

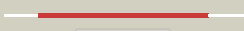





















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1079_(metB)_1204072_1205238
Date	Wed Jul 31 22:05:15 BST 2019
Unique Job ID	a17ea121abb5b8e1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ndnC_</a>	 Alignment		100.0	35	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> o-succinylhomoserine sulfhydrylase; <b>PDBTitle:</b> crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
2	<a href="#">d2ctza1</a>	 Alignment		100.0	34	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
3	<a href="#">c5x5hA_</a>	 Alignment		100.0	63	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cystathionine beta-lyases/cystathionine gamma-synthases; <b>PDBTitle:</b> crystal structure of metb from corynebacterium glutamicum
4	<a href="#">d1y4ia1</a>	 Alignment		100.0	41	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
5	<a href="#">c6cjbA_</a>	 Alignment		100.0	50	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cystathionine beta-lyase; <b>PDBTitle:</b> crystal structure of cystathionine beta-lyase from legionella2 pneumophila philadelphia 1 covalently bound to pyridoxal phosphate
6	<a href="#">d1qgna_</a>	 Alignment		100.0	38	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
7	<a href="#">c2nmpC_</a>	 Alignment		100.0	47	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> cystathionine gamma-lyase; <b>PDBTitle:</b> crystal structure of human cystathionine gamma lyase
8	<a href="#">c2cb1A_</a>	 Alignment		100.0	39	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> o-acetyl homoserine sulfhydrylase; <b>PDBTitle:</b> crystal structure of o-acetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
9	<a href="#">c5dx5B_</a>	 Alignment		100.0	43	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> methionine gamma-lyase; <b>PDBTitle:</b> crystal structure of methionine gamma-lyase from clostridium2 sporogenes
10	<a href="#">d1e5ea_</a>	 Alignment		100.0	40	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
11	<a href="#">c5jigB_</a>	 Alignment		100.0	35	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cys/met metabolism pyridoxal-phosphate-dependent enzyme; <b>PDBTitle:</b> crystal structure of o-acetylhomoserine sulfhydrylase from brucella2 melitensis at 2.0 a resolution

12	<a href="#">d1n8pa_</a>	Alignment		100.0	48	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
13	<a href="#">c2gqnB_</a>	Alignment		100.0	30	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cystathionine beta-lyase; <b>PDBTitle:</b> cystathionine beta-lyase (cbl) from escherichia coli in complex with2 n-hydrazinocarbonylmethyl-2-nitro-benzamide
14	<a href="#">c3qi6B_</a>	Alignment		100.0	86	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cystathionine gamma-synthase metb (cgs); <b>PDBTitle:</b> crystal structure of cystathionine gamma-synthase metb (cgs) from2 mycobacterium ulcerans agy99
15	<a href="#">d1cl1a_</a>	Alignment		100.0	29	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
16	<a href="#">c1i41j_</a>	Alignment		100.0	38	<b>PDB header:</b> lyase <b>Chain:</b> J: <b>PDB Molecule:</b> cystathionine gamma-synthase; <b>PDBTitle:</b> cystathionine gamma-synthase in complex with the inhibitor2 appa
17	<a href="#">d1csl1a_</a>	Alignment		100.0	43	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
18	<a href="#">c3aemD_</a>	Alignment		100.0	40	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> methionine gamma-lyase; <b>PDBTitle:</b> reaction intermediate structure of entamoeba histolytica methionine2 gamma-lyase 1 containing michaelis complex and methionine imine-3 pyridoxamine-5'-phosphate
19	<a href="#">c1ibjC_</a>	Alignment		100.0	42	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> cystathionine beta-lyase; <b>PDBTitle:</b> crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana
20	<a href="#">d1libja_</a>	Alignment		100.0	42	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
21	<a href="#">c4oc9N_</a>	Alignment	not modelled	100.0	35	<b>PDB header:</b> lyase <b>Chain:</b> N: <b>PDB Molecule:</b> putative o-acetylhomoserine (thiol)-lyase; <b>PDBTitle:</b> 2.35 angstrom resolution crystal structure of putative o-2 acetylhomoserine (thiol)-lyase (mety) from campylobacter jejuni3 subsp. jejuni nctc 11168 with n'-pyridoxyl-lysine-5'-monophosphate at4 position 205
22	<a href="#">c3e6gA_</a>	Alignment	not modelled	100.0	56	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cystathionine gamma-lyase-like protein; <b>PDBTitle:</b> crystal structure of xometc, a cystathionine c-lyase-like2 protein from xanthomonas oryzae pv.oryzae
23	<a href="#">c4i0oA_</a>	Alignment	not modelled	100.0	51	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cystathionine gamma-synthase; <b>PDBTitle:</b> structure determination of cystathionine gamma-synthase from2 helicobacter pylori
24	<a href="#">c4q31A_</a>	Alignment	not modelled	100.0	43	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cystathione gamma lyase cale6; <b>PDBTitle:</b> the crystal structure of cystathione gamma lyase (cale6) from2 micromonospora echinospora
25	<a href="#">d1gc0a_</a>	Alignment	not modelled	100.0	43	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
26	<a href="#">c4kamC_</a>	Alignment	not modelled	100.0	40	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> o-acetylhomoserine sulfhydrylase metc; <b>PDBTitle:</b> x-ray crystal structure of o-acetylhomoserine sulfhydrylase metc from2 mycobacterium marinum atcc baa-535 / m
27	<a href="#">c5tt2D_</a>	Alignment	not modelled	100.0	44	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> cystathionine gamma-lyase; <b>PDBTitle:</b> inactive conformation of engineered human cystathionine gamma lyase2 (e59n, r119l, e339v) to depleting methionine
						<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-acetylhomoserine sulfhydrylase;

28	<a href="#">c3ri6A_</a>	Alignment	not modelled	100.0	34	<b>PDBTitle:</b> a novel mechanism of sulfur transfer catalyzed by o-acetylhomoserine2 sulfhydrylase in methionine biosynthetic pathway of wolinnella3 succinogenes <b>PDB header:</b> unknown function
29	<a href="#">c4j8IA_</a>	Alignment	not modelled	100.0	16	<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
30	<a href="#">d1pffa_</a>	Alignment	not modelled	100.0	41	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
31	<a href="#">c3ht4B_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> aluminum resistance protein; <b>PDBTitle:</b> crystal structure of the q81a77_baccr protein from bacillus cereus.2 northeast structural genomics consortium target bcr213
32	<a href="#">c3hvyC_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> cystathionine beta-lyase family protein, ynbb b.subtilis <b>PDBTitle:</b> crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_348457.1) from clostridium acetobutylicum at3 2.00 a resolution
33	<a href="#">c3fd0B_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative cystathionine beta-lyase involved in aluminum <b>PDBTitle:</b> crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_470671.1) from listeria innocua at 2.12 a3 resolution
34	<a href="#">c5w70B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> l-glutamine:2-deoxy-scylo-inosose aminotransferase; <b>PDBTitle:</b> x-ray structure of rbmb from streptomyces ribosidificus
35	<a href="#">c3bcxA_</a>	Alignment	not modelled	100.0	17	<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
36	<a href="#">c4k2bA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ntd biosynthesis operon protein ntda; <b>PDBTitle:</b> crystal structure of ntda from bacillus subtilis in complex with the2 internal aldimine
37	<a href="#">c5k8bA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 8-amino-3,8-dideoxy-alpha-d-manno-octulosonate <b>PDBTitle:</b> x-ray structure of kdna, 8-amino-3,8-dideoxy-alpha-d-manno-2 octulosonate transaminase, from shewanella oneidensis in the presence3 of the external aldimine with plp and glutamate
38	<a href="#">c3gwpA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carbon-sulfur lyase involved in aluminum resistance; <b>PDBTitle:</b> crystal structure of carbon-sulfur lyase involved in aluminum2 resistance (yp_878183.1) from clostridium novyi nt at 2.90 a3 resolution
39	<a href="#">c2po3B_</a>	Alignment	not modelled	100.0	17	<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
40	<a href="#">d1b9ha_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
41	<a href="#">c2c7tA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-2-deoxy-scylo-inosose aminotransferase; <b>PDBTitle:</b> crystal structure of the plp-bound form of bttr, a dual functional2 aminotransferase involved in butirosin biosynthesis.
42	<a href="#">c3ju7B_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative plp-dependent aminotransferase; <b>PDBTitle:</b> crystal structure of putative plp-dependent aminotransferase2 (np_978343.1) from bacillus cereus atcc 10987 at 2.19 a resolution
43	<a href="#">d1o69a_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
44	<a href="#">d1mdoa_</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
45	<a href="#">c2r0tA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxamine 5-phosphate-dependent dehydrase; <b>PDBTitle:</b> crystal structure of gdp-4-keto-6-deoxymannose-3-dehydratase with a2 trapped plp-glutamate geminal diamine
46	<a href="#">c3dr4B_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative perosamine synthetase; <b>PDBTitle:</b> gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
47	<a href="#">c3nysA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase wbpe; <b>PDBTitle:</b> x-ray structure of the k185a mutant of wbpe (wlbe) from pseudomonas2 aeruginosa in complex with plp at 1.45 angstrom resolution
48	<a href="#">c4qgrA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> degt/dnrj/eryc1/strs aminotransferase; <b>PDBTitle:</b> crystal structure of a degt dnrj eryc1 strs aminotransferase from2 brucella abortus
49	<a href="#">c2ogeC_</a>	Alignment	not modelled	100.0	23	<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
50	<a href="#">c3frkB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> qdtb; <b>PDBTitle:</b> x-ray structure of qdtb from t. thermosaccharolyticum in2 complex with a plp:tdp-3-aminoquinovose aldimine

51	<a href="#">c5uidC</a>	Alignment	not modelled	100.0	15	<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
52	<a href="#">c5z0yA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystallization and structure determination of cytoplasm serine2 hydroxymethyltransferase (shmt) from pichia pastoris
53	<a href="#">c3hqtB</a>	Alignment	not modelled	100.0	15	<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
54	<a href="#">c3uwcA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotide-sugar aminotransferase; <b>PDBTitle:</b> structure of an aminotransferase (degt-dnrj-eryc1-strs family) from2 coxiella burnetii in complex with pmp
55	<a href="#">c4ytjC</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> cals13; <b>PDBTitle:</b> crystal structure of sugar aminotransferase cals13 from micromonospora2 echinospora
56	<a href="#">c3caiA</a>	Alignment	not modelled	100.0	17	<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
57	<a href="#">c4xauG</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> putative aminotransferase; <b>PDBTitle:</b> crystal structure of ats13 from actinomadura melliaura
58	<a href="#">c3wy7D</a>	Alignment	not modelled	100.0	21	<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
59	<a href="#">c2w8wA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine palmitoyltransferase; <b>PDBTitle:</b> n100y spt with plp-ser
60	<a href="#">c5u20C</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> putative aminotransferase; <b>PDBTitle:</b> x-ray structure of the wlarg aminotransferase from campylobacter2 jejuni, internal plp-aldimine
61	<a href="#">c4bhel</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> I: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> methanococcus jannaschii serine hydroxymethyltransferase2 in complex with plp
62	<a href="#">c6hrhA</a>	Alignment	not modelled	100.0	14	<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
63	<a href="#">c4wxfC</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of l-serine hydroxymethyltransferase in complex with2 glycine
64	<a href="#">c3ecdC</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> serine hydroxymethyltransferase 2; <b>PDBTitle:</b> crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei
65	<a href="#">c3a2bA</a>	Alignment	not modelled	100.0	13	<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
66	<a href="#">d2fnua1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
67	<a href="#">d2bwna1</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
68	<a href="#">d1bs0a</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
69	<a href="#">c4lc3B</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative udp-4-amino-4-deoxy-l-arabinose-oxoglutarate <b>PDBTitle:</b> x-ray crystal structure of a putative udp-4-amino-4-deoxy-l-arabinose-2-oxoglutarate aminotransferase from burkholderia cenocepacia
70	<a href="#">c5txtA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-aminolevulinate synthase, mitochondrial; <b>PDBTitle:</b> structure of asymmetric apo/holo alas dimer from s. cerevisiae
71	<a href="#">c3lwsF</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> aromatic amino acid beta-eliminating lyase/threonine <b>PDBTitle:</b> crystal structure of putative aromatic amino acid beta-eliminating2 lyase/threonine aldolase. (yp_001813866.1) from exiguobacterium sp.3 255-15 at 2.00 a resolution
72	<a href="#">d1kl1a</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
73	<a href="#">c3pj0D</a>	Alignment	not modelled	100.0	15	<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
74	<a href="#">c4j5uB</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> x-ray crystal structure of a serine hydroxymethyltransferase with2 covalently bound plp from rickettsia rickettsii str. sheila smith
						<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative capsular polysaccharide

75	<a href="#">c6ewqA_</a>	Alignment	not modelled	100.0	17	biosynthesis protein; <b>PDBTitle:</b> putative sugar aminotransferase spr1654 from streptococcus pneumoniae,2 plp-form
76	<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
77	<a href="#">d1vjoa_</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
78	<a href="#">c5vc2A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of a serine hydroxymethyltransferase from2 helicobacter pylori
79	<a href="#">c3w1hB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> l-seryl-trna(sec) selenium transferase; <b>PDBTitle:</b> crystal structure of the selenocysteine synthase sela from aquifex2 aeolicus
80	<a href="#">c3wgcB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> l-allo-threonine aldolase; <b>PDBTitle:</b> aeromonas jandaei l-allo-threonine aldolase h128y/s292r double mutant
81	<a href="#">c5utsC_</a>	Alignment	not modelled	100.0	12	<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
82	<a href="#">c6hnuA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aromatic amino acid aminotransferase i; <b>PDBTitle:</b> crystal structure of the aminotransferase aro8 from c. albicans with2 ligands
83	<a href="#">d1c4ka2</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Ornithine decarboxylase major domain
84	<a href="#">c3vaxA_</a>	Alignment	not modelled	100.0	13	<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
85	<a href="#">c2dkjB_</a>	Alignment	not modelled	100.0	19	<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
86	<a href="#">c3e9kA_</a>	Alignment	not modelled	100.0	11	<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
87	<a href="#">c4iw7A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 8-amino-7-oxonanoate synthase; <b>PDBTitle:</b> crystal structure of 8-amino-7-oxonanoate synthase (biof) from2 francisella tularensis.
88	<a href="#">c3mafB_</a>	Alignment	not modelled	100.0	22	<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)
89	<a href="#">d1qz9a_</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
90	<a href="#">c3n0lA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
91	<a href="#">c4n0wA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> x-ray crystal structure of a serine hydroxymethyltransferase from2 burkholderia cenocepacia with covalently attached pyridoxal phosphate
92	<a href="#">c3hbxB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate decarboxylase 1; <b>PDBTitle:</b> crystal structure of gad1 from arabidopsis thaliana
93	<a href="#">d2hoxa1</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
94	<a href="#">d1jf9a_</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
95	<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
96	<a href="#">c5jayB_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 8-amino-7-oxonanoate synthase; <b>PDBTitle:</b> crystal structure of an 8-amino-7-oxonanoate synthase from2 burkholderia xenovorans
97	<a href="#">c4je5C_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> aromatic/aminoadipate aminotransferase 1; <b>PDBTitle:</b> crystal structure of the aromatic aminotransferase aro8, a putative2 alpha-aminoadipate aminotransferase in saccharomyces cerevisiae
98	<a href="#">c4q6rB_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> lyase/lyase inhibitor <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
99	<a href="#">c3tqxA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-amino-3-ketobutyrate coenzyme a ligase; <b>PDBTitle:</b> structure of the 2-amino-3-ketobutyrate coenzyme a ligase (kbl) from2 coxiella burnetii



100	<a href="#">c2hdyA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> selenocysteine lyase; <b>PDBTitle:</b> structure of human selenocysteine lyase
101	<a href="#">c4lnjA_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> low-specificity l-threonine aldolase; <b>PDBTitle:</b> structure of escherichia coli threonine aldolase in unliganded form
102	<a href="#">d1w7la_</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
103	<a href="#">c5zsqa_</a>	Alignment	not modelled	99.9	13	<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
104	<a href="#">d1fc4a_</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="#">d2v1pa1</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Beta-eliminating lyases
106	<a href="#">d2r5ea1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
107	<a href="#">c3b46B_</a>	Alignment	not modelled	99.9	13	<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
108	<a href="#">c6c3aB_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> o2-, plp-dependent l-arginine hydroxylase rohp 4-hydroxy-2-2 ketoarginine complex
109	<a href="#">c2hzpA_</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> kynureninase; <b>PDBTitle:</b> crystal structure of homo sapiens kynureninase
110	<a href="#">d1m6sa_</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
111	<a href="#">c3eucB_</a>	Alignment	not modelled	99.9	19	<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
112	<a href="#">c4eb5B_</a>	Alignment	not modelled	99.9	14	<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
113	<a href="#">c3kaxB_</a>	Alignment	not modelled	99.9	16	<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
114	<a href="#">c3h14A_</a>	Alignment	not modelled	99.9	16	<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
115	<a href="#">c6hndA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> aromatic-amino-acid:2-oxoglutarate transaminase; <b>PDBTitle:</b> crystal structure of the aromatic aminotransferase aro9 from c.2 albicans
116	<a href="#">c3l8aB_</a>	Alignment	not modelled	99.9	21	<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
117	<a href="#">c3hdoB_</a>	Alignment	not modelled	99.9	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
118	<a href="#">c3jtxB_</a>	Alignment	not modelled	99.9	14	<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
119	<a href="#">c6c9eB_</a>	Alignment	not modelled	99.9	15	<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
120	<a href="#">d3bc8a1</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> SepSecS-like