crystal structure of aminotransferase, class iii from2 deinococcus radiodurans
93	<a href="#">c2z9wA_</a>	Alignment	not modelled	100.0	13	<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
94	<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
95	<a href="#">d1c7ga_</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Beta-eliminating lyases
96	<a href="#">c2eh6A_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetylornithine aminotransferase; <b>PDBTitle:</b> crystal structure of acetylornithine aminotransferase from aquifex2 aeolicus vf5
97	<a href="#">d1dfoa_</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
98	<a href="#">c3mc6C_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> sphingosine-1-phosphate lyase; <b>PDBTitle:</b> crystal structure of scdpl1
99	<a href="#">d1eg5a_</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
100	<a href="#">c3hqtB_</a>	Alignment	not modelled	99.9	16	<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 cqsa
101	<a href="#">d1m6sa_</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
102	<a href="#">d1b9ha_</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like



103	<a href="#">c3islA_</a>	Alignment	not modelled	99.9	13	<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
104	<a href="#">dlvefa1</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
105	<a href="#">d2cfba1</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
106	<a href="#">d1kl1a_</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
107	<a href="#">d2bwna1</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
108	<a href="#">c3nysA_</a>	Alignment	not modelled	99.9	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
109	<a href="#">c2x3lA_</a>	Alignment	not modelled	99.9	11	<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
110	<a href="#">c3pj0D_</a>	Alignment	not modelled	99.9	12	<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
111	<a href="#">c2hdyA_</a>	Alignment	not modelled	99.9	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
112	<a href="#">c3bcxA_</a>	Alignment	not modelled	99.9	12	<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
113	<a href="#">c2huuA_</a>	Alignment	not modelled	99.9	14	<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
114	<a href="#">c3f9tB_</a>	Alignment	not modelled	99.9	13	<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
115	<a href="#">d1qz9a_</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
116	<a href="#">c3a2bA_</a>	Alignment	not modelled	99.9	15	<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
117	<a href="#">c3caiA_</a>	Alignment	not modelled	99.9	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
118	<a href="#">d2ch1a1</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
119	<a href="#">d1bs0a_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
120	<a href="#">c2ordA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetylornithine aminotransferase; <b>PDBTitle:</b> crystal structure of acetylornithine aminotransferase (ec 2.6.1.11)2 (acoat) (tm1785) from thermotoga maritima at 1.40 a resolution