Phyre^2

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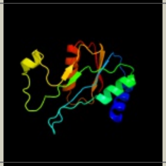
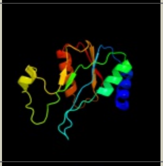
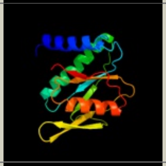
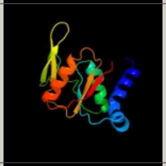
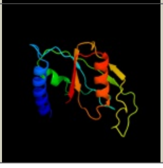
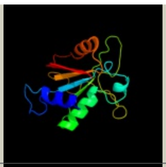
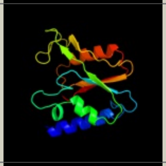
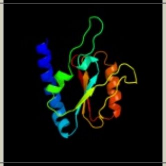
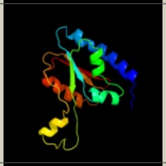
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ecfa1	Alignment		99.8	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
2	c1ecjB_	Alignment		99.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
3	d1gph11	Alignment		99.7	22	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
4	c1gph1_	Alignment		99.7	22	**PDB header:**transferase(glutamine amidotransferase) **Chain:** 1: **PDB Molecule:**glutamine phosphoribosyl-pyrophosphate amidotransferase; **PDBTitle:** structure of the allosteric regulatory enzyme of purine biosynthesis
5	d1wd5a_	Alignment		99.6	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
6	d1g2qa_	Alignment		99.5	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
7	d1zn7a1	Alignment		99.5	26	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
8	d1vcha1	Alignment		99.4	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
9	d1a3ca_	Alignment		99.4	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
10	c2dy0A_	Alignment		99.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenine phosphoribosyltransferase; **PDBTitle:** crystal structure of project jw0458 from escherichia coli
11	c3kb8A_	Alignment		99.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine phosphoribosyltransferase; **PDBTitle:** 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp

12	d1w30a_	Alignment		99.3	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
13	d1tc1a_	Alignment		99.3	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
14	d1yfza1	Alignment		99.3	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
15	c1yfzA_	Alignment		99.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis
16	d1j7ja_	Alignment		99.3	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
17	d1vdma1	Alignment		99.3	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
18	d1mzva_	Alignment		99.3	22	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
19	d1o57a2	Alignment		99.2	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
20	d1g9sa_	Alignment		99.2	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
21	d2igba1	Alignment	not modelled	99.2	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
22	c2wnsB_	Alignment	not modelled	99.2	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** human orotate phosphoribosyltransferase (oprtase) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
23	d1p17b_	Alignment	not modelled	99.2	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
24	d1ufra_	Alignment	not modelled	99.2	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
25	d1hgxa_	Alignment	not modelled	99.2	22	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
26	c1o57A_	Alignment	not modelled	99.2	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**pur operon repressor; **PDBTitle:** crystal structure of the purine operon repressor of2 bacillus subtilis
27	d1y0ba1	Alignment	not modelled	99.2	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
28	c3o7mD_	Alignment	not modelled	99.2	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypoxanthine phosphoribosyltransferase; **PDBTitle:** 1.98 angstrom resolution crystal structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-2) from

						bacillus anthracis str. 'ames3 ancestor'
29	d1pzma_	Alignment	not modelled	99.1	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
30	c3dezA_	Alignment	not modelled	99.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** crystal structure of orotate phosphoribosyltransferase from2 streptococcus mutans
31	c1pzmB_	Alignment	not modelled	99.1	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** crystal structure of hgprt-ase from leishmania tarentolae in complex2 with gmp
32	d2aeea1	Alignment	not modelled	99.1	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
33	c2ywtA_	Alignment	not modelled	99.1	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** crystal structure of hypoxanthine-guanine2 phosphoribosyltransferase with gmp from thermus3 thermophilus hb8
34	d1l1qa_	Alignment	not modelled	99.1	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
35	c3mjdA_	Alignment	not modelled	99.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.9 angstrom crystal structure of orotate2 phosphoribosyltransferase (pyre) francisella tularensis.
36	d1z7ga1	Alignment	not modelled	99.1	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
37	c2p1zA_	Alignment	not modelled	99.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosyltransferase; **PDBTitle:** crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae
38	d1lh0a_	Alignment	not modelled	99.0	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
39	c3efhB_	Alignment	not modelled	99.0	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase 1; **PDBTitle:** crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
40	c2yzkC_	Alignment	not modelled	99.0	24	**PDB header:**transferase **Chain:** C: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** crystal structure of orotate phosphoribosyltransferase from2 aeropyrum pernix
41	d1cjba_	Alignment	not modelled	98.9	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
42	c2c4kD_	Alignment	not modelled	98.9	21	**PDB header:**regulatory protein **Chain:** D: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase- **PDBTitle:** crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
43	d1qb7a_	Alignment	not modelled	98.9	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
44	d1dkua2	Alignment	not modelled	98.9	24	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
45	c3lpnB_	Alignment	not modelled	98.9	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** crystal structure of the phosphoribosylpyrophosphate (prpp) synthetase2 from thermoplasma volcanium in complex with an atp analog (ampcpp).
46	c3m3hA_	Alignment	not modelled	98.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.75 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase from bacillus anthracis str. 'ames3 ancestor'
47	d1u9ya2	Alignment	not modelled	98.9	33	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
48	c3n2lA_	Alignment	not modelled	98.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 2.1 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase (pyre) from vibrio cholerae o1 biovar eltor3 str. n16961
49	c2przB_	Alignment	not modelled	98.8	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**orotate phosphoribosyltransferase 1; **PDBTitle:** s. cerevisiae orotate phosphoribosyltransferase complexed2 with omp
50	c2jkzB_	Alignment	not modelled	98.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'3 -monophosphate) (orthorhombic crystal form)
51	c1dkrB_	Alignment	not modelled	98.8	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase; **PDBTitle:** crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.

52	d2c4ka2_	Alignment	not modelled	98.8	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
53	d1fsga_	Alignment	not modelled	98.8	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
54	c3qw4B_	Alignment	not modelled	98.7	26	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**ump synthase; **PDBTitle:** structure of leishmania donovani ump synthase
55	c3dahB_	Alignment	not modelled	98.7	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
56	c1u9yD_	Alignment	not modelled	98.6	29	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
57	c2jbhA_	Alignment	not modelled	98.4	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosyltransferase domain-containing protein 1; **PDBTitle:** human phosphoribosyl transferase domain containing 1
58	d1nula_	Alignment	not modelled	98.4	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
59	c2ehjA_	Alignment	not modelled	98.1	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** structure of uracil phosphoribosyl transferase
60	d1i5ea_	Alignment	not modelled	98.1	30	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
61	c2e55D_	Alignment	not modelled	98.0	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** structure of aq2163 protein from aquifex aeolicus
62	d1dqna_	Alignment	not modelled	97.9	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
63	d1o5oa_	Alignment	not modelled	97.9	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
64	d1xtta1	Alignment	not modelled	97.8	12	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
65	c3dmpD_	Alignment	not modelled	97.4	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** 2.6 a crystal structure of uracil phosphoribosyltransferase2 from burkholderia pseudomallei
66	d1v9sa1	Alignment	not modelled	97.4	23	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
67	d1bd3a_	Alignment	not modelled	97.2	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
68	d1u9ya1	Alignment	not modelled	92.7	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
69	d2c4ka1	Alignment	not modelled	90.3	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
70	c2kreA_	Alignment		85.5	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin conjugation factor e4 b; **PDBTitle:** solution structure of e4b/ufd2a u-box domain
71	d1dkua1	Alignment	not modelled	83.4	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
72	c2ko5A_	Alignment		83.3	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ring finger protein z; **PDBTitle:** nmr solution structure of lfv-z
73	c1z6uA_	Alignment	not modelled	75.9	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**np95-like ring finger protein isoform b; **PDBTitle:** np95-like ring finger protein isoform b [homo sapiens]
74	c2csyA_	Alignment	not modelled	72.2	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**zinc finger protein 183-like 1; **PDBTitle:** solution structure of the ring domain of the zinc finger2 protein 183-like 1
75	c2k0aA_	Alignment	not modelled	70.8	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor rds3; **PDBTitle:** 1h, 15n and 13c chemical shift assignments for rds3 protein
76	d1wgma_	Alignment	not modelled	69.4	11	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
						PDB header:apoptosis

77	c2ecyA_	Alignment	not modelled	68.1	19	**Chain:** A: **PDB Molecule:**tnf receptor-associated factor 3; **PDBTitle:** solution structure of the zinc finger, c3hc4 type (ring2 finger)" domain of tnf receptor-associated factor 3
78	d2gmga1	Alignment	not modelled	66.1	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF0610-like
79	c3fl2A_	Alignment	not modelled	65.9	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase uhrf1; **PDBTitle:** crystal structure of the ring domain of the e3 ubiquitin-2 protein ligase uhrf1
80	c2f42A_	Alignment	not modelled	64.8	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**stip1 homology and u-box containing protein 1; **PDBTitle:** dimerization and u-box domains of zebrafish c-terminal of hsp702 interacting protein
81	d1wfga_	Alignment	not modelled	64.6	15	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
82	c3eggC_	Alignment	not modelled	64.1	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**spinophilin; **PDBTitle:** crystal structure of a complex between protein phosphatase 1 alpha2 (pp1) and the pp1 binding and pdz domains of spinophilin
83	c2komA_	Alignment	not modelled	63.5	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning defective 3 homolog; **PDBTitle:** solution structure of humar par-3b pdz2 (residues 451-549)
84	d1wifa_	Alignment	not modelled	62.1	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
85	d1t1ha_	Alignment	not modelled	61.9	16	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
86	c2d8tA_	Alignment	not modelled	61.4	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring finger protein 146; **PDBTitle:** solution structure of the ring domain of the human ring2 finger protein 146
87	d1jm7a_	Alignment	not modelled	61.2	21	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
88	c2djbA_	Alignment	not modelled	61.0	20	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**polycomb group ring finger protein 6; **PDBTitle:** solution structure of the ring domain of the human polycomb2 group ring finger protein 6
89	d1ur6b_	Alignment	not modelled	60.5	43	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
90	c3mmnA_	Alignment	not modelled	60.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidine kinase homolog; **PDBTitle:** crystal structure of the receiver domain of the histidine kinase cki12 from arabidopsis thaliana complexed with mg2+
91	d2fiya1	Alignment	not modelled	59.5	31	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
92	d1miob_	Alignment	not modelled	59.1	14	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
93	c2eciA_	Alignment	not modelled	58.8	23	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 6; **PDBTitle:** solution structure of the ring domain of the human tnf2 receptor-associated factor 6 protein
94	d1dgsa1	Alignment	not modelled	58.5	33	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
95	d2baya1	Alignment	not modelled	57.8	10	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
96	d2cssa1	Alignment	not modelled	56.6	15	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
97	c2y43B_	Alignment	not modelled	56.3	30	**PDB header:**ligase **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase rad18; **PDBTitle:** rad18 ubiquitin ligase ring domain structure
98	c2ecmA_	Alignment	not modelled	56.0	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring finger and chy zinc finger domain- **PDBTitle:** solution structure of the ring domain of the ring finger2 and chy zinc finger domain-containing protein 1 from mus3 musculus
99	c3bvoA_	Alignment	not modelled	55.9	27	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb, mitochondrial precursor; **PDBTitle:** crystal structure of human co-chaperone protein hscb
100	d1e4ua_	Alignment	not modelled	55.4	40	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
101	c2cklA_	Alignment	not modelled	54.7	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polycomb group ring finger protein 4; **PDBTitle:** ring1b-bmi1 e3 catalytic domain structure
102	d1iyma_	Alignment	not modelled	54.3	27	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
						PDB header:protein transport

103	c1nsfA_	Alignment	not modelled	54.1	16	**Chain:** A: **PDB Molecule:**n-ethylmaleimide sensitive factor; **PDBTitle:** d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
104	c2i04B_	Alignment	not modelled	53.7	28	**PDB header:**peptide binding protein **Chain:** B: **PDB Molecule:**membrane-associated guanylate kinase, ww and pdz **PDBTitle:** x-ray crystal structure of magi-1 pdz1 bound to the c-2 terminal peptide of hpv18 e6
105	c2jrpA_	Alignment	not modelled	53.6	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** solution nmr structure of yfgj from salmonella typhimurium2 modeled with two zn+2 bound, northeast structural genomics3 consortium target str86
106	c1u37A_	Alignment	not modelled	53.4	8	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**amyloid beta a4 precursor protein-binding, **PDBTitle:** auto-inhibition mechanism of x11s/mints family scaffold2 proteins revealed by the closed conformation of the tandem3 pdz domains
107	c1u38A_	Alignment	not modelled	53.4	8	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**amyloid beta a4 precursor protein-binding, **PDBTitle:** auto-inhibition mechanism of x11s/mints family scaffold2 proteins revealed by the closed conformation of the tandem3 pdz domains
108	c2opgB_	Alignment	not modelled	52.9	21	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** the crystal structure of the 10th pdz domain of mpdz
109	d1weoa_	Alignment	not modelled	52.3	31	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
110	d1vaea_	Alignment	not modelled	51.9	26	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
111	d2c2vv1	Alignment	not modelled	51.6	9	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
112	d1ueqa_	Alignment	not modelled	49.6	25	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
113	d1rmda2	Alignment	not modelled	49.3	26	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
114	c3tsuA_	Alignment	not modelled	49.3	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
115	d1v6ba_	Alignment	not modelled	49.3	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
116	c2hcuA_	Alignment	not modelled	48.5	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** crystal structure of smu.1381 (or leud) from streptococcus2 mutans
117	d1t2ma1	Alignment	not modelled	48.4	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
118	c2owoA_	Alignment	not modelled	48.3	16	**PDB header:**ligase/dna **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
119	c3grfA_	Alignment	not modelled	48.3	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** x-ray structure of ornithine transcarbamoylase from giardia2 lamblia
120	c2vsvB_	Alignment	not modelled	47.1	21	**PDB header:**protein-binding **Chain:** B: **PDB Molecule:**rhophilin-2; **PDBTitle:** crystal structure of the pdz domain of human rhophilin-2