

# Phyre2

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Description	RVBD1613_(trpA)_1812366_1813178
Date	Fri Aug 2 13:30:20 BST 2019
Unique Job ID	d235130ce72cf16e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5tchG_</a>	Alignment		100.0	98	<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
2	<a href="#">c5k9xA_</a>	Alignment		100.0	32	<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
3	<a href="#">c2ekcA_</a>	Alignment		100.0	37	<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
4	<a href="#">c5kzmA_</a>	Alignment		100.0	26	<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
5	<a href="#">c5ey5A_</a>	Alignment		100.0	41	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> lbcats-a; <b>PDBTitle:</b> lbcats
6	<a href="#">c3vndD_</a>	Alignment		100.0	25	<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
7	<a href="#">c3navB_</a>	Alignment		100.0	29	<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
8	<a href="#">d1ujpa_</a>	Alignment		100.0	44	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
9	<a href="#">c5kinC_</a>	Alignment		100.0	31	<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
10	<a href="#">d1qopa_</a>	Alignment		100.0	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
11	<a href="#">c3thaB_</a>	Alignment		100.0	29	<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.

12	<a href="#">d1geqa_</a>	Alignment		100.0	31	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
13	<a href="#">d1rd5a_</a>	Alignment		100.0	33	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
14	<a href="#">d1xcfa_</a>	Alignment		100.0	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
15	<a href="#">c5n2pA_</a>	Alignment		100.0	21	<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
16	<a href="#">c4jejA_</a>	Alignment		100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranylgeranyl phosphate synthase; <b>PDBTitle:</b> gggps from flavobacterium johnsoniae
17	<a href="#">d1viza_</a>	Alignment		100.0	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
18	<a href="#">d2f6ua1</a>	Alignment		100.0	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
19	<a href="#">c4naeA_</a>	Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> heptaprenylglyceryl phosphate synthase; <b>PDBTitle:</b> pcrb from geobacillus kaustophilus, with bound g1p
20	<a href="#">c3w01A_</a>	Alignment		100.0	15	<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
21	<a href="#">c3vkbA_</a>	Alignment	not modelled	100.0	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
22	<a href="#">c6nkeA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranylgeranyl phosphate synthase; <b>PDBTitle:</b> wild-type gggps from thermoplasma volcanium
23	<a href="#">c5b69A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranylgeranyl phosphate synthase; <b>PDBTitle:</b> crystal structure of geranylgeranylgeranyl phosphate synthase2 complexed with an g-1-p from thermoplasma acidophilum
24	<a href="#">d1j5ta_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
25	<a href="#">c3igsB_</a>	Alignment	not modelled	100.0	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 salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
26	<a href="#">c3q58A_</a>	Alignment	not modelled	100.0	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 salmonella2 enterica
27	<a href="#">c2c3zA_</a>	Alignment	not modelled	99.9	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-3-2 glycerol phosphate synthase from sulfobolus solfataricus
28	<a href="#">c4nu7C_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> ribulose-phosphate 3-epimerase;

28	<a href="#">c4lu7C_</a>	Alignment	not modelled	99.9	11	<b>PDBTitle:</b> 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from2 toxoplasma gondii. <b>PDB header:</b> isomerase
29	<a href="#">c5zjnB_</a>	Alignment	not modelled	99.9	17	<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
30	<a href="#">d1rpxa_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
31	<a href="#">d1tqja_</a>	Alignment	not modelled	99.9	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="#">c3qc3B_</a>	Alignment	not modelled	99.9	14	<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
33	<a href="#">c3ct7E_</a>	Alignment	not modelled	99.9	13	<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
34	<a href="#">c5zknA_</a>	Alignment	not modelled	99.9	19	<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
35	<a href="#">d1y0ea_</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> NanE-like
36	<a href="#">d1h1ya_</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
37	<a href="#">d1tqxa_</a>	Alignment	not modelled	99.9	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
38	<a href="#">d1q6oa_</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
39	<a href="#">d1yxya1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> NanE-like
40	<a href="#">c4utwB_</a>	Alignment	not modelled	99.9	14	<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
41	<a href="#">c3jr2D_</a>	Alignment	not modelled	99.9	17	<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
42	<a href="#">d1piia2</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
43	<a href="#">d1dvja_</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
44	<a href="#">c4muzA_</a>	Alignment	not modelled	99.9	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
45	<a href="#">c3f4wA_</a>	Alignment	not modelled	99.9	21	<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
46	<a href="#">c3inpA_</a>	Alignment	not modelled	99.9	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.
47	<a href="#">c3ajxa_</a>	Alignment	not modelled	99.9	18	<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
48	<a href="#">c5umfB_</a>	Alignment	not modelled	99.9	19	<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="#">c5z9yB_</a>	Alignment	not modelled	99.8	17	<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
50	<a href="#">d2czda1</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
51	<a href="#">d2flia1</a>	Alignment	not modelled	99.8	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
52	<a href="#">c4luiB_</a>	Alignment	not modelled	99.8	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
53	<a href="#">c3exsB_</a>	Alignment	not modelled	99.8	14	<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 streptococcus mutans in2

						complex with d-r5p
54	<a href="#">d1i4na_</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
55	<a href="#">d1km4a_</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
56	<a href="#">c4e38A_</a>	Alignment	not modelled	99.7	19	<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)
57	<a href="#">d1vc4a_</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
58	<a href="#">d1vzwa1</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
59	<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
60	<a href="#">c3qjaA_</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
61	<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
62	<a href="#">c4ml9A_</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized tim barrel protein with the2 conserved phosphate binding site fromsebaldeella termitidis
63	<a href="#">c3tsmB_</a>	Alignment	not modelled	99.5	15	<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 bruceella melitensis
64	<a href="#">d1thfd_</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
65	<a href="#">d1wa3a1</a>	Alignment	not modelled	99.5	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
66	<a href="#">d1a53a_</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
67	<a href="#">c6bmaA_</a>	Alignment	not modelled	99.5	11	<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
68	<a href="#">d1w0ma_</a>	Alignment	not modelled	99.5	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
69	<a href="#">d1vhca_</a>	Alignment	not modelled	99.4	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
70	<a href="#">c4axkB_</a>	Alignment	not modelled	99.4	17	<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
71	<a href="#">d1h5ya_</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
72	<a href="#">c4qj1A_</a>	Alignment	not modelled	99.4	21	<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).
73	<a href="#">d1hg3a_</a>	Alignment	not modelled	99.4	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
74	<a href="#">d1wbha1</a>	Alignment	not modelled	99.4	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
75	<a href="#">c4x2rA_</a>	Alignment	not modelled	99.3	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 pria from actinomyces urogenitalis
76	<a href="#">d1mxsa_</a>	Alignment	not modelled	99.3	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
77	<a href="#">c3ru6C_</a>	Alignment	not modelled	99.3	12	<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
78	<a href="#">c5cssA_</a>	Alignment	not modelled	99.3	17	<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
						<b>Fold:</b> TIM beta/alpha-barrel

79	<a href="#">d1xi3a_</a>	Alignment	not modelled	99.2	22	<b>Superfamily:</b> Thiamin phosphate synthase <b>Family:</b> Thiamin phosphate synthase
80	<a href="#">c4iq1B_</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase ii; <b>PDBTitle:</b> crystal structure of porphyromonas gingivalis enoyl-acp reductase ii2 (fabk) with cofactors nadph and fmn
81	<a href="#">c2v82A_</a>	Alignment	not modelled	99.2	22	<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
82	<a href="#">c2y85D_</a>	Alignment	not modelled	99.2	20	<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
83	<a href="#">c3o63B_</a>	Alignment	not modelled	99.2	18	<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
84	<a href="#">c6oviA_</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> keto-deoxy-phosphogluconate aldolase; <b>PDBTitle:</b> crystal structure of kdpg aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
85	<a href="#">d1ka9f_</a>	Alignment	not modelled	99.2	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
86	<a href="#">c5aheA_</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> <b>PDBTitle:</b> crystal structure of salmonella enterica hisa
87	<a href="#">c1piiA_</a>	Alignment	not modelled	99.1	17	<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="#">c3tdnB_</a>	Alignment	not modelled	99.1	11	<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
89	<a href="#">c4mm1E_</a>	Alignment	not modelled	99.0	21	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> geranylgeranyl glyceryl phosphate synthase; <b>PDBTitle:</b> ggpps from methanothermobacter thermautotrophicus
90	<a href="#">c2z6jB_</a>	Alignment	not modelled	99.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> trans-2-enoyl-acp reductase ii; <b>PDBTitle:</b> crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor
91	<a href="#">c4b3yB_</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase; <b>PDBTitle:</b> cryo-em structure of the mycobacterial fatty acid synthase
92	<a href="#">c2cdh1_</a>	Alignment	not modelled	98.9	20	<b>PDB header:</b> transferase <b>Chain:</b> 1: <b>PDB Molecule:</b> enoyl reductase; <b>PDBTitle:</b> architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
93	<a href="#">c4qccA_</a>	Alignment	not modelled	98.9	21	<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
94	<a href="#">c4bk9B_</a>	Alignment	not modelled	98.9	18	<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
95	<a href="#">c6b8sB_</a>	Alignment	not modelled	98.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydroorotate dehydrogenase (quinone); <b>PDBTitle:</b> crystal structure of dihydroorotate dehydrogenase from helicobacter2 pylori with bound fmn
96	<a href="#">c4xq6A_</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotate dehydrogenase (quinone); <b>PDBTitle:</b> crystal structure of dihydroorotate dehydrogenase from mycobacterium2 tuberculosis
97	<a href="#">c2uval_</a>	Alignment	not modelled	98.9	20	<b>PDB header:</b> transferase <b>Chain:</b> I: <b>PDB Molecule:</b> fatty acid synthase beta subunits; <b>PDBTitle:</b> crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
98	<a href="#">c2gjlA_</a>	Alignment	not modelled	98.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pa1024; <b>PDBTitle:</b> crystal structure of 2-nitropropane dioxygenase
99	<a href="#">c2rtdA_</a>	Alignment	not modelled	98.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxyacid oxidase 1; <b>PDBTitle:</b> crystal structure of human glycolate oxidase (go) in complex with cdst
100	<a href="#">c2htmB_</a>	Alignment	not modelled	98.8	23	<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
101	<a href="#">c2vkzH_</a>	Alignment	not modelled	98.8	17	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> fatty acid synthase subunit beta; <b>PDBTitle:</b> structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
102	<a href="#">c4dbeB_</a>	Alignment	not modelled	98.8	11	<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 sulfataricus complexed with inhibitor bmp



103	<a href="#">c3bo9B_</a>	Alignment	not modelled	98.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nitroalkan dioxygenase; <b>PDBTitle:</b> crystal structure of putative nitroalkan dioxygenase (tm0800) from <i>Thermotoga maritima</i> at 2.71 Å resolution
104	<a href="#">c4wd0A_</a>	Alignment	not modelled	98.8	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 hisP from <i>Arthrobacter aurescens</i>
105	<a href="#">c1yadD_</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> regulatory protein Teni; <b>PDBTitle:</b> structure of Teni from <i>Bacillus subtilis</i>
106	<a href="#">c3labA_</a>	Alignment	not modelled	98.8	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative kDpg (2-keto-3-deoxy-6-phosphogluconate) aldolase; <b>PDBTitle:</b> crystal structure of a putative kDpg (2-keto-3-deoxy-6-phosphogluconate) aldolase from <i>Oleispira antarctica</i>
107	<a href="#">c1gthD_</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydropyrimidine dehydrogenase; <b>PDBTitle:</b> dihydropyrimidine dehydrogenase (dpg) from pig, ternary complex with 2 NADPH and 5-iodouracil
108	<a href="#">c2h6rG_</a>	Alignment	not modelled	98.7	18	<b>PDB header:</b> isomerase <b>Chain:</b> G: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase (TIM) from <i>Methanocaldococcus jannaschii</i>
109	<a href="#">d1goxa_</a>	Alignment	not modelled	98.7	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
110	<a href="#">c4zqrD_</a>	Alignment	not modelled	98.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase, inosine-5'- <b>PDBTitle:</b> crystal structure of the catalytic domain of the inosine monophosphate dehydrogenase from <i>Mycobacterium tuberculosis</i>
111	<a href="#">d1tb3a1</a>	Alignment	not modelled	98.7	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
112	<a href="#">d1xm3a_</a>	Alignment	not modelled	98.7	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> ThiG-like <b>Family:</b> ThiG-like
113	<a href="#">d1juba_</a>	Alignment	not modelled	98.7	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
114	<a href="#">d1jcnal</a>	Alignment	not modelled	98.7	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
115	<a href="#">c3tfxB_</a>	Alignment	not modelled	98.7	12	<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 from <i>Lactobacillus acidophilus</i>
116	<a href="#">c5ismF_</a>	Alignment	not modelled	98.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> fmn-dependent nitronate monooxygenase; <b>PDBTitle:</b> crystal structure of nitronate monooxygenase (so_0471) from <i>Shewanella oneidensis</i> MR-1
117	<a href="#">c3w9zA_</a>	Alignment	not modelled	98.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trna-dihydrouridine synthase C; <b>PDBTitle:</b> crystal structure of Dusc
118	<a href="#">d1vrda1</a>	Alignment	not modelled	98.7	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
119	<a href="#">c2a7nA_</a>	Alignment	not modelled	98.7	16	<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
120	<a href="#">c3ivuB_</a>	Alignment	not modelled	98.7	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> homocitrate synthase, mitochondrial; <b>PDBTitle:</b> homocitrate synthase lys4 bound to 2-OG