

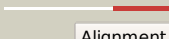
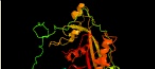

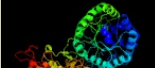
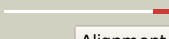
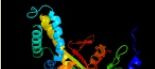
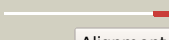








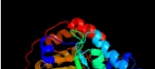



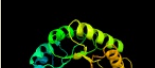





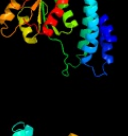


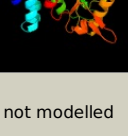


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2124c_(metH)_2382497_2386075
Date	Mon Aug 5 13:25:24 BST 2019
Unique Job ID	f66487ff9dae111b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4cczA_</a>	 Alignment		100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine synthase; <b>PDBTitle:</b> crystal structure of human 5-methyltetrahydrofolate-homocysteine2 methyltransferase, the homocysteine and folate binding domains
2	<a href="#">c1k98A_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine synthase; <b>PDBTitle:</b> adomet complex of meth c-terminal fragment
3	<a href="#">c3bolB_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 5-methyltetrahydrofolate s-homocysteine <b>PDBTitle:</b> cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
4	<a href="#">c2o2kA_</a>	 Alignment		100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine synthase; <b>PDBTitle:</b> crystal structure of the activation domain of human2 methionine synthase isoform/mutant d963e/k1071n
5	<a href="#">d1mska_</a>	 Alignment		100.0	27	<b>Fold:</b> Methionine synthase activation domain-like <b>Superfamily:</b> Methionine synthase activation domain-like <b>Family:</b> Methionine synthase SAM-binding domain
6	<a href="#">d1umya_</a>	 Alignment		100.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Homocysteine S-methyltransferase <b>Family:</b> Homocysteine S-methyltransferase
7	<a href="#">c5vooB_</a>	 Alignment		100.0	49	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 5-methyltetrahydrofolate homocysteine s-methyltransferase; <b>PDBTitle:</b> methionine synthase folate-binding domain with methyltetrahydrofolate2 from thermus thermophilus hb8
8	<a href="#">c3k13A_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methyltetrahydrofolate-homocysteine methyltransferase; <b>PDBTitle:</b> structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
9	<a href="#">d3bofa2</a>	 Alignment		100.0	35	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Homocysteine S-methyltransferase <b>Family:</b> Homocysteine S-methyltransferase
10	<a href="#">d1lt7a_</a>	 Alignment		100.0	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Homocysteine S-methyltransferase <b>Family:</b> Homocysteine S-methyltransferase
11	<a href="#">c4o1fB_</a>	 Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydropteroate synthase dhps; <b>PDBTitle:</b> structure of a methyltransferase component in complex with thf2 involved in o-demethylation

12	<a href="#">c5dmnA_</a>	Alignment		100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homocysteine s-methyltransferase; <b>PDBTitle:</b> crystal structure of the homocysteine methyltransferase mmum from2 escherichia coli, apo form
13	<a href="#">c2yciX_</a>	Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> 5-methyltetrahydrofolate corrinoid/iron sulfur protein <b>PDBTitle:</b> methyltransferase native
14	<a href="#">d3bofa1</a>	Alignment		100.0	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Methyltetrahydrofolate-utilizing methyltransferases
15	<a href="#">d1f6ya_</a>	Alignment		100.0	28	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Methyltetrahydrofolate-utilizing methyltransferases
16	<a href="#">c1bmtB_</a>	Alignment		100.0	35	<b>PDB header:</b> methyltransferase <b>Chain:</b> B: <b>PDB Molecule:</b> methionine synthase; <b>PDBTitle:</b> how a protein binds b12: a 3.0 angstrom x-ray structure of2 the b12-binding domains of methionine synthase
17	<a href="#">c2i2xD_</a>	Alignment		100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> methyltransferase 1; <b>PDBTitle:</b> crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
18	<a href="#">c3ezxA_</a>	Alignment		100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> monomethylamine corrinoid protein 1; <b>PDBTitle:</b> structure of methanosarcina barkeri monomethylamine2 corrinoid protein
19	<a href="#">d3bula2</a>	Alignment		100.0	31	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
20	<a href="#">c4jgiB_</a>	Alignment		100.0	28	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> 1.5 angstrom crystal structure of a novel cobalamin-binding protein2 from desulfitobacterium hafniense dcb-2
21	<a href="#">c1xrsB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> d-lysine 5,6-aminomutase beta subunit; <b>PDBTitle:</b> crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
22	<a href="#">c4hh3C_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> flavoprotein/transcription <b>Chain:</b> C: <b>PDB Molecule:</b> appa protein; <b>PDBTitle:</b> structure of the appa-ppsr2 core complex from rb. sphaeroides
23	<a href="#">c1tx2A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dhps, dihydropteroate synthase; <b>PDBTitle:</b> dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
24	<a href="#">d1tx2a_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
25	<a href="#">d1j6ra_</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Methionine synthase activation domain-like <b>Superfamily:</b> Methionine synthase activation domain-like <b>Family:</b> Hypothetical protein TM0269
26	<a href="#">d1ad1a_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
27	<a href="#">d1ajza_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
28	<a href="#">c5uurA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> xanthomonas albilineans dihydropteroate synthase with 4-aminobenzoic2 acid <b>PDB header:</b> gene regulation

29	<a href="#">c3whpA</a>	Alignment	not modelled	100.0	20	<b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> crystal structure of the c-terminal domain of themus thermophilus litr2 in complex with cobalamin
30	<a href="#">d1xrsb1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
31	<a href="#">c6cluC</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> C: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> staphylococcus aureus dihydropteroate synthase (sadhps) f17l e208k2 double mutant structure
32	<a href="#">c3tr9A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> structure of a dihydropteroate synthase (folp) in complex with pteroi2 acid from coxiella burnetii
33	<a href="#">c2y5aA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
34	<a href="#">c5visB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase,oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> 1.73 angstrom resolution crystal structure of dihydropteroate synthase2 (folp-smz_b27) from soil uncultured bacterium.
35	<a href="#">c6omzA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> crystal structure of dihydropteroate synthase from mycobacterium2 smegmatis with bound 6-hydroxymethylpterin-monophosphate
36	<a href="#">c5uswD</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> the crystal structure of 7,8-dihydropteroate synthase from vibrio2 fischeri es114
37	<a href="#">c2vp8A</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase 2; <b>PDBTitle:</b> structure of mycobacterium tuberculosis rv1207
38	<a href="#">c1y80A</a>	Alignment	not modelled	99.9	37	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> predicted cobalamin binding protein; <b>PDBTitle:</b> structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica
39	<a href="#">c4djdD</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase/vitamin-binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> corrinoid/iron-sulfur protein small subunit; <b>PDBTitle:</b> crystal structure of folate-free corrinoid iron-sulfur protein (cfesp)2 in complex with its methyltransferase (metr)
40	<a href="#">d1leyea</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
41	<a href="#">c2dzaA</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
42	<a href="#">c2h9aB</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> co dehydrogenase/acetyl-coa synthase, iron-sulfur protein; <b>PDBTitle:</b> corrinoid iron-sulfur protein
43	<a href="#">d3bula1</a>	Alignment	not modelled	99.9	44	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Methionine synthase domain <b>Family:</b> Methionine synthase domain
44	<a href="#">c5c8eC</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> C: <b>PDB Molecule:</b> light-dependent transcriptional regulator carh; <b>PDBTitle:</b> crystal structure of thermus thermophilus carh bound to2 adenosylcobalamin and a 26-bp dna segment
45	<a href="#">c2vefB</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> dihydropteroate synthase from streptococcus pneumoniae
46	<a href="#">d7reqa2</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
47	<a href="#">d1ccwa</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
48	<a href="#">d1fmfa</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
49	<a href="#">c4mwaA</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; <b>PDBTitle:</b> 1.85 angstrom crystal structure of gcpe protein from bacillus2 anthracis
50	<a href="#">c2yxbA</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme b12-dependent mutase; <b>PDBTitle:</b> crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
51	<a href="#">c4r3uD</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-hydroxyisobutyryl-coa mutase small subunit; <b>PDBTitle:</b> crystal structure of 2-hydroxyisobutyryl-coa mutase
52	<a href="#">c2h9aA</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> carbon monoxide dehydrogenase corrinoid/iron-sulfur <b>PDBTitle:</b> corrinoid iron-sulfur protein
53	<a href="#">c3mcnA</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine <b>PDBTitle:</b> crystal structure of the 6-hydroxymethyl-7,8-dihydropterin2 pyrophosphokinase dihydropteroate synthase bifunctional enzyme from3 francisella tularensis

54	<a href="#">c4hh0B_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> flavoprotein,signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> appa protein; <b>PDBTitle:</b> dark-state structure of appa c20s without the cys-rich region from rb.2 sphaeroides
55	<a href="#">c4djeE_</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> transferase/vitamin-binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> corrinoide/iron-sulfur protein large subunit; <b>PDBTitle:</b> crystal structure of folate-bound corrinoide iron-sulfur protein2 (cfesp) in complex with its methyltransferase (metr), co-crystallized3 with folate
56	<a href="#">c5z79F_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> hydroxymethyldihydropterin pyrophosphokinase- <b>PDBTitle:</b> crystal structure analysis of the hppk-dhps in complex with substrates
57	<a href="#">c2bmbA_</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> folic acid synthesis protein foll1; <b>PDBTitle:</b> x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropterate synthase from3 saccharomyces cerevisiae
58	<a href="#">c3noyA_</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; <b>PDBTitle:</b> crystal structure of ispg (gcpe)
59	<a href="#">c3bicA_</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> methylmalonyl-coa mutase, mitochondrial precursor; <b>PDBTitle:</b> crystal structure of human methylmalonyl-coa mutase
60	<a href="#">c2yclA_</a>	Alignment	not modelled	98.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carbon monoxide dehydrogenase corrinoide/iron-sulfur <b>PDBTitle:</b> complete structure of the corrinoide,iron-sulfur protein including2 the n-terminal domain with a 4fe-4s cluster
61	<a href="#">c3koxA_</a>	Alignment	not modelled	98.7	23	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-ornithine aminomutase e component; <b>PDBTitle:</b> crystal structure of ornithine 4,5 aminomutase in complex with 2,4-2 diaminobutyrate (anaerobic)
62	<a href="#">c4xc8B_</a>	Alignment	not modelled	98.1	23	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> isobutyryl-coa mutase fused; <b>PDBTitle:</b> isobutyryl-coa mutase fused with bound butyryl-coa, gdp, and mg and2 without cobalamin (apo-icmf/gdp)
63	<a href="#">d1ka9f_</a>	Alignment	not modelled	97.8	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
64	<a href="#">c4i7vD_</a>	Alignment	not modelled	97.7	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> agrobacterium tumefaciens dhps with pyruvate
65	<a href="#">c6h4eB_</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative n-acetylneuraminate lyase; <b>PDBTitle:</b> proteus mirabilis n-acetylneuraminate lyase
66	<a href="#">c4qj1A_</a>	Alignment	not modelled	97.2	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) <b>PDBTitle:</b> crystal structure of 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)2 methylideneamino] imidazole-4-carboxamide isomerase (hisa).
67	<a href="#">c1e1cA_</a>	Alignment	not modelled	97.2	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> methylmalonyl-coa mutase alpha chain; <b>PDBTitle:</b> methylmalonyl-coa mutase h244a mutant
68	<a href="#">c3s5oA_</a>	Alignment	not modelled	97.1	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-2-oxoglutarate aldolase, mitochondrial; <b>PDBTitle:</b> crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate
69	<a href="#">c3noeA_</a>	Alignment	not modelled	96.6	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
70	<a href="#">d1h5ya_</a>	Alignment	not modelled	96.6	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
71	<a href="#">c6daoB_</a>	Alignment	not modelled	96.5	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; <b>PDBTitle:</b> nahe wt selenomethionine
72	<a href="#">c3eb2A_</a>	Alignment	not modelled	96.4	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dihydrodipicolinate synthetase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 2.0a resolution
73	<a href="#">c2ehhE_</a>	Alignment	not modelled	96.3	19	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
74	<a href="#">c5ud6B_</a>	Alignment	not modelled	96.3	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dhps from cyanidioschyzon merolae with lysine2 bound
75	<a href="#">c2r8wB_</a>	Alignment	not modelled	96.2	10	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> agr_c_1641p; <b>PDBTitle:</b> the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
76	<a href="#">c3fluD_</a>	Alignment	not modelled	96.2	13	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
77	<a href="#">c2vc6A_</a>	Alignment	not modelled	96.1	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> structure of mosa from s. meliloti with pyruvate bound
						<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> oxsb protein;

