Phyre^2

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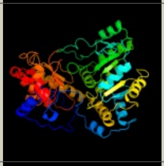
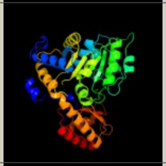
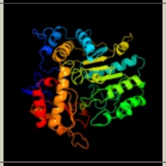
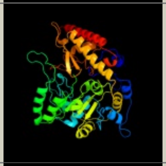
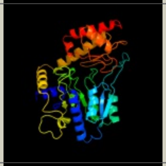
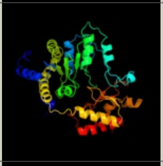
Description	P0A853
Date	Thu Jan 5 11:06:55 GMT 2012
Unique Job ID	2e50dbf18783c6a6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2v1pa1	Alignment		100.0	100	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
2	d1ax4a_	Alignment		100.0	52	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
3	d1c7ga_	Alignment		100.0	44	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
4	d1tpla_	Alignment		100.0	44	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
5	d1m6sa_	Alignment		100.0	20	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
6	c3h7fB_	Alignment		100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase 1; **PDBTitle:** crystal structure of serine hydroxymethyltransferase from2 mycobacterium tuberculosis
7	c3n5mD_	Alignment		100.0	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**adenosylmethionine-8-amino-7-oxononanoate aminotransferase; **PDBTitle:** crystals structure of a bacillus anthracis aminotransferase
8	d1ejia_	Alignment		100.0	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
9	d1bj4a_	Alignment		100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
10	d1wyub1	Alignment		100.0	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Glycine dehydrogenase subunits (GDC-P)
11	c3hmuA_	Alignment		100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase, class iii; **PDBTitle:** crystal structure of a class iii aminotransferase from2 silicibacter pomeroyi

12	d1zoda1	Alignment		100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
13	c3a8uX_	Alignment		100.0	14	**PDB header:**transferase **Chain:** X: **PDB Molecule:**omega-amino acid--pyruvate aminotransferase; **PDBTitle:** crystal structure of omega-amino acid:pyruvate aminotransferase
14	d1rv3a_	Alignment		100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
15	c3n0lA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
16	c3fcrA_	Alignment		100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative aminotransferase; **PDBTitle:** crystal structure of putative aminotransferase (yp_614685.1) from2 silicibacter sp. tm1040 at 1.80 a resolution
17	c3ruyB_	Alignment		100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ornithine aminotransferase; **PDBTitle:** crystal structure of the ornithine-oxo acid transaminase rocd from2 bacillus anthracis
18	d2byla1	Alignment		100.0	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
19	c3i5tB_	Alignment		100.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase prk07036 from rhodobacter2 sphaeroides kd131
20	c1oatB_	Alignment		100.0	12	**PDB header:**aminotransferase **Chain:** B: **PDB Molecule:**ornithine aminotransferase; **PDBTitle:** ornithine aminotransferase
21	d1s0aa_	Alignment	not modelled	100.0	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
22	c2a7vA_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** human mitochondrial serine hydroxymethyltransferase 2
23	d2a7va1	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
24	c3lv2A_	Alignment	not modelled	100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenosylmethionine-8-amino-7-oxononanoate aminotransferase; **PDBTitle:** crystal structure of mycobacterium tuberculosis 7,8-diaminopelargonic2 acid synthase in complex with substrate analog sinefungin
25	c3bs8A_	Alignment	not modelled	100.0	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate-1-semialdehyde 2,1-aminomutase; **PDBTitle:** crystal structure of glutamate 1-semialdehyde aminotransferase2 complexed with pyridoxamine-5'-phosphate from bacillus subtilis
26	c3dxvA_	Alignment	not modelled	100.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alpha-amino-epsilon-caprolactam racemase; **PDBTitle:** the crystal structure of alpha-amino-epsilon-caprolactam racemase from2 achromobacter obae
27	c3dodA_	Alignment	not modelled	100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenosylmethionine-8-amino-7-oxononanoate aminotransferase; **PDBTitle:** crystal structure of plp bound 7,8-diaminopelargonic

						acid synthase in2 bacillus subtilis
28	c3bv0A_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenosylmethionine-8-amino-7-oxononanoate aminotransferase; **PDBTitle:** crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 mycobacterium tuberculosis
29	c2pb2B_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetylornithine/succinyldiaminopimelate aminotransferase; **PDBTitle:** structure of biosynthetic n-acetylornithine aminotransferase from2 salmonella typhimurium: studies on substrate specificity and3 inhibitor binding
30	d1v72a1	Alignment	not modelled	100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
31	c3ecdC_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**serine hydroxymethyltransferase 2; **PDBTitle:** crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei
32	c3nuiA_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate transaminase; **PDBTitle:** crystal structure of omega-transferase from vibrio fluvialis js17
33	c2zsmA_	Alignment	not modelled	100.0	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate-1-semialdehyde 2,1-aminomutase; **PDBTitle:** crystal structure of glutamate-1-semialdehyde 2,1-2 aminomutase from aeropyrum pernix, hexagonal form
34	c2ordA_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylornithine aminotransferase; **PDBTitle:** crystal structure of acetylornithine aminotransferase (ec 2.6.1.11)2 (acoat) (tm1785) from thermotoga maritima at 1.40 a resolution
35	d2gsaa_	Alignment	not modelled	100.0	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
36	d1svva_	Alignment	not modelled	100.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
37	d1kl1a_	Alignment	not modelled	100.0	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
38	d1dfoa_	Alignment	not modelled	100.0	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
39	c3nx3A_	Alignment	not modelled	100.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylornithine aminotransferase; **PDBTitle:** crystal structure of acetylornithine aminotransferase (argd) from2 campylobacter jejuni
40	d1z7da1	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
41	c3bcxA_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3- **PDBTitle:** e1 dehydrase
42	c2e7uA_	Alignment	not modelled	100.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate-1-semialdehyde 2,1-aminomutase; **PDBTitle:** crystal structure of glutamate-1-semialdehyde 2,1-aminomutase from2 thermus thermophilus hb8
43	d1sffa_	Alignment	not modelled	100.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
44	c2eh6A_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylornithine aminotransferase; **PDBTitle:** crystal structure of acetylornithine aminotransferase from aquifex2 aeolicus vf5
45	c2dkjB_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of t.th.hb8 serine hydroxymethyltransferase
46	d1vefa1	Alignment	not modelled	100.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
47	c2cjdA_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**l-lysine-epsilon aminotransferase; **PDBTitle:** lysine aminotransferase from m. tuberculosis in external2 aldimine form
48	c2w8wA_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** n100y spt with plp-ser
49	c3l44A_	Alignment	not modelled	100.0	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate-1-semialdehyde 2,1-aminomutase 1; **PDBTitle:** crystal structure of bacillus anthracis heml-1, glutamate semialdehyde2 aminotransferase
50	c3i4jC_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**aminotransferase, class iii; **PDBTitle:** crystal structure of aminotransferase, class iii from2 deinococcus radiodurans
51	c3oksB_	Alignment	not modelled	100.0	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-aminobutyrate transaminase; **PDBTitle:** crystal structure of 4-aminobutyrate transaminase from mycobacterium2 smegmatis
						Fold:PLP-dependent transferase-like

52	d2cfba1	Alignment	not modelled	100.0	17	**Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
53	c2c7tA_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine-2-deoxy-scyllo-inosose **PDBTitle:** crystal structure of the plp-bound form of btrr,2 a dual functional aminotransferase involved in butirosin3 biosynthesis.
54	c1z7dE_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** E: **PDB Molecule:**ornithine aminotransferase; **PDBTitle:** ornithine aminotransferase py00104 from plasmodium yoelii
55	c2cy8A_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**d-phenylglycine aminotransferase; **PDBTitle:** crystal structure of d-phenylglycine aminotransferase (d-phgat) from2 pseudomonas strutzeri st-201
56	c3pj0D_	Alignment	not modelled	100.0	14	**PDB header:**lyase **Chain:** D: **PDB Molecule:**lmo0305 protein; **PDBTitle:** crystal structure of a putative l-allo-threonine aldolase (lmo0305)2 from listeria monocytogenes egd-e at 1.80 a resolution
57	d2bwna1	Alignment	not modelled	100.0	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
58	d1ohwa_	Alignment	not modelled	100.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
59	c3mafB_	Alignment	not modelled	100.0	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**sphingosine-1-phosphate lyase; **PDBTitle:** crystal structure of stspl (asymmetric form)
60	c3a2bA_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
61	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
62	c2eo5A_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**419aa long hypothetical aminotransferase; **PDBTitle:** crystal structure of 4-aminobutyrate aminotransferase from sulfolobus2 tokodaii strain7
63	d1fc4a_	Alignment	not modelled	100.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
64	c3lwsF_	Alignment	not modelled	100.0	12	**PDB header:**lyase **Chain:** F: **PDB Molecule:**aromatic amino acid beta-eliminating **PDBTitle:** crystal structure of putative aromatic amino acid beta-2 eliminating lyase/threonine aldolase. (yp_001813866.1) from3 exiguobacterium sp. 255-15 at 2.00 a resolution
65	d1c4ka2	Alignment	not modelled	100.0	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Ornithine decarboxylase major domain
66	c3hbxB_	Alignment	not modelled	100.0	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutamate decarboxylase 1; **PDBTitle:** crystal structure of gad1 from arabidopsis thaliana
67	c2jisA_	Alignment	not modelled	100.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cysteine sulfinic acid decarboxylase; **PDBTitle:** human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
68	c3f9tB_	Alignment	not modelled	99.9	14	**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
69	d1bs0a_	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
70	d1b9ha_	Alignment	not modelled	99.9	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
71	c2ogeC_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**transaminase; **PDBTitle:** x-ray structure of s. venezuelae desv in its internal2 aldimine form
72	c2po3B_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-dehydrase; **PDBTitle:** crystal structure analysis of desi in the presence of its2 tdp-sugar product
73	c2r0tA_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxamine 5-phosphate-dependent dehydrase; **PDBTitle:** crystal sructure of gdp-4-keto-6-deoxymannose-3-dehydratase2 with a trapped plp-glutamate geminal diamine
74	d3bc8a1	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SepSecS-like
75	d1wyua1	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Glycine dehydrogenase subunits (GDC-P)
76	c3aemD_	Alignment	not modelled	99.9	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**methionine gamma-lyase; **PDBTitle:** reaction intermediate structure of entamoeba histolytica methionine2 gamma-lyase 1 containing michaelis complex and methionine imine-3 pyridoxamine-5'-phosphate
77	d1qgna_	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like

78	c3nysA_	Alignment	not modelled	99.9	20	**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
79	c2gqnB_	Alignment	not modelled	99.9	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**cystathionine beta-lyase; **PDBTitle:** cystathionine beta-lyase (cbl) from escherichia coli in complex with2 n-hydrazinocarbonylmethyl-2-nitro-benzamide
80	d1o69a_	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
81	c2okkA_	Alignment	not modelled	99.9	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glutamate decarboxylase 2; **PDBTitle:** the x-ray crystal structure of the 65kda isoform of glutamic acid2 decarboxylase (gad65)
82	c2cb1A_	Alignment	not modelled	99.9	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**o-acetyl homoserine sulfhydrylase; **PDBTitle:** crystal structure of o-actetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
83	d1js3a_	Alignment	not modelled	99.9	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Pyridoxal-dependent decarboxylase
84	c3frkB_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**qdtb; **PDBTitle:** x-ray structure of qdtb from t. thermosaccharolyticum in2 complex with a plp:tdp-3-aminoquinovose aldimine
85	d2fnua1	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
86	d2e7ja1	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SepSecS-like
87	c3hl2D_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**o-phosphoseryl-trna(sec) selenium transferase; **PDBTitle:** the crystal structure of the human sepsecs-trnasec complex
88	c3tqxA_	Alignment	not modelled	99.9	17	**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
89	c3ndnC_	Alignment	not modelled	99.9	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**o-succinylhomoserine sulfhydrylase; **PDBTitle:** crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
90	c3uwcA_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleotide-sugar aminotransferase; **PDBTitle:** structure of an aminotransferase (degt-dnrj-eryc1-strs family) from2 coxiella burnetii in complex with pmp
91	c3hvyC_	Alignment	not modelled	99.9	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**cystathionine beta-lyase family protein, ynbb b.subtilis **PDBTitle:** crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_348457.1) from clostridium acetobutylicum at3 2.00 a resolution
92	d1mdoa_	Alignment	not modelled	99.9	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
93	c3k40B_	Alignment	not modelled	99.9	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aromatic-l-amino-acid decarboxylase; **PDBTitle:** crystal structure of drosophila 3,4-dihydroxyphenylalanine2 decarboxylase
94	d1cl1a_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
95	d1pmma_	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Pyridoxal-dependent decarboxylase
96	d1y4ia1	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
97	c3dr4B_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative perosamine synthetase; **PDBTitle:** gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
98	c3b46B_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminotransferase bna3; **PDBTitle:** crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
99	c1i41J_	Alignment	not modelled	99.9	14	**PDB header:**lyase **Chain:** J: **PDB Molecule:**cystathionine gamma-synthase; **PDBTitle:** cystathionine gamma-synthase in complex with the inhibitor2 appa
100	c3nnkC_	Alignment	not modelled	99.9	11	**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
101	d2ch1a1	Alignment	not modelled	99.9	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
						Fold:PLP-dependent transferase-like

102	d2r5ea1	Alignment	not modelled	99.9	13	**Superfamily:**PLP-dependent transferases **Family:**AAT-like
103	d1cs1a_	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
104	d1gc0a_	Alignment	not modelled	99.9	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
105	d2ctza1	Alignment	not modelled	99.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
106	c3fd0B_	Alignment	not modelled	99.9	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative cystathionine beta-lyase involved in aluminum **PDBTitle:** crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_470671.1) from listeria innocua at 2.12 a3 resolution
107	c3mc6C_	Alignment	not modelled	99.9	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**sphingosine-1-phosphate lyase; **PDBTitle:** crystal structure of scdpl1
108	d1vjoa_	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
109	c3ht4B_	Alignment	not modelled	99.9	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aluminum resistance protein; **PDBTitle:** crystal structure of the q81a77_baccr protein from bacillus2 cereus. northeast structural genomics consortium target3 bcr213
110	c1ibjC_	Alignment	not modelled	99.9	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**cystathionine beta-lyase; **PDBTitle:** crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana
111	d1xi9a_	Alignment	not modelled	99.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
112	d1ibja_	Alignment	not modelled	99.9	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
113	c3jtxB_	Alignment	not modelled	99.9	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase (np_283882.1) from neisseria2 meningitidis z2491 at 1.91 a resolution
114	c3ju7B_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative plp-dependent aminotransferase; **PDBTitle:** crystal structure of putative plp-dependent aminotransferase2 (np_978343.1) from bacillus cereus atcc 10987 at 2.19 a resolution
115	c3islA_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine catabolism protein pucg; **PDBTitle:** crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
116	d1w7la_	Alignment	not modelled	99.9	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
117	c2z9wA_	Alignment	not modelled	99.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
118	c3f0hA_	Alignment	not modelled	99.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
119	c3ly1C_	Alignment	not modelled	99.9	14	**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
120	c2hdyA_	Alignment	not modelled	99.9	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**selenocysteine lyase; **PDBTitle:** structure of human selenocysteine lyase