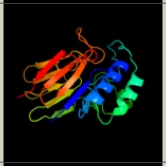
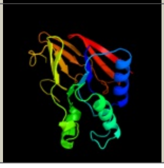
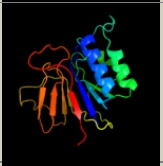
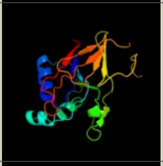
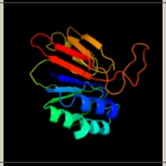
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P67095
Date	Wed Jan 25 15:21:00 GMT 2012
Unique Job ID	09d47189529791cd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1su1A_	Alignment		100.0	99	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yfce; **PDBTitle:** structural and biochemical characterization of yfce, a2 phosphoesterase from e. coli
2	d1su1a_	Alignment		100.0	99	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
3	d1s3la_	Alignment		100.0	27	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
4	c1s3mA_	Alignment		100.0	27	**PDB header:**phosphodiesterase **Chain:** A: **PDB Molecule:**hypothetical protein mj0936; **PDBTitle:** structural and functional characterization of a novel2 archaeal phosphodiesterase
5	d2a22a1	Alignment		100.0	22	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
6	d3ck2a1	Alignment		100.0	26	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
7	d1z2wa1	Alignment		100.0	25	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
8	c2kknA_	Alignment		100.0	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of themotoga maritima protein tm1076:2 northeast structural genomics consortium target vt57
9	c3rqzC_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**metallophosphoesterase; **PDBTitle:** crystal structure of metallophosphoesterase from sphaerobacter2 thermophilus
10	c3qfnA_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
11	d1nnwa_	Alignment		100.0	23	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Phosphoesterase-related

12	d1uf3a_	Alignment		99.9	23	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
13	d2yvta1	Alignment		99.9	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
14	c3av0A_	Alignment		99.9	17	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11-rad50 bound to atp s
15	d1g5ba_	Alignment		99.9	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
16	c3auzA_	Alignment		99.9	20	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11 with manganese
17	d1ii7a_	Alignment		99.9	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DNA double-strand break repair nuclease
18	c2q8uA_	Alignment		99.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exonuclease, putative; **PDBTitle:** crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
19	c3ib7A_	Alignment		99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**icc protein; **PDBTitle:** crystal structure of full length rv0805
20	d1xm7a_	Alignment		99.8	21	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Hypothetical protein aq 1666
21	d3d03a1	Alignment	not modelled	99.8	22	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**GpdQ-like
22	c3qg5D_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mre11; **PDBTitle:** the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
23	c3t1iC_	Alignment	not modelled	99.8	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**double-strand break repair protein mre11a; **PDBTitle:** crystal structure of human mre11: understanding tumorigenic mutations
24	c2qjcA_	Alignment	not modelled	99.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diadenosine tetraphosphatase, putative; **PDBTitle:** crystal structure of a putative diadenosine tetraphosphatase
25	c3rl4A_	Alignment	not modelled	99.7	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallophosphoesterase mpped2; **PDBTitle:** rat metallophosphodiesterase mpped2 g252h mutant
26	d2hy1a1	Alignment	not modelled	99.7	17	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**GpdQ-like
27	c2hy1A_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rv0805; **PDBTitle:** crystal structure of rv0805
28	c2dfjA_	Alignment	not modelled	99.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diadenosinetetraphosphatase; **PDBTitle:** crystal structure of the diadenosine tetraphosphate2 hydrolase from shigella flexneri 2a

29	c2zbmA_	Alignment	not modelled	99.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein-tyrosine-phosphatase; **PDBTitle:** crystal structure of i115m mutant cold-active protein2 tyrosine phosphatase
30	d2nxfa1	Alignment	not modelled	99.6	21	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**ADPRibase-Mn-like
31	c2xmoB_	Alignment	not modelled	99.6	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2642 protein; **PDBTitle:** the crystal structure of lmo2642
32	d3c5wc1	Alignment	not modelled	99.5	23	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
33	d1qhwa_	Alignment	not modelled	99.5	17	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
34	c1qhwA_	Alignment	not modelled	99.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (purple acid phosphatase); **PDBTitle:** purple acid phosphatase from rat bone
35	d1utea_	Alignment	not modelled	99.5	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
36	d1jk7a_	Alignment	not modelled	99.4	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
37	c2jogA_	Alignment	not modelled	99.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**calmodulin-dependent calcineurin a subunit alpha **PDBTitle:** structure of the calcineurin-nfat complex
38	d1auia_	Alignment	not modelled	99.4	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
39	c1auiA_	Alignment	not modelled	99.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine/threonine phosphatase 2b; **PDBTitle:** human calcineurin heterodimer
40	d1s95a_	Alignment	not modelled	99.4	23	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
41	c2p6bC_	Alignment	not modelled	99.3	20	**PDB header:**hydrolase/hydrolase regulator **Chain:** C: **PDB Molecule:**calmodulin-dependent calcineurin a subunit alpha **PDBTitle:** crystal structure of human calcineurin in complex with2 pvivit peptide
42	c1wao4_	Alignment	not modelled	99.3	23	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**serine/threonine protein phosphatase 5; **PDBTitle:** pp5 structure
43	d2p6ba1	Alignment	not modelled	99.3	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
44	d1xzwa2	Alignment	not modelled	99.3	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
45	d1s70a_	Alignment	not modelled	99.3	21	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
46	c1oidA_	Alignment	not modelled	99.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein usha; **PDBTitle:** 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c)
47	c3qfkA_	Alignment	not modelled	99.3	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** 2.05 angstrom crystal structure of putative 5'-nucleotidase from2 staphylococcus aureus in complex with alpha-ketoglutarate
48	d2z1aa2	Alignment	not modelled	99.3	22	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
49	c2z1aA_	Alignment	not modelled	99.2	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-nucleotidase; **PDBTitle:** crystal structure of 5'-nucleotidase precursor from thermus2 thermophilus hb8
50	d1usha2	Alignment	not modelled	99.2	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
51	c3icfB_	Alignment	not modelled	99.2	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine/threonine-protein phosphatase t; **PDBTitle:** structure of protein serine/threonine phosphatase from saccharomyces2 cerevisiae with similarity to human phosphatase pp5
52	d2qfra2	Alignment	not modelled	99.1	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
53	c2wdfA_	Alignment	not modelled	99.1	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sulfur oxidation protein soxb; **PDBTitle:** termus thermophilus sulfate thiohydrolase soxb
54	c3ivdA_	Alignment	not modelled	99.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleotidase; **PDBTitle:** putative 5'-nucleotidase (c4898) from escherichia coli in2 complex with uridine
						PDB header:hydrolase

55	c3zu0A_	Alignment	not modelled	99.0	17	**Chain:** A: **PDB Molecule:**nad nucleotidase; **PDBTitle:** structure of haemophilus influenzae nad nucleotidase (nadn)
56	c3e0jG_	Alignment	not modelled	98.9	14	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna polymerase subunit delta-2; **PDBTitle:** x-ray structure of the complex of regulatory subunits of2 human dna polymerase delta
57	d2z06a1	Alignment	not modelled	98.8	18	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TTHA0625-like
58	c3floG_	Alignment	not modelled	98.8	14	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna polymerase alpha subunit b; **PDBTitle:** crystal structure of the carboxyl-terminal domain of yeast2 dna polymerase alpha in complex with its b subunit
59	d1t71a_	Alignment	not modelled	98.7	21	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DR1281-like
60	d1t70a_	Alignment	not modelled	98.7	19	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DR1281-like
61	d3c9fa2	Alignment	not modelled	98.6	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
62	c1kbpB_	Alignment	not modelled	98.6	18	**PDB header:**hydrolase (phosphoric monoester) **Chain:** B: **PDB Molecule:**purple acid phosphatase; **PDBTitle:** kidney bean purple acid phosphatase
63	c3jyfB_	Alignment	not modelled	98.6	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**2',3'-cyclic nucleotide 2'-phosphodiesterase/3'- **PDBTitle:** the crystal structure of a 2,3-cyclic nucleotide 2-2 phosphodiesterase/3-nucleotidase bifunctional periplasmic precursor3 protein from klebsiella pneumoniae subsp. pneumoniae mgh 78578
64	c3gveB_	Alignment	not modelled	98.6	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yfkn protein; **PDBTitle:** crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
65	c1xzwB_	Alignment	not modelled	98.6	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**purple acid phosphatase; **PDBTitle:** sweet potato purple acid phosphatase/phosphate complex
66	c3c9fB_	Alignment	not modelled	98.2	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**5'-nucleotidase; **PDBTitle:** crystal structure of 5'-nucleotidase from candida albicans sc5314
67	d2nv0a1	Alignment	not modelled	86.8	12	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
68	d1o98a1	Alignment	not modelled	86.6	18	**Fold:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Superfamily:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
69	c2issF_	Alignment	not modelled	81.4	13	**PDB header:**lyase, transferase **Chain:** F: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** structure of the plp synthase holoenzyme from thermotoga maritima
70	c3dnfB_	Alignment	not modelled	77.3	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate reductase; **PDBTitle:** structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
71	d1gg4a1	Alignment	not modelled	71.6	12	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
72	c1o98A_	Alignment	not modelled	68.7	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
73	c3dlaD_	Alignment	not modelled	60.9	12	**PDB header:**ligase **Chain:** D: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
74	c1gshA_	Alignment	not modelled	60.2	21	**PDB header:**glutathione biosynthesis ligase **Chain:** A: **PDB Molecule:**glutathione biosynthetic ligase; **PDBTitle:** structure of escherichia coli glutathione synthetase at ph 7.5
75	c3igzB_	Alignment	not modelled	59.1	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**cofactor-independent phosphoglycerate mutase; **PDBTitle:** crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
76	d1wzca1	Alignment	not modelled	52.3	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
77	c3g13B_	Alignment	not modelled	51.9	9	**PDB header:**recombination **Chain:** B: **PDB Molecule:**putative conjugative transposon recombinase; **PDBTitle:** crystal structure of putative conjugative transposon recombinase from2 clostridium difficile
78	c1b74A_	Alignment	not modelled	49.4	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** glutamate racemase from aquifex pyrophilus

79	d1gsoa2	Alignment	not modelled	46.6	22	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
80	d1j31a_	Alignment	not modelled	40.0	15	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Carbamilase
81	c3n05B_	Alignment	not modelled	37.9	30	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
82	d1rlma_	Alignment	not modelled	37.5	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
83	c3dqqB_	Alignment	not modelled	36.0	33	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative trna synthase; **PDBTitle:** the crystal structure of the putative trna synthase from salmonella2 typhimurium lt2
84	c3hkxA_	Alignment	not modelled	34.8	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidase; **PDBTitle:** crystal structure analysis of an amidase from nesterenkonia sp.
85	c3dzcA_	Alignment	not modelled	34.1	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.35 angstrom resolution structure of wecb (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
86	d1rdua_	Alignment	not modelled	33.7	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
87	c2eklA_	Alignment	not modelled	32.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** structure of st1218 protein from sulfolobus tokodaii
88	c3g23A_	Alignment	not modelled	32.2	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ld-carboxypeptidase a; **PDBTitle:** crystal structure of a ld-carboxypeptidase a (saro_1426) from2 novosphingobium aromaticivorans dsm at 1.89 a resolution
89	c2ywjA_	Alignment	not modelled	32.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
90	c3mpoD_	Alignment	not modelled	31.9	29	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted hydrolase of the had superfamily; **PDBTitle:** the crystal structure of a hydrolase from lactobacillus brevis
91	d1b74a1	Alignment	not modelled	29.3	22	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
92	d2a9va1	Alignment	not modelled	29.1	21	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
93	c3c3wB_	Alignment	not modelled	28.7	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two component transcriptional regulatory protein devr; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
94	d1gsaa1	Alignment	not modelled	28.6	21	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Prokaryotic glutathione synthetase, N-terminal domain
95	c2jfzB_	Alignment	not modelled	28.4	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor
96	d1nn4a_	Alignment	not modelled	28.3	19	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
97	c3ke8A_	Alignment	not modelled	28.2	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate **PDBTitle:** crystal structure of isph:hmbpp-complex
98	c3dojA_	Alignment	not modelled	27.9	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase-like protein; **PDBTitle:** structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1)
99	d2z15a1	Alignment	not modelled	27.6	19	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
100	d2blna2	Alignment	not modelled	27.1	17	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
101	c3ilvA_	Alignment	not modelled	26.8	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
102	d1qdlb_	Alignment	not modelled	26.1	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
103	c3t8yA_	Alignment	not modelled	24.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of the response regulator domain of thermotoga2 maritima cheb
104	c2e11B_	Alignment	not modelled	24.6	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hydrolase; **PDBTitle:** the crystal structure of xc1258 from xanthomonas campestris: a cn-2 hydrolase superfamily protein with an arsenic

						adduct in the active3 site
105	c3l7nA_	Alignment	not modelled	24.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of smu.1228c
106	c1gsoA_	Alignment	not modelled	23.6	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**protein (glycinamide ribonucleotide synthetase); **PDBTitle:** glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.
107	c2p6pB_	Alignment	not modelled	23.2	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase; **PDBTitle:** x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
108	d1o1ya_	Alignment	not modelled	21.6	12	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)