

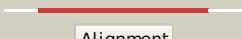













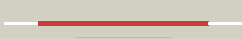







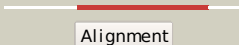





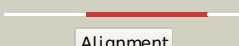

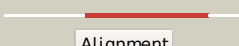

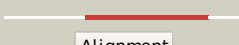









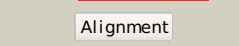
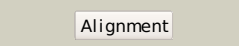



# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0A011
Date	Tue Jul 17 17:05:03 BST 2012
Unique Job ID	0ed864b8d408b2f3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3jrkG_</a>	 Alignment		100.0	72	<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
2	<a href="#">d1to3a_</a>	 Alignment		100.0	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
3	<a href="#">c2qjhH_</a>	 Alignment		100.0	18	<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
4	<a href="#">c3gndC_</a>	 Alignment		100.0	17	<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
5	<a href="#">d1ojxa_</a>	 Alignment		100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
6	<a href="#">c3fokH_</a>	 Alignment		100.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> H; <b>PDB Molecule:</b> uncharacterized protein cgl0159; <b>PDBTitle:</b> crystal structure of cgl0159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural3 genomics target cgr115
7	<a href="#">d1n7ka_</a>	 Alignment		99.1	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
8	<a href="#">d1xi3a_</a>	 Alignment		98.9	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Thiamin phosphate synthase <b>Family:</b> Thiamin phosphate synthase
9	<a href="#">c3ru6C_</a>	 Alignment		98.6	14	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> orotidine 5'-phosphate decarboxylase; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of orotidine 5'-phosphate2 decarboxylase (pyrf) from campylobacter jejuni subsp. jejuni nctc3 11168
10	<a href="#">d2zdra2</a>	 Alignment		98.5	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> NeuB-like
11	<a href="#">c1xuzA_</a>	 Alignment		98.4	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> polysialic acid capsule biosynthesis protein siac; <b>PDBTitle:</b> crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol

12	<a href="#">c3f4wA</a>	 Alignment		98.4	16	<b>PDB header:</b> synthase, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hexulose 6 phosphate synthase; <b>PDBTitle:</b> the 1.65a crystal structure of 3-hexulose-6-phosphate2 synthase from salmonella typhimurium
13	<a href="#">d1a53a</a>	 Alignment		98.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
14	<a href="#">d1i4na</a>	 Alignment		98.4	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
15	<a href="#">d1piia2</a>	 Alignment		98.3	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
16	<a href="#">d1vlia2</a>	 Alignment		98.3	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> NeuB-like
17	<a href="#">c3qjaA</a>	 Alignment		98.2	17	<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
18	<a href="#">c2c3zA</a>	 Alignment		98.2	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 a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
19	<a href="#">d1j5ta</a>	 Alignment		98.2	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
20	<a href="#">c2v82A</a>	 Alignment		98.2	19	<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
21	<a href="#">c1vliA</a>	 Alignment	not modelled	98.2	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> spore coat polysaccharide biosynthesis protein spse; <b>PDBTitle:</b> crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
22	<a href="#">c3o63B</a>	 Alignment	not modelled	98.2	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable thiamine-phosphate pyrophosphorylase; <b>PDBTitle:</b> crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
23	<a href="#">c3q58A</a>	 Alignment	not modelled	98.2	13	<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
24	<a href="#">d2tpsa</a>	 Alignment	not modelled	98.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Thiamin phosphate synthase <b>Family:</b> Thiamin phosphate synthase
25	<a href="#">d1wbha1</a>	 Alignment	not modelled	97.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
26	<a href="#">c4e38A</a>	 Alignment	not modelled	97.9	20	<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 vibrionales bacterium swat-3 (target efi-502156)
27	<a href="#">d1yxa1</a>	 Alignment	not modelled	97.9	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> NanE-like

