Phyre^2

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Description	P04693
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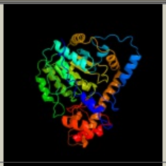
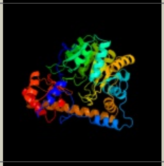
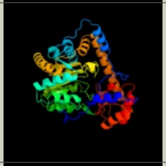
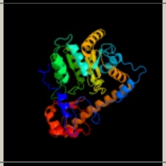
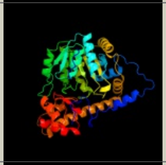
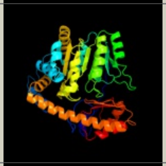
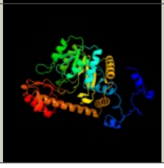
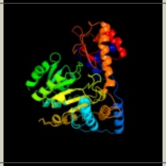
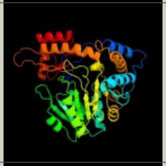
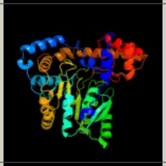
Unique Job ID	72caccff6cd49e42

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3tata_	Alignment		100.0	100	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
2	d2ay1a_	Alignment		100.0	40	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
3	d7aata_	Alignment		100.0	39	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
4	d1yaaa_	Alignment		100.0	36	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
5	d1ajsa_	Alignment		100.0	40	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
6	d2csta_	Alignment		100.0	40	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
7	c3k7yA_	Alignment		100.0	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** aspartate aminotransferase of plasmodium falciparum
8	c3mebB_	Alignment		100.0	35	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** structure of cytoplasmic aspartate aminotransferase from giardia2 lamblia
9	d2q7wa1	Alignment		100.0	42	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
10	c3rq1A_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase class i and ii; **PDBTitle:** crystal structure of aminotransferase class i and ii from veillonella2 parvula
11	c2x5fB_	Alignment		100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartate_tyrosine_phenylalanine pyridoxal-5' **PDBTitle:** crystal structure of the methicillin-resistant2 staphylococcus aureus sar2028, an3 aspartate_tyrosine_phenylalanine pyridoxal-5'-phosphate4 dependent aminotransferase

12	c3t18D_	Alignment		100.0	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**aminotransferase class i and ii; **PDBTitle:** crystal structure of aminotransferase from anaerococcus prevotii dsm2 20548.
13	c3g0tA_	Alignment		100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative aminotransferase; **PDBTitle:** crystal structure of putative aspartate aminotransferase (np_905498.1)2 from porphyromonas gingivalis w83 at 1.75 a resolution
14	c3ihjA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alanine aminotransferase 2; **PDBTitle:** human alanine aminotransferase 2 in complex with plp
15	c1ynuA_	Alignment		100.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**1-aminocyclopropane-1-carboxylate synthase; **PDBTitle:** crystal structure of apple acc synthase in complex with l-vinylglycine
16	c3pplB_	Alignment		100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of an aspartate transaminase (ncgl0237, cgl0240)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.25 a3 resolution
17	c3if2B_	Alignment		100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of putative amino-acid aminotransferase2 (yp_265399.1) from psychrobacter arcticum 273-4 at 2.50 a resolution
18	c3e2yB_	Alignment		100.0	15	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**kynurenine-oxoglutarate transaminase 3; **PDBTitle:** crystal structure of mouse kynurenine aminotransferase iii in complex2 with glutamine
19	c2zc0C_	Alignment		100.0	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**alanine glyoxylate transaminase; **PDBTitle:** crystal structure of an archaeal alanine:glyoxylate aminotransferase
20	d1m7ya_	Alignment		100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
21	d1iaya_	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
22	d1w7la_	Alignment	not modelled	100.0	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
23	d2r5ea1	Alignment	not modelled	100.0	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
24	d1vp4a_	Alignment	not modelled	100.0	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
25	c3ez1A_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase mocr family; **PDBTitle:** crystal structure of putative aminotransferase (mocr family)2 (yp_604413.1) from deinococcus geothermalis dsm 11300 at 2.60 a3 resolution
26	c3qguB_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ll-diaminopimelate aminotransferase; **PDBTitle:** l,l-diaminopimelate aminotransferase from chalmydomonas reinhardtii
27	c3h14A_	Alignment	not modelled	100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase, classes i and ii; **PDBTitle:** crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
28	d1bw0a_	Alignment	not modelled	100.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
						PDB header:transferase

