Phyre2

Email	l.a.kelley@imperial.ac.uk
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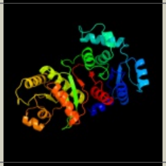
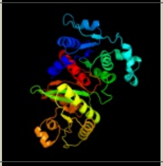
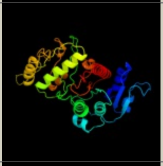
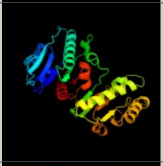
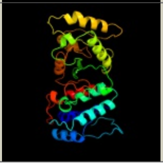
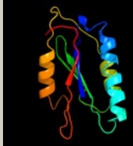
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vmia_	Alignment		100.0	98	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
2	c1vmiA_	Alignment		100.0	98	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative phosphate acetyltransferase; **PDBTitle:** crystal structure of putative phosphate acetyltransferase2 (np_416953.1) from escherichia coli k12 at 2.32 a resolution
3	d1xcoa_	Alignment		100.0	42	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
4	d1r5ja_	Alignment		100.0	41	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
5	d2af4c1	Alignment		100.0	35	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
6	c3tngA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lmo1369 protein; **PDBTitle:** the crystal structure of a possible phosphate acetyl/butaryl2 transferase from listeria monocytogenes egd-e.
7	c1ycoA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**branched-chain phosphotransacylase; **PDBTitle:** crystal structure of a branched-chain phosphotransacylase from2 enterococcus faecalis v583
8	d1vi1a_	Alignment		100.0	21	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PlsX-like
9	d1u7na_	Alignment		100.0	19	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PlsX-like
10	d1ptma_	Alignment		100.0	15	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
11	c1yxoB_	Alignment		99.9	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxythreonine-4-phosphate dehydrogenase 1; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic protein pdxa2 pa0593

12	d1r8ka_	Alignment		99.8	16	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
13	c2hi1A_	Alignment		98.8	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**4-hydroxythreonine-4-phosphate dehydrogenase 2; **PDBTitle:** the structure of a putative 4-hydroxythreonine-4-phosphate2 dehydrogenase from salmonella typhimurium.
14	c3lfhF_	Alignment		73.3	15	**PDB header:**transferase **Chain:** F: **PDB Molecule:**phosphotransferase system, mannose/fructose-specific **PDBTitle:** crystal structure of manxa from thermoanaerobacter tengcongensis
15	c2iueA_	Alignment		70.3	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**pactolus i-domain; **PDBTitle:** pactolus i-domain: functional switching of the rossmann2 fold
16	d3b48a1	Alignment		68.2	11	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
17	d3beda1	Alignment		65.0	12	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**EIIA-man component-like
18	c2ys6A_	Alignment		58.5	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide synthetase; **PDBTitle:** crystal structure of gar synthetase from geobacillus kaustophilus
19	c2yyaB_	Alignment		56.7	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of gar synthetase from aquifex aeolicus
20	c2qk4A_	Alignment		54.9	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trifunctional purine biosynthetic protein adenosine-3; **PDBTitle:** human glycinamide ribonucleotide synthetase
21	c2xd4A_	Alignment	not modelled	51.2	7	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
22	c2vy9A_	Alignment	not modelled	46.4	13	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**anti-sigma-factor antagonist; **PDBTitle:** molecular architecture of the stressosome, a signal2 integration and transduction hub
23	c1gsoA_	Alignment	not modelled	42.7	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**protein (glycinamide ribonucleotide synthetase); **PDBTitle:** glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.
24	c3mtqA_	Alignment	not modelled	29.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative phosphoenolpyruvate-dependent sugar **PDBTitle:** crystal structure of a putative phosphoenolpyruvate-dependent sugar2 phosphotransferase system (pts) permease (kpn_04802) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.70 a resolution
25	c2ip4A_	Alignment	not modelled	27.1	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
26	c3lp8A_	Alignment	not modelled	26.8	8	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine-glycine ligase; **PDBTitle:** crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
27	d2cg4a2	Alignment	not modelled	23.6	8	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
						PDB header:transferase

28	c3dcjA_	Alignment	not modelled	20.9	25	**Chain:** A: **PDB Molecule:**probable 5'-phosphoribosylglycinamide **PDBTitle:** crystal structure of glycinamide formyltransferase (purn)2 from mycobacterium tuberculosis in complex with 5-methyl-5,3 6,7,8-tetrahydrofolic acid derivative
29	d1i1ga2	Alignment	not modelled	20.2	10	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
30	d3bgsa1	Alignment	not modelled	20.1	31	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
31	c2vosA_	Alignment	not modelled	18.6	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**folylpolyglutamate synthase protein folc; **PDBTitle:** mycobacterium tuberculosis folylpolyglutamate synthase2 complexed with adp
32	d1pdoa_	Alignment	not modelled	17.7	9	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**EIIA-man component-like
33	c3ragA_	Alignment	not modelled	16.2	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein aaci_0196 from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
34	c2f3oB_	Alignment	not modelled	15.8	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**pyruvate formate-lyase 2; **PDBTitle:** crystal structure of a glycyl radical enzyme from archaeoglobus2 fulgidus
35	c3n0vD_	Alignment	not modelled	15.8	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
36	d1r9da_	Alignment	not modelled	15.6	19	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
37	c2y8nC_	Alignment	not modelled	15.4	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**4-hydroxyphenylacetate decarboxylase large subunit; **PDBTitle:** crystal structure of glycyl radical enzyme
38	d1e5ma1	Alignment	not modelled	15.0	20	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
39	c2e7xA_	Alignment	not modelled	14.6	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**150aa long hypothetical transcriptional regulator; **PDBTitle:** structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
40	c3louB_	Alignment	not modelled	14.6	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
41	c3ca8B_	Alignment	not modelled	14.0	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydcf; **PDBTitle:** crystal structure of escherichia coli ydcf, an s-adenosyl-l-methionine2 utilizing enzyme
42	c3e7dC_	Alignment	not modelled	13.4	18	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**cobh, precorrin-8x methylmutase; **PDBTitle:** crystal structure of precorrin-8x methyl mutase cbic/cobh from2 brucella melitensis
43	c3lrfA_	Alignment	not modelled	13.4	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-ketoacyl synthase; **PDBTitle:** crystal structure of beta-ketoacyl synthase from brucella2 melitensis
44	c3a0rB_	Alignment	not modelled	13.2	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
45	d1umya_	Alignment	not modelled	13.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
46	d1tqya1	Alignment	not modelled	12.9	23	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
47	c2pjuD_	Alignment	not modelled	12.1	17	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
48	d3ct6a1	Alignment	not modelled	12.0	13	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
49	c2zayA_	Alignment	not modelled	11.1	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
50	d1vrga1	Alignment	not modelled	11.1	14	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
51	c3rhgA_	Alignment	not modelled	10.7	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phophotriesterase; **PDBTitle:** crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
52	c2jtqA_	Alignment	not modelled	10.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phage shock protein e; **PDBTitle:** rhodanese from e.coli
53	d1ou0a_	Alignment	not modelled	10.7	13	**Fold:**Flavodoxin-like **Superfamily:**Precorrin-8X methylmutase CbiC/CobH

						Family: Precorrin-8X methylmutase CbiC/CobH
54	c2l82A_	Alignment	not modelled	10.6	16	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein or32; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or32
55	d2c1ha1	Alignment	not modelled	10.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
56	d1p6qa_	Alignment	not modelled	10.4	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
57	c2nt3A_	Alignment	not modelled	10.3	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator homolog; **PDBTitle:** receiver domain from myxococcus xanthus social motility protein frzs2 (y102a mutant)
58	c2zbcH_	Alignment	not modelled	10.3	12	**PDB header:**transcription **Chain:** H: **PDB Molecule:**83aa long hypothetical transcriptional regulator asnc; **PDBTitle:** crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7.
59	c3gdwA_	Alignment	not modelled	10.3	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sigma-54 interaction domain protein; **PDBTitle:** crystal structure of sigma-54 interaction domain protein from2 enterococcus faecalis
60	d2gfva1	Alignment	not modelled	10.2	23	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
61	c3o1lB_	Alignment	not modelled	9.9	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
62	c2rirA_	Alignment	not modelled	9.6	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase, a chain; **PDBTitle:** crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
63	d2gaxa1	Alignment	not modelled	9.5	9	**Fold:**Peptidyl-tRNA hydrolase II **Superfamily:**Peptidyl-tRNA hydrolase II **Family:**Peptidyl-tRNA hydrolase II
64	d1fmta2	Alignment	not modelled	9.3	23	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
65	d1ofux_	Alignment	not modelled	9.1	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Bacterial cell division inhibitor SulA
66	d2vbaa1	Alignment	not modelled	9.0	18	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
67	c2djwF_	Alignment	not modelled	8.9	12	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**probable transcriptional regulator, asnc family; **PDBTitle:** crystal structure of ttha0845 from thermus thermophilus hb8
68	d3pnpa_	Alignment	not modelled	8.9	29	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
69	c3c97A_	Alignment	not modelled	8.8	13	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**signal transduction histidine kinase; **PDBTitle:** crystal structure of the response regulator receiver domain2 of a signal transduction histidine kinase from aspergillus3 oryzae
70	d1l6sa_	Alignment	not modelled	8.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
71	d1zesa1	Alignment	not modelled	8.8	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
72	c4a1oB_	Alignment	not modelled	8.2	17	**PDB header:**transferase-hydrolase **Chain:** B: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
73	d1p3y1_	Alignment	not modelled	8.2	10	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
74	c2e0cA_	Alignment	not modelled	8.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**409aa long hypothetical nadp-dependent isocitrate **PDBTitle:** crystal structure of isocitrate dehydrogenase from sulfolobus tokodaii2 strain7 at 2.0 a resolution
75	c1yr3A_	Alignment	not modelled	8.1	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xanthosine phosphorylase; **PDBTitle:** escherichia coli purine nucleoside phosphorylase ii, the2 product of the xapa gene
76	d2dx7a1	Alignment	not modelled	7.9	14	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
						Fold: Thiolase-like

77	d2ix4a1	Alignment	not modelled	7.8	36	**Superfamily:**Thiolase-like **Family:**Thiolase-related
78	c2buiC_	Alignment	not modelled	7.7	18	**PDB header:**synthase **Chain:** C: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase i; **PDBTitle:** e.coli beta-ketoacyl (acyl carrier protein) synthase i in2 complex with octanoic acid, 120k
79	c3ktoA_	Alignment	not modelled	7.6	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver protein2 from pseudoalteromonas atlantica
80	c2uv9B_	Alignment	not modelled	7.3	34	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fatty acid synthase alpha subunits; **PDBTitle:** crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the alpha subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
81	c1cr6A_	Alignment	not modelled	7.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
82	c2l2qA_	Alignment	not modelled	7.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, cellobiose-specific iib component (cela); **PDBTitle:** solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
83	c3n53B_	Alignment	not modelled	7.1	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator receiver modulated diguanylate cyclase; **PDBTitle:** crystal structure of a response regulator receiver modulated2 diguanylate cyclase from pelobacter carbinolicus
84	c3p9xB_	Alignment	not modelled	7.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
85	d1vc1a_	Alignment	not modelled	7.0	11	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Anti-sigma factor antagonist SpoIIaa
86	c2e1aD_	Alignment	not modelled	6.9	12	**PDB header:**transcription **Chain:** D: **PDB Molecule:**75aa long hypothetical regulatory protein asnc; **PDBTitle:** crystal structure of ffrp-dm1
87	d1wu2a3	Alignment	not modelled	6.9	33	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
88	d2pjua1	Alignment	not modelled	6.8	16	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
89	c3nhzA_	Alignment	not modelled	6.7	6	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
90	c3ouzA_	Alignment	not modelled	6.6	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
91	d1uz5a3	Alignment	not modelled	6.5	64	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
92	d1gega_	Alignment	not modelled	6.4	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
93	d1gzga_	Alignment	not modelled	6.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
94	d1m3ua_	Alignment	not modelled	6.3	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
95	d1v9ca_	Alignment	not modelled	6.3	30	**Fold:**Flavodoxin-like **Superfamily:**Precorrin-8X methylmutase CbiC/CobH **Family:**Precorrin-8X methylmutase CbiC/CobH
96	c3iprC_	Alignment	not modelled	6.3	10	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pts system, iia component; **PDBTitle:** crystal structure of the enterococcus faecalis gluconate2 specific eiia phosphotransferase system component
97	d1j3na1	Alignment	not modelled	6.3	20	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
98	d1h7na_	Alignment	not modelled	6.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
99	c3tqrA_	Alignment	not modelled	6.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii