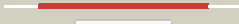



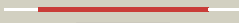





















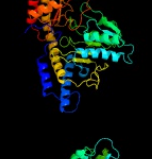

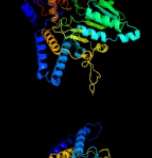

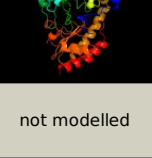


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1464_(csd)_1651524_1652777
Date	Fri Aug 2 13:30:04 BST 2019
Unique Job ID	60520e0854d2693b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1jf9a_</a>	 Alignment		100.0	45	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
2	<a href="#">c6c9eB_</a>	 Alignment		100.0	39	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine desulfurase; <b>PDBTitle:</b> crystal structure of cysteine desulfurase from legionella pneumophila2 philadelphia 1
3	<a href="#">c4w91C_</a>	 Alignment		100.0	48	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of a cysteine desulfurase sufs from brucella suis2 bound to plp
4	<a href="#">c4q76B_</a>	 Alignment		100.0	45	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine desulfurase 2, chloroplastic; <b>PDBTitle:</b> crystal structure of nfs2 c384s mutant, the plastidial cysteine2 desulfurase from arabidopsis thaliana
5	<a href="#">c4lw2C_</a>	 Alignment		100.0	38	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> cysteine sulfinatase desulfurase; <b>PDBTitle:</b> structural changes during cysteine desulfurase csda and sulfur-2 acceptor csde interactions provide insight into the trans-3 persulfuration
6	<a href="#">c5j8qA_</a>	 Alignment		100.0	43	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine desulfurase sufs; <b>PDBTitle:</b> crystal structure of the cysteine desulfurase sufs of bacillus2 subtilis
7	<a href="#">d1t3ia_</a>	 Alignment		100.0	43	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
8	<a href="#">c3caiA_</a>	 Alignment		100.0	24	<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
9	<a href="#">c5b87B_</a>	 Alignment		100.0	42	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine desulfurase; <b>PDBTitle:</b> crystal structure of a cysteine desulfurase from thermococcus2 onnurineus na1 in complex with alanine at 2.3 angstrom resolution
10	<a href="#">c5utsC_</a>	 Alignment		100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> c-s lyase egt2; <b>PDBTitle:</b> carbon sulfoxide lyase, egt2 in the ergothioneine biosynthesis pathway
11	<a href="#">c5vprA_</a>	 Alignment		100.0	37	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine desulfurase; <b>PDBTitle:</b> crystal structure of cysteine desulfurase from elizabethkingia2 anophelis with covalently bound pyridoxal phosphate

12	<a href="#">c3e9kA</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> kynureninase; <b>PDBTitle:</b> crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
13	<a href="#">d1qz9a</a>	Alignment		100.0	23	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
14	<a href="#">c5i90A</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pvdn; <b>PDBTitle:</b> crystal structure of pvdn from pseudomonas aeruginosa
15	<a href="#">c2hzpA</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> kynureninase; <b>PDBTitle:</b> crystal structure of homo sapiens kynureninase
16	<a href="#">c4isyB</a>	Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine desulfurase; <b>PDBTitle:</b> crystal structure of iscs from mycobacterium tuberculosis
17	<a href="#">c2hdyA</a>	Alignment		100.0	23	<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
18	<a href="#">d1elua</a>	Alignment		100.0	25	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
19	<a href="#">c5zsqA</a>	Alignment		100.0	24	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine desulfurase; <b>PDBTitle:</b> nifs from hydrogenimonas thermophila, soaked with l-cysteine for 4 min
20	<a href="#">c4eb5B</a>	Alignment		100.0	23	<b>PDB header:</b> transferase/metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable cysteine desulfurase 2; <b>PDBTitle:</b> a. fulgidus iscs-iscu complex structure
21	<a href="#">d2c0ra1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
22	<a href="#">d1p3wa</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
23	<a href="#">d1eg5a</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
24	<a href="#">c3lvmB</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine desulfurase; <b>PDBTitle:</b> crystal structure of e.coli iscs
25	<a href="#">c3ffrA</a>	Alignment	not modelled	100.0	14	<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
26	<a href="#">d1w23a</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
27	<a href="#">c6czyA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine aminotransferase 1, chloroplastic; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana phosphoserine2 aminotransferase isoform 1 (atpsat1) in complex with pyridoxamine-5'-3 phosphate (pmp)
28	<a href="#">c5kz5M</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase/oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> cysteine desulfurase, mitochondrial; <b>PDBTitle:</b> architecture of the human mitochondrial iron-sulfur

					cluster assembly2 machinery: the complex formed by the iron donor, the sulfur donor,3 and the scaffold
29	<a href="#">c4ixoB</a>	Alignment	not modelled	100.0	19 <b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> nifs-like protein; <b>PDBTitle:</b> x-ray structure of nifs-like protein from rickettsia africae esf-5
30	<a href="#">c3vaxA</a>	Alignment	not modelled	100.0	28 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein dnda; <b>PDBTitle:</b> crystal structure of dnda from streptomyces lividans
31	<a href="#">c5wt2A</a>	Alignment	not modelled	100.0	22 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine desulfurase iscs; <b>PDBTitle:</b> nifs from helicobacter pylori
32	<a href="#">c3m5uA</a>	Alignment	not modelled	100.0	13 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> crystal structure of phosphoserine aminotransferase from2 campylobacter jejuni
33	<a href="#">c4xk1A</a>	Alignment	not modelled	100.0	15 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> crystal structure of a phosphoserine/phosphohydroxythreonine2 aminotransferase (psat) from pseudomonas aeruginosa with cofactor3 pyridoxal phosphate and bound glutamate
34	<a href="#">c2fyfB</a>	Alignment	not modelled	100.0	16 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
35	<a href="#">c3nnkC</a>	Alignment	not modelled	100.0	15 <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
36	<a href="#">c3e77A</a>	Alignment	not modelled	100.0	17 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> human phosphoserine aminotransferase in complex with plp
37	<a href="#">c5usrC</a>	Alignment	not modelled	100.0	24 <b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> cysteine desulfurase, mitochondrial; <b>PDBTitle:</b> crystal structure of human nfs1-isd11 in complex with e. coli acyl-2 carrier protein at 3.09 angstroms
38	<a href="#">c5f8vH</a>	Alignment	not modelled	100.0	14 <b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> aminotransferase, class v family protein; <b>PDBTitle:</b> crystal structure of plp bound phosphoserine aminotransferase (psat)2 from trichomonas vaginalis
39	<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
40	<a href="#">c2z9wA</a>	Alignment	not modelled	100.0	16 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
41	<a href="#">d1bjna</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
42	<a href="#">c3zrrB</a>	Alignment	not modelled	100.0	18 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine-pyruvate aminotransferase (agxt); <b>PDBTitle:</b> crystal structure and substrate specificity of a thermophilic2 archaeal serine : pyruvate aminotransferase from sulfolobus3 solfataricus
43	<a href="#">d1h0ca</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
44	<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
45	<a href="#">c5yb0I</a>	Alignment	not modelled	100.0	16 <b>PDB header:</b> transferase <b>Chain:</b> I: <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> crystal structure of wild type phosphoserine aminotransferase (psat)2 from e. histolytica
46	<a href="#">c4f10A</a>	Alignment	not modelled	100.0	15 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase ald1; <b>PDBTitle:</b> crystal structure of ald1 from arabidopsis thaliana
47	<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
48	<a href="#">c2huuA</a>	Alignment	not modelled	100.0	17 <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 glyoxylate aminotransferase2 in complex with alanine
49	<a href="#">c5usrG</a>	Alignment	not modelled	100.0	23 <b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> cysteine desulfurase, mitochondrial; <b>PDBTitle:</b> crystal structure of human nfs1-isd11 in complex with e. coli acyl-2 carrier protein at 3.09 angstroms
50	<a href="#">d2bkwa1</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
51	<a href="#">d1vjoa</a>	Alignment	not modelled	100.0	17 <b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
52	<a href="#">c3qm2A</a>	Alignment	not modelled	100.0	14 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> 2.25 angstrom crystal structure of phosphoserine aminotransferase2 (serc) from salmonella enterica subsp. enterica serovar typhimurium
					<b>PDB header:</b> lyase/lyase inhibitor

53	<a href="#">c4q6rB_</a>	Alignment	not modelled	100.0	13	<b>Chain:</b> B; <b>PDB Molecule:</b> sphingosine-1-phosphate lyase 1; <b>PDBTitle:</b> crystal structure of human sphingosine-1-phosphate lyase in complex2 with inhibitor 6-[(2r)-4-(4-benzyl-7-chlorophthalazin-1-yl)-2-3 methylpiperazin-1-yl]pyridine-3-carbonitrile
54	<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
55	<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
56	<a href="#">d1m32a_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
57	<a href="#">c3eucB_</a>	Alignment	not modelled	100.0	16	<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
58	<a href="#">c3cbfA_</a>	Alignment	not modelled	100.0	16	<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
59	<a href="#">c3ftbA_</a>	Alignment	not modelled	100.0	11	<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-phosphate aminotransferase2 from clostridium acetobutylicum
60	<a href="#">c3eibB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> ll-diaminopimelate aminotransferase; <b>PDBTitle:</b> crystal structure of k270n variant of ll-diaminopimelate2 aminotransferase from arabidopsis thaliana
61	<a href="#">d1wyua1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Glycine dehydrogenase subunits (GDC-P)
62	<a href="#">c3mafB_</a>	Alignment	not modelled	100.0	19	<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)
63	<a href="#">c3qguB_</a>	Alignment	not modelled	100.0	14	<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
64	<a href="#">c5uidC_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> aminotransferase tlmj; <b>PDBTitle:</b> the crystal structure of an aminotransferase tlmj from2 streptoalloteichus hindustanus
65	<a href="#">d1iuga_</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
66	<a href="#">c3madA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> sphingosine-1-phosphate lyase; <b>PDBTitle:</b> crystal structure of stspl (symmetric form)
67	<a href="#">c2ogeC_</a>	Alignment	not modelled	100.0	18	<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
68	<a href="#">c3g0tA_</a>	Alignment	not modelled	100.0	11	<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
69	<a href="#">c3h14A_</a>	Alignment	not modelled	100.0	17	<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
70	<a href="#">c4wbtA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> probable histidinol-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of histidinol-phosphate aminotransferase from2 sinorhizobium meliloti in complex with pyridoxal-5'-phosphate
71	<a href="#">d1o4sa_</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
72	<a href="#">c5yiiA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> crystal structure of 45 amino acid deleted from n-terminal of2 phosphoserine aminotransferase (psat) of entamoeba histolytica
73	<a href="#">c3bcxA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydrase; <b>PDBTitle:</b> e1 dehydrase
74	<a href="#">d1bw0a_</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
75	<a href="#">c3ly1C_</a>	Alignment	not modelled	100.0	12	<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
76	<a href="#">c3mc6C_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> sphingosine-1-phosphate lyase; <b>PDBTitle:</b> crystal structure of scdp11
						<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> l-tyrosine decarboxylase mfna;

77	<a href="#">c3f9tB_</a>	Alignment	not modelled	100.0	16	<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
78	<a href="#">c3getA_</a>	Alignment	not modelled	100.0	11	<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
79	<a href="#">c5yhvA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of an aminotransferase from mycobacterium2 tuberculosis
80	<a href="#">d1lc5a_</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
81	<a href="#">c5k1rB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> burkholderia pseudomallei sphingosine-1-phosphate lyase <b>PDBTitle:</b> structure of burkholderia pseudomallei k96243 sphingosine-1-phosphate2 lyase bpss2021
82	<a href="#">c2w8wA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine palmitoyltransferase; <b>PDBTitle:</b> n100y spt with plp-ser
83	<a href="#">c2yrrA_</a>	Alignment	not modelled	100.0	18	<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
84	<a href="#">c3kaxB_</a>	Alignment	not modelled	100.0	11	<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
85	<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
86	<a href="#">c4r8dB_</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 rv1600 encoded aminotransferase in complex with2 plp-mes from mycobacterium tuberculosis
87	<a href="#">c3wy7D_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 8-amino-7-oxononanoate synthase; <b>PDBTitle:</b> crystal structure of mycobacterium smegmatis 7-keto-8-aminopelargonic2 acid (kapa) synthase biof
88	<a href="#">c4dgtA_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative pyridoxal phosphate-dependent transferase; <b>PDBTitle:</b> crystal structure of plp-bound putative aminotransferase from2 clostridium difficile 630 crystallized with magnesium formate
89	<a href="#">c3jtxB_</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 aminotransferase (np_283882.1) from neisseria2 meningitidis z2491 at 1.91 a resolution
90	<a href="#">c3b46B_</a>	Alignment	not modelled	100.0	12	<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
91	<a href="#">c3ffhA_</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 histidinol-phosphate aminotransferase from2 listeria innocua clip11262.
92	<a href="#">d1xi9a_</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="#">c6ouxB_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> threonine phosphate decarboxylase-like enzyme; <b>PDBTitle:</b> structure of smul_1544, a decarboxylase from sulfurospirillum2 multivorans
94	<a href="#">c3eleB_</a>	Alignment	not modelled	100.0	15	<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
95	<a href="#">c3l8aB_</a>	Alignment	not modelled	100.0	10	<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
96	<a href="#">d1b5pa_</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
97	<a href="#">c4j8lA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yhfs; <b>PDBTitle:</b> crystal structure of the pyridoxal-5'-phosphate dependent protein yhfs2 from escherichia coli
98	<a href="#">c5z0qG_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> aminotransferase, class i and ii; <b>PDBTitle:</b> crystal structure of ovob
99	<a href="#">d1b9ha_</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
100	<a href="#">c3cq6E_</a>	Alignment	not modelled	100.0	16	<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 )
101	<a href="#">d1bs0a_</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
102	<a href="#">c5iaxB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 8-amino-7-oxononanoate synthase;



102	<a href="#">c3jayB</a>	Alignment	not modelled	100.0	17	<b>PDBTitle:</b> crystal structure of an 8-amino-7-oxononanoate synthase from <i>Burkholderia xenovorans</i> <b>PDB header:</b> transferase
103	<a href="#">c3uwcA</a>	Alignment	not modelled	100.0	16	<b>Chain:</b> A; <b>PDB Molecule:</b> nucleotide-sugar aminotransferase; <b>PDBTitle:</b> structure of an aminotransferase (degt-dnrj-eryc1-strs family) from <i>Coxiella burnetii</i> in complex with pmp
104	<a href="#">c3p1tB</a>	Alignment	not modelled	100.0	17	<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) from <i>Burkholderia pseudomallei</i> K96243 at 2.60 Å resolution
105	<a href="#">d1fg7a</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
106	<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
107	<a href="#">d2bwna1</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
108	<a href="#">c4cvqB</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> glutamate-pyruvate aminotransferase alaA; <b>PDBTitle:</b> crystal structure of an aminotransferase from <i>Escherichia coli</i> at 2.2 Å resolution
109	<a href="#">c3hbxB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> glutamate decarboxylase 1; <b>PDBTitle:</b> crystal structure of gad1 from <i>Arabidopsis thaliana</i>
110	<a href="#">c3pplB</a>	Alignment	not modelled	100.0	13	<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 <i>Corynebacterium glutamicum</i> ATCC 13032 Kitasato at 1.25 Å resolution
111	<a href="#">d2r5ea1</a>	Alignment	not modelled	100.0	11	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
112	<a href="#">c3b1dD</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> lyase <b>Chain:</b> D; <b>PDB Molecule:</b> betac-s lyase; <b>PDBTitle:</b> crystal structure of betac-s lyase from <i>Streptococcus anginosus</i> IN2 complex with L-serine: external aldimine form
113	<a href="#">c3if2B</a>	Alignment	not modelled	100.0	11	<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 <i>Psychrobacter arcticum</i> 273-4 at 2.50 Å resolution
114	<a href="#">d1mdoa</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
115	<a href="#">d1v2da</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
116	<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
117	<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
118	<a href="#">c3fkdC</a>	Alignment	not modelled	100.0	13	<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-phosphate decarboxylase from <i>Porphyromonas gingivalis</i>
119	<a href="#">c6f35B</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> aspartate aminotransferase b; <b>PDBTitle:</b> crystal structure of the aspartate aminotransferase from <i>Rhizobium meliloti</i>
120	<a href="#">c6hrhA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> 5-aminolevulinate synthase, erythroid-specific, <b>PDBTitle:</b> structure of human erythroid-specific 5'-aminolevulinate synthase,2 alas2