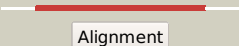



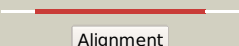





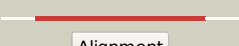













# Phyre2

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 Description RVBD3608c\_folP1\_4049317\_4050159  
 Date Fri Aug 9 18:20:29 BST 2019  
 Unique Job ID 077c1add6934e246

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6omzA_</a>	 Alignment		100.0	74	<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
2	<a href="#">c2bmbA_</a>	 Alignment		100.0	34	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> folic acid synthesis protein fol1; <b>PDBTitle:</b> x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropteroate synthase from3 saccharomyces cerevisiae
3	<a href="#">d1ajza_</a>	 Alignment		100.0	41	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
4	<a href="#">c5z79F_</a>	 Alignment		100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> F; <b>PDB Molecule:</b> hydroxymethyl-dihydropterin pyrophosphokinase- <b>PDBTitle:</b> crystal structure analysis of the hppk-dhps in complex with substrates
5	<a href="#">d1eyea_</a>	 Alignment		100.0	100	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
6	<a href="#">d1ad1a_</a>	 Alignment		100.0	38	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
7	<a href="#">c5uswD_</a>	 Alignment		100.0	32	<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
8	<a href="#">c5visB_</a>	 Alignment		100.0	33	<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.
9	<a href="#">c3tr9A_</a>	 Alignment		100.0	31	<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
10	<a href="#">c1tx2A_</a>	 Alignment		100.0	41	<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
11	<a href="#">d1tx2a_</a>	 Alignment		100.0	41	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase

12	<a href="#">c2y5sA_</a>	Alignment		100.0	39	<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.
13	<a href="#">c5uurA_</a>	Alignment		100.0	43	<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
14	<a href="#">c2vefB_</a>	Alignment		100.0	34	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> dihydropteroate synthase from streptococcus pneumoniae
15	<a href="#">c2dzaA_</a>	Alignment		100.0	43	<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
16	<a href="#">c6cluC_</a>	Alignment		100.0	39	<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
17	<a href="#">c3mcnA_</a>	Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-amino-4-hydroxy-6-hydroxymethyl-dihydropteridine <b>PDBTitle:</b> crystal structure of the 6-hydroxymethyl-7,8-dihydropteridin2 pyrophosphokinase dihydropteroate synthase bifunctional enzyme from3 francisella tularensis
18	<a href="#">c2vp8A_</a>	Alignment		100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase 2; <b>PDBTitle:</b> structure of mycobacterium tuberculosis rv1207
19	<a href="#">c2yciX_</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> 5-methyltetrahydrofolate corrinoid/iron sulfur protein <b>PDBTitle:</b> methyltransferase native
20	<a href="#">d1f6ya_</a>	Alignment		100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Methyltetrahydrofolate-utilizing methyltransferases
21	<a href="#">d3bofa1</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Methyltetrahydrofolate-utilizing methyltransferases
22	<a href="#">c2h9aB_</a>	Alignment	not modelled	100.0	11	<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
23	<a href="#">c4o1fB_</a>	Alignment	not modelled	100.0	19	<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
24	<a href="#">c3bolB_</a>	Alignment	not modelled	100.0	14	<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+
25	<a href="#">c3k13A_</a>	Alignment	not modelled	100.0	16	<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
26	<a href="#">c4cczA_</a>	Alignment	not modelled	100.0	16	<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
27	<a href="#">c4djdD_</a>	Alignment	not modelled	100.0	14	<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)
						<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 5-methyltetrahydrofolate homocysteine s-

28	<a href="#">c5voob_</a>	Alignment	not modelled	100.0	18	methyltransferase; <b>PDBTitle:</b> methionine synthase folate-binding domain with methyltetrahydrofolate2 from thermus thermophilus hb8 <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
29	<a href="#">c4mwaA_</a>	Alignment	not modelled	99.9	16	<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
30	<a href="#">c4djeE_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> carbon monoxide dehydrogenase corrinoide/iron-sulfur <b>PDBTitle:</b> corrinoide iron-sulfur protein
31	<a href="#">c2h9aA_</a>	Alignment	not modelled	99.8	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> crystal structure of ispg (gcpe)
32	<a href="#">c3noyA_</a>	Alignment	not modelled	99.2	16	<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
33	<a href="#">c2yclA_</a>	Alignment	not modelled	99.0	20	<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
34	<a href="#">c2y0fD_</a>	Alignment	not modelled	98.7	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
35	<a href="#">d1qopa_</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase 1; <b>PDBTitle:</b> crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia ambifaria
36	<a href="#">c3t4cD_</a>	Alignment	not modelled	97.6	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> tryptophan synthase subunit alpha from campylobacter jejuni.
37	<a href="#">c3thaB_</a>	Alignment	not modelled	97.5	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> sulfolobus solfataricus tryptophan synthase a
38	<a href="#">c5n2pA_</a>	Alignment	not modelled	97.5	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I DAHP synthetase
39	<a href="#">d1vr6a1</a>	Alignment	not modelled	97.5	14	<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
40	<a href="#">c2ekcA_</a>	Alignment	not modelled	97.5	19	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> biotin and thiamin synthesis associated; <b>PDBTitle:</b> crystal structure of hydg: a maturase of the [fefe]-hydrogenase
41	<a href="#">c4wxcC_</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase; <b>PDBTitle:</b> crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 bruciella melitensis at 1.85a resolution
42	<a href="#">c3fs2A_</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase; <b>PDBTitle:</b> crystal structure of a 2-dehydro-3-deoxyphosphooctonate aldolase from2 legionella pneumophila philadelphia 1
43	<a href="#">c6mdyC_</a>	Alignment	not modelled	97.3	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
44	<a href="#">d1rd5a_</a>	Alignment	not modelled	97.3	16	<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
45	<a href="#">c5kzmA_</a>	Alignment	not modelled	97.2	13	<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
46	<a href="#">c3navB_</a>	Alignment	not modelled	97.1	13	<b>PDB header:</b> lyase/oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> 4-hydroxy-2-oxovalerate aldolase; <b>PDBTitle:</b> crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
47	<a href="#">c1nvmG_</a>	Alignment	not modelled	97.1	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> homocitrate synthase, mitochondrial; <b>PDBTitle:</b> homocitrate synthase lys4 bound to 2-og
48	<a href="#">c3ivuB_</a>	Alignment	not modelled	97.1	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase; <b>PDBTitle:</b> crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis
49	<a href="#">c3stgA_</a>	Alignment	not modelled	97.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
50	<a href="#">d1ps9a1</a>	Alignment	not modelled	97.0	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> HMGL-like
51	<a href="#">d1nvm2</a>	Alignment	not modelled	96.9	17	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate carboxylase;
52	<a href="#">c3hs5C_</a>	Alignment	not modelled	96.9	18	

52	<a href="#">c3bg3C</a>	Alignment	not modelled	96.9	16	<b>PDBTitle:</b> crystal structure of staphylococcus aureus pyruvate carboxylase <b>PDB header:</b> oxidoreductase
53	<a href="#">c4k3zA</a>	Alignment	not modelled	96.9	15	<b>Chain:</b> A; <b>PDB Molecule:</b> d-erythrose 4-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-erythrose 4-phosphate dehydrogenase from2 brucella melitensis, solved by iodide sad <b>PDB header:</b> ligase
54	<a href="#">c3bg3A</a>	Alignment	not modelled	96.8	17	<b>Chain:</b> A; <b>PDB Molecule:</b> pyruvate carboxylase, mitochondrial; <b>PDBTitle:</b> crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
55	<a href="#">c5ey5A</a>	Alignment	not modelled	96.8	20	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> lbcats-a; <b>PDBTitle:</b> lbcats
56	<a href="#">c4lu0A</a>	Alignment	not modelled	96.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase; <b>PDBTitle:</b> crystal structure of 2-keto-3-deoxy-d-manno-octulosonate-8-phosphate2 synthase from pseudomonas aeruginosa.
57	<a href="#">c4qslC</a>	Alignment	not modelled	96.8	17	<b>PDB header:</b> ligase <b>Chain:</b> C; <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of listeria monocytogenes pyruvate carboxylase
58	<a href="#">c3sz8D</a>	Alignment	not modelled	96.8	20	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase 2; <b>PDBTitle:</b> crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
59	<a href="#">c3js3C</a>	Alignment	not modelled	96.7	14	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> 3-dehydroquinate dehydratase; <b>PDBTitle:</b> crystal structure of type i 3-dehydroquinatate dehydratase (arod) from2 clostridium difficile with covalent reaction intermediate
60	<a href="#">c4qslE</a>	Alignment	not modelled	96.7	17	<b>PDB header:</b> ligase <b>Chain:</b> E; <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of listeria monocytogenes pyruvate carboxylase
61	<a href="#">d1geqa</a>	Alignment	not modelled	96.6	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
62	<a href="#">c3q58A</a>	Alignment	not modelled	96.6	19	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> n-acetylmannosamine-6-phosphate 2-epimerase; <b>PDBTitle:</b> structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
63	<a href="#">c4rtbA</a>	Alignment	not modelled	96.6	15	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> hydG protein; <b>PDBTitle:</b> x-ray structure of the fefe-hydrogenase maturase hydG from2 carboxydotherrmus hydrogenoformans
64	<a href="#">c1ps9A</a>	Alignment	not modelled	96.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> 2,4-dienoyl-coa reductase; <b>PDBTitle:</b> the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase
65	<a href="#">c4jn6C</a>	Alignment	not modelled	96.6	17	<b>PDB header:</b> lyase/oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> 4-hydroxy-2-oxovalerate aldolase; <b>PDBTitle:</b> crystal structure of the aldolase-dehydrogenase complex from2 mycobacterium tuberculosis hrv37
66	<a href="#">c3pg8B</a>	Alignment	not modelled	96.5	16	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> phospho-2-dehydro-3-deoxyheptonate aldolase; <b>PDBTitle:</b> truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
67	<a href="#">c5tchG</a>	Alignment	not modelled	96.5	21	<b>PDB header:</b> lyase <b>Chain:</b> G; <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
68	<a href="#">d1d9ea</a>	Alignment	not modelled	96.5	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I DAHP synthetase
69	<a href="#">c5k9xA</a>	Alignment	not modelled	96.5	17	<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 chain from legionella2 pneumophila subsp. pneumophila
70	<a href="#">c3ajxA</a>	Alignment	not modelled	96.5	17	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-hexulose-6-phosphate synthase; <b>PDBTitle:</b> crystal structure of 3-hexulose-6-phosphate synthase
71	<a href="#">c1zcoA</a>	Alignment	not modelled	96.5	17	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphoheptonate aldolase; <b>PDBTitle:</b> crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
72	<a href="#">d1xcfa</a>	Alignment	not modelled	96.4	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
73	<a href="#">c1rr2A</a>	Alignment	not modelled	96.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> transcarboxylase 5s subunit; <b>PDBTitle:</b> propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
74	<a href="#">c4e38A</a>	Alignment	not modelled	96.3	25	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate <b>PDBTitle:</b> crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibionales bacterium swat-3 (target efi-502156)
75	<a href="#">c3bg3B</a>	Alignment	not modelled	96.3	18	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> pyruvate carboxylase, mitochondrial; <b>PDBTitle:</b> crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
76	<a href="#">d2a21a1</a>	Alignment	not modelled	96.2	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase

						<b>Family:</b> Class I DAHP synthetase
77	<a href="#">c3nvtA</a>	Alignment	not modelled	96.2	20	<b>PDB header:</b> transferase/isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; <b>PDBTitle:</b> 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e
78	<a href="#">c3gr7A</a>	Alignment	not modelled	96.2	22	<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
79	<a href="#">c3vndD</a>	Alignment	not modelled	96.1	17	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
80	<a href="#">d1o60a</a>	Alignment	not modelled	96.0	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I DAHP synthetase
81	<a href="#">c2yr1B</a>	Alignment	not modelled	96.0	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-dehydroquinatase; <b>PDBTitle:</b> crystal structure of 3-dehydroquinatase from geobacillus2 kaustophilus hta426
82	<a href="#">c6oviA</a>	Alignment	not modelled	96.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> keto-deoxy-phosphogluconate aldolase; <b>PDBTitle:</b> crystal structure of kdpq aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
83	<a href="#">c2infB</a>	Alignment	not modelled	96.0	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> crystal structure of uroporphyrinogen decarboxylase from bacillus2 subtilis
84	<a href="#">c6ncsB</a>	Alignment	not modelled	95.9	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylneuraminic acid (sialic acid) synthetase; <b>PDBTitle:</b> crystal structure of n-acetylneuraminic acid (sialic acid) synthetase2 from leptospira borgpetersenii serovar hardjo-bovis in complex with3 citrate
85	<a href="#">c4lrtC</a>	Alignment	not modelled	95.9	19	<b>PDB header:</b> lyase/oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 4-hydroxy-2-oxovalerate aldolase; <b>PDBTitle:</b> crystal and solution structures of the bifunctional enzyme2 (aldolase/aldehyde dehydrogenase) from thermomonospora curvata,3 reveal a cofactor-binding domain motion during nad+ and coa4 accommodation within the shared cofactor-binding site
86	<a href="#">c4ph6A</a>	Alignment	not modelled	95.9	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinatase; <b>PDBTitle:</b> structure of 3-dehydroquinatase from enterococcus faecalis
87	<a href="#">c1vs1B</a>	Alignment	not modelled	95.8	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-deoxy-7-phosphoheptulonate synthase; <b>PDBTitle:</b> crystal structure of 3-deoxy-d-arabino-heptulosonate-7-2 phosphate synthase (dahp synthase) from aeropyrum pernix3 in complex with mn2+ and pep
88	<a href="#">c6qkgB</a>	Alignment	not modelled	95.7	18	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> ncr a; <b>PDBTitle:</b> 2-naphthoyl-coa reductase(ncr)
89	<a href="#">d1losc</a>	Alignment	not modelled	95.7	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
90	<a href="#">d1wbha1</a>	Alignment	not modelled	95.7	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
91	<a href="#">c5kinC</a>	Alignment	not modelled	95.7	20	<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
92	<a href="#">d1ka9f</a>	Alignment	not modelled	95.7	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
93	<a href="#">d1vzwa1</a>	Alignment	not modelled	95.6	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
94	<a href="#">c3bleA</a>	Alignment	not modelled	95.6	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> citramalate synthase from leptospira interrogans; <b>PDBTitle:</b> crystal structure of the catalytic domain of licms in complexed with2 malonate
95	<a href="#">c2ze3A</a>	Alignment	not modelled	95.5	17	<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
96	<a href="#">d1h5ya</a>	Alignment	not modelled	95.5	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
97	<a href="#">d1r3sa</a>	Alignment	not modelled	95.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> UROD/MetE-like <b>Family:</b> Uroporphyrinogen decarboxylase, UROD
98	<a href="#">c3igsB</a>	Alignment	not modelled	95.5	23	<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
99	<a href="#">c1vliA</a>	Alignment	not modelled	95.5	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> spore coat polysaccharide biosynthesis protein spse; <b>PDBTitle:</b> crystal structure of spore coat polysaccharide

						biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
100	<a href="#">c4xp7A_</a>	Alignment	not modelled	95.5	8	<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
101	<a href="#">c3ru6C_</a>	Alignment	not modelled	95.4	14	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> orotidine 5'-phosphate decarboxylase; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of orotidine 5'-phosphate2 decarboxylase (pyrf) from campylobacter jejuni subsp. jejuni nctc3 11168
102	<a href="#">c3cixA_</a>	Alignment	not modelled	95.4	16	<b>PDB header:</b> adomet binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fefe-hydrogenase maturase; <b>PDBTitle:</b> x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
103	<a href="#">c5ks8F_</a>	Alignment	not modelled	95.3	16	<b>PDB header:</b> ligase <b>Chain:</b> F: <b>PDB Molecule:</b> pyruvate carboxylase subunit beta; <b>PDBTitle:</b> crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
104	<a href="#">c2ftpA_</a>	Alignment	not modelled	95.3	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa lyase; <b>PDBTitle:</b> crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
105	<a href="#">c5zknA_</a>	Alignment	not modelled	95.3	21	<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
106	<a href="#">c3f4wA_</a>	Alignment	not modelled	95.2	19	<b>PDB header:</b> synthase, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hexulose 6 phosphate synthase; <b>PDBTitle:</b> the 1.65a crystal structure of 3-hexulose-6-phosphate2 synthase from salmonella typhimurium
107	<a href="#">c1zfyA_</a>	Alignment	not modelled	95.2	24	<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
108	<a href="#">d1thfd_</a>	Alignment	not modelled	95.2	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
109	<a href="#">c3hf3A_</a>	Alignment	not modelled	95.1	15	<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
110	<a href="#">c3ffsC_</a>	Alignment	not modelled	95.1	15	<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
111	<a href="#">d1mxsa_</a>	Alignment	not modelled	95.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
112	<a href="#">c6ei9A_</a>	Alignment	not modelled	95.0	15	<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)
113	<a href="#">c4zr8B_</a>	Alignment	not modelled	95.0	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> structure of uroporphyrinogen decarboxylase from acinetobacter2 baumannii
114	<a href="#">c4bk9B_</a>	Alignment	not modelled	94.9	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxo <b>PDBTitle:</b> crystal structure of 2-keto-3-deoxy-6-phospho-gluconate aldolase from2 zymomonas mobilis atcc 29191
115	<a href="#">d1j93a_</a>	Alignment	not modelled	94.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> UROD/MetE-like <b>Family:</b> Uroporphyrinogen decarboxylase, UROD
116	<a href="#">c1djbB_</a>	Alignment	not modelled	94.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> trimethylamine dehydrogenase; <b>PDBTitle:</b> structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
117	<a href="#">c4axkB_</a>	Alignment	not modelled	94.8	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
118	<a href="#">c3t7vA_</a>	Alignment	not modelled	94.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methylornithine synthase pylb; <b>PDBTitle:</b> crystal structure of methylornithine synthase (pylb)
119	<a href="#">c4ay8B_</a>	Alignment	not modelled	94.6	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methylcobalamin): coenzyme m methyltransferase; <b>PDBTitle:</b> semet-derivative of a methyltransferase from m. mazei
120	<a href="#">c3qc3B_</a>	Alignment	not modelled	94.5	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> d-ribulose-5-phosphate-3-epimerase; <b>PDBTitle:</b> crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution