Phyre^2

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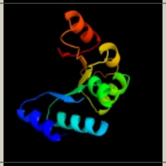
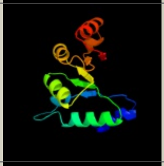
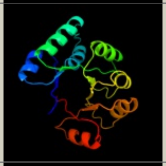
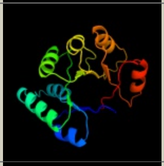
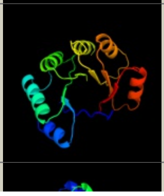
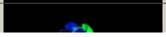
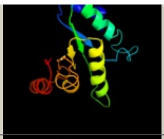
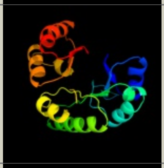
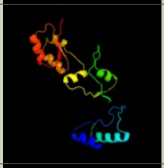
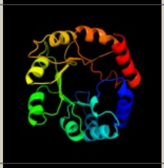
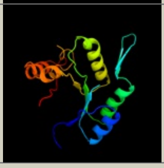
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2bdqA_	Alignment		98.1	18	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**copper homeostasis protein cutc; **PDBTitle:** crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15.
2	c3qjaA_	Alignment		98.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
3	d1xi3a_	Alignment		97.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
4	d1a53a_	Alignment		97.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
5	d1twda_	Alignment		97.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**CutC-like **Family:**CutC-like
6	c2c3zA_	Alignment		97.8	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
7	d1vlia2	Alignment		97.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
8	c1vliA_	Alignment		97.7	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**spore coat polysaccharide biosynthesis protein spse; **PDBTitle:** crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
9	c2ze3A_	Alignment		97.6	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dfa0005; **PDBTitle:** crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
10	d2zdra2	Alignment		97.6	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
11	c1xuzA_	Alignment		97.6	24	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
						

12	c3igsB_	Alignment		97.5	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase 2; **PDBTitle:** structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
13	c3iwpK_	Alignment		97.5	17	**PDB header:**metal binding protein **Chain:** K: **PDB Molecule:**copper homeostasis protein cutc homolog; **PDBTitle:** crystal structure of human copper homeostasis protein cutc
14	c1piiA_	Alignment		97.5	20	**PDB header:**bifunctional(isomerase and synthase) **Chain:** A: **PDB Molecule:**n-(5'phosphoribosyl)anthranilate isomerase; **PDBTitle:** three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase:3 indoleglycerolphosphate synthase from escherichia coli4 refined at 2.0 angstroms resolution
15	c3bleA_	Alignment		97.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citramalate synthase from leptospira interrogans; **PDBTitle:** crystal structure of the catalytic domain of licms in2 complexed with malonate
16	d2tpsa_	Alignment		97.4	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
17	c3ktsA_	Alignment		97.4	19	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**glycerol uptake operon antiterminator regulatory protein; **PDBTitle:** crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365
18	c1yadD_	Alignment		97.4	15	**PDB header:**transcription **Chain:** D: **PDB Molecule:**regulatory protein teni; **PDBTitle:** structure of teni from bacillus subtilis
19	c3fa4D_	Alignment		97.4	12	**PDB header:**lyase **Chain:** D: **PDB Molecule:**2,3-dimethylmalate lyase; **PDBTitle:** crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
20	c3ivuB_	Alignment		97.3	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
21	d1j5ta_	Alignment	not modelled	97.3	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
22	c2ekcA_	Alignment	not modelled	97.3	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
23	d1vc4a_	Alignment	not modelled	97.2	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
24	d1geqa_	Alignment	not modelled	97.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
25	c3q58A_	Alignment	not modelled	97.2	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
26	d1piia2	Alignment	not modelled	97.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
27	c3gr7A_	Alignment	not modelled	97.2	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
28	d1wa3a1	Alignment	not modelled	97.1	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
29	d1i4na_	Alignment	not modelled	97.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel

						Family: Tryptophan biosynthesis enzymes
30	c3lyeA_	Alignment	not modelled	97.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oxaloacetate acetyl hydrolase; **PDBTitle:** crystal structure of oxaloacetate acetylhydrolase
31	c2cw6B_	Alignment	not modelled	97.1	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hydroxymethylglutaryl-coa lyase, mitochondrial; **PDBTitle:** crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
32	d1muma_	Alignment	not modelled	97.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
33	d1ub3a_	Alignment	not modelled	97.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
34	c3ih1A_	Alignment	not modelled	97.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
35	c2ftpA_	Alignment	not modelled	97.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
36	d1e0ta2	Alignment	not modelled	97.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
37	d1h5ya_	Alignment	not modelled	97.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
38	d1ojxa_	Alignment	not modelled	97.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
39	c1e0tD_	Alignment	not modelled	97.0	19	**PDB header:**phosphotransferase **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** r292d mutant of e. coli pyruvate kinase
40	c3eooL_	Alignment	not modelled	96.9	16	**PDB header:**lyase **Chain:** L: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
41	c1zlpA_	Alignment	not modelled	96.9	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**petal death protein; **PDBTitle:** petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
42	d1yxya1	Alignment	not modelled	96.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
43	d1qo2a_	Alignment	not modelled	96.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
44	d1thfd_	Alignment	not modelled	96.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
45	c3oa3A_	Alignment	not modelled	96.9	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aldolase; **PDBTitle:** crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
46	c3q94B_	Alignment	not modelled	96.9	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase, class ii; **PDBTitle:** the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
47	d1o0ya_	Alignment	not modelled	96.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
48	d1vzwa1	Alignment	not modelled	96.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
49	d1jvna1	Alignment	not modelled	96.8	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
50	d1mzha_	Alignment	not modelled	96.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
51	c2iswB_	Alignment	not modelled	96.7	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-1,6-bisphosphate aldolase; **PDBTitle:** structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
52	d1nvma2	Alignment	not modelled	96.7	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**HMGL-like
53	c3sz8D_	Alignment	not modelled	96.7	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 2; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
54	d1geha1	Alignment	not modelled	96.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
55	c3pm6B_	Alignment	not modelled	96.6	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-bisphosphate aldolase;

		Alignment	not modelled			**PDBTitle:** crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
56	d1mxsa_	Alignment	not modelled	96.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
57	c1ydnA_	Alignment	not modelled	96.5	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
58	c3gndC_	Alignment	not modelled	96.5	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
59	c3t7vA_	Alignment	not modelled	96.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylornithine synthase pylb; **PDBTitle:** crystal structure of methylornithine synthase (pylb)
60	c1nvmG_	Alignment	not modelled	96.5	18	**PDB header:**lyase/oxidoreductase **Chain:** G: **PDB Molecule:**4-hydroxy-2-oxovalerate aldolase; **PDBTitle:** crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
61	d1gvfa_	Alignment	not modelled	96.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
62	d1y0ea_	Alignment	not modelled	96.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
63	c3ngjC_	Alignment	not modelled	96.4	12	**PDB header:**lyase **Chain:** C: **PDB Molecule:**deoxyribose-phosphate aldolase; **PDBTitle:** crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
64	d1d9ea_	Alignment	not modelled	96.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
65	d1wbha1	Alignment	not modelled	96.3	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
66	c3b8iF_	Alignment	not modelled	96.3	15	**PDB header:**lyase **Chain:** F: **PDB Molecule:**pa4872 oxaloacetate decarboxylase; **PDBTitle:** crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
67	c3ng3A_	Alignment	not modelled	96.3	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**deoxyribose-phosphate aldolase; **PDBTitle:** crystal structure of deoxyribose phosphate aldolase from mycobacterium2 avium 104 in a schiff base with an unknown aldehyde
68	c2y85D_	Alignment	not modelled	96.3	18	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**phosphoribosyl isomerase a; **PDBTitle:** crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
69	d1ps9a1	Alignment	not modelled	96.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
70	d1ujqa_	Alignment	not modelled	96.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
71	c3bg3B_	Alignment	not modelled	96.2	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase, mitochondrial; **PDBTitle:** crystal structure of human pyruvate carboxylase (missing2 the biotin carboxylase domain at the n-terminus)
72	d1tqxa_	Alignment	not modelled	96.2	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
73	c2htmB_	Alignment	not modelled	96.2	15	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**thiazole biosynthesis protein thig; **PDBTitle:** crystal structure of ttha0676 from thermus thermophilus hb8
74	d1n7ka_	Alignment	not modelled	96.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
75	c3g8rA_	Alignment	not modelled	96.2	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**probable spore coat polysaccharide biosynthesis protein e; **PDBTitle:** crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
76	c2z6jB_	Alignment	not modelled	96.2	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**trans-2-enoyl-acp reductase ii; **PDBTitle:** crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor
77	c2zyfA_	Alignment	not modelled	96.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homocitrate synthase; **PDBTitle:** crystal structure of homocitrate synthase from thermus thermophilus2 complexed with magnesuim ion and alpha-ketoglutarate
78	d1vhca_	Alignment	not modelled	96.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
79	c3gnnA_	Alignment	not modelled	96.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide2 pyrophosphorylase from burkholderi pseudomallei
						PDB header:transferase **Chain:** B: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate

80	c3pg8B_	Alignment	not modelled	96.1	14	aldolase; **PDBTitle:** truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
81	d1w0ma_	Alignment	not modelled	96.1	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
82	d1ujpa_	Alignment	not modelled	96.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
83	c2qjhH_	Alignment	not modelled	96.1	15	**PDB header:**lyase **Chain:** H: **PDB Molecule:**putative aldolase mj0400; **PDBTitle:** m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
84	d1o60a_	Alignment	not modelled	96.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
85	d1rpxa_	Alignment	not modelled	96.1	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
86	c3tqvA_	Alignment	not modelled	96.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
87	c2h6rG_	Alignment	not modelled	96.1	20	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
88	c1ydoC_	Alignment	not modelled	96.0	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hmg-coa lyase; **PDBTitle:** crystal structure of the bacillis subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
89	c3inpA_	Alignment		96.0	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**d-ribulose-phosphate 3-epimerase; **PDBTitle:** 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
90	c3labA_	Alignment	not modelled	96.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative kdpg (2-keto-3-deoxy-6-phosphogluconate) **PDBTitle:** crystal structure of a putative kdpg (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
91	c2yw3E_	Alignment	not modelled	96.0	20	**PDB header:**lyase **Chain:** E: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase/2-deydro-3- **PDBTitle:** crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1
92	c2nx9B_	Alignment	not modelled	96.0	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxaloacetate decarboxylase 2, subunit alpha; **PDBTitle:** crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
93	c3r2gA_	Alignment	not modelled	95.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine 5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
94	d1h1ya_	Alignment	not modelled	95.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
95	c2z1kA_	Alignment	not modelled	95.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**(neo)pullulanase; **PDBTitle:** crystal structure of ttha1563 from thermus thermophilus hb8
96	d1rvga_	Alignment	not modelled	95.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
97	c3pajA_	Alignment	not modelled	95.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase, carboxylating; **PDBTitle:** 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
98	c1zfjA_	Alignment	not modelled	95.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
99	c2w6rA_	Alignment	not modelled	95.8	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**imidazole glycerol phosphate synthase subunit **PDBTitle:** crystal structure of an artificial (ba)8-barrel protein2 designed from identical half barrels
100	c1qpoA_	Alignment	not modelled	95.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**quinolinate acid phosphoribosyl transferase; **PDBTitle:** quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
101	c3b0vD_	Alignment	not modelled	95.8	12	**PDB header:**oxidoreductase/rna **Chain:** D: **PDB Molecule:**trna-dihydrouridine synthase; **PDBTitle:** trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
102	c3l0gD_	Alignment	not modelled	95.8	8	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide

						pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
103	d1ka9f_	Alignment	not modelled	95.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
104	c3navB_	Alignment	not modelled	95.7	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
105	c1qhoA_	Alignment	not modelled	95.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
106	c3elfA_	Alignment	not modelled	95.7	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** structural characterization of tetrameric mycobacterium tuberculosis2 fructose 1,6-bisphosphate aldolase - substrate binding and catalysis3 mechanism of a class iia bacterial aldolase
107	d1eepa_	Alignment	not modelled	95.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
108	c2hjpA_	Alignment	not modelled	95.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonopyruvate hydrolase; **PDBTitle:** crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
109	c1o4uA_	Alignment	not modelled	95.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type ii quinolic acid phosphoribosyltransferase; **PDBTitle:** crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
110	c3thaB_	Alignment	not modelled	95.7	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** tryptophan synthase subunit alpha from campylobacter jejuni.
111	c2jbmA_	Alignment	not modelled	95.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** qprtase structure from human
112	d1qpoa1	Alignment	not modelled	95.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
113	d1qopa_	Alignment	not modelled	95.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
114	c2v5jB_	Alignment	not modelled	95.6	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; **PDBTitle:** apo class ii aldolase hpch
115	d2flia1	Alignment	not modelled	95.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
116	c2h90A_	Alignment	not modelled	95.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xenobiotic reductase a; **PDBTitle:** xenobiotic reductase a in complex with coumarin
117	d1u5ha_	Alignment	not modelled	95.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
118	c3bmwA_	Alignment	not modelled	95.5	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cyclomaltodextrin glucanotransferase; **PDBTitle:** cyclodextrin glycosyl transferase from thermoanerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
119	c3cixA_	Alignment	not modelled	95.5	13	**PDB header:**adomet binding protein **Chain:** A: **PDB Molecule:**fefe-hydrogenase maturase; **PDBTitle:** x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
120	c2gjlA_	Alignment	not modelled	95.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein pa1024; **PDBTitle:** crystal structure of 2-nitropropane dioxygenase