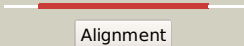

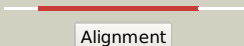

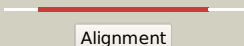







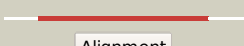




















# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD3109\_(moaA1)\_3477646\_3478725  
 Date Thu Aug 8 16:20:29 BST 2019  
 Unique Job ID 46f40e796196d289

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1tv8a_</a>	 Alignment		100.0	38	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Radical SAM enzymes <b>Family:</b> MoCo biosynthesis proteins
2	<a href="#">c6efnA_</a>	 Alignment		100.0	21	<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
3	<a href="#">c4wxcC_</a>	 Alignment		100.0	13	<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 [fe]-hydrogenase
4	<a href="#">c5v1tA_</a>	 Alignment		100.0	17	<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 suib bound to precursor2 peptide sua
5	<a href="#">c4k39A_</a>	 Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> anaerobic sulfatase-maturing enzyme; <b>PDBTitle:</b> native ansmece with bound adomet and cp18cys peptide
6	<a href="#">c5wggA_</a>	 Alignment		100.0	16	<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
7	<a href="#">c5vslB_</a>	 Alignment		100.0	19	<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)
8	<a href="#">c6b4cH_</a>	 Alignment		100.0	16	<b>PDB header:</b> antiviral protein <b>Chain:</b> H: <b>PDB Molecule:</b> viperin; <b>PDBTitle:</b> structure of viperin from trichoderma virens
9	<a href="#">c6c8vA_</a>	 Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme pqq synthesis protein e; <b>PDBTitle:</b> x-ray structure of pqqe from methylobacterium extorquens
10	<a href="#">c2yx0A_</a>	 Alignment		99.9	16	<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
11	<a href="#">c5th5C_</a>	 Alignment		99.9	14	<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

12	<a href="#">c3rfaB</a>	Alignment		99.9	19	<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
13	<a href="#">c4m7tA</a>	Alignment		99.9	19	<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-doia
14	<a href="#">c3c8fA</a>	Alignment		99.9	18	<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
15	<a href="#">c3t7vA</a>	Alignment		99.9	14	<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)
16	<a href="#">c6fz6B</a>	Alignment		99.8	18	<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
17	<a href="#">c5exkG</a>	Alignment		99.8	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
18	<a href="#">c4u0pB</a>	Alignment		99.8	14	<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
19	<a href="#">c3rfaA</a>	Alignment		99.8	19	<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
20	<a href="#">c2a5hC</a>	Alignment		99.8	17	<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).
21	<a href="#">c1r30A</a>	Alignment	not modelled	99.8	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
22	<a href="#">d1r30a</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Radical SAM enzymes <b>Family:</b> Biotin synthase
23	<a href="#">c4jc0B</a>	Alignment	not modelled	99.8	13	<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
24	<a href="#">c3cixA</a>	Alignment	not modelled	99.8	18	<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
25	<a href="#">c4rtbA</a>	Alignment	not modelled	99.8	14	<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
26	<a href="#">c2z2uA</a>	Alignment	not modelled	99.8	21	<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
27	<a href="#">d1olta</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Radical SAM enzymes <b>Family:</b> Oxygen-independent coproporphyrinogen III oxidase HemN
28	<a href="#">c3canA</a>	Alignment	not modelled	99.8	18	<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

29	<a href="#">c6nhbB</a>	Alignment	not modelled	99.8	27	<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
30	<a href="#">c4njka</a>	Alignment	not modelled	99.8	22	<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 complex2 with adomet, 7-carboxy-7-deazaguanine, and mg2+
31	<a href="#">c6fd2B</a>	Alignment	not modelled	99.7	18	<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
32	<a href="#">c4r33A</a>	Alignment	not modelled	99.5	16	<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
33	<a href="#">c5l7ja</a>	Alignment	not modelled	99.4	13	<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
34	<a href="#">c5ul4A</a>	Alignment	not modelled	99.4	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
35	<a href="#">c6qk7C</a>	Alignment	not modelled	99.3	13	<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
36	<a href="#">c2qgqF</a>	Alignment	not modelled	99.3	13	<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
37	<a href="#">c6iazA</a>	Alignment	not modelled	99.0	15	<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)
38	<a href="#">c4fheA</a>	Alignment	not modelled	99.0	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> spore photoproduct lyase; <b>PDBTitle:</b> spore photoproduct lyase c140a mutant
39	<a href="#">c3rmjB</a>	Alignment	not modelled	97.6	12	<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
40	<a href="#">c3ivuB</a>	Alignment	not modelled	97.6	14	<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
41	<a href="#">c6e1jB</a>	Alignment	not modelled	97.6	18	<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
42	<a href="#">c3ewbX</a>	Alignment	not modelled	97.1	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
43	<a href="#">c3bleA</a>	Alignment	not modelled	96.8	16	<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
44	<a href="#">c3eegB</a>	Alignment	not modelled	96.6	15	<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
45	<a href="#">c2ftpA</a>	Alignment	not modelled	96.1	14	<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
46	<a href="#">c1nvmG</a>	Alignment	not modelled	95.9	18	<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="#">c1sr9A</a>	Alignment	not modelled	95.5	12	<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
48	<a href="#">c2cw6B</a>	Alignment	not modelled	95.3	18	<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
49	<a href="#">c5zmyF</a>	Alignment	not modelled	95.1	13	<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
50	<a href="#">c3hpxB</a>	Alignment	not modelled	94.7	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis leua active site2 domain 1-425 (truncation mutant delta:426-644)
51	<a href="#">c1ydcC</a>	Alignment	not modelled	94.4	15	<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.
52	<a href="#">c4jn6C</a>	Alignment	not modelled	94.4	16	<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
53	<a href="#">c4nvaA</a>	Alignment	not modelled	94.3	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> isopropylmalate synthase;

53	<a href="#">c40v3A</a>	Alignment	not modelled	94.2	11	<b>PDBTitle:</b> structure of isopropylmalate synthase binding with alpha-2 isopropylmalate <b>PDB header:</b> lyase
54	<a href="#">c1ydnA</a>	Alignment	not modelled	94.1	14	<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.
55	<a href="#">d1nvma2</a>	Alignment	not modelled	93.8	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> HMGL-like
56	<a href="#">d1eyea</a>	Alignment	not modelled	93.4	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
57	<a href="#">c2p0oA</a>	Alignment	not modelled	91.3	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein duf871; <b>PDBTitle:</b> crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function
58	<a href="#">c5ks8D</a>	Alignment	not modelled	90.6	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
59	<a href="#">c4lrtC</a>	Alignment	not modelled	85.8	17	<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
60	<a href="#">c1rr2A</a>	Alignment	not modelled	85.0	16	<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
61	<a href="#">c3vteA</a>	Alignment	not modelled	83.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tetrahydrocannabinolic acid synthase; <b>PDBTitle:</b> crystal structure of tetrahydrocannabinolic acid synthase from2 cannabis sativa
62	<a href="#">c2zyfA</a>	Alignment	not modelled	83.3	13	<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
63	<a href="#">d1n7ka</a>	Alignment	not modelled	81.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
64	<a href="#">c3w9zA</a>	Alignment	not modelled	80.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trna-dihydrouridine synthase c; <b>PDBTitle:</b> crystal structure of dusc
65	<a href="#">c2nx9B</a>	Alignment	not modelled	79.4	16	<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
66	<a href="#">c6omzA</a>	Alignment	not modelled	74.7	15	<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
67	<a href="#">d1vyra</a>	Alignment	not modelled	74.0	9	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
68	<a href="#">c3hf3A</a>	Alignment	not modelled	72.4	16	<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
69	<a href="#">d1rqba2</a>	Alignment	not modelled	72.2	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> HMGL-like
70	<a href="#">c3c6cA</a>	Alignment	not modelled	72.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-keto-5-aminoheptanoate cleavage enzyme; <b>PDBTitle:</b> crystal structure of a putative 3-keto-5-aminoheptanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
71	<a href="#">c2zq0B</a>	Alignment	not modelled	71.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-glucosidase (alpha-glucosidase sub); <b>PDBTitle:</b> crystal structure of sub complexed with acarbose
72	<a href="#">c3dxiB</a>	Alignment	not modelled	70.7	13	<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
73	<a href="#">c3a9iA</a>	Alignment	not modelled	68.8	14	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> homocitrate synthase; <b>PDBTitle:</b> crystal structure of homocitrate synthase from thermus thermophilus2 complexed with lys
74	<a href="#">c3lotC</a>	Alignment	not modelled	68.3	14	<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) from2 archaeoglobus fulgidus at 1.89 a resolution
75	<a href="#">d1o0ya</a>	Alignment	not modelled	67.9	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
76	<a href="#">d1rvka1</a>	Alignment	not modelled	67.6	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
77	<a href="#">c1ps9A</a>	Alignment	not modelled	67.4	17	<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

78	<a href="#">c3ndcB</a>	Alignment	not modelled	65.3	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> precocorrin-4 c(11)-methyltransferase; <b>PDBTitle:</b> crystal structure of precocorrin-4 c11-methyltransferase from2 rhodobacter capsulatus
79	<a href="#">c3bg5C</a>	Alignment	not modelled	63.9	11	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of staphylococcus aureus pyruvate carboxylase
80	<a href="#">c4ot7A</a>	Alignment	not modelled	63.6	11	<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
81	<a href="#">c3bg3A</a>	Alignment	not modelled	63.1	12	<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)
82	<a href="#">c3oa3A</a>	Alignment	not modelled	63.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> aldolase; <b>PDBTitle:</b> crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
83	<a href="#">c4ay8B</a>	Alignment	not modelled	62.5	12	<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
84	<a href="#">c1pjtB</a>	Alignment	not modelled	62.2	25	<b>PDB header:</b> transferase/oxidoreductase/lyase <b>Chain:</b> B: <b>PDB Molecule:</b> siroheme synthase; <b>PDBTitle:</b> the structure of the ser128ala point-mutant variant of cysg, the2 multifunctional methyltransferase/dehydrogenase/ferrochelatae for3 siroheme synthesis
85	<a href="#">c6f73B</a>	Alignment	not modelled	61.8	21	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> mtvao615; <b>PDBTitle:</b> crystal structure of vao-type flavoprotein mtvao615 at ph 5.0 from2 myceliophthora thermophila c1
86	<a href="#">d1ps9a1</a>	Alignment	not modelled	61.6	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
87	<a href="#">c3no5C</a>	Alignment	not modelled	60.2	10	<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
88	<a href="#">d1yx1a1</a>	Alignment	not modelled	60.1	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> KguE-like
89	<a href="#">c3a24A</a>	Alignment	not modelled	59.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-galactosidase; <b>PDBTitle:</b> crystal structure of bt1871 retaining glycosidase
90	<a href="#">c3bg3B</a>	Alignment	not modelled	59.8	14	<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)
91	<a href="#">c3gr7A</a>	Alignment	not modelled	59.7	9	<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
92	<a href="#">d1z41a1</a>	Alignment	not modelled	59.3	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
93	<a href="#">c4ml9A</a>	Alignment	not modelled	59.1	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized tim barrel protein with the2 conserved phosphate binding site fromsebaldeella termitidis
94	<a href="#">c5visB</a>	Alignment	not modelled	58.9	16	<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.
95	<a href="#">d1bxba</a>	Alignment	not modelled	58.7	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
96	<a href="#">c2y7eA</a>	Alignment	not modelled	58.4	15	<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)
97	<a href="#">d1qt1a</a>	Alignment	not modelled	57.7	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
98	<a href="#">c3e02A</a>	Alignment	not modelled	57.6	20	<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 (bx_e_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
99	<a href="#">c3e49A</a>	Alignment	not modelled	57.3	13	<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 (bx_e_c0966) from burkholderia xenovorans lb4003 at 1.75 a resolution
100	<a href="#">c3khdC</a>	Alignment	not modelled	56.9	12	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure of pff1300w.
101	<a href="#">d1s4da</a>	Alignment	not modelled	56.7	18	<b>Fold:</b> Tetrapyrrole methylase <b>Superfamily:</b> Tetrapyrrole methylase <b>Family:</b> Tetrapyrrole methylase
102	<a href="#">c4nc1F</a>	Alignment	not modelled	56.5	10	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> pyruvate carboxylase;

102	<a href="#">c4qslE</a>	Alignment	not modelled	56.5	10	<b>PDBTitle:</b> crystal structure of listeria monocytogenes pyruvate carboxylase <b>PDB header:</b> lyase
103	<a href="#">c3b4uB</a>	Alignment	not modelled	56.4	19	<b>Chain:</b> B; <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
104	<a href="#">d1xima</a>	Alignment	not modelled	55.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
105	<a href="#">c3u9iA</a>	Alignment	not modelled	54.9	16	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme, c-terminal <b>PDBTitle:</b> the crystal structure of mandelate racemase/muconate lactonizing2 enzyme from roseiflexus sp.
106	<a href="#">c3atyA</a>	Alignment	not modelled	54.3	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> prostaglandin f2a synthase; <b>PDBTitle:</b> crystal structure of tcoye
107	<a href="#">c3qfeB</a>	Alignment	not modelled	54.0	16	<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
108	<a href="#">c3chvA</a>	Alignment	not modelled	54.0	13	<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
109	<a href="#">d1ajza</a>	Alignment	not modelled	53.9	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
110	<a href="#">c1zfyA</a>	Alignment	not modelled	53.1	10	<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
111	<a href="#">c3ngjC</a>	Alignment	not modelled	53.0	13	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> deoxyribose-phosphate aldolase; <b>PDBTitle:</b> crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
112	<a href="#">c3h7uA</a>	Alignment	not modelled	53.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> aldo-keto reductase; <b>PDBTitle:</b> crystal structure of the plant stress-response enzyme akr4c9
113	<a href="#">d1qwka</a>	Alignment	not modelled	52.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> NAD(P)-linked oxidoreductase <b>Family:</b> Aldo-keto reductases (NADP)
114	<a href="#">c3vndD</a>	Alignment	not modelled	52.5	13	<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
115	<a href="#">d1vcva1</a>	Alignment	not modelled	52.3	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
116	<a href="#">c2h90A</a>	Alignment	not modelled	52.2	12	<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
117	<a href="#">c3lciA</a>	Alignment	not modelled	51.9	12	<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
118	<a href="#">c5ocsB</a>	Alignment	not modelled	51.8	14	<b>PDB header:</b> flavoprotein <b>Chain:</b> B; <b>PDB Molecule:</b> putative nadh-dependent flavin oxidoreductase; <b>PDBTitle:</b> ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans
119	<a href="#">c6daoB</a>	Alignment	not modelled	51.6	15	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; <b>PDBTitle:</b> nahe wt selenomethionine
120	<a href="#">c5uurA</a>	Alignment	not modelled	51.3	22	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> xanthomonas albilineans dihydropteroate synthase with 4-aminobenzoic2 acid