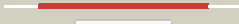



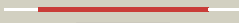







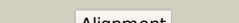











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1438_(tpiA)_1615570_1616355
Date	Wed Jul 31 22:05:54 BST 2019
Unique Job ID	c99d3f7823ea5066

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3gvqA_</a>	 Alignment		100.0	100	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from mycobacterium2 tuberculosis
2	<a href="#">c4y9aB_</a>	 Alignment		100.0	67	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from streptomyces2 coelicolor
3	<a href="#">d1m6ja_</a>	 Alignment		100.0	36	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
4	<a href="#">c1yyaA_</a>	 Alignment		100.0	50	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of tt0473, putative triosephosphate isomerase from2 thermus thermophilus hb8
5	<a href="#">d1b9ba_</a>	 Alignment		100.0	45	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
6	<a href="#">d1aw1a_</a>	 Alignment		100.0	41	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
7	<a href="#">d1trea_</a>	 Alignment		100.0	42	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
8	<a href="#">c4y96B_</a>	 Alignment		100.0	45	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from gemmata2 obscuriglobus
9	<a href="#">c2dp3A_</a>	 Alignment		100.0	39	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of a double mutant (c202a/a198v) of triosephosphate2 isomerase from giardia lamblia
10	<a href="#">d1mo0a_</a>	 Alignment		100.0	40	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
11	<a href="#">c3m9yB_</a>	 Alignment		100.0	44	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from methicillin2 resistant staphylococcus aureus at 1.9 angstrom resolution

12	<a href="#">d2btma_</a>	Alignment		100.0	45	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
13	<a href="#">c5zg5B_</a>	Alignment		100.0	43	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase sadsubaa mutant from2 opisthorchis viverrini
14	<a href="#">d1kv5a_</a>	Alignment		100.0	38	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
15	<a href="#">d1n55a_</a>	Alignment		100.0	40	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
16	<a href="#">c4y8fA_</a>	Alignment		100.0	43	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from clostridium2 perfringens
17	<a href="#">c4mknA_</a>	Alignment		100.0	41	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of chloroplastic triosephosphate isomerase from2 chlamydomonas reinhardtii at 1.1 a of resolution
18	<a href="#">d1suxa_</a>	Alignment		100.0	40	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
19	<a href="#">c4x22A_</a>	Alignment		100.0	40	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of leptospira interrogans triosephosphate isomerase2 (litim)
20	<a href="#">c4obtA_</a>	Alignment		100.0	43	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase, cytosolic; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana cytosolic triose phosphate2 isomerase
21	<a href="#">c5uprA_</a>	Alignment	not modelled	100.0	42	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> x-ray structure of a putative triosephosphate isomerase from2 toxoplasma gondii me49
22	<a href="#">d1sw3a_</a>	Alignment	not modelled	100.0	39	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
23	<a href="#">c3qstA_</a>	Alignment	not modelled	100.0	40	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase, putative; <b>PDBTitle:</b> crystal structure of trichomonas vaginalis triosephosphate isomerase2 tvag_096350 gene (val-45 variant)
24	<a href="#">c3krsB_</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> structure of triosephosphate isomerase from cryptosporidium parvum at2 1.55a resolution
25	<a href="#">d1r2ra_</a>	Alignment	not modelled	100.0	39	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
26	<a href="#">c4ohqB_</a>	Alignment	not modelled	100.0	41	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase, chloroplastic; <b>PDBTitle:</b> crystal structure of chloroplast triose phosphate isomerase from2 arabidopsis thaliana
27	<a href="#">c4g1kB_</a>	Alignment	not modelled	100.0	45	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from burkholderia2 thailandensis
28	<a href="#">c5ibxB_</a>	Alignment	not modelled	100.0	46	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> 1.65 angstrom crystal structure of triosephosphate isomerase (tim)2 from streptococcus pneumoniae
						<b>Fold:</b> TIM beta/alpha-barrel

29	<a href="#">d1o5xa_</a>	Alignment	not modelled	100.0	36	<b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
30	<a href="#">c4y90B_</a>	Alignment	not modelled	100.0	49	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from deinococcus2 radiodurans
31	<a href="#">c5ujwD_</a>	Alignment	not modelled	100.0	42	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from francisella2 tularensis subsp. tularensis schu s4
32	<a href="#">c5eywB_</a>	Alignment	not modelled	100.0	36	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of liopenaeus vannamei triosephosphate isomerase2 complexed with 2-phosphoglycolic acid
33	<a href="#">d1neya_</a>	Alignment	not modelled	100.0	40	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
34	<a href="#">c6bveA_</a>	Alignment	not modelled	100.0	44	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> triosephosphate isomerase of synechocystis in complex with 2-2 phosphoglycolic acid
35	<a href="#">c3th6B_</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from rhipicephalus2 (boophilus) microplus.
36	<a href="#">c4nvtD_</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from brucella2 melitensis
37	<a href="#">c3s6dA_</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of a putative triosephosphate isomerase from2 coccidioides immitis
38	<a href="#">d1ttja_</a>	Alignment	not modelled	100.0	38	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
39	<a href="#">c3kxqB_</a>	Alignment	not modelled	100.0	38	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from bartonella2 henselae at 1.6a resolution
40	<a href="#">c2jqgB_</a>	Alignment	not modelled	100.0	34	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> kinetics and structural properties of triosephosphate2 isomerase from helicobacter pylori
41	<a href="#">d1hg3a_</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
42	<a href="#">d1w0ma_</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
43	<a href="#">c5cssA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from thermoplasma2 acidophilum with glycerol 3-phosphate
44	<a href="#">c2h6rG_</a>	Alignment	not modelled	100.0	24	<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
45	<a href="#">d1rpxa_</a>	Alignment	not modelled	98.6	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
46	<a href="#">d1tqja_</a>	Alignment	not modelled	97.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
47	<a href="#">c4nu7C_</a>	Alignment	not modelled	97.9	16	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> ribulose-phosphate 3-epimerase; <b>PDBTitle:</b> 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from2 toxoplasma gondii.
48	<a href="#">c5umfB_</a>	Alignment	not modelled	97.8	15	<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
49	<a href="#">c3ct7E_</a>	Alignment	not modelled	97.7	18	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> d-allulose-6-phosphate 3-epimerase; <b>PDBTitle:</b> crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
50	<a href="#">c3qjaA_</a>	Alignment	not modelled	97.5	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
51	<a href="#">d1qopa_</a>	Alignment	not modelled	97.4	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
52	<a href="#">d1j5ta_</a>	Alignment	not modelled	97.4	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
53	<a href="#">c5n2pA_</a>	Alignment	not modelled	97.4	9	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> sulfobolus solfataricus tryptophan synthase a
54	<a href="#">d1tqxa_</a>	Alignment	not modelled	97.4	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
55	<a href="#">d2flia1</a>	Alignment	not modelled	97.3	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase

56	<a href="#">c3inpA</a>	Alignment	not modelled	97.3	17	<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.
57	<a href="#">c3tsmB</a>	Alignment	not modelled	97.2	12	<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
58	<a href="#">d1rd5a</a>	Alignment	not modelled	97.1	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
59	<a href="#">c2c3zA</a>	Alignment	not modelled	97.0	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
60	<a href="#">c3qc3B</a>	Alignment	not modelled	97.0	13	<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
61	<a href="#">d1a53a</a>	Alignment	not modelled	96.9	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
62	<a href="#">c3f4wA</a>	Alignment	not modelled	96.9	20	<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
63	<a href="#">d1h1ya</a>	Alignment	not modelled	96.9	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
64	<a href="#">c4utwB</a>	Alignment	not modelled	96.6	15	<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
65	<a href="#">c5zknA</a>	Alignment	not modelled	96.6	13	<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
66	<a href="#">d1q6oa</a>	Alignment	not modelled	96.6	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
67	<a href="#">d1i4na</a>	Alignment	not modelled	96.6	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
68	<a href="#">c6bmaA</a>	Alignment	not modelled	96.4	15	<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
69	<a href="#">c5zjnB</a>	Alignment	not modelled	96.3	14	<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
70	<a href="#">c3q58A</a>	Alignment	not modelled	96.2	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylmannosamine-6-phosphate 2-epimerase; <b>PDBTitle:</b> structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
71	<a href="#">d1xcfa</a>	Alignment	not modelled	96.1	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
72	<a href="#">c4e38A</a>	Alignment	not modelled	96.1	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 vibriionales bacterium swat-3 (target efi-502156)
73	<a href="#">d1vc4a</a>	Alignment	not modelled	96.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
74	<a href="#">c3ajxA</a>	Alignment	not modelled	95.9	20	<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
75	<a href="#">c3igsB</a>	Alignment	not modelled	95.9	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
76	<a href="#">c3thaB</a>	Alignment	not modelled	95.9	12	<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.
77	<a href="#">d1yxya1</a>	Alignment	not modelled	95.8	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> NanE-like
78	<a href="#">c4axkB</a>	Alignment	not modelled	95.7	18	<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
79	<a href="#">d1h5ya</a>	Alignment	not modelled	95.5	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
80	<a href="#">d1wv2a</a>	Alignment	not modelled	95.3	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> ThiG-like

						Family:ThiG-like
81	<a href="#">c2bdqA</a>	Alignment	not modelled	95.3	16	<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 from <i>Streptococcus agalactiae</i> , northeast structural genomics target sar15.
82	<a href="#">c3navB</a>	Alignment	not modelled	95.3	20	<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 from <i>Vibrio cholerae</i> O1 biovar el tor str. n16961
83	<a href="#">d1vzwa1</a>	Alignment	not modelled	95.0	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
84	<a href="#">c3vndD</a>	Alignment	not modelled	95.0	20	<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 the <i>Psychrophile Shewanella frigidimarina</i> K14-2
85	<a href="#">c4x2rA</a>	Alignment	not modelled	94.9	15	<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 Prib from <i>Actinomyces urogenitalis</i>
86	<a href="#">d1geqa</a>	Alignment	not modelled	94.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
87	<a href="#">d1ka9f</a>	Alignment	not modelled	94.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
88	<a href="#">c5b69A</a>	Alignment	not modelled	94.6	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranylgeranyl phosphate synthase; <b>PDBTitle:</b> crystal structure of geranylgeranylgeranyl phosphate synthase 2 complexed with an G-1-P from <i>Thermoplasma acidophilum</i>
89	<a href="#">c6hyeF</a>	Alignment	not modelled	94.2	24	<b>PDB header:</b> plant protein <b>Chain:</b> F: <b>PDB Molecule:</b> pyridoxal 5'-phosphate synthase subunit pdx1.3; <b>PDBTitle:</b> pdx1.2/pdx1.3 complex (pdx1.3:k97a)
90	<a href="#">c6nkeA</a>	Alignment	not modelled	94.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranylgeranyl phosphate synthase; <b>PDBTitle:</b> wild-type ggpps from <i>Thermoplasma volcanium</i>
91	<a href="#">d1piia2</a>	Alignment	not modelled	94.1	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
92	<a href="#">c3tdmD</a>	Alignment	not modelled	94.1	14	<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
93	<a href="#">c5ey5A</a>	Alignment	not modelled	94.0	24	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lbcats-a; <b>PDBTitle:</b> lbcats
94	<a href="#">c2y85D</a>	Alignment	not modelled	93.8	16	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosyl isomerase a; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis phosphoribosyl isomerase with bound rcdp
95	<a href="#">c4gj1A</a>	Alignment	not modelled	93.7	23	<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).
96	<a href="#">c4ml9A</a>	Alignment	not modelled	93.1	21	<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 the 2 conserved phosphate binding site from <i>Sebalidella termitidis</i>
97	<a href="#">c5tchG</a>	Alignment	not modelled	93.1	31	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase from <i>M. tuberculosis</i> -2 ligand-free form, trpa-g66v mutant
98	<a href="#">d1wa3a1</a>	Alignment	not modelled	93.1	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
99	<a href="#">c4jejA</a>	Alignment	not modelled	93.1	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranylgeranyl phosphate synthase; <b>PDBTitle:</b> ggpps from <i>Flavobacterium johnsoniae</i>
100	<a href="#">c5aheA</a>	Alignment	not modelled	92.9	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> <b>PDBTitle:</b> crystal structure of <i>Salmonella enterica</i> hisa
101	<a href="#">d1y0ea</a>	Alignment	not modelled	92.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> NanE-like
102	<a href="#">c3exsB</a>	Alignment	not modelled	92.4	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> rmppd (hexulose-6-phosphate synthase); <b>PDBTitle:</b> crystal structure of kgpdc from <i>Streptococcus mutans</i> in 2 complex with d-r5p
103	<a href="#">c2nv2U</a>	Alignment	not modelled	92.3	22	<b>PDB header:</b> lyase/transferase <b>Chain:</b> U: <b>PDB Molecule:</b> pyridoxal biosynthesis lyase pdxs; <b>PDBTitle:</b> structure of the plp synthase complex pdx1/2 (yaad/e) from <i>Bacillus subtilis</i>
104	<a href="#">c6hxgE</a>	Alignment	not modelled	92.3	19	<b>PDB header:</b> plant protein <b>Chain:</b> E: <b>PDB Molecule:</b> pyridoxal 5'-phosphate synthase-like subunit pdx1.2; <b>PDBTitle:</b> pdx1.2/pdx1.3 complex (intermediate)
105	<a href="#">d1jvna1</a>	Alignment	not modelled	92.1	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes

106	<a href="#">c4wd0A_</a>	Alignment	not modelled	91.8	17	<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 hisap form arthrobacter aurescens
107	<a href="#">c4adsF_</a>	Alignment	not modelled	91.8	24	<b>PDB header:</b> transferase/transferase <b>Chain:</b> F: <b>PDB Molecule:</b> pyridoxine biosynthetic enzyme pdx1 homologue, putative; <b>PDBTitle:</b> crystal structure of plasmodial plp synthase complex
108	<a href="#">c4a3uB_</a>	Alignment	not modelled	91.8	13	<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)
109	<a href="#">c3gkaB_</a>	Alignment	not modelled	91.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> n-ethylmaleimide reductase; <b>PDBTitle:</b> crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
110	<a href="#">c4b5nA_</a>	Alignment	not modelled	91.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, frn-binding; <b>PDBTitle:</b> crystal structure of oxidized shewanella yellow enzyme 4 (sye4)
111	<a href="#">c2zbtB_</a>	Alignment	not modelled	91.3	27	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxal biosynthesis lyase pdxs; <b>PDBTitle:</b> crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
112	<a href="#">c4r9xB_</a>	Alignment	not modelled	91.3	20	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> copper homeostasis protein cutc; <b>PDBTitle:</b> crystal structure of putative copper homeostasis protein cutc from2 bacillus anthracis
113	<a href="#">c5kzmA_</a>	Alignment	not modelled	91.2	14	<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
114	<a href="#">d1znna1</a>	Alignment	not modelled	91.2	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> PdxS-like
115	<a href="#">d1viza_</a>	Alignment	not modelled	91.1	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
116	<a href="#">d1xi3a_</a>	Alignment	not modelled	91.1	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Thiamin phosphate synthase <b>Family:</b> Thiamin phosphate synthase
117	<a href="#">c2ekcA_</a>	Alignment	not modelled	91.1	19	<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
118	<a href="#">c6oviA_</a>	Alignment	not modelled	91.1	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> keto-deoxy-phosphogluconate aldolase; <b>PDBTitle:</b> crystal structure of kdpq aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
119	<a href="#">c3tdnB_</a>	Alignment	not modelled	91.1	13	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> f1r symmetric alpha-beta tim barrel; <b>PDBTitle:</b> computationally designed two-fold symmetric tim-barrel protein, f1r
120	<a href="#">c6mywA_</a>	Alignment	not modelled	91.0	14	<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