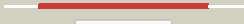



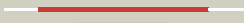



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2225_(panB)_2497750_2498595
Date	Mon Aug 5 13:25:35 BST 2019
Unique Job ID	7edf5c6ebe24fbe9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1o66a_</a>	 Alignment		100.0	47	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Ketopantoate hydroxymethyltransferase PanB
2	<a href="#">d1oy0a_</a>	 Alignment		100.0	100	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Ketopantoate hydroxymethyltransferase PanB
3	<a href="#">d1m3ua_</a>	 Alignment		100.0	45	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Ketopantoate hydroxymethyltransferase PanB
4	<a href="#">c3ez4B_</a>	 Alignment		100.0	46	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-methyl-2-oxobutanoate hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of 3-methyl-2-oxobutanoate hydroxymethyltransferase2 from burkholderia pseudomallei
5	<a href="#">d1ujqa_</a>	 Alignment		100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/Isocitrate lyase-like
6	<a href="#">d1muma_</a>	 Alignment		100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/Isocitrate lyase-like
7	<a href="#">c1zlpA_</a>	 Alignment		100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> petal death protein; <b>PDBTitle:</b> petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
8	<a href="#">c2ze3A_</a>	 Alignment		100.0	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dfa0005; <b>PDBTitle:</b> crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
9	<a href="#">c4lsbA_</a>	 Alignment		100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lyase/mutase; <b>PDBTitle:</b> crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315
10	<a href="#">c3eool_</a>	 Alignment		100.0	16	<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
11	<a href="#">c3ih1A_</a>	 Alignment		100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis

12	<a href="#">c4mg4G_</a>	Alignment		100.0	18	<b>PDB header:</b> unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> phosphonomutase; <b>PDBTitle:</b> crystal structure of a putative phosphonomutase from burkholderia2 cenocepacia j2315
13	<a href="#">c2hjpA_</a>	Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphonopyruvate hydrolase; <b>PDBTitle:</b> crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
14	<a href="#">c2qiwA_</a>	Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pep phosphonomutase; <b>PDBTitle:</b> crystal structure of a putative phosphonopyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
15	<a href="#">c3b8iF_</a>	Alignment		100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> pa4872 oxaloacetate decarboxylase; <b>PDBTitle:</b> crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
16	<a href="#">c3fa4D_</a>	Alignment		100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> 2,3-dimethylmalate lyase; <b>PDBTitle:</b> crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
17	<a href="#">c5uncB_</a>	Alignment		100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoenolpyruvate phosphomutase; <b>PDBTitle:</b> the crystal structure of phosphoenolpyruvate phosphomutase from2 streptomyces platensis subsp. rosaceus
18	<a href="#">c3lyeA_</a>	Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oxaloacetate acetyl hydrolase; <b>PDBTitle:</b> crystal structure of oxaloacetate acetylhydrolase
19	<a href="#">d1s2wa_</a>	Alignment		100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like
20	<a href="#">c3i4eA_</a>	Alignment		99.9	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> isocitrate lyase; <b>PDBTitle:</b> crystal structure of isocitrate lyase from burkholderia2 pseudomallei
21	<a href="#">d1f61a_</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like
22	<a href="#">c3e5bB_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> isocitrate lyase; <b>PDBTitle:</b> 2.4 a crystal structure of isocitrate lyase from brucella melitensis
23	<a href="#">d1igwa_</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like
24	<a href="#">c3eolB_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> isocitrate lyase; <b>PDBTitle:</b> 2.0a crystal structure of isocitrate lyase from brucella melitensis2 (p43212)
25	<a href="#">c5e9fD_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> isocitrate lyase; <b>PDBTitle:</b> structural insights of isocitrate lyases from magnaporthe oryzae
26	<a href="#">d1dqua_</a>	Alignment	not modelled	99.4	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like
27	<a href="#">c6g1oA_</a>	Alignment	not modelled	98.7	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> isocitrate lyase; <b>PDBTitle:</b> structure of pseudomonas aeruginosa isocitrate lyase, icl
28	<a href="#">d1xcfa_</a>	Alignment	not modelled	98.4	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
29	<a href="#">c3vndD_</a>	Alignment	not modelled	97.9	14	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophan synthase alpha chain;

29	<a href="#">c3vhdD_</a>	Alignment	not modelled	97.9	14	<b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2 <b>PDB header:</b> hydrolase
30	<a href="#">c2p10D_</a>	Alignment	not modelled	97.8	22	<b>Chain:</b> D: <b>PDB Molecule:</b> mlI9387 protein; <b>PDBTitle:</b> crystal structure of a putative phosphonopyruvate hydrolase (mlI9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
31	<a href="#">d2p10a1</a>	Alignment	not modelled	97.7	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> MIl9387-like
32	<a href="#">d1qopa_</a>	Alignment	not modelled	97.6	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
33	<a href="#">c3navB_</a>	Alignment	not modelled	97.6	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
34	<a href="#">c2z6jB_</a>	Alignment	not modelled	97.5	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> trans-2-enoyl-acyl reductase ii; <b>PDBTitle:</b> crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor
35	<a href="#">c4iqjB_</a>	Alignment	not modelled	97.5	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase ii; <b>PDBTitle:</b> crystal structure of porphyromonas gingivalis enoyl-acyl reductase ii2 (fabk) with cofactors nadph and fmn
36	<a href="#">c6nkeA_</a>	Alignment	not modelled	97.4	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranylglyceryl phosphate synthase; <b>PDBTitle:</b> wild-type gggps from thermoplasma volcanium
37	<a href="#">c3w9zA_</a>	Alignment	not modelled	97.4	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trna-dihydrouridine synthase c; <b>PDBTitle:</b> crystal structure of dusc
38	<a href="#">c5kzmA_</a>	Alignment	not modelled	97.3	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
39	<a href="#">d1xm3a_</a>	Alignment	not modelled	97.3	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> ThiG-like <b>Family:</b> ThiG-like
40	<a href="#">c3hf3A_</a>	Alignment	not modelled	97.3	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> chromate reductase; <b>PDBTitle:</b> old yellow enzyme from thermus scotoductus sa-01
41	<a href="#">c2htmB_</a>	Alignment	not modelled	97.1	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> thiazole biosynthesis protein thiG; <b>PDBTitle:</b> crystal structure of ttha0676 from thermus thermophilus hb8
42	<a href="#">c4utwB_</a>	Alignment	not modelled	97.1	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative n-acetylmannosamine-6-phosphate 2-epimerase; <b>PDBTitle:</b> structural characterisation of nane, mannac6p c2 epimerase,2 from clostridium perfringens
43	<a href="#">c3bw2A_</a>	Alignment	not modelled	97.1	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-nitropropane dioxygenase; <b>PDBTitle:</b> crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
44	<a href="#">c5zjnB_</a>	Alignment	not modelled	97.1	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative n-acetylmannosamine-6-phosphate 2-epimerase; <b>PDBTitle:</b> structure of n-acetylmannosamine-6-phosphate-2-epimerase from vibrio2 cholerae with n-acetylmannosamine-6-phosphate
45	<a href="#">c4fq5B_</a>	Alignment	not modelled	97.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> maleate cis-trans isomerase; <b>PDBTitle:</b> crystal structure of the maleate isomerase iso(c200a) from pseudomonas2 putida s16 with maleate
46	<a href="#">d1wv2a_</a>	Alignment	not modelled	96.9	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> ThiG-like <b>Family:</b> ThiG-like
47	<a href="#">d1rd5a_</a>	Alignment	not modelled	96.8	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
48	<a href="#">c4n6eA_</a>	Alignment	not modelled	96.8	24	<b>PDB header:</b> lyase/biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative thiosugar synthase; <b>PDBTitle:</b> crystal structure of amycolatopsis orientalis bexx/cyso complex
49	<a href="#">c3igsB_</a>	Alignment	not modelled	96.8	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylmannosamine-6-phosphate 2-epimerase 2; <b>PDBTitle:</b> structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
50	<a href="#">c2vlbC_</a>	Alignment	not modelled	96.8	12	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> arylmalonate decarboxylase; <b>PDBTitle:</b> structure of unliganded arylmalonate decarboxylase
51	<a href="#">c6ofuC_</a>	Alignment	not modelled	96.7	16	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> ydji aldolase; <b>PDBTitle:</b> x-ray crystal structure of the ydji aldolase from escherichia coli k12
52	<a href="#">c4xp7A_</a>	Alignment	not modelled	96.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trna-dihydrouridine(20) synthase [nad(p+)]-like; <b>PDBTitle:</b> crystal structure of human trna dihydrouridine synthase 2
53	<a href="#">c2eq5D_</a>	Alignment	not modelled	96.7	13	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> 228aa long hypothetical hydantoin racemase; <b>PDBTitle:</b> crystal structure of hydantoin racemase from pyrococcus horikoshii ot3
						<b>PDB header:</b> lyase

54	<a href="#">c5afdA_</a>	Alignment	not modelled	96.7	19	<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 alivibrio salmonicida
55	<a href="#">c2ekcA_</a>	Alignment	not modelled	96.7	17	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> structural study of project id aq_1548 from aquifex aeolicus vf5
56	<a href="#">c2qjIA_</a>	Alignment	not modelled	96.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein pa1024; <b>PDBTitle:</b> crystal structure of 2-nitropropane dioxygenase
57	<a href="#">c4zqrD_</a>	Alignment	not modelled	96.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase,inosine-5'- <b>PDBTitle:</b> crystal structure of the catalytic domain of the inosine monophosphate2 dehydrogenase from mycobacterium tuberculosis
58	<a href="#">c3fkkA_</a>	Alignment	not modelled	96.6	18	<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
59	<a href="#">c2hmcA_</a>	Alignment	not modelled	96.6	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
60	<a href="#">c3tsdA_</a>	Alignment	not modelled	96.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of inosine-5'-monophosphate dehydrogenase from2 bacillus anthracis str. ames complexed with xmp
61	<a href="#">c4z87B_</a>	Alignment	not modelled	96.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> structure of the imp dehydrogenase from ashbya gossypii bound to gdp
62	<a href="#">c5lsmF_</a>	Alignment	not modelled	96.5	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F; <b>PDB Molecule:</b> fmn-dependent nitronate monooxygenase; <b>PDBTitle:</b> crystal structure of nitronate monooxygenase (so_0471) from shewanella2 oneidensis mr-1
63	<a href="#">c2rfgB_</a>	Alignment	not modelled	96.5	28	<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
64	<a href="#">c3fluD_</a>	Alignment	not modelled	96.4	23	<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
65	<a href="#">c4af0B_</a>	Alignment	not modelled	96.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of cryptococcal inosine monophosphate2 dehydrogenase
66	<a href="#">c2xecD_</a>	Alignment	not modelled	96.4	16	<b>PDB header:</b> isomerase <b>Chain:</b> D; <b>PDB Molecule:</b> putative maleate isomerase; <b>PDBTitle:</b> nocardia farcinica maleate cis-trans isomerase bound to2 tris
67	<a href="#">c3s5oA_</a>	Alignment	not modelled	96.4	24	<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
68	<a href="#">d1zfa1</a>	Alignment	not modelled	96.4	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
69	<a href="#">c2h90A_</a>	Alignment	not modelled	96.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> xenobiotic reductase a; <b>PDBTitle:</b> xenobiotic reductase a in complex with coumarin
70	<a href="#">c5zknA_</a>	Alignment	not modelled	96.4	11	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> putative n-acetylmannosamine-6-phosphate 2-epimerase; <b>PDBTitle:</b> structure of n-acetylmannosamine-6-phosphate 2-epimerase from2 fusobacterium nucleatum
71	<a href="#">d1xxa1</a>	Alignment	not modelled	96.3	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
72	<a href="#">c6daoB_</a>	Alignment	not modelled	96.3	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
73	<a href="#">c4xkyC_</a>	Alignment	not modelled	96.3	24	<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
74	<a href="#">c4fxsA_</a>	Alignment	not modelled	96.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed2 with imp and mycophenolic acid
75	<a href="#">c6mqbA_</a>	Alignment	not modelled	96.3	21	<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
76	<a href="#">c2v9dB_</a>	Alignment	not modelled	96.2	29	<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
77	<a href="#">c3n2xB_</a>	Alignment	not modelled	96.2	29	<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

78	<a href="#">c3lciA</a>	Alignment	not modelled	96.2	28	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylneuraminate lyase; <b>PDBTitle:</b> the d-sialic acid aldolase mutant v251w
79	<a href="#">c5b69A</a>	Alignment	not modelled	96.2	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranylglyceryl phosphate synthase; <b>PDBTitle:</b> crystal structure of geranylgeranylglyceryl phosphate synthase2 complexed with an g-1-p from thermoplasma acidophilum
80	<a href="#">d1geqa</a>	Alignment	not modelled	96.2	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
81	<a href="#">d1hl2a</a>	Alignment	not modelled	96.2	28	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
82	<a href="#">c4dqwb</a>	Alignment	not modelled	96.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> crystal structure analysis of pa3770
83	<a href="#">c5kinC</a>	Alignment	not modelled	96.2	18	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
84	<a href="#">c3ffsC</a>	Alignment	not modelled	96.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> inosine-5-monophosphate dehydrogenase; <b>PDBTitle:</b> the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
85	<a href="#">c2nuxB</a>	Alignment	not modelled	96.2	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate <b>PDBTitle:</b> 2-keto-3-deoxygluconate aldolase from sulfobolus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
86	<a href="#">c1zfa</a>	Alignment	not modelled	96.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine monophosphate dehydrogenase; <b>PDBTitle:</b> inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
87	<a href="#">c3g0sA</a>	Alignment	not modelled	96.1	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> dihydrodipicolinate synthase from salmonella typhimurium lt2
88	<a href="#">d2a6na1</a>	Alignment	not modelled	96.1	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
89	<a href="#">c3pueA</a>	Alignment	not modelled	96.1	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
90	<a href="#">c5ocsB</a>	Alignment	not modelled	96.1	27	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadh-depentdent flavin oxidoreductase; <b>PDBTitle:</b> ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans
91	<a href="#">d1w3ia</a>	Alignment	not modelled	96.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
92	<a href="#">d1gvfa</a>	Alignment	not modelled	96.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class II FBP aldolase
93	<a href="#">c4ix1B</a>	Alignment	not modelled	96.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of hypothetical protein opag_01669 from rhodococcus2 opacus pd630, target 016205
94	<a href="#">c3na8A</a>	Alignment	not modelled	96.0	26	<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
95	<a href="#">c6ei9A</a>	Alignment	not modelled	96.0	21	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> trna-dihydrouridine synthase b; <b>PDBTitle:</b> crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
96	<a href="#">c6h4eB</a>	Alignment	not modelled	96.0	19	<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
97	<a href="#">c3gr7A</a>	Alignment	not modelled	96.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh dehydrogenase; <b>PDBTitle:</b> structure of oye from geobacillus kaustophilus, hexagonal crystal form
98	<a href="#">c4xtia</a>	Alignment	not modelled	96.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase,inosine-5'- <b>PDBTitle:</b> structure of imp dehydrogenase of ashbya gossypii with imp bound to2 the active site
99	<a href="#">c2qjhH</a>	Alignment	not modelled	96.0	20	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> putative aldolase mj0400; <b>PDBTitle:</b> m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
100	<a href="#">c3cprB</a>	Alignment	not modelled	95.9	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthetase; <b>PDBTitle:</b> the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
101	<a href="#">c5ey5A</a>	Alignment	not modelled	95.9	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lbcats-a; <b>PDBTitle:</b> lbcats
102	<a href="#">c2dgdD</a>	Alignment	not modelled	95.9	14	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> 223aa long hypothetical arylmalonate decarboxylase; <b>PDBTitle:</b> crystal structure of st0656, a function unknown protein

						from2 sulfobolus tokodaii
103	<a href="#">c3lerA_</a>	Alignment	not modelled	95.9	26	<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
104	<a href="#">c4i7vD_</a>	Alignment	not modelled	95.8	28	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> agrobacterium tumefaciens dhdps with pyruvate
105	<a href="#">c3qvjB_</a>	Alignment	not modelled	95.7	20	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative hydantoin racemase; <b>PDBTitle:</b> allantoin racemase from klebsiella pneumoniae
106	<a href="#">c4icnB_</a>	Alignment	not modelled	95.7	24	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> dihydrodipicolinate synthase from shewanella benthica
107	<a href="#">c5z9yB_</a>	Alignment	not modelled	95.7	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thiazole synthase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis thiazole synthase2 (thig) complexed with dxp
108	<a href="#">d1to3a_</a>	Alignment	not modelled	95.7	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
109	<a href="#">c2r94B_</a>	Alignment	not modelled	95.7	22	<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
110	<a href="#">d1y0ea_</a>	Alignment	not modelled	95.6	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> NanE-like
111	<a href="#">c3noeA_</a>	Alignment	not modelled	95.6	15	<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
112	<a href="#">d1jr1a1</a>	Alignment	not modelled	95.6	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
113	<a href="#">c3pm6B_</a>	Alignment	not modelled	95.6	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative fructose-bisphosphate aldolase; <b>PDBTitle:</b> crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
114	<a href="#">d1ojxa_</a>	Alignment	not modelled	95.6	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
115	<a href="#">c3qfeB_</a>	Alignment	not modelled	95.5	20	<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
116	<a href="#">c3si9B_</a>	Alignment	not modelled	95.5	29	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
117	<a href="#">c5ktlA_</a>	Alignment	not modelled	95.5	24	<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.
118	<a href="#">c2ehhE_</a>	Alignment	not modelled	95.5	25	<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
119	<a href="#">c1jcnA_</a>	Alignment	not modelled	95.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine monophosphate dehydrogenase i; <b>PDBTitle:</b> binary complex of human type-i inosine monophosphate dehydrogenase2 with 6-cl-imp
120	<a href="#">c6bkaA_</a>	Alignment	not modelled	95.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitronate monooxygenase; <b>PDBTitle:</b> crystal structure of nitronate monooxygenase from cyberlindnera2 saturnus