28	<a href="#">d1vc4a_</a>	Alignment	not modelled	97.9	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
29	<a href="#">c3exsB_</a>	Alignment	not modelled	97.9	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> rmpp (hexulose-6-phosphate synthase); <b>PDBTitle:</b> crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p
30	<a href="#">c3ajxA_</a>	Alignment	not modelled	97.9	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hexulose-6-phosphate synthase; <b>PDBTitle:</b> crystal structure of 3-hexulose-6-phosphate synthase
31	<a href="#">d1h1ya_</a>	Alignment	not modelled	97.9	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
32	<a href="#">c3g8rA_</a>	Alignment	not modelled	97.8	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable spore coat polysaccharide biosynthesis protein e; <b>PDBTitle:</b> crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
33	<a href="#">d1o60a_</a>	Alignment	not modelled	97.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I DAHP synthetase
34	<a href="#">c3stgA_</a>	Alignment	not modelled	97.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase; <b>PDBTitle:</b> crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis
35	<a href="#">c1yadD_</a>	Alignment	not modelled	97.8	20	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> regulatory protein teni; <b>PDBTitle:</b> structure of teni from bacillus subtilis
36	<a href="#">d1wa3a1</a>	Alignment	not modelled	97.8	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
37	<a href="#">d1y0ea_</a>	Alignment	not modelled	97.8	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> NanE-like
38	<a href="#">d1q6oa_</a>	Alignment	not modelled	97.7	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
39	<a href="#">c3pg8B_</a>	Alignment	not modelled	97.7	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phospho-2-dehydro-3-deoxyheptonate aldolase; <b>PDBTitle:</b> truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
40	<a href="#">d1d9ea_</a>	Alignment	not modelled	97.6	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I DAHP synthetase
41	<a href="#">d1o0ya_</a>	Alignment	not modelled	97.6	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
42	<a href="#">d1mxsa_</a>	Alignment	not modelled	97.6	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
43	<a href="#">c3igsB_</a>	Alignment	not modelled	97.6	13	<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
44	<a href="#">d1zfja1</a>	Alignment	not modelled	97.5	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
45	<a href="#">c3ngjC_</a>	Alignment	not modelled	97.5	15	<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
46	<a href="#">c3jr2D_</a>	Alignment	not modelled	97.5	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> hexulose-6-phosphate synthase sgbh; <b>PDBTitle:</b> x-ray crystal structure of the mg-bound 3-keto-l-gulonate-6-phosphate2 decarboxylase from vibrio cholerae o1 biovar el tor str. n16961
47	<a href="#">c3mbfA_</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> fructose-bisphosphate aldolase; <b>PDBTitle:</b> crystal structure of fructose bisphosphate aldolase from2 encephalitozoon cuniculi, bound to fructose 1,6-bisphosphate
48	<a href="#">c1piiA_</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> bifunctional (isomerase and synthase) <b>Chain:</b> A: <b>PDB Molecule:</b> n-(5'-phosphoribosyl)anthranilate isomerase; <b>PDBTitle:</b> three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase:3 indoleglycerolphosphate synthase from escherichia coli4 refined at 2.0 angstroms resolution
49	<a href="#">d1vhca_</a>	Alignment	not modelled	97.4	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
50	<a href="#">d1ub3a_</a>	Alignment	not modelled	97.3	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
51	<a href="#">c3sz8D_</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase 2; <b>PDBTitle:</b> crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei

52	<a href="#">c3oa3A</a>	Alignment	not modelled	97.3	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
53	<a href="#">d1mzha</a>	Alignment	not modelled	97.3	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
54	<a href="#">c3ng3A</a>	Alignment	not modelled	97.2	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> deoxyribose-phosphate aldolase; <b>PDBTitle:</b> crystal structure of deoxyribose phosphate aldolase from mycobacterium2 avium 104 in a schiff base with an unknown aldehyde
55	<a href="#">c3t4cD</a>	Alignment	not modelled	97.2	23	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooc-tonate aldolase 1; <b>PDBTitle:</b> crystal structure of 2-dehydro-3-deoxyphosphooc-tonate aldolase from2 burkholderia ambifaria
56	<a href="#">d1rpxa</a>	Alignment	not modelled	97.1	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
57	<a href="#">d2qapa1</a>	Alignment	not modelled	97.1	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
58	<a href="#">d1xcfa</a>	Alignment	not modelled	97.1	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
59	<a href="#">c4ff0B</a>	Alignment	not modelled	97.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> inosine 5'-monophosphate dehydrogenase from vibrio cholerae, deletion2 mutant, complexed with imp
60	<a href="#">d1eixa</a>	Alignment	not modelled	97.0	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
61	<a href="#">c1vs1B</a>	Alignment	not modelled	97.0	21	<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
62	<a href="#">d1eepa</a>	Alignment	not modelled	97.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
63	<a href="#">d1dbta</a>	Alignment	not modelled	97.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
64	<a href="#">d1dvja</a>	Alignment	not modelled	97.0	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
65	<a href="#">c1zjfA</a>	Alignment	not modelled	96.9	21	<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
66	<a href="#">c3inpA</a>	Alignment	not modelled	96.9	15	<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.
67	<a href="#">d1vrda1</a>	Alignment	not modelled	96.9	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
68	<a href="#">c1zcoA</a>	Alignment	not modelled	96.9	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphoheptonate aldolase; <b>PDBTitle:</b> crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
69	<a href="#">c3fs2A</a>	Alignment	not modelled	96.9	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooc-tonate aldolase; <b>PDBTitle:</b> crystal structure of 2-dehydro-3-deoxyphosphooc-tonate2 aldolase from bruciella melitensis at 1.85a resolution
70	<a href="#">c2y85D</a>	Alignment	not modelled	96.9	9	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosyl isomerase a; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
71	<a href="#">d1z41a1</a>	Alignment	not modelled	96.8	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
72	<a href="#">c3gr7A</a>	Alignment	not modelled	96.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph dehydrogenase; <b>PDBTitle:</b> structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
73	<a href="#">d1uuma</a>	Alignment	not modelled	96.8	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
74	<a href="#">c3qc3B</a>	Alignment	not modelled	96.7	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> d-ribulose-5-phosphate-3-epimerase; <b>PDBTitle:</b> crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
75	<a href="#">c1rldB</a>	Alignment	not modelled	96.7	16	<b>PDB header:</b> lyase(carbon-carbon) <b>Chain:</b> B: <b>PDB Molecule:</b> ribulose 1,5 bisphosphate carboxylase/oxygenase (large) <b>PDBTitle:</b> solid-state phase transition in the crystal structure of ribulose 1,5-2 biphosphate carboxylase(/slash)oxygenase
76	<a href="#">c1vrda</a>	Alignment	not modelled	96.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase;

76	<a href="#">c1v9A</a>	Alignment	not modelled	96.7	16	<b>PDBTitle:</b> crystal structure of inosine-5'-monophosphate dehydrogenase (tm1347)2 from thermotoga maritima at 2.18 a resolution
77	<a href="#">c2qapC</a>	Alignment	not modelled	96.7	16	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> fructose-1,6-bisphosphate aldolase; <b>PDBTitle:</b> fructose-1,6-bisphosphate aldolase from leishmania mexicana
78	<a href="#">d1wv2a</a>	Alignment	not modelled	96.7	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> ThiG-like <b>Family:</b> ThiG-like
79	<a href="#">c3mmtC</a>	Alignment	not modelled	96.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> fructose-bisphosphate aldolase; <b>PDBTitle:</b> crystal structure of fructose bisphosphate aldolase from bartonella2 henselae, bound to fructose bisphosphate
80	<a href="#">c2yw3E</a>	Alignment	not modelled	96.6	20	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3- <b>PDBTitle:</b> crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1
81	<a href="#">c3khjE</a>	Alignment	not modelled	96.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> inosine-5-monophosphate dehydrogenase; <b>PDBTitle:</b> c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
82	<a href="#">d1w0ma</a>	Alignment	not modelled	96.6	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
83	<a href="#">d1jr1a1</a>	Alignment	not modelled	96.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
84	<a href="#">d1f2ja</a>	Alignment	not modelled	96.5	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
85	<a href="#">d1ep3a</a>	Alignment	not modelled	96.5	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
86	<a href="#">c3b4uB</a>	Alignment	not modelled	96.4	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
87	<a href="#">c3ffsC</a>	Alignment	not modelled	96.4	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> inosine-5-monophosphate dehydrogenase; <b>PDBTitle:</b> the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
88	<a href="#">d1vzwa1</a>	Alignment	not modelled	96.4	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
89	<a href="#">c2h90A</a>	Alignment	not modelled	96.4	14	<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
90	<a href="#">d1jcna1</a>	Alignment	not modelled	96.2	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
91	<a href="#">c2h6rG</a>	Alignment	not modelled	96.1	20	<b>PDB header:</b> isomerase <b>Chain:</b> G: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
92	<a href="#">c1djnb</a>	Alignment	not modelled	96.1	15	<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)
93	<a href="#">c3ldvB</a>	Alignment	not modelled	96.0	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> orotidine 5'-phosphate decarboxylase; <b>PDBTitle:</b> 1.77 angstrom resolution crystal structure of orotidine 5'-2 phosphate decarboxylase from vibrio cholerae o1 biovar3 eltor str. n16961
94	<a href="#">c3kx6C</a>	Alignment	not modelled	96.0	16	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> fructose-bisphosphate aldolase; <b>PDBTitle:</b> crystal structure of fructose-1,6-bisphosphate aldolase from babesia2 bovis at 2.1a resolution
95	<a href="#">d1djqa1</a>	Alignment	not modelled	96.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
96	<a href="#">d1km4a</a>	Alignment	not modelled	96.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
97	<a href="#">c1jcna</a>	Alignment	not modelled	96.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine monophosphate dehydrogenase i; <b>PDBTitle:</b> binary complex of human type-i inosine monophosphate dehydrogenase2 with 6-cl-imp
98	<a href="#">d1qt1a</a>	Alignment	not modelled	95.9	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
99	<a href="#">c3hf3A</a>	Alignment	not modelled	95.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> chromate reductase; <b>PDBTitle:</b> old yellow enzyme from thermus scotoductus sa-01
100	<a href="#">d1gvfa</a>	Alignment	not modelled	95.8	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class II FBP aldolase
						<b>Fold:</b> TIM beta/alpha-barrel

101	<a href="#">d8ruca1</a>	Alignment	not modelled	95.8	14	<b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
102	<a href="#">c2qr6A</a>	Alignment	not modelled	95.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> imp dehydrogenase/gmp reductase; <b>PDBTitle:</b> crystal structure of imp dehydrogenase/gmp reductase-like protein2 (np_599840.1) from corynebacterium glutamicum atcc 13032 kitasato at3 1.50 a resolution
103	<a href="#">c2a7nA</a>	Alignment	not modelled	95.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l(+)-mandelate dehydrogenase; <b>PDBTitle:</b> crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
104	<a href="#">c3tfxB</a>	Alignment	not modelled	95.8	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> orotidine 5'-phosphate decarboxylase; <b>PDBTitle:</b> crystal structure of orotidine 5'-phosphate decarboxylase from2 lactobacillus acidophilus
105	<a href="#">c2ze3A</a>	Alignment	not modelled	95.7	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
106	<a href="#">c3labA</a>	Alignment	not modelled	95.7	16	<b>PDB header:</b> <b>PDB COMPND:</b>
107	<a href="#">d1muwa</a>	Alignment	not modelled	95.7	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
108	<a href="#">c2iswB</a>	Alignment	not modelled	95.7	20	<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-bisphosphate aldolase in2 complex with phosphoglycolohydroxamate
109	<a href="#">d1qo5b</a>	Alignment	not modelled	95.7	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
110	<a href="#">c3kruC</a>	Alignment	not modelled	95.6	18	<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
111	<a href="#">c2ehhE</a>	Alignment	not modelled	95.6	17	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
112	<a href="#">d2a21a1</a>	Alignment	not modelled	95.5	9	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I DAHP synthetase
113	<a href="#">d1gk8a1</a>	Alignment	not modelled	95.5	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
114	<a href="#">d1rd5a</a>	Alignment	not modelled	95.5	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
115	<a href="#">c3l52A</a>	Alignment	not modelled	95.4	12	<b>PDB header:</b> <b>PDB COMPND:</b>
116	<a href="#">c3navB</a>	Alignment	not modelled	95.3	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
117	<a href="#">d1vhna</a>	Alignment	not modelled	95.3	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
118	<a href="#">c3tr2A</a>	Alignment	not modelled	95.3	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> orotidine 5'-phosphate decarboxylase; <b>PDBTitle:</b> structure of a orotidine 5'-phosphate decarboxylase (pyrf) from2 coxiella burnetii
119	<a href="#">d1p4ca</a>	Alignment	not modelled	95.2	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
120	<a href="#">d1tqja</a>	Alignment	not modelled	95.2	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase