Phyre^2

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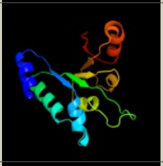
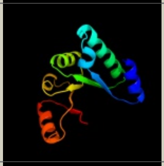
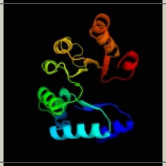
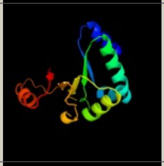
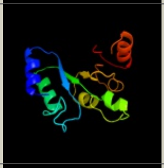
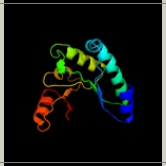
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qjaA_	Alignment		98.1	14	**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
2	c3iwpK_	Alignment		98.0	18	**PDB header:**metal binding protein **Chain:** K: **PDB Molecule:**copper homeostasis protein cutc homolog; **PDBTitle:** crystal structure of human copper homeostasis protein cutc
3	c2bdqA_	Alignment		97.9	21	**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.
4	d1a53a_	Alignment		97.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
5	c2c3zA_	Alignment		97.8	16	**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
6	d1twda_	Alignment		97.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**CutC-like **Family:**CutC-like
7	c3igsB_	Alignment		97.5	10	**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
8	c2ze3A_	Alignment		97.4	21	**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
9	d1vlia2	Alignment		97.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
10	d2zdra2	Alignment		97.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
11	c1vliA_	Alignment		97.4	20	**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

12	d1xi3a_	Alignment		97.4	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
13	d1piia2	Alignment		97.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
14	d1j5ta_	Alignment		97.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
15	c1xuzA_	Alignment		97.2	15	**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
16	d1i4na_	Alignment		97.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
17	c3q58A_	Alignment		97.2	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
18	d1h5ya_	Alignment		97.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
19	d1n7ka_	Alignment		97.1	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
20	d1vc4a_	Alignment		97.1	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
21	c3lyeA_	Alignment	not modelled	97.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oxaloacetate acetyl hydrolase; **PDBTitle:** crystal structure of oxaloacetate acetylhydrolase
22	d1jvna1	Alignment	not modelled	97.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
23	c2ftpA_	Alignment	not modelled	96.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
24	c1zlpA_	Alignment	not modelled	96.9	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**petal death protein; **PDBTitle:** petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
25	d1qo2a_	Alignment	not modelled	96.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
26	c3q94B_	Alignment	not modelled	96.8	21	**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'
27	d1wa3a1	Alignment	not modelled	96.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
28	d1yxya1	Alignment	not modelled	96.7	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
						Fold:TIM beta/alpha-barrel

29	d1thfd_	Alignment	not modelled	96.7	16	**Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
30	c3ivuB_	Alignment	not modelled	96.7	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
31	c2iswB_	Alignment	not modelled	96.7	22	**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
32	d1vzwa1	Alignment	not modelled	96.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
33	d1gvfa_	Alignment	not modelled	96.6	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
34	c3ktsA_	Alignment	not modelled	96.5	16	**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
35	c3bleA_	Alignment	not modelled	96.5	18	**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
36	d1o0ya_	Alignment	not modelled	96.5	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
37	c3fa4D_	Alignment	not modelled	96.3	16	**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
38	c3oa3A_	Alignment	not modelled	96.3	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aldolase; **PDBTitle:** crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
39	c2z6jB_	Alignment	not modelled	96.2	19	**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
40	c2ekcA_	Alignment	not modelled	96.2	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
41	d1ub3a_	Alignment	not modelled	96.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
42	c2y85D_	Alignment	not modelled	96.1	20	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**phosphoribosyl isomerase a; **PDBTitle:** crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
43	c3eooL_	Alignment	not modelled	96.1	19	**PDB header:**lyase **Chain:** L: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
44	d1muma_	Alignment	not modelled	96.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
45	c1ydnA_	Alignment	not modelled	96.1	13	**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.
46	d1ka9f_	Alignment	not modelled	96.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
47	d1tqxa_	Alignment	not modelled	96.0	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
48	c3ih1A_	Alignment	not modelled	96.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
49	c3gr7A_	Alignment	not modelled	95.9	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
50	d1ujqa_	Alignment	not modelled	95.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
51	c1jvnB_	Alignment	not modelled	95.8	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional histidine biosynthesis protein hishf; **PDBTitle:** crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
52	d2tpsa_	Alignment	not modelled	95.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
53	c3b8iF_	Alignment	not modelled	95.8	20	**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+.
						PDB header:transferase

54	c3t7vA_	Alignment	not modelled	95.8	16	**Chain:** A: **PDB Molecule:**methylornithine synthase pylb; **PDBTitle:** crystal structure of methylornithine synthase (pylb)
55	d1mxsa_	Alignment	not modelled	95.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
56	c1yadD_	Alignment	not modelled	95.7	12	**PDB header:**transcription **Chain:** D: **PDB Molecule:**regulatory protein teni; **PDBTitle:** structure of teni from bacillus subtilis
57	c3pm6B_	Alignment	not modelled	95.7	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
58	c3cixA_	Alignment	not modelled	95.7	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
59	c2w6rA_	Alignment	not modelled	95.7	15	**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
60	c3elfA_	Alignment	not modelled	95.6	13	**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
61	c2hjpA_	Alignment	not modelled	95.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonopyruvate hydrolase; **PDBTitle:** crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
62	d1mzha_	Alignment	not modelled	95.5	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
63	d1rvga_	Alignment	not modelled	95.5	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
64	d1rpxa_	Alignment	not modelled	95.5	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
65	d1u5ha_	Alignment	not modelled	95.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
66	c3ng3A_	Alignment	not modelled	95.5	22	**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
67	c2gjlA_	Alignment	not modelled	95.4	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein pa1024; **PDBTitle:** crystal structure of 2-nitropropane dioxygenase
68	d1e0ta2	Alignment	not modelled	95.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
69	c3thaB_	Alignment	not modelled	95.4	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** tryptophan synthase subunit alpha from campylobacter jejuni.
70	c3ngjC_	Alignment	not modelled	95.4	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**deoxyribose-phosphate aldolase; **PDBTitle:** crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
71	c3bo9B_	Alignment	not modelled	95.2	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nitroalkan dioxygenase; **PDBTitle:** crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution
72	c1u5vA_	Alignment	not modelled	95.1	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cite; **PDBTitle:** structure of cite complexed with triphosphate group of atp2 form mycobacterium tuberculosis
73	c1r30A_	Alignment	not modelled	95.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**biotin synthase; **PDBTitle:** the crystal structure of biotin synthase, an s-2 adenosylmethionine-dependent radical enzyme
74	d1r30a_	Alignment	not modelled	95.1	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Biotin synthase
75	c3navB_	Alignment	not modelled	95.1	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
76	c3c52B_	Alignment	not modelled	95.1	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** class ii fructose-1,6-bisphosphate aldolase from2 helicobacter pylori in complex with3 phosphoglycolohydroxamic acid, a competitive inhibitor
77	c3hf3A_	Alignment	not modelled	95.1	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
78	c3pg8B_	Alignment	not modelled	95.1	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate aldolase; **PDBTitle:** truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
79	d1wbha1	Alignment	not modelled	95.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase

						Family: Class I aldolase
80	d1y0ea_	Alignment	not modelled	94.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
81	c2dh3A_	Alignment	not modelled	94.9	21	**PDB header:**transport protein, signaling protein **Chain:** A: **PDB Molecule:**4f2 cell-surface antigen heavy chain; **PDBTitle:** crystal structure of human ed-4f2hc
82	d1geqa_	Alignment	not modelled	94.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
83	d1vhca_	Alignment	not modelled	94.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
84	d1nvma2	Alignment	not modelled	94.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**HMGL-like
85	d2flia1	Alignment	not modelled	94.8	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
86	c3r2gA_	Alignment	not modelled	94.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine 5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
87	c2pz0B_	Alignment	not modelled	94.7	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
88	c3ewbX_	Alignment	not modelled	94.7	9	**PDB header:**transferase **Chain:** X: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of n-terminal domain of putative 2-2 isopropylmalate synthase from listeria monocytogenes
89	c2v82A_	Alignment	not modelled	94.6	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase; **PDBTitle:** kdpgal complexed to kdpgal
90	c3gndC_	Alignment	not modelled	94.5	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
91	c3l12A_	Alignment	not modelled	94.4	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (yp_165505.1) from silicibacter pomeroyi dss-3 at3 1.60 a resolution
92	c1nvmG_	Alignment	not modelled	94.3	15	**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
93	d1qopa_	Alignment	not modelled	94.3	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
94	c2cw6B_	Alignment	not modelled	94.3	13	**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
95	c3inpA_	Alignment		94.2	15	**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.
96	d1o60a_	Alignment	not modelled	94.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
97	c3g8rA_	Alignment	not modelled	94.2	20	**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
98	d1ojxa_	Alignment	not modelled	94.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
99	c3sz8D_	Alignment	not modelled	94.1	8	**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
100	c3rlgA_	Alignment	not modelled	94.1	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sphingomyelin phosphodiesterase d lisictox-alphaia1a; **PDBTitle:** crystal structure of loxosceles intermedia phospholipase d isoform 12 h12a mutant
101	d1xcfa_	Alignment	not modelled	94.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
102	c3ffsC_	Alignment	not modelled	94.0	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**inosine-5-monophosphate dehydrogenase;

						PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
103	d1w3ia_	Alignment	not modelled	93.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
104	c2nx9B_	Alignment	not modelled	93.9	19	**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
105	c3ez4B_	Alignment	not modelled	93.8	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-methyl-2-oxobutanoate hydroxymethyltransferase; **PDBTitle:** crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
106	c3bg3B_	Alignment	not modelled	93.7	20	**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)
107	c1rr2A_	Alignment	not modelled	93.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarboxylase 5s subunit; **PDBTitle:** propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
108	c1piiA_	Alignment	not modelled	93.6	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
109	d1ps9a1	Alignment	not modelled	93.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
110	c1qpoA_	Alignment	not modelled	93.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**quinolinate acid phosphoribosyl transferase; **PDBTitle:** quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
111	d1dxea_	Alignment	not modelled	93.5	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
112	d1d9ea_	Alignment	not modelled	93.5	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
113	c3eegB_	Alignment	not modelled	93.4	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
114	c2z1kA_	Alignment	not modelled	93.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**(neo)pullulanase; **PDBTitle:** crystal structure of ttha1563 from thermus thermophilus hb8
115	d1o4ua1	Alignment	not modelled	93.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
116	d1qpoa1	Alignment	not modelled	93.3	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
117	d1p1xa_	Alignment	not modelled	93.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
118	d1m3ua_	Alignment	not modelled	93.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
119	c2r94B_	Alignment	not modelled	93.1	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxy-(6-phospho-)gluconate aldolase; **PDBTitle:** crystal structure of kd(p)ga from t.tenax
120	c3bmwA_	Alignment	not modelled	93.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cyclomaltodextrin glucanotransferase; **PDBTitle:** cyclodextrin glycosyl transferase from thermoanerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor