Phyre^2

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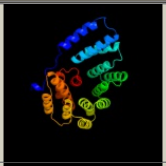
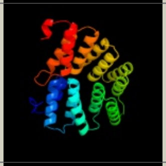
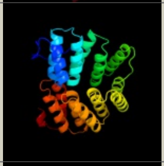
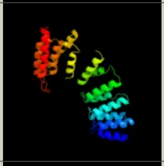
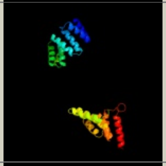
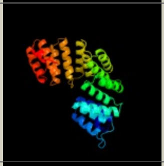
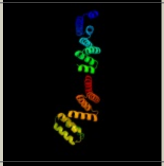
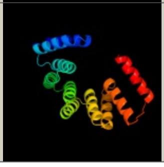
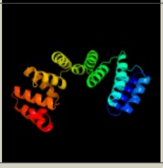
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xnfa_	Alignment		100.0	99	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
2	d1w3ba_	Alignment		100.0	19	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
3	c1fchB_	Alignment		99.9	18	**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
4	c2y4tA_	Alignment		99.9	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 3; **PDBTitle:** crystal structure of the human co-chaperone p58(ipk)
5	d1fcha_	Alignment		99.9	17	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
6	d1dcea1	Alignment		99.9	13	**Fold:**alpha-alpha superhelix **Superfamily:**Protein prenylyltransferase **Family:**Protein prenylyltransferase
7	c3iegB_	Alignment		99.9	16	**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
8	c2xpiA_	Alignment		99.9	16	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**anaphase-promoting complex subunit cut9; **PDBTitle:** crystal structure of apc/c hetero-tetramer cut9-hcn1
9	c3cvpA_	Alignment		99.9	16	**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)
10	c3fp4A_	Alignment		99.9	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tpr repeat-containing protein yhr117w; **PDBTitle:** crystal structure of tom71 complexed with ssa1 c-terminal2 fragment
11	c3pe3D_	Alignment		99.9	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

12	c2gw1A_	Alignment		99.9	25	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**mitochondrial precursor proteins import receptor; **PDBTitle:** crystal structure of the yeast tom70
13	c3q75A_	Alignment		99.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**farnesyltransferase alpha subunit; **PDBTitle:** cryptococcus neoformans protein farnesyltransferase in complex with2 fpt-ii and tkcvvm peptide
14	d1d8da_	Alignment		99.9	13	**Fold:**alpha-alpha superhelix **Superfamily:**Protein prenylyltransferase **Family:**Protein prenylyltransferase
15	d2h6fa1	Alignment		99.9	13	**Fold:**alpha-alpha superhelix **Superfamily:**Protein prenylyltransferase **Family:**Protein prenylyltransferase
16	c3draA_	Alignment		99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein **PDBTitle:** candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp
17	c1tnoI_	Alignment		99.9	13	**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
18	c3urzB_	Alignment		99.9	11	**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
19	c3hymB_	Alignment		99.9	11	**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
20	c2ho1B_	Alignment		99.9	16	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**type 4 fimbrial biogenesis protein pilf; **PDBTitle:** functional characterization of pseudomonas aeruginosa pilf
21	c3as5A_	Alignment	not modelled	99.9	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**mama; **PDBTitle:** mama amb-1 p212121
22	c2q7fA_	Alignment	not modelled	99.9	14	**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
23	c2vq2A_	Alignment	not modelled	99.9	14	**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
24	c2pl2A_	Alignment	not modelled	99.9	20	**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
25	c3sf4B_	Alignment	not modelled	99.8	11	**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
26	c3mkrA_	Alignment	not modelled	99.8	11	**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
27	d1hz4a_	Alignment	not modelled	99.8	12	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Transcription factor MalT domain III
28	d2c2la1	Alignment	not modelled	99.8	13	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)

29	c2hyzA_	Alignment	not modelled	99.8	32	**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)
30	d1hh8a_	Alignment	not modelled	99.8	20	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
31	c3mv3B_	Alignment	not modelled	99.8	13	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**coatomer subunit epsilon; **PDBTitle:** crystal structure of a-cop in complex with e-cop
32	c3q15A_	Alignment	not modelled	99.8	11	**PDB header:**hydrolase/kinase **Chain:** A: **PDB Molecule:**response regulator aspartate phosphatase h; **PDBTitle:** crystal structure of raph complexed with spo0f
33	c2r5sB_	Alignment	not modelled	99.8	16	**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
34	c2ifuA_	Alignment	not modelled	99.8	11	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**gamma-snap; **PDBTitle:** crystal structure of a gamma-snap from danio rerio
35	d2ooea1	Alignment	not modelled	99.7	9	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**HAT/Suf repeat
36	c1wao4_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**serine/threonine protein phosphatase 5; **PDBTitle:** pp5 structure
37	c2uy1A_	Alignment	not modelled	99.7	11	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**cleavage stimulation factor 77; **PDBTitle:** crystal structure of cstf-77
38	c2c2lD_	Alignment	not modelled	99.7	13	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**carboxy terminus of hsp70-interacting protein; **PDBTitle:** crystal structure of the chip u-box e3 ubiquitin ligase
39	c3nf1A_	Alignment	not modelled	99.7	16	**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
40	c2vyiA_	Alignment	not modelled	99.7	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**sgta protein; **PDBTitle:** crystal structure of the tpr domain of human sgt
41	d1qsaa1	Alignment	not modelled	99.7	10	**Fold:**alpha-alpha superhelix **Superfamily:**Bacterial muramidases **Family:**Bacterial muramidases
42	c2e2eA_	Alignment	not modelled	99.7	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
43	c3gw4B_	Alignment	not modelled	99.7	15	**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.
44	d1elwa_	Alignment	not modelled	99.7	21	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
45	c2yhcA_	Alignment	not modelled	99.7	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**upf0169 lipoprotein yfio; **PDBTitle:** structure of bamd from e. coli
46	c2xcbA_	Alignment	not modelled	99.7	14	**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
47	c3ceqB_	Alignment	not modelled	99.6	18	**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)
48	c3qkyA_	Alignment	not modelled	99.6	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane assembly lipoprotein yfio; **PDBTitle:** crystal structure of rhodothermus marinus bamd
49	c3gyzB_	Alignment	not modelled	99.6	11	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone protein ipgc; **PDBTitle:** crystal structure of ipgc from shigella flexneri
50	d1a17a_	Alignment	not modelled	99.6	17	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
51	c3sz7A_	Alignment	not modelled	99.6	19	**PDB header:**chaperone regulator **Chain:** A: **PDB Molecule:**hsc70 cochaperone (sgt); **PDBTitle:** crystal structure of the sgt2 tpr domain from aspergillus fumigatus
52	c3rkvA_	Alignment	not modelled	99.6	21	**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
53	c2kckA_	Alignment	not modelled	99.6	16	**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
54	d2buga1	Alignment	not modelled	99.6	17	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)

55	c3q49B_	Alignment	not modelled	99.6	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
56	c2dbaA_	Alignment	not modelled	99.5	20	**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
57	d1hxia_	Alignment	not modelled	99.5	20	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
58	d1zu2a1	Alignment	not modelled	99.5	19	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
59	c3ly8A_	Alignment	not modelled	99.5	6	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**transcriptional activator cadc; **PDBTitle:** crystal structure of mutant d471e of the periplasmic domain of cadc
60	d2hr2a1	Alignment	not modelled	99.5	14	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**CT2138-like
61	d1kt1a1	Alignment	not modelled	99.5	22	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
62	c2vsnB_	Alignment	not modelled	99.5	16	**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
63	c1ihgA_	Alignment	not modelled	99.5	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**cyclophilin 40; **PDBTitle:** bovine cyclophilin 40, monoclinic form
64	c3qdnA_	Alignment	not modelled	99.5	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin protein; **PDBTitle:** putative thioredoxin protein from salmonella typhimurium
65	d1p5qa1	Alignment	not modelled	99.5	23	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
66	d1qqea_	Alignment	not modelled	99.5	13	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
67	d1elra_	Alignment	not modelled	99.5	13	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
68	d2fbna1	Alignment	not modelled	99.4	21	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
69	c2fbnA_	Alignment	not modelled	99.4	21	**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
70	c3k9iA_	Alignment	not modelled	99.4	13	**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
71	c1xi4D_	Alignment	not modelled	99.4	12	**PDB header:**endocytosis/exocytosis **Chain:** D: **PDB Molecule:**clathrin heavy chain; **PDBTitle:** clathrin d6 coat
72	c1kt0A_	Alignment	not modelled	99.4	18	**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
73	d1ihga1	Alignment	not modelled	99.4	18	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
74	c1na3A_	Alignment	not modelled	99.4	31	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein ctpr2; **PDBTitle:** design of stable alpha-helical arrays from an idealized tpr2 motif
75	c1ltxA_	Alignment	not modelled	99.4	11	**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
76	c1qz2B_	Alignment	not modelled	99.4	23	**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
77	c2xevB_	Alignment	not modelled	99.4	23	**PDB header:**metal binding **Chain:** B: **PDB Molecule:**ybgf; **PDBTitle:** crystal structure of the tpr domain of xanthomonas2 campestris ybgf
78	d2onda1	Alignment	not modelled	99.3	11	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**HAT/Suf repeat
79	c2l6jA_	Alignment	not modelled	99.3	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tpr repeat-containing protein associated with hsp90; **PDBTitle:** tah1 complexed by meevd
						PDB header:structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein;

80	c2katA_	Alignment	not modelled	99.3	20	**PDBTitle:** solution structure of protein bpp2914 from bordetella2 parapertussis. northeast structural genomics consortium3 target bpr206
81	c2if4A_	Alignment	not modelled	99.3	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**atfkbp42; **PDBTitle:** crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana
82	d1nzna_	Alignment	not modelled	99.3	9	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
83	c2vgxA_	Alignment	not modelled	99.3	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone sycd; **PDBTitle:** structure of the yersinia enterocolitica type iii secretion2 translocator chaperone sycd
84	c2avpA_	Alignment	not modelled	99.3	31	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**synthetic consensus tpr protein; **PDBTitle:** crystal structure of an 8 repeat consensus tpr superhelix
85	d1iyga_	Alignment	not modelled	99.3	9	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
86	c2kcvA_	Alignment	not modelled	99.2	14	**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
87	d1pc2a_	Alignment	not modelled	99.2	10	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
88	c3fflC_	Alignment	not modelled	99.2	13	**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
89	d1zbpa1	Alignment	not modelled	99.1	10	**Fold:**ImpE-like **Superfamily:**ImpE-like **Family:**ImpE-like
90	d1ouva_	Alignment	not modelled	99.1	15	**Fold:**alpha-alpha superhelix **Superfamily:**HCP-like **Family:**HCP-like
91	c3q3hA_	Alignment	not modelled	99.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hmw1c-like glycosyltransferase; **PDBTitle:** crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
92	c1slyA_	Alignment	not modelled	99.0	8	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**70-kda soluble lytic transglycosylase; **PDBTitle:** complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
93	d1tjca_	Alignment	not modelled	99.0	27	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
94	c2kc7A_	Alignment	not modelled	98.9	16	**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
95	d1y8ma1	Alignment	not modelled	98.8	11	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
96	c3beeB_	Alignment	not modelled	98.7	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative yfre protein; **PDBTitle:** crystal structure of putative yfre protein from vibrio2 parahaemolyticus
97	c3n71A_	Alignment	not modelled	98.7	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**histone lysine methyltransferase smyd1; **PDBTitle:** crystal structure of cardiac specific histone methyltransferase smyd1
98	c3e4bD_	Alignment	not modelled	98.5	13	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**algk; **PDBTitle:** crystal structure of algk from pseudomonas fluorescens wcs374r
99	d2pqrb1	Alignment	not modelled	98.3	12	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
100	d2ff4a2	Alignment	not modelled	98.2	20	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**BTAD-like
101	c3txmA_	Alignment	not modelled	98.0	9	**PDB header:**hydrolase, protein binding **Chain:** A: **PDB Molecule:**26s proteasome regulatory complex subunit p42b; **PDBTitle:** crystal structure of rpn6 from drosophila melanogaster, gd(3+) complex
102	c2qfcB_	Alignment	not modelled	98.0	12	**PDB header:**transcription regulation **Chain:** B: **PDB Molecule:**plcr protein; **PDBTitle:** crystal structure of bacillus thuringiensis plcr complexed with papr
103	c2xm6A_	Alignment	not modelled	98.0	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein corresponding to locus c5321 from cft073 e.coli **PDBTitle:** crystal structure of the protein corresponding to locus c5321 from2 cft073 e.coli strain
104	c3mekA_	Alignment	not modelled	97.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**set and mynd domain-containing protein 3; **PDBTitle:** crystal structure of human histone-lysine n-2 methyltransferase smyd3 in complex with s-adenosyl-l-3 methionine
						PDB header:transferase **Chain:** A: **PDB Molecule:**set and mynd domain-containing protein

105	c3qwvA_	Alignment	not modelled	97.8	9	2; **PDBTitle:** crystal structure of histone lysine methyltransferase smyd2 in complex2 with the cofactor product adohcy
106	c3oxgA_	Alignment	not modelled	97.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**set and mynd domain-containing protein 3; **PDBTitle:** human lysine methyltransferase smyd3 in complex with adohcy (form iii)
107	d1iipa1	Alignment	not modelled	97.5	18	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
108	c3rjvA_	Alignment	not modelled	96.9	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**putative sel1 repeat protein; **PDBTitle:** crystal structure of a putative sel1 repeat protein (kpn_04481) from2 klebsiella pneumoniae subsp. pneumoniae at 1.65 a resolution
109	d1ya0a1	Alignment	not modelled	95.5	16	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
110	c2lahA_	Alignment	not modelled	95.5	13	**PDB header:**cell cycle, apoptosis **Chain:** A: **PDB Molecule:**mitotic checkpoint serine/threonine-protein kinase bub1; **PDBTitle:** solution nmr structure of mitotic checkpoint serine/threonine-protein2 kinase bub1 n-terminal domain from homo sapiens, northeast structural3 genomics consortium target hr5460a (methods development)
111	c2ff4B_	Alignment	not modelled	95.4	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable regulatory protein embr; **PDBTitle:** mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide
112	c3lvhA_	Alignment	not modelled	94.1	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**clathrin heavy chain 1; **PDBTitle:** crystal structure of a clathrin heavy chain and clathrin light chain2 complex
113	c1b89A_	Alignment	not modelled	93.3	16	**PDB header:**clathrin **Chain:** A: **PDB Molecule:**protein (clathrin heavy chain); **PDBTitle:** clathrin heavy chain proximal leg segment (bovine)
114	d1b89a_	Alignment	not modelled	93.3	16	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Clathrin heavy chain proximal leg segment
115	c2wviA_	Alignment	not modelled	93.3	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mitotic checkpoint serine/threonine-protein **PDBTitle:** crystal structure of the n-terminal domain of bubr1
116	d2crba1	Alignment	not modelled	90.3	16	**Fold:**Spectrin repeat-like **Superfamily:**MIT domain-like **Family:**MIT domain
117	c3mkqA_	Alignment	not modelled	90.3	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**coatomer beta'-subunit; **PDBTitle:** crystal structure of yeast alpha/betaprime-cop subcomplex of the copi2 vesicular coat
118	c3eslA_	Alignment	not modelled	79.2	12	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**checkpoint serine/threonine-protein kinase bub1; **PDBTitle:** crystal structure of the conserved n-terminal domain of the2 mitotic checkpoint component bub1
119	d1klxa_	Alignment	not modelled	77.5	13	**Fold:**alpha-alpha superhelix **Superfamily:**HCP-like **Family:**HCP-like
120	c2w2uA_	Alignment	not modelled	77.3	16	**PDB header:**hydrolase/transport **Chain:** A: **PDB Molecule:**hypothetical p60 katanin; **PDBTitle:** structural insight into the interaction between archaeal2 escrt-iii and aaa-atpase