29	c3jtxB_	Alignment	not modelled	100.0	16	**Chain:** B: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase (np_283882.1) from neisseria2 meningitidis z2491 at 1.91 a resolution
30	d1wsta1	Alignment	not modelled	100.0	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
31	d1u08a_	Alignment	not modelled	100.0	21	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
32	c3b46B_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminotransferase bna3; **PDBTitle:** crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
33	c3l8aB_	Alignment	not modelled	100.0	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative aminotransferase, probable beta-cystathionase; **PDBTitle:** crystal structure of metc from streptococcus mutans
34	c3dzzB_	Alignment	not modelled	100.0	16	**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
35	d1o4sa_	Alignment	not modelled	100.0	19	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
36	d1x0ma1	Alignment	not modelled	100.0	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
37	c3ezsB_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminotransferase aspb; **PDBTitle:** crystal structure of aminotransferase aspb (np_207418.1) from2 helicobacter pylori 26695 at 2.19 a resolution
38	d1xi9a_	Alignment	not modelled	100.0	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
39	d1gdea_	Alignment	not modelled	100.0	21	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
40	c3d6kB_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative aminotransferase; **PDBTitle:** the crystal structure of a putative aminotransferase from2 corynebacterium diphtheriae
41	c3eibB_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ll-diaminopimelate aminotransferase; **PDBTitle:** crystal structure of k270n variant of ll-diaminopimelate2 aminotransferase from arabidopsis thaliana
42	c2o0rA_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rv0858c (n-succinyldiaminopimelate aminotransferase); **PDBTitle:** the three-dimensional structure of n-succinyldiaminopimelate2 aminotransferase from mycobacterium tuberculosis
43	d1j32a_	Alignment	not modelled	100.0	19	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
44	c3eleB_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**amino transferase; **PDBTitle:** crystal structure of amino transferase (rer070207001803) from2 eubacterium rectale at 2.10 a resolution
45	d1b5pa_	Alignment	not modelled	100.0	21	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
46	d1c7na_	Alignment	not modelled	100.0	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
47	c2zy3A_	Alignment	not modelled	100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-aspartate beta-decarboxylase; **PDBTitle:** dodecameric l-aspartate beta-decarboxylase
48	c3nraA_	Alignment	not modelled	100.0	20	**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
49	c2o1bA_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase, class i; **PDBTitle:** structure of aminotransferase from staphylococcus aureus
50	c3kaxB_	Alignment	not modelled	100.0	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aminotransferase, classes i and ii; **PDBTitle:** crystal structure of a putative c-s lyase from bacillus anthracis
51	c2x5dD_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**probable aminotransferase; **PDBTitle:** crystal structure of a probable aminotransferase from2 pseudomonas aeruginosa
52	c3dc1A_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**kynurenine/alpha-aminoadipate aminotransferase **PDBTitle:** crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate
53	c3asaA_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ll-diaminopimelate aminotransferase; **PDBTitle:** crystal structure of apo-ll-diaminopimelate aminotransferase from2 chlamydia trachomatis
						PDB header:transferase

54	c3f6tA_	Alignment	not modelled	100.0	16	**Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of aspartate aminotransferase (e.c. 2.6.1.1)2 (yp_194538.1) from lactobacillus acidophilus ncfm at 2.15 a3 resolution
55	d2gb3a1	Alignment	not modelled	100.0	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
56	c3fdbA_	Alignment	not modelled	100.0	10	**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
57	c3g7qA_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**valine-pyruvate aminotransferase; **PDBTitle:** crystal structure of valine-pyruvate aminotransferase avta2 (np_462565.1) from salmonella typhimurium lt2 at 1.80 a resolution
58	c2douA_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable n-succinyldiaminopimelate aminotransferase; **PDBTitle:** probable n-succinyldiaminopimelate aminotransferase (ttha0342) from2 thermus thermophilus hb8
59	c3dydB_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**tyrosine aminotransferase; **PDBTitle:** human tyrosine aminotransferase
60	d1v2da_	Alignment	not modelled	100.0	22	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
61	c3pdxA_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine aminotransferase; **PDBTitle:** crystal structural of mouse tyrosine aminotransferase
62	c1d2fB_	Alignment	not modelled	100.0	15	**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
63	d1d2fa_	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
64	c2z61A_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable aspartate aminotransferase 2; **PDBTitle:** crystal structure of mj0684 from methanococcus jannaschii2 reveals its similarity in the active site to kynurenine3 aminotransferases
65	c3ly1C_	Alignment	not modelled	100.0	20	**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
66	c3cbfA_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-aminodipate aminotransferase; **PDBTitle:** crystal structure of lysn, alpha-aminoadipate2 aminotransferase, from thermus thermophilus hb27
67	c3cq6E_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** E: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound)
68	c3eucB_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**histidinol-phosphate aminotransferase 2; **PDBTitle:** crystal structure of histidinol-phosphate aminotransferase2 (yp_297314.1) from ralstonia eutropha jmp134 at 2.05 a resolution
69	c3op7A_	Alignment	not modelled	100.0	18	**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
70	c3getA_	Alignment	not modelled	100.0	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
71	c3bwnF_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** F: **PDB Molecule:**l-tryptophan aminotransferase; **PDBTitle:** l-tryptophan aminotransferase
72	d2f8ja1	Alignment	not modelled	100.0	20	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
73	d1fg7a_	Alignment	not modelled	100.0	20	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
74	d1lc5a_	Alignment	not modelled	100.0	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
75	c3hdoB_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
76	d2hoxa1	Alignment	not modelled	100.0	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
77	c3ffhA_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** the crystal structure of histidinol-phosphate

						aminotransferase from2 listeria innocua clip11262.
78	c3p1tB_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of a putative aminotransferase (bpsl1724) from2 burkholderia pseudomallei k96243 at 2.60 a resolution
79	c3fkdC_	Alignment	not modelled	100.0	16	**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
80	c3ftbA_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** the crystal structure of the histidinol-phosphate2 aminotransferase from clostridium acetobutylicum
81	d2aeua1	Alignment	not modelled	100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SelA-like
82	d1tpla_	Alignment	not modelled	100.0	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
83	d1svva_	Alignment	not modelled	100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
84	d2e7ja1	Alignment	not modelled	100.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SepSecS-like
85	c3f0hA_	Alignment	not modelled	100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
86	d1vjoa_	Alignment	not modelled	100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
87	d1v72a1	Alignment	not modelled	100.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
88	c2dkjB_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of t.th.hb8 serine hydroxymethyltransferase
89	c3nnkC_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ureidoglycine-glyoxylate aminotransferase; **PDBTitle:** biochemical and structural characterization of a ureidoglycine2 aminotransferase in the klebsiella pneumoniae uric acid catabolic3 pathway
90	c3hqtB_	Alignment	not modelled	100.0	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cai-1 autoinducer synthase; **PDBTitle:** plp-dependent acyl-coa transferase cqsa
91	c3ffrA_	Alignment	not modelled	100.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase serc; **PDBTitle:** crystal structure of a phosphoserine aminotransferase serc (chu_0995)2 from cytophaga hutchinsonii atcc 33406 at 1.75 a resolution
92	d2bwna1	Alignment	not modelled	100.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
93	d1c7ga_	Alignment	not modelled	100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
94	c3i4jC_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**aminotransferase, class iii; **PDBTitle:** crystal structure of aminotransferase, class iii from2 deinococcus radiodurans
95	c2z9wA_	Alignment	not modelled	100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
96	d1dfoa_	Alignment	not modelled	100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
97	d1eg5a_	Alignment	not modelled	100.0	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
98	d1m6sa_	Alignment	not modelled	100.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
99	c3islA_	Alignment	not modelled	100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine catabolism protein pucg; **PDBTitle:** crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
100	c2po3B_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-dehydrase; **PDBTitle:** crystal structure analysis of desi in the presence of its2 tdp-sugar product
101	c3a2bA_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
102	d1h0ca_	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like

103	c2huuA_	Alignment	not modelled	100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alanine glyoxylate aminotransferase; **PDBTitle:** crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine
104	c3mafB_	Alignment	not modelled	100.0	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**sphingosine-1-phosphate lyase; **PDBTitle:** crystal structure of stspl (asymmetric form)
105	c2eh6A_	Alignment	not modelled	100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylornithine aminotransferase; **PDBTitle:** crystal structure of acetylornithine aminotransferase from aquifex2 aeolicus vf5
106	d1kl1a_	Alignment	not modelled	100.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
107	d1b9ha_	Alignment	not modelled	100.0	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
108	d1vefa1	Alignment	not modelled	100.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
109	d2ch1a1	Alignment	not modelled	100.0	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
110	c2hdyA_	Alignment	not modelled	100.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**selenocysteine lyase; **PDBTitle:** structure of human selenocysteine lyase
111	c3mc6C_	Alignment	not modelled	100.0	10	**PDB header:**lyase **Chain:** C: **PDB Molecule:**sphingosine-1-phosphate lyase; **PDBTitle:** crystal structure of scdpl1
112	c3tqxA_	Alignment	not modelled	100.0	13	**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
113	c2w8wA_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** n100y spt with plp-ser
114	c3f9tB_	Alignment	not modelled	100.0	11	**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
115	c3caiA_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible aminotransferase; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv3778c2 protein
116	d2cfba1	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
117	c3e9kA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**kynureninase; **PDBTitle:** crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
118	d1bs0a_	Alignment	not modelled	100.0	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
119	c3nysA_	Alignment	not modelled	99.9	16	**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
120	c2yrrA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase, class v; **PDBTitle:** hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8