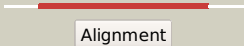

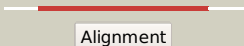

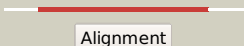







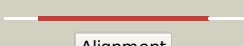











# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD1605\_(hisF)\_1804860\_1805663  
 Date Fri Aug 2 13:30:19 BST 2019  
 Unique Job ID c09b3b3f46329a46

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1jvna1</a>	 Alignment		100.0	41	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
2	<a href="#">c1jvnB_</a>	 Alignment		100.0	43	<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
3	<a href="#">d1thfd_</a>	 Alignment		100.0	53	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
4	<a href="#">d1ka9f_</a>	 Alignment		100.0	60	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
5	<a href="#">d1h5ya_</a>	 Alignment		100.0	56	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
6	<a href="#">d1qo2a_</a>	 Alignment		100.0	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
7	<a href="#">c4axkB_</a>	 Alignment		100.0	27	<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
8	<a href="#">c4x2rA_</a>	 Alignment		100.0	30	<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
9	<a href="#">c2y85D_</a>	 Alignment		100.0	25	<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 rcdp
10	<a href="#">c4gj1A_</a>	 Alignment		100.0	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 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)2 methylideneamino] imidazole-4-carboxamide isomerase (hisa).
11	<a href="#">c5aheA_</a>	 Alignment		100.0	28	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> <b>PDBTitle:</b> crystal structure of salmonella enterica hisa

12	<a href="#">c3tdnB_</a>	Alignment		100.0	31	<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
13	<a href="#">c4wd0A_</a>	Alignment		100.0	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 hisp form arthrobacter aurescens
14	<a href="#">d1vzwa1</a>	Alignment		100.0	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
15	<a href="#">c2agkA_</a>	Alignment		100.0	16	<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
16	<a href="#">c2w6rA_</a>	Alignment		100.0	33	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> imidazole glycerol phosphate synthase subunit <b>PDBTitle:</b> crystal structure of an artificial (ba)8-barrel protein2 designed from identical half barrels
17	<a href="#">c1znnF_</a>	Alignment		100.0	18	<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
18	<a href="#">d1znnal</a>	Alignment		100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> PdxS-like
19	<a href="#">c4ml9A_</a>	Alignment		100.0	18	<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
20	<a href="#">c3tsmB_</a>	Alignment		100.0	20	<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
21	<a href="#">c3qjaA_</a>	Alignment	not modelled	100.0	27	<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
22	<a href="#">c6bmaA_</a>	Alignment	not modelled	99.9	23	<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
23	<a href="#">d1vc4a_</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
24	<a href="#">d1a53a_</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
25	<a href="#">c2c3zA_</a>	Alignment	not modelled	99.9	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
26	<a href="#">c1piiA_</a>	Alignment	not modelled	99.9	19	<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
27	<a href="#">d2flia1</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
28	<a href="#">c3igsB_</a>	Alignment	not modelled	99.9	22	<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-phosphate 2-epimerase
29	<a href="#">d1i4na_</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
30	<a href="#">c5umfB_</a>	Alignment	not modelled	99.9	26	<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
31	<a href="#">d1piaa2</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
32	<a href="#">d1j5ta_</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
33	<a href="#">c3q58A_</a>	Alignment	not modelled	99.8	21	<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
34	<a href="#">c5zjnB_</a>	Alignment	not modelled	99.8	23	<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
35	<a href="#">d1tqja_</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
36	<a href="#">d1h1ya_</a>	Alignment	not modelled	99.8	21	<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="#">c4utwB_</a>	Alignment	not modelled	99.8	18	<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
38	<a href="#">d1rpxa_</a>	Alignment	not modelled	99.8	17	<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="#">d1y0ea_</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> NanE-like
40	<a href="#">c3inpA_</a>	Alignment	not modelled	99.8	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.
41	<a href="#">c3ct7E_</a>	Alignment	not modelled	99.8	20	<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
42	<a href="#">d1yxa1</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> NanE-like
43	<a href="#">c5zknA_</a>	Alignment	not modelled	99.8	18	<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
44	<a href="#">c3tdmD_</a>	Alignment	not modelled	99.8	41	<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
45	<a href="#">c3cu2A_</a>	Alignment	not modelled	99.8	14	<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
46	<a href="#">c4nu7C_</a>	Alignment	not modelled	99.7	19	<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.
47	<a href="#">c3qc3B_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> d-ribulose-5-phosphate-3-epimerase; <b>PDBTitle:</b> crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
48	<a href="#">c5n2pA_</a>	Alignment	not modelled	99.7	13	<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
49	<a href="#">d1tqxa_</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
50	<a href="#">d1qopa_</a>	Alignment	not modelled	99.6	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
51	<a href="#">c4e38A_</a>	Alignment	not modelled	99.6	14	<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)
52	<a href="#">d1wbha1</a>	Alignment	not modelled	99.6	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
						<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranylgluceryl phosphate

53	<a href="#">c5b69A_</a>	Alignment	not modelled	99.6	15	synthase; <b>PDBTitle:</b> crystal structure of geranylgeranylglyceryl phosphate synthase2 complexed with an g-1-p from thermoplasma acidophilum
54	<a href="#">c1zfiA_</a>	Alignment	not modelled	99.6	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine monophosphate dehydrogenase; <b>PDBTitle:</b> inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
55	<a href="#">c4n6eA_</a>	Alignment	not modelled	99.6	15	<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
56	<a href="#">c3cwoX_</a>	Alignment	not modelled	99.6	38	<b>PDB header:</b> de novo protein <b>Chain:</b> X: <b>PDB Molecule:</b> beta/alpha-barrel protein based on 1thf and 1tmy; <b>PDBTitle:</b> a beta/alpha-barrel built by the combination of fragments from2 different folds
57	<a href="#">d1rd5a_</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
58	<a href="#">c6oviA_</a>	Alignment	not modelled	99.6	19	<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
59	<a href="#">d1xm3a_</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> ThiG-like <b>Family:</b> ThiG-like
60	<a href="#">d1geqa_</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
61	<a href="#">c3vkbA_</a>	Alignment	not modelled	99.6	12	<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
62	<a href="#">d1xcfa_</a>	Alignment	not modelled	99.5	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
63	<a href="#">c4fxsA_</a>	Alignment	not modelled	99.5	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed2 with imp and mycophenolic acid
64	<a href="#">d1vhca_</a>	Alignment	not modelled	99.5	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
65	<a href="#">c4z87B_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> structure of the imp dehydrogenase from ashbya gossypii bound to gdp
66	<a href="#">c3vndD_</a>	Alignment	not modelled	99.5	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 the2 psychrophile shewanella frigidimarina k14-2
67	<a href="#">c5kzmA_</a>	Alignment	not modelled	99.5	18	<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
68	<a href="#">c2v82A_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; <b>PDBTitle:</b> kdpgal complexed to kdpgal
69	<a href="#">c3navB_</a>	Alignment	not modelled	99.5	24	<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
70	<a href="#">d1wa3a1</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
71	<a href="#">c5z9yB_</a>	Alignment	not modelled	99.5	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
72	<a href="#">d2tpsa_</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Thiamin phosphate synthase <b>Family:</b> Thiamin phosphate synthase
73	<a href="#">d1mxsa_</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
74	<a href="#">c2ekcA_</a>	Alignment	not modelled	99.4	16	<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
75	<a href="#">c6nkeA_</a>	Alignment	not modelled	99.4	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranylglyceryl phosphate synthase; <b>PDBTitle:</b> wild-type gggps from thermoplasma volcanium
76	<a href="#">c3ajxA_</a>	Alignment	not modelled	99.4	21	<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
77	<a href="#">c4qccA_</a>	Alignment	not modelled	99.4	17	<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
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inosine-5'-monophosphate

78	<a href="#">c4af0B_</a>	Alignment	not modelled	99.4	27	dehydrogenase; <b>PDBTitle:</b> crystal structure of cryptococcal inosine monophosphate2 dehydrogenase
79	<a href="#">c4bk9B_</a>	Alignment	not modelled	99.4	20	<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
80	<a href="#">c5x8oA_</a>	Alignment	not modelled	99.4	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate
81	<a href="#">d1xi3a_</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Thiamin phosphate synthase <b>Family:</b> Thiamin phosphate synthase
82	<a href="#">c2z6jB_</a>	Alignment	not modelled	99.4	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> trans-2-enoyl-acyl reductase ii; <b>PDBTitle:</b> crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor
83	<a href="#">c3w9zA_</a>	Alignment	not modelled	99.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trna-dihydrouridine synthase c; <b>PDBTitle:</b> crystal structure of dusc
84	<a href="#">d1zfja1</a>	Alignment	not modelled	99.3	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
85	<a href="#">c3f4wA_</a>	Alignment	not modelled	99.3	12	<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
86	<a href="#">c3tsdA_</a>	Alignment	not modelled	99.3	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of inosine-5'-monophosphate dehydrogenase from2 bacillus anthracis str. ames complexed with xmp
87	<a href="#">c5ey5A_</a>	Alignment	not modelled	99.3	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lbcats-a; <b>PDBTitle:</b> lbcats
88	<a href="#">d1vhna_</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
89	<a href="#">c5upxA_</a>	Alignment	not modelled	99.3	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of the catalytic domain of the inosine monophosphate2 dehydrogenase from listeria monocytogenes in the presence of3 xanthosine monophosphate
90	<a href="#">c3thaB_</a>	Alignment	not modelled	99.3	14	<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.
91	<a href="#">c4dqwb_</a>	Alignment	not modelled	99.3	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> crystal structure analysis of pa3770
92	<a href="#">c3labA_</a>	Alignment	not modelled	99.3	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-6-2 phosphogluconate) aldolase from oleispira antarctica
93	<a href="#">c4iqjB_</a>	Alignment	not modelled	99.3	25	<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-acyl reductase ii2 (fabk) with cofactors nadph and fmn
94	<a href="#">c4zqrD_</a>	Alignment	not modelled	99.3	31	<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 monophosphate2 dehydrogenase from mycobacterium tuberculosis
95	<a href="#">c6ei9A_</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> trna-dihydrouridine synthase b; <b>PDBTitle:</b> crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
96	<a href="#">c1yadD_</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> regulatory protein teni; <b>PDBTitle:</b> structure of teni from bacillus subtilis
97	<a href="#">d1jcna1</a>	Alignment	not modelled	99.3	26	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
98	<a href="#">c3o63B_</a>	Alignment	not modelled	99.3	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
99	<a href="#">d1jr1a1</a>	Alignment	not modelled	99.3	30	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
100	<a href="#">c5tchG_</a>	Alignment	not modelled	99.3	17	<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
101	<a href="#">c5k9xA_</a>	Alignment	not modelled	99.3	21	<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
						<b>PDB header:</b> oxidoreductase

102	<a href="#">c1jcnA_</a>	Alignment	not modelled	99.3	28	<b>Chain:</b> A: <b>PDB Molecule:</b> inosine monophosphate dehydrogenase ; <b>PDBTitle:</b> binary complex of human type-i inosine monophosphate dehydrogenase2 with 6-cl-imp
103	<a href="#">c3bo9B_</a>	Alignment	not modelled	99.3	20	<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) from2 thermotoga maritima at 2.71 a resolution
104	<a href="#">c3khjE_</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> inosine-5-monophosphate dehydrogenase; <b>PDBTitle:</b> c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
105	<a href="#">c6gk9C_</a>	Alignment	not modelled	99.3	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> inhibited structure of impdh from pseudomonas aeruginosa
106	<a href="#">c5kinC_</a>	Alignment	not modelled	99.3	16	<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
107	<a href="#">c2qr6A_</a>	Alignment	not modelled	99.3	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> imp dehydrogenase/gmp reductase; <b>PDBTitle:</b> crystal structure of imp dehydrogenase/gmp reductase-like protein2 (np_599840.1) from corynebacterium glutamicum atcc 13032 kitasato at3 1.50 a resolution
108	<a href="#">c2gjlA_</a>	Alignment	not modelled	99.3	27	<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
109	<a href="#">c2zrvC_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> isopentenyl-diphosphate delta-isomerase; <b>PDBTitle:</b> crystal structure of sulfolobus shibatae isopentenyl diphosphate2 isomerase in complex with reduced fmn.
110	<a href="#">d1wv2a_</a>	Alignment	not modelled	99.3	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> ThiG-like <b>Family:</b> ThiG-like
111	<a href="#">c4q33F_</a>	Alignment	not modelled	99.2	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of inosine 5'-monophosphate dehydrogenase from2 clostridium perfringens complexed with imp and a110
112	<a href="#">c4ff0B_</a>	Alignment	not modelled	99.2	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> inosine 5'-monophosphate dehydrogenase from vibrio cholerae, deletion2 mutant, complexed with imp
113	<a href="#">c2rdtA_</a>	Alignment	not modelled	99.2	24	<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
114	<a href="#">c2zbtB_</a>	Alignment	not modelled	99.2	18	<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
115	<a href="#">c4xtiA_</a>	Alignment	not modelled	99.2	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase,inosine-5'- <b>PDBTitle:</b> structure of imp dehydrogenase of ashbya gossypii with imp bound to2 the active site
116	<a href="#">d1w0ma_</a>	Alignment	not modelled	99.2	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
117	<a href="#">c4mz1A_</a>	Alignment	not modelled	99.2	26	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of the inosine 5'-monophosphate dehydrogenase, with2 a internal deletion of cbs domain from campylobacter jejuni complexed3 with inhibitor compound p12
118	<a href="#">c5cssA_</a>	Alignment	not modelled	99.2	14	<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
119	<a href="#">c4jejA_</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranyl glyceryl phosphate synthase; <b>PDBTitle:</b> gggps from flavobacterium johnsoniae
120	<a href="#">c6dvhF_</a>	Alignment	not modelled	99.2	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> lactate 2-monooxygenase; <b>PDBTitle:</b> lactate monooxygenase from mycobacterium smegmatis - c203a mutant