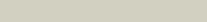
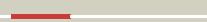


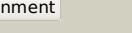
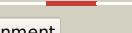
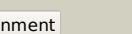
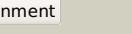
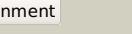
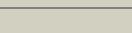
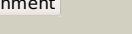
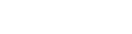
# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD1173_(fblC)_1302936_1305506
Date	Wed Jul 31 22:05:26 BST 2019
Unique Job ID	02e017f26b80b3e8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3cixA</a>			100.0	21	<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 hyd from2 thermotoga maritima in complex with thiocyanate
2	<a href="#">c4rtbA</a>			100.0	16	<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 hyd from2 carboxydothermus hydrogenoformans
3	<a href="#">c3t7vA</a>			100.0	20	<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)
4	<a href="#">c4r33A</a>			100.0	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> :nosl; <b>PDBTitle:</b> x-ray structure of the tryptophan lyase nosl with tryptophan and s-2 adenosyl-l-homocysteine bound
5	<a href="#">c4wcxC</a>			100.0	17	<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
6	<a href="#">c1r30A</a>			100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> biotin synthase; <b>PDBTitle:</b> the crystal structure of biotin synthase, an s-adenosylmethionine-2 dependent radical enzyme
7	<a href="#">d1r30a</a>			100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Radical SAM enzymes <b>Family:</b> Biotin synthase
8	<a href="#">c4u0pB</a>			99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lipoyl synthase 2; <b>PDBTitle:</b> the crystal structure of lipoyl synthase in complex with s-adenosyl2 homocysteine
9	<a href="#">c5exkG</a>			99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> lipoyl synthase; <b>PDBTitle:</b> crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate
10	<a href="#">c5zmyF</a>			99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> cis-epoxysuccinate hydrolase; <b>PDBTitle:</b> crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids
11	<a href="#">c4jc0B</a>			99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal protein s12 methylthiotransferase rimo; <b>PDBTitle:</b> crystal structure of thermotoga maritima holo rimo in complex with2 pentasulfide, northeast structural genomics consortium target vr77

12	<a href="#">d1olta_</a>			99.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Radical SAM enzymes <b>Family:</b> Oxygen-independent coproporphyrinogen III oxidase HemN
13	<a href="#">c6fd2B_</a>			99.8	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative apramycin biosynthetic oxidoreductase 4; <b>PDBTitle:</b> radical sam 1,2-diol dehydratase aprd4 in complex with its substrate2 paromamine
14	<a href="#">c5l7jA_</a>			99.7	12	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> elp3 family; <b>PDBTitle:</b> crystal structure of elp3 from dehalococcoides mccartyi
15	<a href="#">c2qqqF_</a>			99.6	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> protein tm_1862; <b>PDBTitle:</b> crystal structure of tm_1862 from thermotoga maritima. northeast2 structural genomics consortium target vr77
16	<a href="#">c6qk7C_</a>			99.6	9	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> elongator complex protein 3; <b>PDBTitle:</b> elongator catalytic subcomplex elp123 lobe
17	<a href="#">d1tv8a_</a>			99.6	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Radical SAM enzymes <b>Family:</b> MoCo biosynthesis proteins
18	<a href="#">c6iazA_</a>			99.5	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone acetyltransferase, elp3 family; <b>PDBTitle:</b> the archaeal methanocaldococcus infernus elp3 with n-terminus deletion2 (1-46)
19	<a href="#">c3rfaB_</a>			99.2	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase n; <b>PDBTitle:</b> x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
20	<a href="#">c5vslB_</a>			99.2	16	<b>PDB header:</b> antiviral protein <b>Chain:</b> B: <b>PDB Molecule:</b> radical s-adenosyl methionine domain-containing protein 2; <b>PDBTitle:</b> crystal structure of viperin with bound [4fe-4s] cluster and s-2 adenosylhomocysteine (sah)
21	<a href="#">c5v1tA_</a>		not modelled	99.2	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> radical sam; <b>PDBTitle:</b> crystal structure of streptococcus suis suis bound to precursor2 peptide suis
22	<a href="#">c5ul4A_</a>		not modelled	99.2	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> oxsb protein; <b>PDBTitle:</b> structure of cobalamin-dependent s-adenosylmethionine radical enzyme2 oxsb with aqua-cobalamin and s-adenosylmethionine bound
23	<a href="#">c6efnA_</a>		not modelled	99.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sporulation killing factor maturation protein skfb; <b>PDBTitle:</b> structure of a ripp maturase, skfb
24	<a href="#">c6b4ch_</a>		not modelled	99.2	13	<b>PDB header:</b> antiviral protein <b>Chain:</b> H: <b>PDB Molecule:</b> viperin; <b>PDBTitle:</b> structure of viperin from trichoderma virens
25	<a href="#">c3rfaA_</a>		not modelled	99.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase n; <b>PDBTitle:</b> x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
26	<a href="#">c3c8fA_</a>		not modelled	99.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate formate-lyase 1-activating enzyme; <b>PDBTitle:</b> 4fe-4s-pyruvate formate-lyase activating enzyme with partially2 disordered adomet
27	<a href="#">c6fz6B_</a>		not modelled	99.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable dual-specificity rna methyltransferase rlmn; <b>PDBTitle:</b> crystal structure of a radical sam methyltransferase from2 sphaerobacter thermophilus
						<b>PDB header:</b> oxidoreductase

28	<a href="#">c4k39A</a>		Alignment	not modelled	99.0	11	<p><b>PDB header:</b>anaerobic sulfatase-maturating enzyme; <b>PDBTitle:</b> native ansmecpe with bound adomet and cp18cys peptide</p>
29	<a href="#">c4m7tA</a>		Alignment	not modelled	98.8	10	<p><b>PDB header:</b>metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b>btrn; <b>PDBTitle:</b> crystal structure of btrn in complex with adomet and 2-dioa</p>
30	<a href="#">c2a5hC</a>		Alignment	not modelled	98.6	13	<p><b>PDB header:</b>isomerase <b>Chain:</b> C: <b>PDB Molecule:</b>l-lysine 2,3-aminomutase; <b>PDBTitle:</b> 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).</p>
31	<a href="#">c2yx0A</a>		Alignment	not modelled	98.4	12	<p><b>PDB header:</b>metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b>radical sam enzyme; <b>PDBTitle:</b> crystal structure of p. horikoshii tyw1</p>
32	<a href="#">c4fheA</a>		Alignment	not modelled	98.4	9	<p><b>PDB header:</b>lyase <b>Chain:</b> A: <b>PDB Molecule:</b>spore photoproduct lyase; <b>PDBTitle:</b> spore photoproduct lyase c140a mutant</p>
33	<a href="#">c5wggA</a>		Alignment	not modelled	98.3	9	<p><b>PDB header:</b>peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b>radical sam domain protein; <b>PDBTitle:</b> structural insights into thioether bond formation in the biosynthesis2 of sactipeptides</p>
34	<a href="#">c5th5C</a>		Alignment	not modelled	98.1	10	<p><b>PDB header:</b>lyase <b>Chain:</b> C: <b>PDB Molecule:</b>7-carboxy-7-deazaguanine synthase; <b>PDBTitle:</b> crystal structure of quee from bacillus subtilis with 6-carboxypterin-2 5'-deoxyadenosyl ester bound</p>
35	<a href="#">c6c8vA</a>		Alignment	not modelled	98.0	15	<p><b>PDB header:</b>oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b>coenzyme pqg synthesis protein e; <b>PDBTitle:</b> x-ray structure of pqge from methylobacterium extorquens</p>
36	<a href="#">c3e02A</a>		Alignment	not modelled	98.0	16	<p><b>PDB header:</b>metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b>uncharacterized protein duf849; <b>PDBTitle:</b> crystal structure of a duf849 family protein (bxe_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution</p>
37	<a href="#">c3e49A</a>		Alignment	not modelled	97.8	19	<p><b>PDB header:</b>metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b>uncharacterized protein duf849 with a tim barrel fold; <b>PDBTitle:</b> crystal structure of a prokaryotic domain of unknown function (duf849)2 with a tim barrel fold (bxe_c0966) from burkholderia xenovorans lb400 at 1.75 a resolution</p>
38	<a href="#">c3chvA</a>		Alignment	not modelled	97.8	18	<p><b>PDB header:</b>metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b>prokaryotic domain of unknown function (duf849) with a tim <b>PDBTitle:</b> crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution</p>
39	<a href="#">c3no5C</a>		Alignment	not modelled	97.8	18	<p><b>PDB header:</b>structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b>uncharacterized protein; <b>PDBTitle:</b> crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution</p>
40	<a href="#">c3c6cA</a>		Alignment	not modelled	97.7	14	<p><b>PDB header:</b>hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b>3-keto-5-aminohexanoate cleavage enzyme; <b>PDBTitle:</b> crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution</p>
41	<a href="#">c2y7eA</a>		Alignment	not modelled	97.7	16	<p><b>PDB header:</b>lyase <b>Chain:</b> A: <b>PDB Molecule:</b>3-keto-5-aminohexanoate cleavage enzyme; <b>PDBTitle:</b> crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)</p>
42	<a href="#">c3lotC</a>		Alignment	not modelled	97.6	16	<p><b>PDB header:</b>structure genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b>uncharacterized protein; <b>PDBTitle:</b> crystal structure of protein of unknown function (np_070038.1) from archaeoglobus fulgidus at 1.89 a resolution</p>
43	<a href="#">c1nvmG</a>		Alignment	not modelled	97.5	14	<p><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</p>
44	<a href="#">d1ka9f</a>		Alignment	not modelled	97.2	16	<p><b>Fold:</b>TIM beta/alpha-barrel <b>Superfamily:</b>Ribulose-phosphate binding barrel <b>Family:</b>Histidine biosynthesis enzymes</p>
45	<a href="#">c3ivuB</a>		Alignment	not modelled	97.1	11	<p><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</p>
46	<a href="#">c2nx9B</a>		Alignment	not modelled	96.9	13	<p><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</p>
47	<a href="#">c4jn6C</a>		Alignment	not modelled	96.8	16	<p><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 from mycobacterium tuberculosis hrv37</p>
48	<a href="#">c2cw6B</a>		Alignment	not modelled	96.8	9	<p><b>PDB header:</b>lyase <b>Chain:</b> B: <b>PDB Molecule:</b>hydroxymethylglutaryl-coa lyase, mitochondrial; <b>PDBTitle:</b> crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria</p>
49	<a href="#">c3eegB</a>		Alignment	not modelled	96.8	14	<p><b>PDB header:</b>transferase <b>Chain:</b> B: <b>PDB Molecule:</b>2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii</p>
50	<a href="#">c4njka</a>		Alignment	not modelled	96.6	14	<p><b>PDB header:</b>lyase <b>Chain:</b> A: <b>PDB Molecule:</b>7-carboxy-7-deazaguanine synthase; <b>PDBTitle:</b> crystal structure of quee from burkholderia multivorans in</p>

						complex2 with adomet, 7-carboxy-7-deazaguanine, and mg2+
51	<a href="#">d1nvma2</a>	Alignment	not modelled	96.5	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> HMGL-like
52	<a href="#">c1rr2A_</a>	Alignment	not modelled	96.5	12	<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
53	<a href="#">c3canA_</a>	Alignment	not modelled	96.5	14	<b>PDB header:</b> lyase activator <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate-formate lyase-activating enzyme; <b>PDBTitle:</b> crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
54	<a href="#">c3bleA_</a>	Alignment	not modelled	96.4	9	<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
55	<a href="#">c2ftpA_</a>	Alignment	not modelled	96.4	11	<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
56	<a href="#">c5ks8D_</a>	Alignment	not modelled	96.3	14	<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
57	<a href="#">c1ydnA_</a>	Alignment	not modelled	96.2	10	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa lyase; <b>PDBTitle:</b> crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
58	<a href="#">c3labA_</a>	Alignment	not modelled	96.2	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative kdpg (2-keto-3-deoxy-6-phosphogluconate) aldolase; <b>PDBTitle:</b> crystal structure of a putative kdpg (2-keto-3-deoxy-6-phosphogluconate) aldolase from oleispira antarctica
59	<a href="#">c6e1jB_</a>	Alignment	not modelled	96.0	10	<b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> 2-isopropylmalate synthase, a genome specific 1; <b>PDBTitle:</b> crystal structure of methylthioalkylmalate synthase (bjumam1.1) from2 brassica juncea
60	<a href="#">d1thfd_</a>	Alignment	not modelled	96.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
