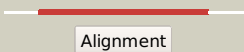

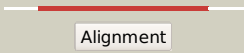



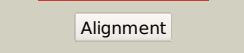



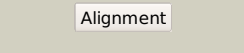

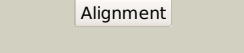



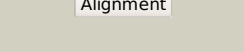

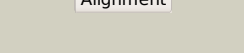

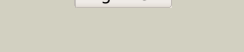



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1385_(pyrF)_1560451_1561275
Date	Wed Jul 31 22:05:49 BST 2019
Unique Job ID	9b7c0bb767ae7e1b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3l52A_</a>	 Alignment		100.0	50	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> orotidine 5'-phosphate decarboxylase; <b>PDBTitle:</b> crystal structure of putative orotidine 5'-phosphate decarboxylase2 from streptomyces avermitilis ma-4680
2	<a href="#">d2ffca1</a>	 Alignment		100.0	26	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
3	<a href="#">d2q8za1</a>	 Alignment		100.0	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
4	<a href="#">c3r89A_</a>	 Alignment		100.0	28	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> orotidine 5'-phosphate decarboxylase; <b>PDBTitle:</b> crystal structure of orotidine 5-phosphate decarboxylase from2 anaerococcus prevotii dsm 20548
5	<a href="#">d2fdsa1</a>	 Alignment		100.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
6	<a href="#">c2fdaA_</a>	 Alignment		100.0	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> orotidine-monophosphate-decarboxylase; <b>PDBTitle:</b> crystal structure of plasmodium berghei orotidine 5'-monophosphate2 decarboxylase (ortholog of plasmodium falciparum pf10_0225)
7	<a href="#">c3qw4B_</a>	 Alignment		100.0	38	<b>PDB header:</b> transferase, lyase <b>Chain:</b> B: <b>PDB Molecule:</b> ump synthase; <b>PDBTitle:</b> structure of leishmania donovani ump synthase
8	<a href="#">c4mjzA_</a>	 Alignment		100.0	33	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> orotidine 5'-phosphate decarboxylase; <b>PDBTitle:</b> 2.75 angstrom resolution crystal structure of putative orotidine-2 monophosphate-decarboxylase from toxoplasma gondii.
9	<a href="#">c3qw3B_</a>	 Alignment		100.0	37	<b>PDB header:</b> transferase, lyase <b>Chain:</b> B: <b>PDB Molecule:</b> orotidine-5-phosphate decarboxylase/orotate <b>PDBTitle:</b> structure of leishmania donovani omp decarboxylase
10	<a href="#">c3bvjA_</a>	 Alignment		100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uridine 5'-monophosphate synthase; <b>PDBTitle:</b> crystal structure of human orotidine 5'-monophosphate decarboxylase2 complexed with xmp
11	<a href="#">c2qcnA_</a>	 Alignment		100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uridine 5'-monophosphate synthase; <b>PDBTitle:</b> covalent complex of the orotidine-5'-monophosphate decarboxylase2 domain of human ump synthase with 6-iodo-ump

12	<a href="#">d1dqwa_</a>	Alignment		100.0	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
13	<a href="#">d1dbta_</a>	Alignment		100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
14	<a href="#">d1eixa_</a>	Alignment		100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
15	<a href="#">c4dbeB_</a>	Alignment		100.0	20	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> orotidine 5'-phosphate decarboxylase; <b>PDBTitle:</b> crystal structure of orotidine 5'-monophosphate decarboxylase from2 sulfolobus solfataricus complexed with inhibitor bmp
16	<a href="#">c3ldvB_</a>	Alignment		100.0	19	<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'-phosphate2 decarboxylase from vibrio cholerae o1 biovar eltor str. n16961
17	<a href="#">c3ru6C_</a>	Alignment		100.0	15	<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
18	<a href="#">c3tfxB_</a>	Alignment		100.0	16	<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
19	<a href="#">d1dvja_</a>	Alignment		100.0	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
20	<a href="#">d1km4a_</a>	Alignment		100.0	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
21	<a href="#">c3tr2A_</a>	Alignment	not modelled	100.0	18	<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
22	<a href="#">c2yytA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> orotidine 5'-phosphate decarboxylase; <b>PDBTitle:</b> crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
23	<a href="#">d1losc_</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
24	<a href="#">c4luiB_</a>	Alignment	not modelled	100.0	24	<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'-monophosphate decarboxylase from2 methanocaldococcus jannaschii
25	<a href="#">c3ve9B_</a>	Alignment	not modelled	100.0	22	<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'-monophosphate decarboxylase from2 metallospiraera sedula
26	<a href="#">c4df1B_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> orotidine 5'-phosphate decarboxylase; <b>PDBTitle:</b> crystal structure of orotidine 5'-monophosphate decarboxylase from2 thermoproteus neutrophilus complexed with inhibitor bmp
27	<a href="#">c4muza_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> orotidine 5'-phosphate decarboxylase; <b>PDBTitle:</b> crystal structure of orotidine 5'-monophosphate decarboxylase from2 archaeoglobus fulgidus complexed with inhibitor bmp
28	<a href="#">d2czda1</a>	Alianment	not modelled	100.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel

					<b>Family:</b> Decarboxylase
29	<a href="#">d1vqta1</a>	Alignment	not modelled	100.0	20 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
30	<a href="#">d1q6oa_</a>	Alignment	not modelled	99.9	21 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
31	<a href="#">c3exsB_</a>	Alignment	not modelled	99.9	14 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> rrmpd (hexulose-6-phosphate synthase); <b>PDBTitle:</b> crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p
32	<a href="#">c3jr2D_</a>	Alignment	not modelled	99.9	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
33	<a href="#">c3ajxA_</a>	Alignment	not modelled	99.9	17 <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
34	<a href="#">c3f4wA_</a>	Alignment	not modelled	99.9	19 <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
35	<a href="#">d1ojxa_</a>	Alignment	not modelled	99.7	18 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
36	<a href="#">c3gndC_</a>	Alignment	not modelled	99.4	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
37	<a href="#">c2qjhH_</a>	Alignment	not modelled	99.4	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
38	<a href="#">d1h1ya_</a>	Alignment	not modelled	98.8	15 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
39	<a href="#">c4nu7C_</a>	Alignment	not modelled	98.7	17 <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.
40	<a href="#">c3inpA_</a>	Alignment	not modelled	98.5	10 <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.
41	<a href="#">d2flia1</a>	Alignment	not modelled	98.4	19 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
42	<a href="#">d1tqxa_</a>	Alignment	not modelled	98.4	10 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
43	<a href="#">c3qc3B_</a>	Alignment	not modelled	98.3	15 <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
44	<a href="#">c5umfB_</a>	Alignment	not modelled	98.1	13 <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
45	<a href="#">c3ct7E_</a>	Alignment	not modelled	98.0	19 <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
46	<a href="#">d1rpxa_</a>	Alignment	not modelled	97.6	16 <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="#">d1tqja_</a>	Alignment	not modelled	97.2	13 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
48	<a href="#">c5n2pA_</a>	Alignment	not modelled	96.9	13 <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
49	<a href="#">c2ze3A_</a>	Alignment	not modelled	96.6	19 <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
50	<a href="#">c3igsB_</a>	Alignment	not modelled	96.2	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
51	<a href="#">d1j5ta_</a>	Alignment	not modelled	95.6	17 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
52	<a href="#">d1i4na_</a>	Alignment	not modelled	94.9	17 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
53	<a href="#">c4n6eA_</a>	Alignment	not modelled	94.3	14 <b>PDB header:</b> lyase/biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative thiosugar synthase; <b>PDBTitle:</b> crystal structure of amycolatopsis orientalis bexx/cyso complex
					<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> H: <b>PDB Molecule:</b> uncharacterized protein cgl0159;

54	<a href="#">c3fokH_</a>	Alignment	not modelled	94.1	19	<b>PDBTitle:</b> crystal structure of cgl0159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural3 genomics target cgr115
55	<a href="#">c5zknA_</a>	Alignment	not modelled	93.8	14	<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
56	<a href="#">c3gkaB_</a>	Alignment	not modelled	93.7	13	<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
57	<a href="#">c2htmB_</a>	Alignment	not modelled	93.6	25	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> thiazole biosynthesis protein thig; <b>PDBTitle:</b> crystal structure of ttha0676 from thermus thermophilus hb8
58	<a href="#">c4ot7A_</a>	Alignment	not modelled	93.2	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
59	<a href="#">c3navB_</a>	Alignment	not modelled	92.9	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
60	<a href="#">d1piia2</a>	Alignment	not modelled	92.7	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
61	<a href="#">d1vyra_</a>	Alignment	not modelled	92.2	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
62	<a href="#">c5z9yB_</a>	Alignment	not modelled	92.1	14	<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
63	<a href="#">c3q58A_</a>	Alignment	not modelled	92.1	15	<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
64	<a href="#">c3hf3A_</a>	Alignment	not modelled	91.4	13	<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
65	<a href="#">c4e38A_</a>	Alignment	not modelled	90.7	15	<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)
66	<a href="#">c4mg4G_</a>	Alignment	not modelled	89.5	15	<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
67	<a href="#">d3bofa2</a>	Alignment	not modelled	89.2	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Homocysteine S-methyltransferase <b>Family:</b> Homocysteine S-methyltransferase
68	<a href="#">c3qjaA_</a>	Alignment	not modelled	88.8	13	<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
69	<a href="#">d1wv2a_</a>	Alignment	not modelled	88.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> ThiG-like <b>Family:</b> ThiG-like
70	<a href="#">d1xm3a_</a>	Alignment	not modelled	88.5	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> ThiG-like <b>Family:</b> ThiG-like
71	<a href="#">c4a3uB_</a>	Alignment	not modelled	88.3	16	<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)
72	<a href="#">c2ekcA_</a>	Alignment	not modelled	87.8	14	<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
73	<a href="#">c2c3zA_</a>	Alignment	not modelled	87.6	18	<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
74	<a href="#">c4qnwA_</a>	Alignment	not modelled	87.3	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> chanoclavine-i aldehyde reductase; <b>PDBTitle:</b> crystal structure of easa, an old yellow enzyme from aspergillus2 fumigatus
75	<a href="#">c4lsbA_</a>	Alignment	not modelled	86.8	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
76	<a href="#">d1xcfa_</a>	Alignment	not modelled	85.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
77	<a href="#">d1zna1</a>	Alignment	not modelled	85.4	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> PdxS-like
78	<a href="#">c4utwB_</a>	Alignment	not modelled	85.1	10	<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
79	<a href="#">c1znnF_</a>	Alignment	not modelled	84.6	12	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> F: <b>PDB Molecule:</b> plp synthase;

						<b>PDBTitle:</b> structure of the synthase subunit of plp synthase
80	<a href="#">d1q45a_</a>	Alignment	not modelled	83.0	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
81	<a href="#">d1m3ua_</a>	Alignment	not modelled	82.7	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Ketopantoate hydroxymethyltransferase PanB
82	<a href="#">c6mywA_</a>	Alignment	not modelled	82.6	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
83	<a href="#">d1ujpa_</a>	Alignment	not modelled	82.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
84	<a href="#">d1xi3a_</a>	Alignment	not modelled	82.4	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Thiamin phosphate synthase <b>Family:</b> Thiamin phosphate synthase
85	<a href="#">c5ey5A_</a>	Alignment	not modelled	81.5	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lbcats-a; <b>PDBTitle:</b> lbcats
86	<a href="#">c1yadD_</a>	Alignment	not modelled	81.2	12	<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
87	<a href="#">d1icpa_</a>	Alignment	not modelled	78.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
88	<a href="#">c2wskA_</a>	Alignment	not modelled	76.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycogen debranching enzyme; <b>PDBTitle:</b> crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
89	<a href="#">d1vjia_</a>	Alignment	not modelled	76.5	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
90	<a href="#">c2ya0A_</a>	Alignment	not modelled	75.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative alkaline amylopullulanase; <b>PDBTitle:</b> catalytic module of the multi-modular glycogen-degrading pneumococcal2 virulence factor spua
91	<a href="#">d1qopa_</a>	Alignment	not modelled	75.3	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
92	<a href="#">c4mozC_</a>	Alignment	not modelled	74.9	17	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> fructose-bisphosphate aldolase; <b>PDBTitle:</b> fructose-bisphosphate aldolase from slackia heliotrinireducens dsm2 20476
93	<a href="#">c5zjnB_</a>	Alignment	not modelled	74.4	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
94	<a href="#">c2h90A_</a>	Alignment	not modelled	74.0	21	<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
95	<a href="#">d8ruca1</a>	Alignment	not modelled	72.4	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
96	<a href="#">c6bmaA_</a>	Alignment	not modelled	72.0	16	<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
97	<a href="#">c2e8yA_</a>	Alignment	not modelled	71.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amylx protein; <b>PDBTitle:</b> crystal structure of pullulanase type i from bacillus subtilis str.2 168
98	<a href="#">c3lyeA_</a>	Alignment	not modelled	70.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oxaloacetate acetyl hydrolase; <b>PDBTitle:</b> crystal structure of oxaloacetate acetylhydrolase
99	<a href="#">c5ocsB_</a>	Alignment	not modelled	70.6	19	<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
100	<a href="#">d1to3a_</a>	Alignment	not modelled	70.2	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
101	<a href="#">d1a53a_</a>	Alignment	not modelled	70.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
102	<a href="#">c3cu2A_</a>	Alignment	not modelled	69.9	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribulose-5-phosphate 3-epimerase; <b>PDBTitle:</b> crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
103	<a href="#">c2ya1A_</a>	Alignment	not modelled	69.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative alkaline amylopullulanase; <b>PDBTitle:</b> product complex of a multi-modular glycogen-degrading pneumococcal2 virulence factor spua
104	<a href="#">d1wa3a1</a>	Alignment	not modelled	69.0	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
105	<a href="#">c2x4bA_</a>	Alignment	not modelled	69.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> limit dextrinase; <b>PDBTitle:</b> barley limit dextrinase in complex with beta-cyclodextrin

106	<a href="#">c3wdjA_</a>	Alignment	not modelled	68.6	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> type i pullulanase; <b>PDBTitle:</b> crystal structure of pullulanase complexed with maltotetraose from2 anoxybacillus sp. Im18-11
107	<a href="#">dlyxya1</a>	Alignment	not modelled	68.1	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> NanE-like
108	<a href="#">c1hvxA_</a>	Alignment	not modelled	68.1	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> bacillus stearothermophilus alpha-amylase
109	<a href="#">d1hx0a2</a>	Alignment	not modelled	67.9	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
110	<a href="#">c3o63B_</a>	Alignment	not modelled	67.7	19	<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
111	<a href="#">c1jdaA_</a>	Alignment	not modelled	67.6	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-alpha maltotetrahydrolase; <b>PDBTitle:</b> maltotetraose-forming exo-amylase
112	<a href="#">c1ud8A_</a>	Alignment	not modelled	67.6	42	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amylase; <b>PDBTitle:</b> crystal structure of amyk38 with lithium ion
113	<a href="#">c1mwoA_</a>	Alignment	not modelled	67.5	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha amylase; <b>PDBTitle:</b> crystal structure analysis of the hyperthermostable2 pyrococcus woesei alpha-amylase
114	<a href="#">c4jcmA_</a>	Alignment	not modelled	67.3	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclodextrin glucanotransferase; <b>PDBTitle:</b> crystal structure of gamma-cgtase from alkalophilic bacillus clarkii2 at 1.65 angstrom resolution
115	<a href="#">c1bwvA_</a>	Alignment	not modelled	67.0	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (ribulose bisphosphate carboxylase); <b>PDBTitle:</b> activated ribulose 1,5-bisphosphate carboxylase/oxygenase (rubisco)2 complexed with the reaction intermediate analogue 2-carboxyarabinitol3 1,5-bisphosphate
116	<a href="#">d1svda1</a>	Alignment	not modelled	66.9	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
117	<a href="#">d1lekqa_</a>	Alignment	not modelled	66.5	13	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
118	<a href="#">c3faxA_</a>	Alignment	not modelled	66.3	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> reticulocyte binding protein; <b>PDBTitle:</b> the crystal structure of gbs pullulanase sap in complex with2 maltotetraose
119	<a href="#">c1bf2A_</a>	Alignment	not modelled	65.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> isoamylase; <b>PDBTitle:</b> structure of pseudomonas isoamylase
120	<a href="#">d1gcya2</a>	Alignment	not modelled	65.8	38	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain