

























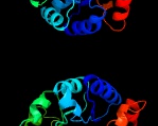






# Phyre2

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 Description RVBD1408\_(rpe)\_1584505\_1585203  
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 Unique Job ID b432d59e0c128c17

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3cu2A_</a>	 Alignment		100.0	22	<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
2	<a href="#">c3ct7E_</a>	 Alignment		100.0	34	<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
3	<a href="#">c3qc3B_</a>	 Alignment		100.0	43	<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 d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
4	<a href="#">d1rpxa_</a>	 Alignment		100.0	44	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
5	<a href="#">c5umfB_</a>	 Alignment		100.0	48	<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
6	<a href="#">c4nu7C_</a>	 Alignment		100.0	43	<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 from 2 toxoplasma gondii.
7	<a href="#">d1tqxa_</a>	 Alignment		100.0	38	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
8	<a href="#">d2flia1</a>	 Alignment		100.0	45	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
9	<a href="#">d1h1ya_</a>	 Alignment		100.0	50	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
10	<a href="#">c3inpA_</a>	 Alignment		100.0	40	<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.
11	<a href="#">d1tqja_</a>	 Alignment		100.0	44	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase

12	<a href="#">c4muzA</a>	Alignment		100.0	17	<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
13	<a href="#">d1q6oa</a>	Alignment		100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
14	<a href="#">c3ajxA</a>	Alignment		100.0	22	<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
15	<a href="#">c3jr2D</a>	Alignment		100.0	22	<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
16	<a href="#">c3exsB</a>	Alignment		100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> rmpd (hexulose-6-phosphate synthase); <b>PDBTitle:</b> crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p
17	<a href="#">c3thaB</a>	Alignment		100.0	11	<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.
18	<a href="#">c3f4wA</a>	Alignment		100.0	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
19	<a href="#">c5n2pA</a>	Alignment		100.0	18	<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
20	<a href="#">d1qopa</a>	Alignment		100.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
21	<a href="#">d1rd5a</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
22	<a href="#">c3vndD</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
23	<a href="#">c5kzmA</a>	Alignment	not modelled	100.0	16	<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
24	<a href="#">c4luiB</a>	Alignment	not modelled	100.0	15	<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="#">d2czda1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
26	<a href="#">c5k9xA</a>	Alignment	not modelled	100.0	23	<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 chain from legionella2 pneumophila subsp. pneumophila
27	<a href="#">d1eixa</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
28	<a href="#">c5tchG</a>	Alignment	not modelled	100.0	16	<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 m. tuberculosis -2 ligand-free form, trpa-g66v mutant
						<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> orotidine 5'-phosphate decarboxylase;

29	<a href="#">c3ru6C_</a>	Alignment	not modelled	100.0	15	<b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of orotidine 5'-phosphate2 decarboxylase (pyrf) from campylobacter jejuni subsp. jejuni nctc3 11168 <b>PDB header:</b> lyase
30	<a href="#">c3navB_</a>	Alignment	not modelled	100.0	20	<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
31	<a href="#">c5ey5A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lbcats-a; <b>PDBTitle:</b> lbcats
32	<a href="#">c2ekcA_</a>	Alignment	not modelled	100.0	15	<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
33	<a href="#">d1km4a_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
34	<a href="#">d1ujpa_</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
35	<a href="#">c3ve9B_</a>	Alignment	not modelled	99.9	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'-monophosphate decarboxylase from2 metallosphaera sedula
36	<a href="#">d1geqa_</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
37	<a href="#">c5kinC_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
38	<a href="#">d1vqta1</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
39	<a href="#">d1dvja_</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
40	<a href="#">c3tfxB_</a>	Alignment	not modelled	99.9	19	<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
41	<a href="#">c2bdqA_</a>	Alignment	not modelled	99.9	12	<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 from2 streptococcus agalactiae, northeast structural genomics target sar15.
42	<a href="#">c3tr2A_</a>	Alignment	not modelled	99.9	17	<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
43	<a href="#">c3ldvB_</a>	Alignment	not modelled	99.9	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
44	<a href="#">d1xcfa_</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
45	<a href="#">c2yytA_</a>	Alignment	not modelled	99.9	19	<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
46	<a href="#">c4axkB_</a>	Alignment	not modelled	99.9	22	<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
47	<a href="#">d1dbta_</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
48	<a href="#">d1j5ta_</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
49	<a href="#">c2y85D_</a>	Alignment	not modelled	99.9	21	<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
50	<a href="#">d1thfd_</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
51	<a href="#">c4gj1A_</a>	Alignment	not modelled	99.9	16	<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).
52	<a href="#">d1losc_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
53	<a href="#">c4x2rA_</a>	Alignment	not modelled	99.9	24	<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
						<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> orotidine 5'-phosphate decarboxylase;

54	<a href="#">c4df1B_</a>	Alignment	not modelled	99.9	18	<b>PDBTitle:</b> crystal structure of orotidine 5'-monophosphate decarboxylase from <i>Thermoproteus neutrophilus</i> complexed with inhibitor bmp
55	<a href="#">c6bmaA_</a>	Alignment	not modelled	99.8	19	<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 from <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> nctc 11168
56	<a href="#">c2c3zA_</a>	Alignment	not modelled	99.8	12	<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-glycerol phosphate synthase from <i>Sulfolobus solfataricus</i>
57	<a href="#">d1ka9f_</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
58	<a href="#">d1h5ya_</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
59	<a href="#">c3tsmB_</a>	Alignment	not modelled	99.8	19	<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 from <i>Brucella melitensis</i>
60	<a href="#">c3qjaA_</a>	Alignment	not modelled	99.8	19	<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-glycerol phosphate synthase (trpc) in apo form
61	<a href="#">c4dbeB_</a>	Alignment	not modelled	99.8	16	<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 from <i>Sulfolobus solfataricus</i> complexed with inhibitor bmp
62	<a href="#">d1vc4a_</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
63	<a href="#">c4ml9A_</a>	Alignment	not modelled	99.8	17	<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 sites from <i>Seibaldella termitidis</i>
64	<a href="#">c4wd0A_</a>	Alignment	not modelled	99.8	18	<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 HisP from <i>Arthrobacter aurescens</i>
65	<a href="#">d1i4na_</a>	Alignment	not modelled	99.8	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
66	<a href="#">d1a53a_</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
67	<a href="#">c5b69A_</a>	Alignment	not modelled	99.8	17	<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>
68	<a href="#">c5aheA_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> HisA <b>PDBTitle:</b> crystal structure of <i>Salmonella enterica</i> HisA
69	<a href="#">d1piai2</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
70	<a href="#">d1vzwa1</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
71	<a href="#">c4e38A_</a>	Alignment	not modelled	99.8	17	<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 from <i>Vibrionales bacterium</i> swat-3 (target efi-502156)
72	<a href="#">c6nkeA_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> geranylgeranylgeranyl phosphate synthase; <b>PDBTitle:</b> wild-type GGGPS from <i>Thermoplasma volcanium</i>
73	<a href="#">c3igsB_</a>	Alignment	not modelled	99.7	16	<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 <i>Salmonella enterica</i> n-acetylmannosamine-6-phosphate 2-epimerase
74	<a href="#">d1wa3a1</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
75	<a href="#">c5zknA_</a>	Alignment	not modelled	99.7	15	<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 from <i>Fusobacterium nucleatum</i>
76	<a href="#">c3q58A_</a>	Alignment	not modelled	99.7	16	<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 <i>Salmonella enterica</i>
77	<a href="#">d1dqwa_</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
78	<a href="#">d1yxya1</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> NanE-like
						<b>Fold:</b> TIM beta/alpha-barrel

79	<a href="#">d1y0ea_</a>	Alignment	not modelled	99.7	17	<b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> NanE-like
80	<a href="#">c3tdnB_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> flr symmetric alpha-beta tim barrel; <b>PDBTitle:</b> computationally designed two-fold symmetric tim-barrel protein, flr
81	<a href="#">d1wbha1</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
82	<a href="#">c2qcnA_</a>	Alignment	not modelled	99.7	16	<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
83	<a href="#">c3bvjA_</a>	Alignment	not modelled	99.7	16	<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
84	<a href="#">c4n6eA_</a>	Alignment	not modelled	99.7	16	<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
85	<a href="#">c6oviA_</a>	Alignment	not modelled	99.7	15	<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 with 2 pyruvate captured at low ph as a covalent carbinolamine intermediate
86	<a href="#">d1xi3a_</a>	Alignment	not modelled	99.7	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Thiamin phosphate synthase <b>Family:</b> Thiamin phosphate synthase
87	<a href="#">c1piiA_</a>	Alignment	not modelled	99.7	16	<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: indoleglycerolphosphate3 synthase from escherichia coli refined at 2.0 angstroms resolution
88	<a href="#">c2v82A_</a>	Alignment	not modelled	99.7	15	<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
89	<a href="#">c3o63B_</a>	Alignment	not modelled	99.6	22	<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
90	<a href="#">c5zjnB_</a>	Alignment	not modelled	99.6	20	<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
91	<a href="#">c4utwB_</a>	Alignment	not modelled	99.6	17	<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
92	<a href="#">d2tpsa_</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Thiamin phosphate synthase <b>Family:</b> Thiamin phosphate synthase
93	<a href="#">c1yadD_</a>	Alignment	not modelled	99.6	18	<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
94	<a href="#">d1qo2a_</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
95	<a href="#">d1jvna1</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
96	<a href="#">d1w0ma_</a>	Alignment	not modelled	99.6	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
97	<a href="#">c1znnF_</a>	Alignment	not modelled	99.6	16	<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
98	<a href="#">d1znaa1</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> PdxS-like
99	<a href="#">c4bk9B_</a>	Alignment	not modelled	99.6	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxo <b>PDBTitle:</b> crystal structure of 2-keto-3-deoxy-6-phospho-gluconate aldolase from2 zymomonas mobilis atcc 29191
100	<a href="#">c1jvnB_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional histidine biosynthesis protein hishf; <b>PDBTitle:</b> crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
101	<a href="#">c3vkbA_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> moeo5; <b>PDBTitle:</b> crystal structure of moeo5 soaked with fspp overnight
102	<a href="#">c4jejA_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranyl glyceryl phosphate synthase; <b>PDBTitle:</b> gggps from flavobacterium johnsoniae <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> imidazole glycerol phosphate synthase

103	<a href="#">c2w6rA_</a>	Alignment	not modelled	99.5	16	subunit <b>PDBTitle:</b> crystal structure of an artificial (ba)8-barrel protein2 designed from identical half barrels
104	<a href="#">d1vhca_</a>	Alignment	not modelled	99.5	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
105	<a href="#">c4qccA_</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> structural protein, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxy-6-phosphogalactonate aldolase, peptidyl- <b>PDBTitle:</b> structure of a cube-shaped, highly porous protein cage designed by2 fusing symmetric oligomeric domains
106	<a href="#">c3nm3D_</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> thiamine biosynthetic bifunctional enzyme; <b>PDBTitle:</b> the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosynthesis of eukaryotes
107	<a href="#">c5cssA_</a>	Alignment	not modelled	99.5	13	<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
108	<a href="#">d1hg3a_</a>	Alignment	not modelled	99.5	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
109	<a href="#">c2agkA_</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) <b>PDBTitle:</b> structure of s. cerevisiae his6 protein
110	<a href="#">d1mxsa_</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
111	<a href="#">c5z9yB_</a>	Alignment	not modelled	99.4	24	<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
112	<a href="#">c3qw3B_</a>	Alignment	not modelled	99.4	15	<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
113	<a href="#">c3gndC_</a>	Alignment	not modelled	99.4	14	<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
114	<a href="#">c3labA_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative kdpq (2-keto-3-deoxy-6-phosphogluconate) aldolase; <b>PDBTitle:</b> crystal structure of a putative kdpq (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
115	<a href="#">d1viza_</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
116	<a href="#">d1ojxa_</a>	Alignment	not modelled	99.3	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
117	<a href="#">c3w01A_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> heptaprenylglyceryl phosphate synthase; <b>PDBTitle:</b> crystal structure of pcrb complexed with peg from staphylococcus2 aureus subsp. aureus mu3
118	<a href="#">c2h6rG_</a>	Alignment	not modelled	99.3	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
119	<a href="#">c2yw3E_</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3- <b>PDBTitle:</b> crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 dehydro-3-deoxyphosphogluconate aldolase from tthb1
120	<a href="#">c2htmB_</a>	Alignment	not modelled	99.3	20	<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