Phyre^2

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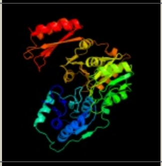
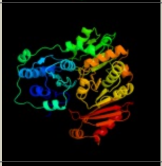
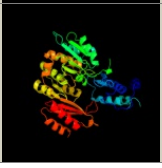
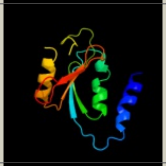
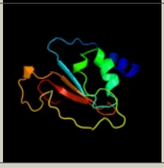
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pdkB_	Alignment		100.0	46	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucosamine mutase; **PDBTitle:** crystal structure of phosphoglucosamine mutase from b. anthracis
2	c1wqaB_	Alignment		100.0	33	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phospho-sugar mutase; **PDBTitle:** crystal structure of pyrococcus horikoshii2 phosphomannomutase/phosphoglucomutase complexed with mg2+
3	c2f7lA_	Alignment		100.0	28	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**455aa long hypothetical phospho-sugar mutase; **PDBTitle:** crystal structure of sulfolobus tokodaii2 phosphomannomutase/phosphoglucomutase
4	c3i3wB_	Alignment		100.0	43	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucosamine mutase; **PDBTitle:** structure of a phosphoglucosamine mutase from francisella tularensis
5	c3c04A_	Alignment		100.0	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphomannomutase/phosphoglucomutase; **PDBTitle:** structure of the p368g mutant of pmm/pgm from p. aeruginosa
6	c1tuoA_	Alignment		100.0	27	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative phosphomannomutase; **PDBTitle:** crystal structure of putative phosphomannomutase from2 thermus thermophilus hb8
7	c2fuvB_	Alignment		100.0	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucomutase; **PDBTitle:** phosphoglucomutase from salmonella typhimurium.
8	c1c4gB_	Alignment		100.0	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (alpha-d-glucose 1-phosphate **PDBTitle:** phosphoglucomutase vanadate based transition state analog2 complex
9	c2z0fA_	Alignment		100.0	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphoglucomutase; **PDBTitle:** crystal structure of putative phosphoglucomutase from thermus2 thermophilus hb8
10	c1kfiA_	Alignment		100.0	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoglucomutase 1; **PDBTitle:** crystal structure of the exocytosis-sensitive2 phosphoprotein, pp63/parafusin (phosphoglucomutase) from3 paramecium
11	c2dkdA_	Alignment		100.0	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoacetylglucosamine mutase; **PDBTitle:** crystal structure of n-acetylglucosamine-phosphate mutase,2 a member of the alpha-d-phosphohexomutase superfamily, in3 the product complex

12	d1p5dx1	Alignment		100.0	26	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
13	d1kfia1	Alignment		100.0	26	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
14	d3pmga1	Alignment		100.0	27	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
15	d1p5dx3	Alignment		99.9	19	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
16	d3pmga3	Alignment		99.9	17	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
17	d1p5dx2	Alignment		99.9	40	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
18	d1kfia3	Alignment		99.9	18	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
19	d3pmga2	Alignment		99.9	29	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
20	d1kfia2	Alignment		99.8	20	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
21	d1p5dx4	Alignment	not modelled	99.6	19	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
22	d1wjwa_	Alignment	not modelled	99.4	18	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
23	d1kfia4	Alignment	not modelled	95.2	18	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
24	d3pmga4	Alignment	not modelled	94.9	18	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
25	c3he8A_	Alignment	not modelled	90.8	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
26	d1nn4a_	Alignment	not modelled	89.2	28	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
27	c3s5pA_	Alignment	not modelled	89.2	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
28	c3k7pA_	Alignment	not modelled	88.8	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
29	c3m1pA_	Alignment	not modelled	87.5	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase;

29	c3m1pA_	Alignment	not modelled	87.5	24	**PDBTitle:** structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
30	d3bula2	Alignment	not modelled	86.6	14	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
31	d2vvpa1	Alignment	not modelled	84.2	28	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
32	c3qayC_	Alignment	not modelled	77.5	18	**PDB header:**lyase **Chain:** C: **PDB Molecule:**endolysin; **PDBTitle:** catalytic domain of cd27l endolysin targeting clostridia difficile
33	c1k98A_	Alignment	not modelled	75.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionine synthase; **PDBTitle:** adomet complex of meth c-terminal fragment
34	c2g04B_	Alignment	not modelled	72.4	30	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**probable fatty-acid-coa racemase far; **PDBTitle:** crystal structure of fatty acid-coa racemase from mycobacterium2 tuberculosis h37rv
35	c2yxbA_	Alignment	not modelled	71.4	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
36	d1ycga1	Alignment	not modelled	71.1	27	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
37	d1o1xa_	Alignment	not modelled	71.0	25	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
38	d1ccwa_	Alignment	not modelled	69.7	18	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
39	d1x74a1	Alignment	not modelled	68.3	39	**Fold:**CoA-transferase family III (CaiB/BaiF) **Superfamily:**CoA-transferase family III (CaiB/BaiF) **Family:**CoA-transferase family III (CaiB/BaiF)
40	c1bmtB_	Alignment	not modelled	67.4	13	**PDB header:**methyltransferase **Chain:** B: **PDB Molecule:**methionine synthase; **PDBTitle:** how a protein binds b12: a 3.0 angstrom x-ray structure of2 the b12-binding domains of methionine synthase
41	c3sz8D_	Alignment	not modelled	66.6	9	**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
42	d1xk7a1	Alignment	not modelled	66.3	33	**Fold:**CoA-transferase family III (CaiB/BaiF) **Superfamily:**CoA-transferase family III (CaiB/BaiF) **Family:**CoA-transferase family III (CaiB/BaiF)
43	c2i2xD_	Alignment	not modelled	64.0	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**methyltransferase 1; **PDBTitle:** crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
44	c3hlyA_	Alignment	not modelled	63.3	14	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavodoxin-like domain; **PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
45	c2ppwA_	Alignment	not modelled	63.2	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
46	c2ohiB_	Alignment	not modelled	63.0	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**type a flavoprotein fpra; **PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
47	c1xa3B_	Alignment	not modelled	62.8	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**crotonobetainyl-coa:carnitine coa-transferase; **PDBTitle:** crystal structure of caib, a type iii coa transferase in2 carnitine metabolism
48	c3qd5B_	Alignment	not modelled	62.7	26	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of a putative ribose-5-phosphate isomerase from2 coccidioides immitis solved by combined iodide ion sad and mr
49	d2vjma1	Alignment	not modelled	60.5	30	**Fold:**CoA-transferase family III (CaiB/BaiF) **Superfamily:**CoA-transferase family III (CaiB/BaiF) **Family:**CoA-transferase family III (CaiB/BaiF)
50	d1e5da1	Alignment	not modelled	58.8	20	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
51	c1y80A_	Alignment	not modelled	58.3	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted cobalamin binding protein; **PDBTitle:** structure of a corrinoid (factor iiim)-binding protein from2 moorella thermoacetica
52	d1q7ea_	Alignment	not modelled	57.9	30	**Fold:**CoA-transferase family III (CaiB/BaiF) **Superfamily:**CoA-transferase family III (CaiB/BaiF) **Family:**CoA-transferase family III (CaiB/BaiF)
53	c3c5yD_	Alignment	not modelled	56.5	17	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
54	c3ne8A_	Alignment	not modelled	54.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** the crystal structure of a domain from n-acetylmuramoyl-

						l-alanine2 amidase of bartonella henselae str. houston-1
55	c2q9uB_	Alignment	not modelled	53.4	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
56	c3nvtA_	Alignment	not modelled	49.1	12	**PDB header:**transferase/isomerase **Chain:** A: **PDB Molecule:**3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; **PDBTitle:** 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e
57	d1b1ca_	Alignment	not modelled	48.1	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
58	c2yh5A_	Alignment	not modelled	46.0	13	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**dapx protein; **PDBTitle:** structure of the c-terminal domain of bamc
59	d1dxha2	Alignment	not modelled	43.8	15	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
60	c1e5dA_	Alignment	not modelled	42.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
61	d1d9ea_	Alignment	not modelled	41.6	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
62	c3ezxA_	Alignment	not modelled	40.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**monomethylamine corrinoid protein 1; **PDBTitle:** structure of methanosarcina barkeri monomethylamine2 corrinoid protein
63	c3fniA_	Alignment	not modelled	38.7	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative diflavin flavoprotein a 3; **PDBTitle:** crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
64	d3eeqa2	Alignment	not modelled	38.2	10	**Fold:**CbiG N-terminal domain-like **Superfamily:**CbiG N-terminal domain-like **Family:**CbiG N-terminal domain-like
65	d1xrsb1	Alignment	not modelled	37.5	13	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
66	d1vmea1	Alignment	not modelled	35.2	9	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
67	c2pfsA_	Alignment	not modelled	34.3	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** crystal structure of universal stress protein from nitrosomonas2 europaea
68	c1xrsB_	Alignment	not modelled	33.6	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**d-lysine 5,6-aminomutase beta subunit; **PDBTitle:** crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
69	c3onoA_	Alignment	not modelled	32.4	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus
70	c3lopA_	Alignment	not modelled	32.1	16	**PDB header:**substrate binding protein **Chain:** A: **PDB Molecule:**substrate binding periplasmic protein; **PDBTitle:** crystal structure of substrate-binding periplasmic protein2 (pbp) from ralstonia solanacearum
71	c2rejA_	Alignment	not modelled	31.6	6	**PDB header:**choline-binding protein **Chain:** A: **PDB Molecule:**putative glycine betaine abc transporter protein; **PDBTitle:** abc-transporter choline binding protein in unliganded semi-2 closed conformation
72	d7reqa2	Alignment	not modelled	31.0	10	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
73	c3n0wA_	Alignment	not modelled	30.6	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc branched chain amino acid family transporter, **PDBTitle:** crystal structure of a branched chain amino acid abc transporter2 periplasmic ligand-binding protein (bxe_c0949) from burkholderia3 xenovorans lb400 at 1.88 a resolution
74	c2zkiH_	Alignment	not modelled	30.2	16	**PDB header:**transcription **Chain:** H: **PDB Molecule:**199aa long hypothetical trp repressor binding **PDBTitle:** crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
75	d2cc0a1	Alignment	not modelled	29.0	20	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
76	d1fmfa_	Alignment	not modelled	28.0	22	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
77	d1ws6a1	Alignment	not modelled	27.1	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
78	d1tubb1	Alignment	not modelled	27.0	4	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
79	c2zf8A_	Alignment	not modelled	27.0	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**component of sodium-driven polar

79	c2zf8A_	Alignment	not modelled	27.0	9	flagellar motor; **PDBTitle:** crystal structure of moty
80	d2p1ra1	Alignment	not modelled	24.7	17	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
81	c3k6qB_	Alignment	not modelled	24.5	13	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**putative ligand binding protein; **PDBTitle:** crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
82	c3qqzA_	Alignment	not modelled	24.3	0	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein yjik; **PDBTitle:** crystal structure of the c-terminal domain of the yjik protein from2 escherichia coli cft073
83	d1duvg2	Alignment	not modelled	23.9	14	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
84	d2ebfx2	Alignment	not modelled	22.5	10	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**PMT domain-like
85	d2btoa1	Alignment	not modelled	22.5	10	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
86	d1ml4a2	Alignment	not modelled	22.2	17	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
87	d1qo0a_	Alignment	not modelled	22.2	14	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
88	d1q77a_	Alignment	not modelled	21.8	4	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
89	c3ff1B_	Alignment	not modelled	21.4	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** structure of glucose 6-phosphate isomerase from staphylococcus aureus
90	d1a9xa4	Alignment	not modelled	21.4	25	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
91	c3hjtB_	Alignment	not modelled	21.3	15	**PDB header:**cell adhesion, transport protein **Chain:** B: **PDB Molecule:**lmb; **PDBTitle:** structure of laminin binding protein (lmb) of streptococcus2 agalactiae a bifunctional protein with adhesin and metal3 transporting activity
92	d2a5la1	Alignment	not modelled	21.1	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
93	c3s3tD_	Alignment	not modelled	20.6	5	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**nucleotide-binding protein, universal stress protein uspa **PDBTitle:** universal stress protein uspa from lactobacillus plantarum
94	d2z3va1	Alignment	not modelled	20.3	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
95	d1yt8a4	Alignment	not modelled	19.9	13	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
96	d1vp8a_	Alignment	not modelled	19.8	20	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
97	c2x41A_	Alignment	not modelled	19.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
98	d1of8a_	Alignment	not modelled	19.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
99	d1ak2a1	Alignment	not modelled	19.5	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases