Phyre^2

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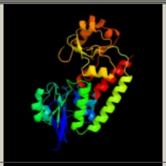
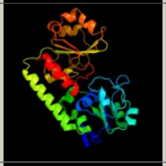
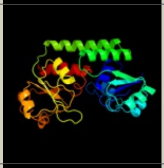
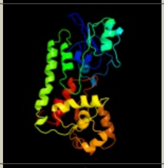
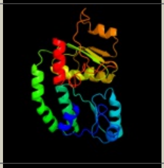
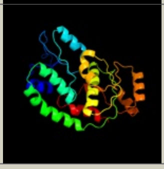
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3eiwA_	Alignment		100.0	37	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**htsa protein; **PDBTitle:** crystal structure of staphylococcus aureus lipoprotein, htsa
2	d2chua1	Alignment		100.0	22	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TM0189-like
3	c3pshA_	Alignment		100.0	18	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**protein hi_1472; **PDBTitle:** classification of a haemophilus influenzae abc transporter hi1470/712 through its cognate molybdate periplasmic binding protein mola (mola3 bound to molybdate)
4	c3gfvA_	Alignment		100.0	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**uncharacterized abc transporter solute-binding **PDBTitle:** crystal structure of petrobactin-binding protein yclq from2 bacillu subtilis
5	c3be5D_	Alignment		100.0	20	**PDB header:**metal transport **Chain:** D: **PDB Molecule:**putative iron compound-binding protein of abc transporter **PDBTitle:** crystal structure of fite (crystal form 1), a group iii periplasmic2 siderophore binding protein
6	d2phza1	Alignment		100.0	14	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TM0189-like
7	c2phzA_	Alignment		100.0	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**iron-uptake system-binding protein; **PDBTitle:** crystal structure of iron-uptake system-binding protein2 feua from bacillus subtilis. northeast structural genomics3 target sr580.
8	c2q8pA_	Alignment		100.0	17	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**iron-regulated surface determinant e; **PDBTitle:** crystal structure of selenomethionine labelled s. aureus isde2 complexed with heme
9	c2r79A_	Alignment		100.0	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic binding protein; **PDBTitle:** crystal structure of a periplasmic heme binding protein from2 pseudomonas aeruginosa
10	c3mwgA_	Alignment		100.0	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**iron-regulated abc transporter siderophore-binding protein **PDBTitle:** crystal structure of staphylococcus aureus sira
11	d1esza_	Alignment		100.0	17	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Periplasmic ferric siderophore binding protein FhuD

12	c3md9A_	Alignment		100.0	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hemin-binding periplasmic protein hmut; **PDBTitle:** structure of apo form of a periplasmic heme binding protein
13	c2r7aC_	Alignment		100.0	17	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bacterial heme binding protein; **PDBTitle:** crystal structure of a periplasmic heme binding protein2 from shigella dysenteriae
14	c2x4lA_	Alignment		100.0	17	**PDB header:**transport **Chain:** A: **PDB Molecule:**ferric-siderophore receptor protein; **PDBTitle:** crystal structure of dese, a ferric-siderophore receptor2 protein from streptomyces coelicolor
15	d1n2za_	Alignment		100.0	17	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
16	c3g9qA_	Alignment		100.0	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ferrichrome-binding protein; **PDBTitle:** crystal structure of the fhud fold-family bsu3320, a periplasmic2 binding protein component of a fep/fec-like ferrichrome abc3 transporter from bacillus subtilis. northeast structural genomics4 consortium target sr577a
17	d2etva1	Alignment		100.0	14	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TM0189-like
18	d1qh8a_	Alignment		96.3	14	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
19	d1m1na_	Alignment		96.1	11	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
20	c3aerC_	Alignment		95.6	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**light-independent protochlorophyllide reductase subunit n; **PDBTitle:** structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
21	c3pdiG_	Alignment	not modelled	94.9	13	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nife; **PDBTitle:** precursor bound nifen
22	d1mioa_	Alignment	not modelled	93.4	12	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
23	d1qh8b_	Alignment	not modelled	93.0	17	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
24	c3eywA_	Alignment	not modelled	91.8	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux **PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
25	d1m1nb_	Alignment	not modelled	91.7	24	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
26	d1miob_	Alignment	not modelled	89.0	13	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
27	c2xdqB_	Alignment	not modelled	88.8	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**light-independent protochlorophyllide reductase subunit b; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-2 chlb)2 complex
28	c3pdiB_	Alignment	not modelled	73.6	15	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nifn; **PDBTitle:** precursor bound nifen

29	d1gmla_	Alignment	not modelled	66.5	20	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
30	d7reqa2	Alignment	not modelled	65.4	13	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
31	c3aerB_	Alignment	not modelled	65.2	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**light-independent protochlorophyllide reductase subunit b; **PDBTitle:** structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
32	c2xdqA_	Alignment	not modelled	64.6	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase subunit n; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-2 chlb)2 complex
33	d1q3qa2	Alignment	not modelled	64.5	8	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
34	c3obiC_	Alignment	not modelled	62.4	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
35	c1z7eC_	Alignment	not modelled	62.1	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of full length arna
36	d1assa_	Alignment	not modelled	61.0	8	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
37	d1a6db2	Alignment	not modelled	58.8	8	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
38	d2blna2	Alignment	not modelled	52.4	24	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
39	c1yrwA_	Alignment	not modelled	45.4	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of e.coli arna transformylase domain
40	d1a9xb2	Alignment	not modelled	43.4	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
41	c3k8zD_	Alignment	not modelled	39.7	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nad-specific glutamate dehydrogenase; **PDBTitle:** crystal structure of gudb1 a decryptified secondary glutamate2 dehydrogenase from b. subtilis
42	c2r8rB_	Alignment	not modelled	38.5	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the n-terminal region (19..243) of sensor protein2 kdpd from pseudomonas syringae pv. tomato str. dc3000
43	c3cx3A_	Alignment	not modelled	37.3	10	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**lipoprotein; **PDBTitle:** crystal structure analysis of the streptococcus pneumoniae2 adcaii protein
44	c2ov3A_	Alignment	not modelled	37.1	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic binding protein component of an abc **PDBTitle:** crystal structure of 138-173 znua deletion mutant plus zinc2 bound
45	c3hg7A_	Alignment	not modelled	34.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-isomer specific 2-hydroxyacid dehydrogenase family **PDBTitle:** crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 family protein from aeromonas salmonicida subsp. salmonicida a449
46	c3q0iA_	Alignment	not modelled	32.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** methionyl-trna formyltransferase from vibrio cholerae
47	d1fyea_	Alignment	not modelled	32.3	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Aspartyl dipeptidase PepE
48	c2yxbA_	Alignment	not modelled	31.8	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
49	d1fmta2	Alignment	not modelled	29.0	18	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
50	c3tqrA_	Alignment	not modelled	28.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
51	c3hjtB_	Alignment	not modelled	27.8	16	**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
52	c3tqqA_	Alignment	not modelled	26.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** structure of the methionyl-trna formyltransferase (fmt) from coxiella2 burnetii
						PDB header:formyltransferase

53	c1fmtA_	Alignment	not modelled	26.1	18	**Chain:** A: **PDB Molecule:**methionyl-trna fmet formyltransferase; **PDBTitle:** methionyl-trnafmet formyltransferase from escherichia coli
54	c2waoA_	Alignment	not modelled	24.7	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase e; **PDBTitle:** structure of a family two carbohydrate esterase from2 clostridium thermocellum in complex with cellohexaose
55	c3p9xB_	Alignment	not modelled	23.8	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
56	d1s3ia2	Alignment	not modelled	22.8	17	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
57	d1zgha2	Alignment	not modelled	22.6	10	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
58	c3o1lB_	Alignment	not modelled	21.8	10	**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
59	c3lo3E_	Alignment	not modelled	21.5	9	**PDB header:**structure genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved functionally unknown2 protein from colwellia psychrerythraea 34h.
60	d1psza_	Alignment	not modelled	21.2	11	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
61	c1s3iA_	Alignment	not modelled	21.1	15	**PDB header:**hydrolase, oxidoreductase **Chain:** A: **PDB Molecule:**10-formyltetrahydrofolate dehydrogenase; **PDBTitle:** crystal structure of the n terminal hydrolase domain of 10-2 formyltetrahydrofolate dehydrogenase
62	d1bvua1	Alignment	not modelled	20.6	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
63	d2bw0a2	Alignment	not modelled	19.2	15	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
64	c2ywrA_	Alignment	not modelled	18.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of gar transformylase from aquifex2 aeolicus
65	c1bvuF_	Alignment	not modelled	18.7	11	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**protein (glutamate dehydrogenase); **PDBTitle:** glutamate dehydrogenase from thermococcus litoralis
66	c3ndjA_	Alignment	not modelled	18.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
67	c3en0A_	Alignment	not modelled	17.9	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyanophycinase; **PDBTitle:** the structure of cyanophycinase
68	c3louB_	Alignment	not modelled	17.6	12	**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
69	c1ulzA_	Alignment	not modelled	17.0	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase n-terminal domain; **PDBTitle:** crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
70	c3cu5B_	Alignment	not modelled	16.5	7	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**two component transcriptional regulator, arac family; **PDBTitle:** crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg
71	c3rfoA_	Alignment	not modelled	15.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** crystal structure of methyionyl-trna formyltransferase from bacillus2 anthracis
72	c1keeH_	Alignment	not modelled	15.6	23	**PDB header:**ligase **Chain:** H: **PDB Molecule:**carbamoyl-phosphate synthetase small chain; **PDBTitle:** inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
73	d1fmfa_	Alignment	not modelled	15.2	16	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
74	c2gm2A_	Alignment	not modelled	15.1	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** nmr structure of xanthomonas campestris xcc1710: northeast2 structural genomics consortium target xcr35
75	c2okxB_	Alignment	not modelled	15.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rhamnosidase b; **PDBTitle:** crystal structure of gh78 family rhamnosidase of bacillus sp. gl1 at2 1.9 a
76	c3nrbD_	Alignment	not modelled	15.0	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
77	d2q4ga1	Alignment	not modelled	14.9	6	**Fold:**MTH938-like **Superfamily:**MTH938-like

						Family:MTH938-like
78	c1zghA_	Alignment	not modelled	14.6	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** methionyl-trna formyltransferase from clostridium thermocellum
79	c3n0vD_	Alignment	not modelled	14.2	14	**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
80	d2fiua1	Alignment	not modelled	13.4	12	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Atu0297-like
81	d1b26a1	Alignment	not modelled	13.3	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
82	d2ji7a1	Alignment	not modelled	12.5	9	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
83	c1bmtB_	Alignment	not modelled	12.2	14	**PDB header:**methyltransferase **Chain:** B: **PDB Molecule:**methionine synthase; **PDBTitle:** how a protein binds b12: a 3.o angstrom x-ray structure of2 the b12-binding domains of methionine synthase
84	c2ps3A_	Alignment	not modelled	12.0	10	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**high-affinity zinc uptake system protein znua; **PDBTitle:** structure and metal binding properties of znua, a2 periplasmic zinc transporter from escherichia coli
85	c3gg9C_	Alignment	not modelled	11.9	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase oxidoreductase protein; **PDBTitle:** crystal structure of putative d-3-phosphoglycerate dehydrogenase2 oxidoreductase from ralstonia solanacearum
86	c3aogA_	Alignment	not modelled	11.8	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** crystal structure of glutamate dehydrogenase (gdhb) from thermus2 thermophilus (glu bound form)
87	d1pq4a_	Alignment	not modelled	11.7	13	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
88	d2cyja1	Alignment	not modelled	10.9	15	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
89	c3dcjA_	Alignment	not modelled	10.7	22	**PDB header:**transferase **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
90	c2zwrA_	Alignment	not modelled	10.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallo-beta-lactamase superfamily protein; **PDBTitle:** crystal structure of ttha1623 from thermus thermophilus hb8
91	c1y80A_	Alignment	not modelled	9.6	11	**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
92	c2j6iC_	Alignment	not modelled	9.6	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
93	c3chgB_	Alignment	not modelled	9.1	20	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**glycine betaine-binding protein; **PDBTitle:** the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
94	c3l4eA_	Alignment	not modelled	9.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized peptidase lmo0363; **PDBTitle:** 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
95	c2w2kB_	Alignment	not modelled	9.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**d-mandelate dehydrogenase; **PDBTitle:** crystal structure of the apo forms of rhodotorula graminis2 d-mandelate dehydrogenase at 1.8a.
96	d1ihna_	Alignment	not modelled	9.0	40	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
97	c2dzdB_	Alignment	not modelled	8.8	10	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of the biotin carboxylase domain of2 pyruvate carboxylase
98	c3cihA_	Alignment	not modelled	8.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alpha-rhamnosidase; **PDBTitle:** crystal structure of a putative alpha-rhamnosidase from2 bacteroides thetaiotaomicron
99	d2a9pa1	Alignment	not modelled	8.6	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related