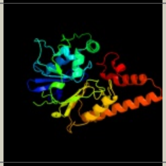
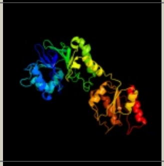
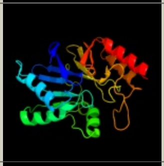
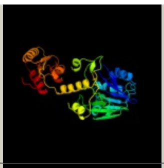
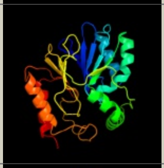
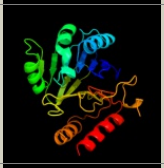
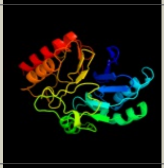
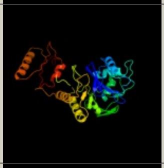
Phyre^{2}

Email	l.a.kelley@imperial.ac.uk
Description	P32717
Date	Thu Jan 5 11:50:40 GMT 2012
Unique Job ID	187506d7713eff93

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2cfuA_	Alignment		100.0	45	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sdsa1; **PDBTitle:** crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
2	d2cfua2	Alignment		100.0	47	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Alkylsulfatase-like
3	d2q0ia1	Alignment		100.0	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**PqsE-like
4	c3spuB_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase ndm-1; **PDBTitle:** apo ndm-1 crystal structure
5	c2zo4A_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallo-beta-lactamase family protein; **PDBTitle:** crystal structure of metallo-beta-lactamase family protein ttha14292 from thermus thermophilus hb8
6	c1ychD_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitric oxide reductase; **PDBTitle:** x-ray crystal structures of moorella thermoacetica fpra.2 novel diiron site structure and mechanistic insights into3 a scavenging nitric oxide reductase
7	c2ohiB_	Alignment		100.0	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**type a flavoprotein fpra; **PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
8	d1jjta_	Alignment		100.0	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
9	d1m2xa_	Alignment		100.0	15	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
10	d1ko3a_	Alignment		100.0	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
11	c3sd9B_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of serratia fonticola sfh-i: source of the2 nucleophile in the catalytic mechanism of mono-zinc metallo-beta-3 lactamases

12	c1e5dA_	Alignment		100.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
13	d1x8ha_	Alignment		100.0	22	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
14	c2q9uB_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
15	c2fhxB_	Alignment		100.0	16	**PDB header:**hydrolase, metal binding protein **Chain:** B: **PDB Molecule:**spm-1; **PDBTitle:** pseudomonas aeruginosa spm-1 metallo-beta-lactamase
16	d1e5da2	Alignment		100.0	18	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
17	c3rkjA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase ndm-1; **PDBTitle:** crystal structure of new delhi metallo-beta-lactamase-1 from2 klebsiella pnueumoniae
18	d1znba_	Alignment		100.0	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
19	c1vmeB_	Alignment		100.0	20	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
20	d1mqoa_	Alignment		100.0	14	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
21	c2yz3B_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**metallo-beta-lactamase; **PDBTitle:** crystallographic investigation of inhibition mode of the2 vim-2 metallo-beta-lactamase from pseudomonas aeruginosa3 with mercaptocarboxylate inhibitor
22	c3l6nA_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallo-beta-lactamase; **PDBTitle:** crystal structure of metallo-beta-lactamase ind-7
23	d2cfua1	Alignment	not modelled	100.0	36	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**Alkylsulfatase C-terminal domain-like
24	d2gmna1	Alignment	not modelled	99.9	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
25	d2aioa1	Alignment	not modelled	99.9	20	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
26	c3lvzA_	Alignment	not modelled	99.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**blr6230 protein; **PDBTitle:** new refinement of the crystal structure of bjp-1, a subclass b32 metallo-beta-lactamase of bradyrhizobium japonicum
27	c3hnnD_	Alignment	not modelled	99.9	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**putative diflavin flavoprotein a 5; **PDBTitle:** crystal structure of putative diflavin flavoprotein a 5 (fragment 1-2 254) from nostoc sp. pcc 7120, northeast structural genomics3 consortium target nsr435a
28	d1k07a_	Alignment	not modelled	99.9	14	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase

29	d1ycga2	Alignment	not modelled	99.9	19	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
30	c3adrA_	Alignment	not modelled	99.9	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein st1585; **PDBTitle:** the first crystal structure of an archaeal metallo-beta-lactamase2 superfamily protein; st1585 from sulfolobus tokodaii
31	d1vmea2	Alignment	not modelled	99.9	26	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
32	d1xm8a_	Alignment	not modelled	99.9	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
33	c3aj3A_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**4-pyridoxolactonase; **PDBTitle:** crystal structure of selenomethionine substituted 4-pyridoxolactonase2 from mesorhizobium loti
34	d2qeda1	Alignment	not modelled	99.8	19	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
35	c3r2uC_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**metallo-beta-lactamase family protein; **PDBTitle:** 2.1 angstrom resolution crystal structure of metallo-beta-lactamase2 from staphylococcus aureus subsp. aureus col
36	c2r2dC_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**zn-dependent hydrolases; **PDBTitle:** structure of a quorum-quenching lactonase (aiib) from agrobacterium2 tumefaciens
37	c2zwrA_	Alignment	not modelled	99.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallo-beta-lactamase superfamily protein; **PDBTitle:** crystal structure of ttha1623 from thermus thermophilus hb8
38	d2p97a1	Alignment	not modelled	99.8	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Ava3068-like
39	d1qh5a_	Alignment	not modelled	99.8	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
40	c2xf4A_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydroxyacylglutathione hydrolase; **PDBTitle:** crystal structure of salmonella enterica serovar2 typhimurium ycbl
41	c2gcuD_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative hydroxyacylglutathione hydrolase 3; **PDBTitle:** x-ray structure of gene product from arabidopsis thaliana2 at1g53580
42	c3tp9B_	Alignment	not modelled	99.8	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase and rhodanese domain protein; **PDBTitle:** crystal structure of alicyclobacillus acidocaldarius protein with2 beta-lactamase and rhodanese domains
43	c3eshB_	Alignment	not modelled	99.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein similar to metal-dependent hydrolase; **PDBTitle:** crystal structure of a probable metal-dependent hydrolase2 from staphylococcus aureus. northeast structural genomics3 target zr314
44	c2p18A_	Alignment	not modelled	99.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glyoxalase ii; **PDBTitle:** crystal structure of the leishmania infantum glyoxalase ii
45	c2br6A_	Alignment	not modelled	99.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aiia-like protein; **PDBTitle:** crystal structure of quorum-quenching n-acyl homoserine2 lactone lactonase
46	c1p9eA_	Alignment	not modelled	99.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methyl parathion hydrolase; **PDBTitle:** crystal structure analysis of methyl parathion hydrolase from2 pseudomonas sp wbc-3
47	d1p9ea_	Alignment	not modelled	99.7	14	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Methyl parathion hydrolase
48	c2p4zA_	Alignment	not modelled	99.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metal-dependent hydrolases of the beta-lactamase **PDBTitle:** a ferredoxin-like metallo-beta-lactamase superfamily protein from2 thermoanaerobacter tengcongensis
49	d1ztca1	Alignment	not modelled	99.5	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**TM0894-like
50	c3h3eA_	Alignment	not modelled	99.4	15	**PDB header:**structural genomics, metal binding prote **Chain:** A: **PDB Molecule:**uncharacterized protein tm1679; **PDBTitle:** crystal structure of tm1679, a metal-dependent hydrolase of2 the beta-lactamase superfamily
51	c3bdqB_	Alignment	not modelled	99.4	16	**PDB header:**lipid transport **Chain:** B: **PDB Molecule:**sterol carrier protein 2-like 2; **PDBTitle:** room tempreture crystal structure of sterol carrier protein-2 2 like-2
52	c3zq4C_	Alignment	not modelled	99.3	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ribonuclease j 1; **PDBTitle:** unusual, dual endo- and exo-nuclease activity in the degradosome2 explained by crystal structure analysis of rnase j1
53	d1ikta_	Alignment	not modelled	99.3	16	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**Sterol carrier protein, SCP

54	d1c44a_	Alignment	not modelled	99.2	16	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**Sterol carrier protein, SCP
55	c3bk2A_	Alignment	not modelled	99.2	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metal dependent hydrolase; **PDBTitle:** crystal structure analysis of the rnase j/ump complex
56	d2i7ta1	Alignment	not modelled	99.1	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
57	c2az4A_	Alignment	not modelled	99.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ef2904; **PDBTitle:** crystal structure of a protein of unknown function from enterococcus2 faecalis v583
58	d1pz4a_	Alignment	not modelled	99.1	14	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**Sterol carrier protein, SCP
59	c1zkpD_	Alignment	not modelled	99.1	14	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein ba1088; **PDBTitle:** 1.5a resolution crystal structure of a metallo beta lactamase family2 protein, the elac homolgue of bacillus anthracis, a putative3 ribonuclease
60	d2dkfa1	Alignment	not modelled	99.0	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
61	d2az4a1	Alignment	not modelled	99.0	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
62	c3g1pA_	Alignment	not modelled	99.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**protein phnp; **PDBTitle:** crystals structure of phnp from e.coli k-12
63	c3bn8A_	Alignment	not modelled	98.9	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative sterol carrier protein 2; **PDBTitle:** crystal structure of a putative sterol carrier protein type 2 (af1534)2 from archaeoglobus fulgidus dsm 4304 at 2.11 a resolution
64	c3af5A_	Alignment	not modelled	98.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1404; **PDBTitle:** the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii
65	d1zkpa1	Alignment	not modelled	98.9	15	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**YhfI-like
66	c3zwfA_	Alignment	not modelled	98.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc phosphodiesterase elac protein 1; **PDBTitle:** crystal structure of human trnase z, short form (elac1).
67	c2bibA_	Alignment	not modelled	98.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**teichoic acid phosphorylcholine esterase/ choline binding **PDBTitle:** crystal structure of the complete modular teichioic acid2 phosphorylcholine esterase pce (cbpe) from streptococcus3 pneumoniae
68	d1y44a1	Alignment	not modelled	98.8	15	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**RNase Z-like
69	c3kl7A_	Alignment	not modelled	98.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative metal-dependent hydrolase; **PDBTitle:** crystal structure of putative metal-dependent hydrolase2 (yp_001302908.1) from parabacteroides distasonis atcc 8503 at 2.30 a3 resolution
70	c2ycbA_	Alignment	not modelled	98.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cleavage and polyadenylation specificity factor; **PDBTitle:** structure of the archaeal beta-casp protein with n-terminal2 kh domains from methanothermobacter thermautotrophicus
71	c2xr1A_	Alignment	not modelled	98.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cleavage and polyadenylation specificity factor 100 kd **PDBTitle:** dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
72	d2e7ya1	Alignment	not modelled	98.7	12	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**RNase Z-like
73	c3md7A_	Alignment	not modelled	98.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase-like; **PDBTitle:** crystal structure of a beta-lactamase-like protein bound to gmp from2 brucella melitensis
74	c2xr1B_	Alignment	not modelled	98.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cleavage and polyadenylation specificity factor 100 kd **PDBTitle:** dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
75	d1wraa1	Alignment	not modelled	98.6	13	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Pce catalytic domain-like
76	d2cbna1	Alignment	not modelled	98.5	13	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**RNase Z-like
77	c3bkrA_	Alignment	not modelled	98.4	21	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**sterol carrier protein-2 like-3; **PDBTitle:** crystal structure of sterol carrier protein-2 like-3 (scp2-2 l3) from aedes aegypti

78	c2wylF_	Alignment	not modelled	98.4	15	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**l-ascorbate-6-phosphate lactonase ulag; **PDBTitle:** apo structure of a metallo-b-lactamase
79	d2i7xa1	Alignment	not modelled	98.3	14	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
80	c2i7xA_	Alignment	not modelled	98.3	14	**PDB header:**rna binding protein, protein binding **Chain:** A: **PDB Molecule:**protein cft2; **PDBTitle:** structure of yeast cpsf-100 (ydh1p)
81	c3bv6D_	Alignment	not modelled	98.1	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**metal-dependent hydrolase; **PDBTitle:** crystal structure of uncharacterized metallo protein from vibrio2 cholerae with beta-lactamase like fold
82	d1xtoa_	Alignment	not modelled	98.1	14	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Coenzyme PQQ synthesis protein B, PqqB
83	d1vjna_	Alignment	not modelled	98.0	24	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Hypothetical protein TM0207
84	c3rpcD_	Alignment	not modelled	97.6	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**possible metal-dependent hydrolase; **PDBTitle:** the crystal structure of a possible metal-dependent hydrolase from2 veillonella parvula dsm 2008
85	d1wfra_	Alignment	not modelled	97.5	16	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**Sterol carrier protein, SCP
86	d2ozga1	Alignment	not modelled	96.6	13	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**EF1021 C-terminal domain-like
87	c3r1kA_	Alignment	not modelled	96.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**enhanced intracellular survival protein; **PDBTitle:** crystal structure of acetyltransferase eis from mycobacterium2 tuberculosis h37rv in complex with coa and an acetamide moiety
88	c2ozgA_	Alignment	not modelled	95.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gcn5-related n-acetyltransferase; **PDBTitle:** crystal structure of gcn5-related n-acetyltransferase (yp_325469.1)2 from anabaena variabilis atcc 29413 at 2.00 a resolution
89	d2hv2a1	Alignment	not modelled	95.5	10	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**EF1021 C-terminal domain-like
90	d2i00a1	Alignment	not modelled	95.2	10	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**EF1021 C-terminal domain-like
91	c3n7zD_	Alignment	not modelled	95.2	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyltransferase, gnat family; **PDBTitle:** crystal structure of acetyltransferase from bacillus anthracis
92	c2hv2D_	Alignment	not modelled	94.5	10	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of conserved protein of unknown function from2 enterococcus faecalis v583 at 2.4 a resolution, probable n-3 acyltransferase
93	c2i00D_	Alignment	not modelled	94.5	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyltransferase, gnat family; **PDBTitle:** crystal structure of acetyltransferase (gnat family) from enterococcus2 faecalis
94	d1y8ma1	Alignment	not modelled	93.3	10	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
95	d1pc2a_	Alignment	not modelled	93.2	16	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
96	d1iyga_	Alignment	not modelled	92.7	16	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
97	d2pqrb1	Alignment	not modelled	92.5	10	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
98	c2r5sB_	Alignment	not modelled	92.4	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein vp0806; **PDBTitle:** the crystal structure of a domain of protein vp0806 (unknown function)2 from vibrio parahaemolyticus rimd 2210633
99	d1nzna_	Alignment	not modelled	92.2	17	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
100	c3hymB_	Alignment	not modelled	91.9	16	**PDB header:**cell cycle, ligase **Chain:** B: **PDB Molecule:**cell division cycle protein 16 homolog; **PDBTitle:** insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure
101	c2y4tA_	Alignment	not modelled	91.6	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 3; **PDBTitle:** crystal structure of the human co-chaperone p58(ipk)
102	c1wao4_	Alignment	not modelled	91.5	16	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**serine/threonine protein phosphatase 5; **PDBTitle:** pp5 structure
103	c3qdnA_	Alignment	not modelled	91.2	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin protein; **PDBTitle:** putative thioredoxin protein from salmonella typhimurium
						PDB header:chaperone

104	c3iegB_	Alignment	not modelled	91.2	14	**Chain:** B: **PDB Molecule:**dnaj homolog subfamily c member 3; **PDBTitle:** crystal structure of p58(ipk) tpr domain at 2.5 a
105	c2kc7A_	Alignment	not modelled	90.6	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bfr218_protein; **PDBTitle:** solution nmr structure of bacteroides fragilis protein2 bf1650. northeast structural genomics consortium target3 bfr218
106	c2owyB_	Alignment	not modelled	90.1	15	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**recombination-associated protein rdgc; **PDBTitle:** the recombination-associated protein rdgc adopts a novel toroidal2 architecture for dna binding
107	c2owlA_	Alignment	not modelled	89.9	21	**PDB header:**recombination **Chain:** A: **PDB Molecule:**recombination-associated protein rdgc; **PDBTitle:** crystal structure of e. coli rdgc
108	d1w3ba_	Alignment	not modelled	89.0	17	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
109	c1na3A_	Alignment	not modelled	88.9	25	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein ctpr2; **PDBTitle:** design of stable alpha-helical arrays from an idealized tpr2 motif
110	c2l6jA_	Alignment	not modelled	88.8	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tpr repeat-containing protein associated with hsp90; **PDBTitle:** tah1 complexed by meevd
111	c2ff4B_	Alignment	not modelled	88.4	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable regulatory protein embr; **PDBTitle:** mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide
112	d2ff4a2	Alignment	not modelled	88.2	9	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**BTAD-like
113	c3fp4A_	Alignment	not modelled	87.6	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tpr repeat-containing protein yhr117w; **PDBTitle:** crystal structure of tom71 complexed with ssa1 c-terminal2 fragment
114	d1fcha_	Alignment	not modelled	87.3	10	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
115	c2k49A_	Alignment	not modelled	87.3	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0339 protein so_3888; **PDBTitle:** solution nmr structure of upf0339 protein so3888 from shewanella2 oneidensis. northeast structural genomics consortium target sor190
116	c3cvpA_	Alignment	not modelled	87.2	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**peroxisome targeting signal 1 receptor pex5; **PDBTitle:** structure of peroxisomal targeting signal 1 (pts1) binding2 domain of trypanosoma brucei peroxin 5 (tbpex5)complexed3 to pts1 peptide (10-skl)
117	c2xcbA_	Alignment	not modelled	85.8	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**regulatory protein pcrh; **PDBTitle:** crystal structure of pcrh in complex with the chaperone2 binding region of popd
118	c3qkyA_	Alignment	not modelled	85.5	22	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane assembly lipoprotein yfio; **PDBTitle:** crystal structure of rhodothermus marinus bamd
119	d1zbpa1	Alignment	not modelled	84.7	24	**Fold:**ImpE-like **Superfamily:**ImpE-like **Family:**ImpE-like
120	c1fchB_	Alignment	not modelled	84.6	10	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**peroxisomal targeting signal 1 receptor; **PDBTitle:** crystal structure of the pts1 complexed to the tpr region2 of human pex5