61	<a href="#">c3rmjB_</a>	Alignment	not modelled	95.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
62	<a href="#">c3bg3B_</a>	Alignment	not modelled	95.8	21	<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)
63	<a href="#">c1ydoC_</a>	Alignment	not modelled	95.6	9	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> hmg-coa lyase; <b>PDBTitle:</b> crystal structure of the bacillus subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
64	<a href="#">c5kzmA_</a>	Alignment	not modelled	95.5	18	<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
65	<a href="#">d1h5ya_</a>	Alignment	not modelled	95.5	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
66	<a href="#">c4nnca_</a>	Alignment	not modelled	95.5	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> obca, oxalate biosynthetic component a; <b>PDBTitle:</b> ternary complex of obca with c4-coa adduct and oxalate
67	<a href="#">d1wbha1</a>	Alignment	not modelled	95.4	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
68	<a href="#">d1m5wa_</a>	Alignment	not modelled	95.3	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Pyridoxine 5'-phosphate synthase <b>Family:</b> Pyridoxine 5'-phosphate synthase
69	<a href="#">c5dlcC_</a>	Alignment	not modelled	95.1	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pyridoxine 5'-phosphate synthase; <b>PDBTitle:</b> x-ray crystal structure of a pyridoxine 5-prime-phosphate synthase2 from pseudomonas aeruginosa
70	<a href="#">c4lrc_</a>	Alignment	not modelled	95.0	16	<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 whithin the shared cofactor-binding site
71	<a href="#">c3dxiB_</a>	Alignment	not modelled	94.8	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative aldolase; <b>PDBTitle:</b> crystal structure of the n-terminal domain of a putative2 aldolase (bvu_2661) from bacteroides vulgatus
72	<a href="#">d1rqba2</a>	Alignment	not modelled	94.7	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> HMGL-like
73	<a href="#">d1rvka1</a>	Alignment	not modelled	94.4	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
74	<a href="#">c3ewbX_</a>	Alignment	not modelled	94.3	14	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of n-terminal domain of putative 2-isopropylmalate2 synthase from listeria monocytogenes
						<b>Fold:</b> TIM beta/alpha-barrel

75	<a href="#">d1tx2a_</a>	Alignment	not modelled	94.2	16	<b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
76	<a href="#">c1tx2A_</a>	Alignment	not modelled	94.2	16	<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
77	<a href="#">c1vs1B_</a>	Alignment	not modelled	94.0	15	<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
78	<a href="#">c3gk0H_</a>	Alignment	not modelled	93.8	16	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> pyridoxine 5'-phosphate synthase; <b>PDBTitle:</b> crystal structure of pyridoxal phosphate biosynthetic protein from2 burkholderia pseudomallei
79	<a href="#">c5vooB_</a>	Alignment	not modelled	93.6	16	<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
80	<a href="#">c3obkH_</a>	Alignment	not modelled	93.5	17	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> delta-aminolevulinic acid dehydratase; <b>PDBTitle:</b> crystal structure of delta-aminolevulinic acid dehydratase2 (porphobilinogen synthase) from toxoplasma gondii me49 in complex3 with the reaction product porphobilinogen
81	<a href="#">c1zcoA_</a>	Alignment	not modelled	93.4	14	<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
82	<a href="#">d1mxsa_</a>	Alignment	not modelled	93.4	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
83	<a href="#">c6oviA_</a>	Alignment	not modelled	92.8	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> keto-deoxy-phosphogluconate aldolase; <b>PDBTitle:</b> crystal structure of kdpg aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
84	<a href="#">d1pv8a_</a>	Alignment	not modelled	92.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
85	<a href="#">c3vndD_</a>	Alignment	not modelled	92.6	15	<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
86	<a href="#">d2c1ha1</a>	Alignment	not modelled	92.3	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
87	<a href="#">c5visB_</a>	Alignment	not modelled	92.3	21	<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 (flop-smz_b27) from soil uncultured bacterium.
88	<a href="#">c2vefB_</a>	Alignment	not modelled	92.1	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> dihydropteroate synthase from streptococcus pneumoniae
89	<a href="#">c2z2uA_</a>	Alignment	not modelled	92.1	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> upf0026 protein mj0257; <b>PDBTitle:</b> crystal structure of archaeal tyw1
90	<a href="#">c3fs2A_</a>	Alignment	not modelled	92.1	12	<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 brucella melitensis at 1.85a resolution
91	<a href="#">d1ad1a_</a>	Alignment	not modelled	92.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
92	<a href="#">c5ks8F_</a>	Alignment	not modelled	92.0	12	<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
93	<a href="#">d2a21a1</a>	Alignment	not modelled	91.9	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I DAHP synthetase
94	<a href="#">c3bg3A_</a>	Alignment	not modelled	91.7	22	<b>PDB header:</b> ligase <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)
95	<a href="#">d1ajza_</a>	Alignment	not modelled	91.4	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
96	<a href="#">d1h7na_</a>	Alignment	not modelled	91.3	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
97	<a href="#">c2bdqA_</a>	Alignment	not modelled	91.1	13	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> copper homeostasis protein cutc; <b>PDBTitle:</b> crystal structure of the putative copper homeostasis protein cutc from2 streptococcus agalactiae, northeast strucral genomics target sar15.
98	<a href="#">c1sr9A_</a>	Alignment	not modelled	90.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of leuA from mycobacterium tuberculosis
99	<a href="#">d1g7ca_</a>	Alignment	not modelled	90.7	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase

99	<a href="#">u1yqA</a>	Alignment	not modelled	90.7	17	<b>Family:</b> 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
100	<a href="#">d2flia1</a>	Alignment	not modelled	90.6	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
101	<a href="#">c2zyfA</a>	Alignment	not modelled	90.4	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homocitrate synthase; <b>PDBTitle:</b> crystal structure of homocitrate synthase from thermus thermophilus2 complexed with magnesium ion and alpha-ketoglutarate
102	<a href="#">c2v82A</a>	Alignment	not modelled	90.3	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; <b>PDBTitle:</b> kdpgal complexed to kdpgal
103	<a href="#">c2ekcA</a>	Alignment	not modelled	90.1	16	<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
104	<a href="#">c3w9zA</a>	Alignment	not modelled	90.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tRNA-dihydrouridine synthase c; <b>PDBTitle:</b> crystal structure of dusc
105	<a href="#">d1l6sa</a>	Alignment	not modelled	89.9	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
106	<a href="#">c6nhIB</a>	Alignment	not modelled	89.8	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 7-carboxy-7-deazaguanine synthase; <b>PDBTitle:</b> crystal structure of quee from escherichia coli
107	<a href="#">c4e38A</a>	Alignment	not modelled	89.7	11	<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 from 2 vibrionales bacterium swat-3 (target efi-502156)
108	<a href="#">d1qopa</a>	Alignment	not modelled	89.6	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
109	<a href="#">c5umfB</a>	Alignment	not modelled	89.4	11	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ribulose-phosphate 3-epimerase; <b>PDBTitle:</b> crystal structure of a ribulose-phosphate 3-epimerase from neisseria2 gonorrhoeae with bound phosphate
110	<a href="#">c6fnuA</a>	Alignment	not modelled	88.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methylenetetrahydrofolate reductase 1; <b>PDBTitle:</b> structure of s. cerevisiae methylenetetrahydrofolate reductase 1,2 catalytic domain
111	<a href="#">d1h1ya</a>	Alignment	not modelled	88.8	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
112	<a href="#">c5uurA</a>	Alignment	not modelled	88.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> xanthomonas albilineans dihydropteroate synthase with 4-aminobenzoic acid
113	<a href="#">d1vhca</a>	Alignment	not modelled	88.4	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
114	<a href="#">d1bqga1</a>	Alignment	not modelled	88.2	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
115	<a href="#">d1ub3a</a>	Alignment	not modelled	88.2	30	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
116	<a href="#">c4z1bA</a>	Alignment	not modelled	88.0	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase; <b>PDBTitle:</b> structure of h204a mutant kdo8ps from h.pylori
117	<a href="#">c6cluC</a>	Alignment	not modelled	87.9	20	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> C: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> staphylococcus aureus dihydropteroate synthase (sadhp) f17l e208k2 double mutant structure
118	<a href="#">c3tdmD</a>	Alignment	not modelled	87.9	15	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> computationally designed two-fold symmetric tim-barrel <b>PDBTitle:</b> computationally designed tim-barrel protein, halfflr
119	<a href="#">c4ot7A</a>	Alignment	not modelled	87.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh:flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> x-structure of a variant of ncr from zymomonas mobilis
120	<a href="#">d1jdfa1</a>	Alignment	not modelled	87.1	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like