78	<a href="#">c5ul4A</a>	Alignment	not modelled	96.1	16	<b>PDBTitle:</b> structure of cobalamin-dependent s-adenosylmethionine radical enzyme2 oxsb with aqua-cobalamin and s-adenosylmethionine bound
79	<a href="#">c3n2xB</a>	Alignment	not modelled	96.0	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yage; <b>PDBTitle:</b> crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
80	<a href="#">c3lerA</a>	Alignment	not modelled	95.9	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
81	<a href="#">d1o5ka</a>	Alignment	not modelled	95.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
82	<a href="#">c4axkB</a>	Alignment	not modelled	95.8	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 1-(5-phosphoribosyl)-5-((5'-phosphoribosylamino) <b>PDBTitle:</b> crystal structure of subhisa from the thermophile corynebacterium2 efficiens
83	<a href="#">c2y0fD</a>	Alignment	not modelled	95.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; <b>PDBTitle:</b> structure of gcpe (ispg) from thermus thermophilus hb27
84	<a href="#">c3eool</a>	Alignment	not modelled	95.6	23	<b>PDB header:</b> lyase <b>Chain:</b> L: <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
85	<a href="#">c4xkyC</a>	Alignment	not modelled	95.6	14	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> structure of dihydrodipicolinate synthase from the commensal bacterium2 bacteroides thetaiotaomicron at 2.1 a resolution
86	<a href="#">c5c54D</a>	Alignment	not modelled	95.5	14	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase/n-acetylneuraminatase lyase; <b>PDBTitle:</b> crystal structure of a novel n-acetylneuraminic acid lyase from2 corynebacterium glutamicum
87	<a href="#">c3fkkA</a>	Alignment	not modelled	95.4	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-2-keto-3-deoxyarabonate dehydratase; <b>PDBTitle:</b> structure of l-2-keto-3-deoxyarabonate dehydratase
88	<a href="#">c3dz1A</a>	Alignment	not modelled	95.3	9	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 1.87a resolution
89	<a href="#">c2v9dB</a>	Alignment	not modelled	95.3	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> yage; <b>PDBTitle:</b> crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12
90	<a href="#">d1muma</a>	Alignment	not modelled	95.2	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/Isocitrate lyase-like
91	<a href="#">c3na8A</a>	Alignment	not modelled	95.1	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dihydrodipicolinate synthetase; <b>PDBTitle:</b> crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
92	<a href="#">c4nq1B</a>	Alignment	not modelled	95.1	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate synthase; <b>PDBTitle:</b> legionella pneumophila dihydrodipicolinate synthase with first2 substrate pyruvate bound in the active site
93	<a href="#">c6mqhA</a>	Alignment	not modelled	95.1	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of 4-hydroxy-tetrahydrodipicolinate synthase (htpa2 synthase) from burkholderia mallei
94	<a href="#">d1xxa1</a>	Alignment	not modelled	95.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
95	<a href="#">c5afdA</a>	Alignment	not modelled	95.0	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylneuraminatase lyase; <b>PDBTitle:</b> native structure of n-acetylneuraminatase lyase (sialic acid aldolase)2 from aliivibrio salmonicida
96	<a href="#">c5kt1A</a>	Alignment	not modelled	94.6	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate synthase; <b>PDBTitle:</b> dihydrodipicolinate synthase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
97	<a href="#">c3qfeB</a>	Alignment	not modelled	94.6	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative dihydrodipicolinate synthase family protein; <b>PDBTitle:</b> crystal structures of a putative dihydrodipicolinate synthase family2 protein from coccidioides immitis
98	<a href="#">c3e96B</a>	Alignment	not modelled	94.3	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
99	<a href="#">c2y85D</a>	Alignment	not modelled	94.2	24	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosyl isomerase a; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdp
100	<a href="#">c6reqB</a>	Alignment	not modelled	94.1	12	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (methylmalonyl-coa mutase); <b>PDBTitle:</b> methylmalonyl-coa mutase, 3-carboxypropyl-coa inhibitor complex
101	<a href="#">c2fdaA</a>	Alignment	not modelled	94.0	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> orotidine-monophosphate-decarboxylase; <b>PDBTitle:</b> crystal structure of plasmodium berghei orotidine 5'-monophosphate2 decarboxylase (ortholog of plasmodium falciparum pf10 0225)
102	<a href="#">d2fda1</a>	Alignment	not modelled	94.0	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase

103	<a href="#">c3bi8A_</a>	Alignment	not modelled	93.9	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> structure of dihydrodipicolinate synthase from clostridium2 botulinum
104	<a href="#">c5ks8D_</a>	Alignment	not modelled	93.9	16	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate carboxylase subunit beta; <b>PDBTitle:</b> crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
105	<a href="#">c2r94B_</a>	Alignment	not modelled	93.8	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-keto-3-deoxy-(6-phospho-)gluconate aldolase; <b>PDBTitle:</b> crystal structure of kd(p)ga from t.tenax
106	<a href="#">d1thfd_</a>	Alignment	not modelled	93.8	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
107	<a href="#">c2qw5B_</a>	Alignment	not modelled	93.7	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> xylose isomerase-like tim barrel; <b>PDBTitle:</b> crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
108	<a href="#">d1jvna1</a>	Alignment	not modelled	93.7	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
109	<a href="#">c3d0cB_</a>	Alignment	not modelled	93.4	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
110	<a href="#">d2ffca1</a>	Alignment	not modelled	93.3	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
111	<a href="#">c3daqB_</a>	Alignment	not modelled	93.1	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
112	<a href="#">d1bwva1</a>	Alignment	not modelled	93.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
113	<a href="#">c2rfqB_</a>	Alignment	not modelled	92.9	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
114	<a href="#">d1h7na_</a>	Alignment	not modelled	92.6	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
115	<a href="#">d2c1ha1</a>	Alignment	not modelled	92.5	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
116	<a href="#">d1l6sa_</a>	Alignment	not modelled	92.4	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
117	<a href="#">c6daqA_</a>	Alignment	not modelled	92.4	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phdj; <b>PDBTitle:</b> phdj bound to substrate intermediate
118	<a href="#">c1jvnB_</a>	Alignment	not modelled	92.3	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional histidine biosynthesis protein hish3f; <b>PDBTitle:</b> crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
119	<a href="#">c2nx9B_</a>	Alignment	not modelled	92.2	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> oxaloacetate decarboxylase 2, subunit alpha; <b>PDBTitle:</b> crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
120	<a href="#">c4uxdC_</a>	Alignment	not modelled	92.1	12	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-dehydro-3-deoxy-d-gluconate/2-dehydro-3-deoxy- <b>PDBTitle:</b> 2-keto 3-deoxygluconate aldolase from picrophilus torridus