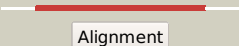



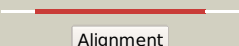





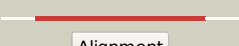
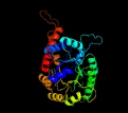







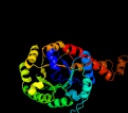




# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD0363c\_(fba)\_441266\_442300  
 Date Tue Jul 23 14:50:43 BST 2019  
 Unique Job ID c522673c4bce48fc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3elfA_</a>	 Alignment		100.0	100	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> fructose-bisphosphate aldolase; <b>PDBTitle:</b> structural characterization of tetrameric mycobacterium tuberculosis2 fructose 1,6-bisphosphate aldolase - substrate binding and catalysis3 mechanism of a class iia bacterial aldolase
2	<a href="#">d1dosa_</a>	 Alignment		100.0	40	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class II FBP aldolase
3	<a href="#">c3qm3C_</a>	 Alignment		100.0	38	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> fructose-bisphosphate aldolase; <b>PDBTitle:</b> 1.85 angstrom resolution crystal structure of fructose-bisphosphate2 aldolase (fba) from campylobacter jejuni
4	<a href="#">c5u4nA_</a>	 Alignment		100.0	32	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> fructose-1; <b>PDBTitle:</b> crystal structure of a fructose-bisphosphate aldolase from neisseria2 gonorrhoeae
5	<a href="#">c3q94B_</a>	 Alignment		100.0	29	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> fructose-bisphosphate aldolase, class ii; <b>PDBTitle:</b> the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
6	<a href="#">d1gvfa_</a>	 Alignment		100.0	26	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class II FBP aldolase
7	<a href="#">d1rvga_</a>	 Alignment		100.0	32	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class II FBP aldolase
8	<a href="#">c3c52B_</a>	 Alignment		100.0	29	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> fructose-bisphosphate aldolase; <b>PDBTitle:</b> class ii fructose-1,6-bisphosphate aldolase from helicobacter pylori2 in complex with phosphoglycolohydroxamic acid, a competitive3 inhibitor
9	<a href="#">c6ofuC_</a>	 Alignment		100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> ydji aldolase; <b>PDBTitle:</b> x-ray crystal structure of the ydji aldolase from escherichia coli k12
10	<a href="#">c2iswB_</a>	 Alignment		100.0	30	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative fructose-1,6-bisphosphate aldolase; <b>PDBTitle:</b> structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
11	<a href="#">c3pm6B_</a>	 Alignment		100.0	27	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative fructose-bisphosphate aldolase; <b>PDBTitle:</b> crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr

12	<a href="#">c4mg4G_</a>	Alignment		99.6	12	<b>PDB header:</b> unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> phosphonomutase; <b>PDBTitle:</b> crystal structure of a putative phosphonomutase from burkholderia2 cenocepacia j2315
13	<a href="#">d2fiqa1</a>	Alignment		99.4	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> GatZ-like
14	<a href="#">c2qjhH_</a>	Alignment		99.0	17	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> putative aldolase mj0400; <b>PDBTitle:</b> m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
15	<a href="#">d1ps9a1</a>	Alignment		98.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
16	<a href="#">c4utwB_</a>	Alignment		98.4	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative n-acetylmannosamine-6-phosphate 2-epimerase; <b>PDBTitle:</b> structural characterisation of nane, mannac6p c2 epimerase,2 from clostridium perfringens
17	<a href="#">c5ocsB_</a>	Alignment		98.1	11	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadh-depentdent flavin oxidoreductase; <b>PDBTitle:</b> ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans
18	<a href="#">c4ot7A_</a>	Alignment		98.1	13	<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
19	<a href="#">c3gr7A_</a>	Alignment		98.1	15	<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
20	<a href="#">c2h90A_</a>	Alignment		98.1	19	<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
21	<a href="#">c5zknA_</a>	Alignment	not modelled	98.0	16	<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
22	<a href="#">c3k30B_</a>	Alignment	not modelled	97.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> histamine dehydrogenase; <b>PDBTitle:</b> histamine dehydrogenase from nocardiodes simplex
23	<a href="#">d1thfd_</a>	Alignment	not modelled	97.8	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
24	<a href="#">c3gndC_</a>	Alignment	not modelled	97.8	16	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> aldolase lsrf; <b>PDBTitle:</b> crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
25	<a href="#">c5n2pA_</a>	Alignment	not modelled	97.8	12	<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
26	<a href="#">d1vyra_</a>	Alignment	not modelled	97.8	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
27	<a href="#">c3kruC_</a>	Alignment	not modelled	97.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh:flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
28	<a href="#">c2ze3A_</a>	Alignment	not modelled	97.6	14	<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

29	<a href="#">c3l5aA_</a>	Alignment	not modelled	97.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh/flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
30	<a href="#">c4xp7A_</a>	Alignment	not modelled	97.6	17	<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
31	<a href="#">c3q58A_</a>	Alignment	not modelled	97.5	17	<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
32	<a href="#">c3b8fF_</a>	Alignment	not modelled	97.5	12	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> pa4872 oxaloacetate decarboxylase; <b>PDBTitle:</b> crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
33	<a href="#">d1z41a1</a>	Alignment	not modelled	97.4	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
34	<a href="#">c4a3uB_</a>	Alignment	not modelled	97.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh\flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> x-structure of the old yellow enzyme homologue from zymomonas mobilis2 (ncr)
35	<a href="#">c4jicB_</a>	Alignment	not modelled	97.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gtn reductase; <b>PDBTitle:</b> glycerol trinitrate reductase nera from agrobacterium radiobacter
36	<a href="#">c1ps9A_</a>	Alignment	not modelled	97.4	12	<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
37	<a href="#">d1a53a_</a>	Alignment	not modelled	97.3	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
38	<a href="#">c2c3zA_</a>	Alignment	not modelled	97.2	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase; <b>PDBTitle:</b> crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
39	<a href="#">c4lsbA_</a>	Alignment	not modelled	97.2	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lyase/mutase; <b>PDBTitle:</b> crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315
40	<a href="#">c3hf3A_</a>	Alignment	not modelled	97.1	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
41	<a href="#">c2cw6B_</a>	Alignment	not modelled	97.1	20	<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
42	<a href="#">c3eooL_</a>	Alignment	not modelled	96.9	13	<b>PDB header:</b> lyase <b>Chain:</b> L: <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
43	<a href="#">d1i4na_</a>	Alignment	not modelled	96.9	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
44	<a href="#">d1muma_</a>	Alignment	not modelled	96.9	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/Isocitrate lyase-like
45	<a href="#">c3igsB_</a>	Alignment	not modelled	96.9	15	<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
46	<a href="#">d1ujqa_</a>	Alignment	not modelled	96.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/Isocitrate lyase-like
47	<a href="#">d1ojxa_</a>	Alignment	not modelled	96.9	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
48	<a href="#">c3w9zA_</a>	Alignment	not modelled	96.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trna-dihydrouridine synthase c; <b>PDBTitle:</b> crystal structure of dusc
49	<a href="#">d1tqxa_</a>	Alignment	not modelled	96.9	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
50	<a href="#">d1j5ta_</a>	Alignment	not modelled	96.7	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
51	<a href="#">d1y0ea_</a>	Alignment	not modelled	96.7	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> NanE-like
52	<a href="#">d1rd5a_</a>	Alignment	not modelled	96.7	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
53	<a href="#">c6ei9A_</a>	Alignment	not modelled	96.7	13	<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)
						<b>Fold:</b> TIM beta/alpha-barrel

54	<a href="#">d1h1ya_</a>	Alignment	not modelled	96.6	15	<b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
55	<a href="#">c3qjaA_</a>	Alignment	not modelled	96.6	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
56	<a href="#">c2gq8A_</a>	Alignment	not modelled	96.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, frn-binding; <b>PDBTitle:</b> structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone
57	<a href="#">c6bmaA_</a>	Alignment	not modelled	96.4	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase; <b>PDBTitle:</b> the crystal structure of indole-3-glycerol phosphate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
58	<a href="#">c5zjnB_</a>	Alignment	not modelled	96.4	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative n-acetylmannosamine-6-phosphate 2-epimerase; <b>PDBTitle:</b> structure of n-acetylmannosamine-6-phosphate-2-epimerase from vibrio2 cholerae with n-acetylmannosamine-6-phosphate
59	<a href="#">d1h5ya_</a>	Alignment	not modelled	96.4	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
60	<a href="#">c2ftpA_</a>	Alignment	not modelled	96.3	17	<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
61	<a href="#">c3tdmD_</a>	Alignment	not modelled	96.3	18	<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
62	<a href="#">c3ih1A_</a>	Alignment	not modelled	96.3	10	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
63	<a href="#">c2nx9B_</a>	Alignment	not modelled	96.2	13	<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
64	<a href="#">d1gwja_</a>	Alignment	not modelled	96.1	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
65	<a href="#">c6mywA_</a>	Alignment	not modelled	96.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> n-ethylmaleimide reductase; <b>PDBTitle:</b> gluconobacter ene-reductase (gluer) mutant - t36a
66	<a href="#">c1ydcC_</a>	Alignment	not modelled	95.9	19	<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.
67	<a href="#">c3tsmB_</a>	Alignment	not modelled	95.9	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase; <b>PDBTitle:</b> crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
68	<a href="#">c5z9yB_</a>	Alignment	not modelled	95.9	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thiazole synthase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis thiazole synthase2 (thig) complexed with dxp
69	<a href="#">c4q33F_</a>	Alignment	not modelled	95.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of inosine 5'-monophosphate dehydrogenase from2 clostridium perfringens complexed with imp and a110
70	<a href="#">c3dxiB_</a>	Alignment	not modelled	95.8	14	<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 (bv_2661) from bacteroides vulgatus
71	<a href="#">c2qiwaA_</a>	Alignment	not modelled	95.8	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pep phosphonomutase; <b>PDBTitle:</b> crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncg1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
72	<a href="#">c1djinB_</a>	Alignment	not modelled	95.7	13	<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)
73	<a href="#">d1qopa_</a>	Alignment	not modelled	95.7	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
74	<a href="#">d1wbha1</a>	Alignment	not modelled	95.6	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
75	<a href="#">c4x2rA_</a>	Alignment	not modelled	95.5	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)] <b>PDBTitle:</b> crystal structure of pria from actinomyces urogenitalis
76	<a href="#">c5ks8D_</a>	Alignment	not modelled	95.5	15	<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
77	<a href="#">d1piia2</a>	Alignment	not modelled	95.4	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
78	<a href="#">c3bleA_</a>	Alignment	not modelled	95.4	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
79	<a href="#">c4axkB_</a>	Alignment	not modelled	95.4	19	<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
80	<a href="#">c3jrkG_</a>	Alignment	not modelled	95.4	14	<b>PDB header:</b> lyase <b>Chain:</b> G; <b>PDB Molecule:</b> tagatose 1,6-diphosphate aldolase 2; <b>PDBTitle:</b> a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
81	<a href="#">c5ks8F_</a>	Alignment	not modelled	95.3	14	<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
82	<a href="#">d1vhca_</a>	Alignment	not modelled	95.2	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
83	<a href="#">d1xcfa_</a>	Alignment	not modelled	95.2	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
84	<a href="#">d1rpxa_</a>	Alignment	not modelled	95.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
85	<a href="#">d1xya1</a>	Alignment	not modelled	95.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> NanE-like
86	<a href="#">c3ivuB_</a>	Alignment	not modelled	95.0	13	<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
87	<a href="#">c3lyeA_</a>	Alignment	not modelled	94.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> oxaloacetate acetyl hydrolase; <b>PDBTitle:</b> crystal structure of oxaloacetate acetylhydrolase
88	<a href="#">c3fa4D_</a>	Alignment	not modelled	94.8	14	<b>PDB header:</b> lyase <b>Chain:</b> D; <b>PDB Molecule:</b> 2,3-dimethylmalate lyase; <b>PDBTitle:</b> crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
89	<a href="#">c5d88A_</a>	Alignment	not modelled	94.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> predicted protease of the collagenase family; <b>PDBTitle:</b> the structure of the u32 peptidase mk0906
90	<a href="#">c4ml9A_</a>	Alignment	not modelled	94.8	15	<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
91	<a href="#">c4wd0A_</a>	Alignment	not modelled	94.7	19	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> 1-(5-phosphoribosyl)-5-[(5'-phosphoribosylamino)] <b>PDBTitle:</b> crystal structure of hisa from arthrobacter aurescens
92	<a href="#">c6qkqB_</a>	Alignment	not modelled	94.7	13	<b>PDB header:</b> flavoprotein <b>Chain:</b> B; <b>PDB Molecule:</b> ncr a; <b>PDBTitle:</b> 2-naphthoyl-coa reductase(ncr)
93	<a href="#">c3thaB_</a>	Alignment	not modelled	94.6	15	<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.
94	<a href="#">d1vjia_</a>	Alignment	not modelled	94.4	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
95	<a href="#">c5umfB_</a>	Alignment	not modelled	94.4	14	<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
96	<a href="#">c3bo9B_</a>	Alignment	not modelled	94.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> putative nitroalkan dioxygenase; <b>PDBTitle:</b> crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution
97	<a href="#">c2cdh1_</a>	Alignment	not modelled	94.2	13	<b>PDB header:</b> transferase <b>Chain:</b> 1; <b>PDB Molecule:</b> enoyl reductase; <b>PDBTitle:</b> architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
98	<a href="#">c4gj1A_</a>	Alignment	not modelled	94.2	20	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> 1-(5-phosphoribosyl)-5-[(5'-phosphoribosylamino)] <b>PDBTitle:</b> crystal structure of 1-(5-phosphoribosyl)-5-[(5'-phosphoribosylamino)]2 methylideneamino] imidazole-4-carboxamide isomerase (hisa).
99	<a href="#">c3r2gA_</a>	Alignment	not modelled	94.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> inosine 5'-monophosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
100	<a href="#">c1ydnA_</a>	Alignment	not modelled	94.1	17	<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.
101	<a href="#">c5aheA_</a>	Alignment	not modelled	93.8	13	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> <b>PDBTitle:</b> crystal structure of salmonella enterica hisa
102	<a href="#">c3inpA_</a>	Alignment	not modelled	93.8	18	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> d-ribulose-phosphate 3-epimerase; <b>PDBTitle:</b> 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
103	<a href="#">d2mnra1</a>	Alignment	not modelled	93.8	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like

104	<a href="#">d1djqa1</a>	Alignment	not modelled	93.8	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
105	<a href="#">c5epdA</a>	Alignment	not modelled	93.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol trinitrate reductase; <b>PDBTitle:</b> crystal structure of glycerol trinitrate reductase xdpb from2 agrobacterium sp. r89-1 (apo form)
106	<a href="#">c2w6rA</a>	Alignment	not modelled	93.5	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> imidazole glycerol phosphate synthase subunit <b>PDBTitle:</b> crystal structure of an artificial (ba)8-barrel protein2 designed from identical half barrels
107	<a href="#">d1vzwa1</a>	Alignment	not modelled	93.5	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
108	<a href="#">d1ka9f</a>	Alignment	not modelled	93.2	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
109	<a href="#">d2flia1</a>	Alignment	not modelled	93.2	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
110	<a href="#">d1vc4a</a>	Alignment	not modelled	93.1	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
111	<a href="#">d1xi3a</a>	Alignment	not modelled	93.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Thiamin phosphate synthase <b>Family:</b> Thiamin phosphate synthase
112	<a href="#">c2z6jB</a>	Alignment	not modelled	92.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> trans-2-enoyl-acyl reductase ii; <b>PDBTitle:</b> crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor
113	<a href="#">d1tqja</a>	Alignment	not modelled	92.5	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
114	<a href="#">c4iqjB</a>	Alignment	not modelled	92.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase ii; <b>PDBTitle:</b> crystal structure of porphyromonas gingivalis enoyl-acyl reductase ii2 (fabk) with cofactors nadph and fmn
115	<a href="#">d1s2wa</a>	Alignment	not modelled	92.4	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/Isocitrate lyase-like
116	<a href="#">c1f9cA</a>	Alignment	not modelled	92.3	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (muconate cycloisomerase i); <b>PDBTitle:</b> crystal structure of mle d178n variant
117	<a href="#">d1wv2a</a>	Alignment	not modelled	92.3	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> ThiG-like <b>Family:</b> ThiG-like
118	<a href="#">c5uncB</a>	Alignment	not modelled	92.2	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoenolpyruvate phosphomutase; <b>PDBTitle:</b> the crystal structure of phosphoenolpyruvate phosphomutase from2 streptomyces platensis subsp. rosaceus
119	<a href="#">c4e38A</a>	Alignment	not modelled	92.0	16	<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 vibriionales bacterium swat-3 (target efi-502156)
120	<a href="#">c3qz6A</a>	Alignment	not modelled	92.0	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hpch/hpai aldolase; <b>PDBTitle:</b> the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2