Phyre^2

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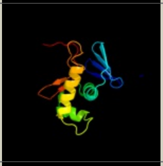
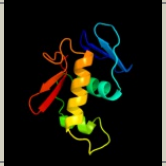
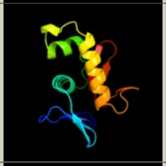
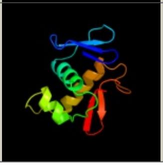
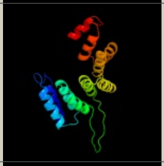
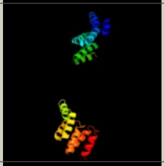
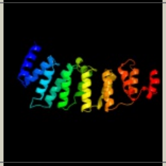
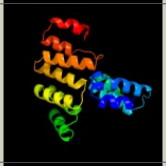
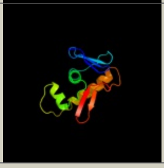
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ly8A_	Alignment		100.0	100	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**transcriptional activator cadc; **PDBTitle:** crystal structure of mutant d471e of the periplasmic domain of cadc
2	c2jzyA_	Alignment		99.9	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein pcor; **PDBTitle:** solution structure of c-terminal effector domain of2 putative two-component-system response regulator involved3 in copper resistance from klebsiella pneumoniae
3	d1opca_	Alignment		99.9	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
4	c2hqnA_	Alignment		99.9	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
5	d1ys7a1	Alignment		99.9	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
6	d1p2fa1	Alignment		99.9	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
7	c2hwvA_	Alignment		99.8	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-binding response regulator vicr; **PDBTitle:** crystal structure of an essential response regulator dna binding2 domain, vicrc in enterococcus faecalis, a member of the yycf3 subfamily.
8	d1gxqa_	Alignment		99.8	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
9	c2pmuD_	Alignment		99.8	24	**PDB header:**transcription regulation **Chain:** D: **PDB Molecule:**response regulator phop; **PDBTitle:** crystal structure of the dna-binding domain of phop
10	c3q9vB_	Alignment		99.8	27	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna-binding response regulator; **PDBTitle:** crystal structure of rra c-terminal domain(123-221) from deinococcus2 radiodurans
11	c2zxjB_	Alignment		99.8	26	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein walr; **PDBTitle:** crystal structure of yycf dna-binding domain from staphylococcus2 aureus

12	d1kgsa1	Alignment		99.8	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
13	c3pe3D_	Alignment		99.8	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine--peptide n- **PDBTitle:** structure of human o-glcnac transferase and its complex with a peptide2 substrate
14	c2k4jA_	Alignment		99.8	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** arsr dna binding domain
15	c2xpiA_	Alignment		99.7	12	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**anaphase-promoting complex subunit cut9; **PDBTitle:** crystal structure of apc/c hetero-tetramer cut9-hcn1
16	d1w3ba_	Alignment		99.7	30	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
17	c3cvpA_	Alignment		99.7	24	**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)
18	d1d8da_	Alignment		99.6	10	**Fold:**alpha-alpha superhelix **Superfamily:**Protein prenylyltransferase **Family:**Protein prenylyltransferase
19	c1fchB_	Alignment		99.6	25	**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
20	c1ys7B_	Alignment		99.6	29	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulatory protein prra; **PDBTitle:** crystal structure of the response regulator protein prra comlexed with2 mg2+
21	c3as5A_	Alignment	not modelled	99.6	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**mama; **PDBTitle:** mama amb-1 p212121
22	c2oqrA_	Alignment	not modelled	99.6	31	**PDB header:**transcription,signaling protein **Chain:** A: **PDB Molecule:**sensory transduction protein regx3; **PDBTitle:** the structure of the response regulator regx3 from mycobacterium2 tuberculosis
23	d2h6fa1	Alignment	not modelled	99.6	11	**Fold:**alpha-alpha superhelix **Superfamily:**Protein prenylyltransferase **Family:**Protein prenylyltransferase
24	c2q7fA_	Alignment	not modelled	99.6	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**yrrb protein; **PDBTitle:** crystal structure of yrrb: a tpr protein with an unusual peptide-2 binding site
25	c1tnol_	Alignment	not modelled	99.6	11	**PDB header:**transferase **Chain:** I: **PDB Molecule:**geranylgeranyltransferase type i alpha subunit; **PDBTitle:** rat protein geranylgeranyltransferase type-i complexed with2 a ggpp analog and a kkksktkcvim peptide derived from k-3 ras4b
26	c2y4tA_	Alignment	not modelled	99.6	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 3; **PDBTitle:** crystal structure of the human co-chaperone p58(ipk)
27	c2pl2A_	Alignment	not modelled	99.6	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**hypothetical conserved protein ttc0263; **PDBTitle:** crystal structure of ttc0263: a thermophilic tpr protein in thermus2 thermophilus hb27
28	c2ho1B_	Alignment	not modelled	99.6	22	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**type 4 fimbrial biogenesis protein pilf; **PDBTitle:** functional characterization of pseudomonas aeruginosa

						pilf
29	d1fcha_	Alignment	not modelled	99.6	26	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
30	d1hh8a_	Alignment	not modelled	99.6	9	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
31	c2vq2A_	Alignment	not modelled	99.6	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**putative fimbrial biogenesis and twitching **PDBTitle:** crystal structure of pilw, widely conserved type iv pilus2 biogenesis factor
32	c3hymB_	Alignment	not modelled	99.6	18	**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
33	c2hqrA_	Alignment	not modelled	99.5	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
34	c3iegB_	Alignment	not modelled	99.5	20	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**dnaj homolog subfamily c member 3; **PDBTitle:** crystal structure of p58(ipk) tpr domain at 2.5 a
35	c2hyzA_	Alignment	not modelled	99.5	18	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**synthetic consensus tpr protein; **PDBTitle:** crystal structure of an 8 repeat consensus tpr superhelix2 (orthorombic crystal form)
36	c3urzB_	Alignment	not modelled	99.5	9	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical protein (bacova_03105) from2 bacteroides ovatus atcc 8483 at 2.19 a resolution
37	d1dcea1	Alignment	not modelled	99.5	6	**Fold:**alpha-alpha superhelix **Superfamily:**Protein prenylyltransferase **Family:**Protein prenylyltransferase
38	c2gwrA_	Alignment	not modelled	99.5	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**dna-binding response regulator mtra; **PDBTitle:** crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
39	c3fp4A_	Alignment	not modelled	99.5	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tpr repeat-containing protein yhr117w; **PDBTitle:** crystal structure of tom71 complexed with ssa1 c-terminal2 fragment
40	d2ff4a1	Alignment	not modelled	99.5	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
41	d1zu2a1	Alignment	not modelled	99.5	9	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
42	c3q75A_	Alignment	not modelled	99.4	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**farnesyltransferase alpha subunit; **PDBTitle:** cryptococcus neoformans protein farnesyltransferase in complex with2 fpt-ii and tkcvvm peptide
43	c2r5sB_	Alignment	not modelled	99.4	14	**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
44	c2e2eA_	Alignment	not modelled	99.4	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**formate-dependent nitrite reductase complex nrfg subunit; **PDBTitle:** tpr domain of nrfg mediates the complex formation between heme lyase2 and formate-dependent nitrite reductase in escherichia coli o157:h7
45	c3gyzB_	Alignment	not modelled	99.4	8	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone protein ipgc; **PDBTitle:** crystal structure of ipgc from shigella flexneri
46	c1wao4_	Alignment	not modelled	99.4	14	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**serine/threonine protein phosphatase 5; **PDBTitle:** pp5 structure
47	d2c2la1	Alignment	not modelled	99.4	11	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
48	c3mv3B_	Alignment	not modelled	99.4	11	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**coatomer subunit epsilon; **PDBTitle:** crystal structure of a-cop in complex with e-cop
49	c3draA_	Alignment	not modelled	99.4	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein **PDBTitle:** candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp
50	c2xcbA_	Alignment	not modelled	99.4	8	**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
51	c2gw1A_	Alignment	not modelled	99.3	9	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**mitochondrial precursor proteins import receptor; **PDBTitle:** crystal structure of the yeast tom70
52	c2c2lD_	Alignment	not modelled	99.3	16	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**carboxy terminus of hsp70-interacting protein; **PDBTitle:** crystal structure of the chip u-box e3 ubiquitin ligase
53	c3sz7A_	Alignment	not modelled	99.3	11	**PDB header:**chaperone regulator **Chain:** A: **PDB Molecule:**hsc70 cochaperone (sgt); **PDBTitle:** crystal structure of the sgt2 tpr domain from aspergillus fumigatus

54	c1p2fA_	Alignment	not modelled	99.3	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure analysis of response regulator drrb, a2 thermotoga maritima ompr/phob homolog
55	c3r0jA_	Alignment	not modelled	99.3	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**possible two component system response transcriptional **PDBTitle:** structure of phop from mycobacterium tuberculosis
56	c2kckA_	Alignment	not modelled	99.3	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tpr repeat; **PDBTitle:** nmr solution structure of the northeast structural genomics2 consortium (nesg) target mrr121a
57	d1a17a_	Alignment	not modelled	99.3	13	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
58	c3mkrA_	Alignment	not modelled	99.3	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**coatomer subunit epsilon; **PDBTitle:** crystal structure of yeast alpha/epsilon-cop subcomplex of the copi2 vesicular coat
59	d1xnfa_	Alignment	not modelled	99.3	12	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
60	c3gw4B_	Alignment	not modelled	99.3	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein from deinococcus2 radiodurans. northeast structural genomics consortium target drr162b.
61	c2uy1A_	Alignment	not modelled	99.3	9	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**cleavage stimulation factor 77; **PDBTitle:** crystal structure of cstf-77
62	d1qsaa1	Alignment	not modelled	99.3	8	**Fold:**alpha-alpha superhelix **Superfamily:**Bacterial muramidases **Family:**Bacterial muramidases
63	c2vyiA_	Alignment	not modelled	99.2	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**sgta protein; **PDBTitle:** crystal structure of the tpr domain of human sgt
64	c1ihgA_	Alignment	not modelled	99.2	7	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**cyclophilin 40; **PDBTitle:** bovine cyclophilin 40, monoclinic form
65	c2vsnB_	Alignment	not modelled	99.2	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**xcogt; **PDBTitle:** structure and topological arrangement of an o-glcnac2 transferase homolog: insight into molecular control of3 intracellular glycosylation
66	d1ihga1	Alignment	not modelled	99.2	6	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
67	d1elwa_	Alignment	not modelled	99.2	15	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
68	d1hz4a_	Alignment	not modelled	99.2	10	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Transcription factor MalT domain III
69	c3qdnA_	Alignment	not modelled	99.2	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin protein; **PDBTitle:** putative thioredoxin protein from salmonella typhimurium
70	c1kt0A_	Alignment	not modelled	99.2	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**51 kda fk506-binding protein; **PDBTitle:** structure of the large fkbp-like protein, fkbp51, involved in steroid2 receptor complexes
71	d2ooea1	Alignment	not modelled	99.2	6	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**HAT/Suf repeat
72	c1kgsA_	Alignment	not modelled	99.2	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna binding response regulator d; **PDBTitle:** crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
73	c3rkvA_	Alignment	not modelled	99.2	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative peptidylprolyl isomerase; **PDBTitle:** c-terminal domain of protein c56c10.10, a putative peptidylprolyl2 isomerase, from caenorhabditis elegans
74	c1ltxA_	Alignment	not modelled	99.1	8	**PDB header:**transferase/protein binding **Chain:** A: **PDB Molecule:**rab geranylgeranyltransferase alpha subunit; **PDBTitle:** structure of rab escort protein-1 in complex with rab2 geranylgeranyl transferase and isoprenoid
75	d1hxia_	Alignment	not modelled	99.1	16	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
76	c2dbaA_	Alignment	not modelled	99.1	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**smooth muscle cell associated protein-1, isoform **PDBTitle:** the solution structure of the tetratrico peptide repeat of2 human smooth muscle cell associated protein-1, isoform 2
77	c2vgxA_	Alignment	not modelled	99.1	10	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone sycd; **PDBTitle:** structure of the yersinia enterocolitica type iii secretion2 translocator chaperone sycd
78	d1zbpa1	Alignment	not modelled	99.1	14	**Fold:**ImpE-like **Superfamily:**ImpE-like **Family:**ImpE-like
79	c2katA_	Alignment	not modelled	99.1	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of protein bpp2914 from bordetella2

						parapertussis. northeast structural genomics consortium3 target bpr206
80	d2buga1	Alignment	not modelled	99.1	13	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
81	c2yhcA_	Alignment	not modelled	99.1	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**upf0169 lipoprotein yfio; **PDBTitle:** structure of bamd from e. coli
82	c3sf4B_	Alignment	not modelled	99.1	22	**PDB header:**signaling protein/protein binding **Chain:** B: **PDB Molecule:**g-protein-signaling modulator 2; **PDBTitle:** crystal structure of the complex between the conserved cell polarity2 proteins inscuteable and lgn
83	c2kcvA_	Alignment	not modelled	99.1	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tetratricopeptide repeat domain protein; **PDBTitle:** solution nmr structure of tetratricopeptide repeat domain2 protein sru_0103 from salinibacter ruber, northeast3 structural genomics consortium (nesg) target srr115c
84	c3q49B_	Alignment	not modelled	99.1	16	**PDB header:**ligase/chaperone **Chain:** B: **PDB Molecule:**stip1 homology and u box-containing protein 1; **PDBTitle:** crystal structure of the tpr domain of chip complexed with hsp70-c2 peptide
85	d1elra_	Alignment	not modelled	99.1	13	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
86	d1p5qa1	Alignment	not modelled	99.0	10	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
87	d1iyga_	Alignment	not modelled	99.0	6	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
88	d1kt1a1	Alignment	not modelled	99.0	8	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
89	c1na3A_	Alignment	not modelled	99.0	20	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein ctpr2; **PDBTitle:** design of stable alpha-helical arrays from an idealized tpr2 motif
90	c2ifuA_	Alignment	not modelled	99.0	8	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**gamma-snap; **PDBTitle:** crystal structure of a gamma-snap from danio rerio
91	c1qz2B_	Alignment	not modelled	99.0	10	**PDB header:**isomerase/chaperone **Chain:** B: **PDB Molecule:**fk506-binding protein 4; **PDBTitle:** crystal structure of fkbp52 c-terminal domain complex with2 the c-terminal peptide meevd of hsp90
92	c2ff4B_	Alignment	not modelled	99.0	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable regulatory protein embr; **PDBTitle:** mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide
93	c3k9iA_	Alignment	not modelled	99.0	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**bh0479 protein; **PDBTitle:** crystal structure of putative protein binding protein (np_241345.1)2 from bacillus halodurans at 2.71 a resolution
94	c2if4A_	Alignment	not modelled	99.0	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**atfkbp42; **PDBTitle:** crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana
95	d1pc2a_	Alignment	not modelled	99.0	8	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
96	d1nzna_	Alignment	not modelled	98.9	9	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
97	c2avpA_	Alignment	not modelled	98.9	23	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**synthetic consensus tpr protein; **PDBTitle:** crystal structure of an 8 repeat consensus tpr superhelix
98	d1qqea_	Alignment	not modelled	98.9	12	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
99	d2fbna1	Alignment	not modelled	98.9	16	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
100	c2fbnA_	Alignment	not modelled	98.9	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**70 kda peptidylprolyl isomerase, putative; **PDBTitle:** plasmodium falciparum putative fk506-binding protein2 pfl2275c, c-terminal tpr-containing domain
101	c3q15A_	Alignment	not modelled	98.9	12	**PDB header:**hydrolase/kinase **Chain:** A: **PDB Molecule:**response regulator aspartate phosphatase h; **PDBTitle:** crystal structure of raph complexed with spo0f
102	d2hr2a1	Alignment	not modelled	98.9	9	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**CT2138-like
103	c3q9sA_	Alignment	not modelled	98.8	27	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding response regulator; **PDBTitle:** crystal structure of rra(1-215) from deinococcus radiodurans
104	c2xevB_	Alignment	not modelled	98.8	12	**PDB header:**metal binding **Chain:** B: **PDB Molecule:**ybgf; **PDBTitle:** crystal structure of the tpr domain of xanthomonas2 campestris ybgf
						Fold:alpha-alpha superhelix

105	d1tjca_	Alignment	not modelled	98.8	12	**Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
106	c3ulqA_	Alignment	not modelled	98.8	12	**PDB header:**gene regulation/transcription activator **Chain:** A: **PDB Molecule:**response regulator aspartate phosphatase f; **PDBTitle:** crystal structure of the anti-activator rapf complexed with the2 response regulator coma dna binding domain
107	c2kc7A_	Alignment	not modelled	98.8	20	**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
108	c3nf1A_	Alignment	not modelled	98.7	24	**PDB header:**motor protein, transport protein **Chain:** A: **PDB Molecule:**kinesin light chain 1; **PDBTitle:** crystal structure of the tpr domain of kinesin light chain 1
109	c3fflC_	Alignment	not modelled	98.7	9	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**anaphase-promoting complex subunit 7; **PDBTitle:** crystal structure of the n-terminal domain of anaphase-2 promoting complex subunit 7
110	c2l6jA_	Alignment	not modelled	98.7	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tpr repeat-containing protein associated with hsp90; **PDBTitle:** tah1 complexed by meevd
111	c3qkyA_	Alignment	not modelled	98.7	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane assembly lipoprotein yfio; **PDBTitle:** crystal structure of rhodothermus marinus bamd
112	d2onda1	Alignment	not modelled	98.7	9	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**HAT/Suf repeat
113	c1slyA_	Alignment	not modelled	98.6	17	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**70-kda soluble lytic transglycosylase; **PDBTitle:** complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
114	c3beeB_	Alignment	not modelled	98.5	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative yfre protein; **PDBTitle:** crystal structure of putative yfre protein from vibrio2 parahaemolyticus
115	d1y8ma1	Alignment	not modelled	98.5	9	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
116	c3n71A_	Alignment	not modelled	98.5	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**histone lysine methyltransferase smyd1; **PDBTitle:** crystal structure of cardiac specific histone methyltransferase smyd1
117	c3ceqB_	Alignment	not modelled	98.4	28	**PDB header:**motor protein, transport protein **Chain:** B: **PDB Molecule:**kinesin light chain 2; **PDBTitle:** the tpr domain of human kinesin light chain 2 (hklc2)
118	d2ff4a2	Alignment	not modelled	98.4	15	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**BTAD-like
119	c1xi4D_	Alignment	not modelled	98.3	8	**PDB header:**endocytosis/exocytosis **Chain:** D: **PDB Molecule:**clathrin heavy chain; **PDBTitle:** clathrin d6 coat
120	c2qfcB_	Alignment	not modelled	98.2	12	**PDB header:**transcription regulation **Chain:** B: **PDB Molecule:**plcr protein; **PDBTitle:** crystal structure of bacillus thuringiensis plcr complexed with papr