



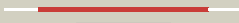




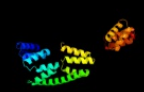





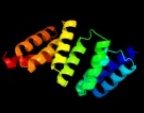

















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1w3ba_</a>	 Alignment		99.9	14	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
2	<a href="#">c2xpiA_</a>	 Alignment		99.9	7	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> anaphase-promoting complex subunit cut9; <b>PDBTitle:</b> crystal structure of apc/c hetero-tetramer cut9-hcn1
3	<a href="#">c3hymB_</a>	 Alignment		99.9	11	<b>PDB header:</b> cell cycle, ligase <b>Chain:</b> B: <b>PDB Molecule:</b> cell division cycle protein 16 homolog; <b>PDBTitle:</b> insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure
4	<a href="#">c2y4tA_</a>	 Alignment		99.9	11	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> dnaj homolog subfamily c member 3; <b>PDBTitle:</b> crystal structure of the human co-chaperone p58(ipk)
5	<a href="#">c3iegB_</a>	 Alignment		99.9	12	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> dnaj homolog subfamily c member 3; <b>PDBTitle:</b> crystal structure of p58(ipk) tpr domain at 2.5 a
6	<a href="#">d1dcea1</a>	 Alignment		99.9	9	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Protein prenyltransferase <b>Family:</b> Protein prenyltransferase
7	<a href="#">c1fchB_</a>	 Alignment		99.8	12	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal targeting signal 1 receptor; <b>PDBTitle:</b> crystal structure of the pts1 complexed to the tpr region2 of human pex5
8	<a href="#">c3pe3D_</a>	 Alignment		99.8	13	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine--peptide n- <b>PDBTitle:</b> structure of human o-glcna transferase and its complex with a peptide2 substrate
9	<a href="#">c3fp4A_</a>	 Alignment		99.8	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> tpr repeat-containing protein yhr117w; <b>PDBTitle:</b> crystal structure of tom71 complexed with ssa1 c-terminal2 fragment
10	<a href="#">c2q7fA_</a>	 Alignment		99.8	13	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> yrrb protein; <b>PDBTitle:</b> crystal structure of yrrb: a tpr protein with an unusual peptide-2 binding site
11	<a href="#">c3cvpA_</a>	 Alignment		99.8	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisome targeting signal 1 receptor pex5; <b>PDBTitle:</b> structure of peroxisomal targeting signal 1 (pts1) binding2 domain of trypanosoma brucei peroxin 5 (tpex5)complexed3 to pts1 peptide (10-skl)

12	<a href="#">dlfcha_</a>	Alignment		99.8	12	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
13	<a href="#">c3mkrA_</a>	Alignment		99.8	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> coatamer subunit epsilon; <b>PDBTitle:</b> crystal structure of yeast alpha/epsilon-cop subcomplex of the cop2 vesicular coat
14	<a href="#">dlxnfa_</a>	Alignment		99.8	10	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
15	<a href="#">c1wao4_</a>	Alignment		99.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> 4: <b>PDB Molecule:</b> serine/threonine protein phosphatase 5; <b>PDBTitle:</b> pp5 structure
16	<a href="#">d1d8da_</a>	Alignment		99.8	8	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Protein prenyltransferase <b>Family:</b> Protein prenyltransferase
17	<a href="#">c2ho1B_</a>	Alignment		99.8	10	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> type 4 fimbrial biogenesis protein pilf; <b>PDBTitle:</b> functional characterization of pseudomonas aeruginosa pilf
18	<a href="#">d2h6fa1</a>	Alignment		99.8	8	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Protein prenyltransferase <b>Family:</b> Protein prenyltransferase
19	<a href="#">c3as5A_</a>	Alignment		99.8	11	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> mama; <b>PDBTitle:</b> mama amb-1 p212121
20	<a href="#">c1tnol_</a>	Alignment		99.8	9	<b>PDB header:</b> transferase <b>Chain:</b> I: <b>PDB Molecule:</b> geranylgeranyltransferase type i alpha subunit; <b>PDBTitle:</b> rat protein geranylgeranyltransferase type-i complexed with2 a ggpp analog and a kkskstkcvim peptide derived from k-3 ras4b
21	<a href="#">c2pl2A_</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical conserved protein ttc0263; <b>PDBTitle:</b> crystal structure of ttc0263: a thermophilic tpr protein in thermus2 thermophilus hb27
22	<a href="#">c3urzB_</a>	Alignment	not modelled	99.7	9	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a hypothetical protein (bacova_03105) from2 bacteroides ovatus atcc 8483 at 2.19 a resolution
23	<a href="#">c2vq2A_</a>	Alignment	not modelled	99.7	9	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative fimbrial biogenesis and twitching <b>PDBTitle:</b> crystal structure of pilw, widely conserved type iv pilus2 biogenesis factor
24	<a href="#">c2xcba_</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein pcrh; <b>PDBTitle:</b> crystal structure of pcrh in complex with the chaperone2 binding region of popd
25	<a href="#">c2dbaA_</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> smooth muscle cell associated protein-1, isoform <b>PDBTitle:</b> the solution structure of the tetratrico peptide repeat of2 human smooth muscle cell associated protein-1, isoform 2
26	<a href="#">c2gw1A_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial precursor proteins import receptor; <b>PDBTitle:</b> crystal structure of the yeast tom70
27	<a href="#">c3gyzB_</a>	Alignment	not modelled	99.7	9	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> chaperone protein ipgc; <b>PDBTitle:</b> crystal structure of ipgc from shigella flexneri
						<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical conserved protein ttc0263; <b>PDBTitle:</b> crystal structure of ttc0263: a thermophilic tpr protein in thermus2 thermophilus hb27

28	<a href="#">c3k9iA_</a>	Alignment	not modelled	99.7	9	<b>Chain:</b> A: <b>PDB Molecule:</b> bnu4/9 protein; <b>PDBTitle:</b> crystal structure of putative protein binding protein (np_241345.1)2 from bacillus halodurans at 2.71 a resolution
29	<a href="#">d1elwa_</a>	Alignment	not modelled	99.7	7	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
30	<a href="#">c1kt0A_</a>	Alignment	not modelled	99.7	8	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 51 kda fk506-binding protein; <b>PDBTitle:</b> structure of the large fkbp-like protein, fkbp51, involved in steroid2 receptor complexes
31	<a href="#">c3ly8A_</a>	Alignment	not modelled	99.7	9	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional activator cadc; <b>PDBTitle:</b> crystal structure of mutant d471e of the periplasmic domain of cadc
32	<a href="#">c2c2lD_</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> carboxy terminus of hsp70-interacting protein; <b>PDBTitle:</b> crystal structure of the chip u-box e3 ubiquitin ligase
33	<a href="#">d2buga1</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
34	<a href="#">c3q75A_</a>	Alignment	not modelled	99.7	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> farnesyltransferase alpha subunit; <b>PDBTitle:</b> cryptococcus neoformans protein farnesyltransferase in complex with2 fpt-ii and tkcvvm peptide
35	<a href="#">d1zu2a1</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
36	<a href="#">d2c2la1</a>	Alignment	not modelled	99.7	9	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
37	<a href="#">c1ihgA_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclophilin 40; <b>PDBTitle:</b> bovine cyclophilin 40, monoclinic form
38	<a href="#">c3draA_</a>	Alignment	not modelled	99.7	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein <b>PDBTitle:</b> candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp
39	<a href="#">c2vyiA_</a>	Alignment	not modelled	99.7	8	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> sgta protein; <b>PDBTitle:</b> crystal structure of the tpr domain of human sgt
40	<a href="#">c1na3A_</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> designed protein ctrp2; <b>PDBTitle:</b> design of stable alpha-helical arrays from an idealized tpr2 motif
41	<a href="#">d1a17a_</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
42	<a href="#">c3sz7A_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> chaperone regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hsc70 cochaperone (sgt); <b>PDBTitle:</b> crystal structure of the sgt2 tpr domain from aspergillus fumigatus
43	<a href="#">d1nzna_</a>	Alignment	not modelled	99.7	11	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
44	<a href="#">c2katA_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of protein bpp2914 from bordetella2 parapertussis. northeast structural genomics consortium3 target bpr206
45	<a href="#">c3rkva_</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative peptidylprolyl isomerase; <b>PDBTitle:</b> c-terminal domain of protein c56c10.10, a putative peptidylprolyl2 isomerase, from caenorhabditis elegans
46	<a href="#">d1p5qa1</a>	Alignment	not modelled	99.6	9	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
47	<a href="#">c2hyza_</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> synthetic consensus tpr protein; <b>PDBTitle:</b> crystal structure of an 8 repeat consensus tpr superhelix2 (orthorhombic crystal form)
48	<a href="#">c1qz2B_</a>	Alignment	not modelled	99.6	9	<b>PDB header:</b> isomerase/chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> fk506-binding protein 4; <b>PDBTitle:</b> crystal structure of fkbp52 c-terminal domain complex with2 the c-terminal peptide meevd of hsp90
49	<a href="#">c2kckA_</a>	Alignment	not modelled	99.6	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tpr repeat; <b>PDBTitle:</b> nmr solution structure of the northeast structural genomics2 consortium (nesg) target mrr121a
50	<a href="#">d1iyga_</a>	Alignment	not modelled	99.6	12	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
51	<a href="#">c3mv3B_</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> coatomer subunit epsilon; <b>PDBTitle:</b> crystal structure of a-cop in complex with e-cop
52	<a href="#">d1ktla1</a>	Alignment	not modelled	99.6	9	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
53	<a href="#">c2uy1A_</a>	Alignment	not modelled	99.6	7	<b>PDB header:</b> rna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cleavage stimulation factor 77; <b>PDBTitle:</b> crystal structure of cstf-77
54	<a href="#">c2kc7A_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bfr218_protein; <b>PDBTitle:</b> solution nmr structure of bacteroides fragilis protein2

					bf1650. northeast structural genomics consortium target3 bfr218
55	<a href="#">d1pc2a_</a>	Alignment	not modelled	99.6	12 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
56	<a href="#">d1ihga1</a>	Alignment	not modelled	99.6	13 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
57	<a href="#">c3q49B_</a>	Alignment	not modelled	99.6	10 <b>PDB header:</b> ligase/chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> stip1 homology and u box-containing protein 1; <b>PDBTitle:</b> crystal structure of the tpr domain of chip complexed with hsp70-c2 peptide
58	<a href="#">c2vsnB_</a>	Alignment	not modelled	99.6	12 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> xcogt; <b>PDBTitle:</b> structure and topological arrangement of an o-glcna2 transferase homolog: insight into molecular control of3 intracellular glycosylation
59	<a href="#">c2e2eA_</a>	Alignment	not modelled	99.6	7 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> formate-dependent nitrite reductase complex nrfg subunit; <b>PDBTitle:</b> tpr domain of nrfg mediates the complex formation between heme lyase2 and formate-dependent nitrite reductase in escherichia coli o157:h7
60	<a href="#">c2kcvA_</a>	Alignment	not modelled	99.6	16 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tetratricopeptide repeat domain protein; <b>PDBTitle:</b> solution nmr structure of tetratricopeptide repeat domain2 protein sru_0103 from salinibacter ruber, northeast3 structural genomics consortium (nesg) target srr115c
61	<a href="#">c2r5sB_</a>	Alignment	not modelled	99.6	12 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein vp0806; <b>PDBTitle:</b> the crystal structure of a domain of protein vp0806 (unknown function)2 from vibrio parahaemolyticus rimd 2210633
62	<a href="#">c2avpA_</a>	Alignment	not modelled	99.6	13 <b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> synthetic consensus tpr protein; <b>PDBTitle:</b> crystal structure of an 8 repeat consensus tpr superhelix
63	<a href="#">d1hh8a_</a>	Alignment	not modelled	99.6	13 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
64	<a href="#">c2fbaA_</a>	Alignment	not modelled	99.6	9 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 70 kda peptidylprolyl isomerase, putative; <b>PDBTitle:</b> plasmodium falciparum putative fk506-binding protein2 pfl2275c, c-terminal tpr-containing domain
65	<a href="#">d2fbna1</a>	Alignment	not modelled	99.6	9 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
66	<a href="#">d1hxia_</a>	Alignment	not modelled	99.5	12 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
67	<a href="#">c2xevB_</a>	Alignment	not modelled	99.5	14 <b>PDB header:</b> metal binding <b>Chain:</b> B: <b>PDB Molecule:</b> ybgf; <b>PDBTitle:</b> crystal structure of the tpr domain of xanthomonas2 campestris ybgf
68	<a href="#">d2o0ea1</a>	Alignment	not modelled	99.5	9 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> HAT/Suf repeat
69	<a href="#">d1y8ma1</a>	Alignment	not modelled	99.5	10 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
70	<a href="#">c2l6jA_</a>	Alignment	not modelled	99.5	10 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> tpr repeat-containing protein associated with hsp90; <b>PDBTitle:</b> tah1 complexed by meevd
71	<a href="#">d1elra_</a>	Alignment	not modelled	99.5	6 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
72	<a href="#">d1tjca_</a>	Alignment	not modelled	99.5	14 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
73	<a href="#">d1hz4a_</a>	Alignment	not modelled	99.5	11 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Transcription factor MalT domain III
74	<a href="#">c2if4A_</a>	Alignment	not modelled	99.5	15 <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> atfkbp42; <b>PDBTitle:</b> crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana
75	<a href="#">c3gw4B_</a>	Alignment	not modelled	99.4	8 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein from deinococcus2 radiodurans. northeast structural genomics consortium target drr162b.
76	<a href="#">c3beeB_</a>	Alignment	not modelled	99.4	12 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative yfre protein; <b>PDBTitle:</b> crystal structure of putative yfre protein from vibrio2 parahaemolyticus
77	<a href="#">c2vgxA_</a>	Alignment	not modelled	99.4	12 <b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone sycd; <b>PDBTitle:</b> structure of the yersinia enterocolitica type iii secretion2 translocator chaperone sycd
78	<a href="#">c3qkyA_</a>	Alignment	not modelled	99.4	9 <b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane assembly lipoprotein yfio; <b>PDBTitle:</b> crystal structure of rhodothermus marinus bamd
79	<a href="#">d2hr2a1</a>	Alignment	not modelled	99.4	13 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like

					<b>Family:</b> CT2138-like
80	<a href="#">dlqsaa1</a>	Alignment	not modelled	99.4	8 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Bacterial muramidases <b>Family:</b> Bacterial muramidases
81	<a href="#">c3sf4B_</a>	Alignment	not modelled	99.4	16 <b>PDB header:</b> signaling protein/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> g-protein-signaling modulator 2; <b>PDBTitle:</b> crystal structure of the complex between the conserved cell polarity2 proteins inscuteable and lgn
82	<a href="#">c3fflC_</a>	Alignment	not modelled	99.4	16 <b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> anaphase-promoting complex subunit 7; <b>PDBTitle:</b> crystal structure of the n-terminal domain of anaphase-2 promoting complex subunit 7
83	<a href="#">d2pqrbl</a>	Alignment	not modelled	99.3	7 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
84	<a href="#">c2yhca_</a>	Alignment	not modelled	99.3	10 <b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> upf0169 lipoprotein yfio; <b>PDBTitle:</b> structure of bamd from e. coli
85	<a href="#">c3q15A_</a>	Alignment	not modelled	99.3	11 <b>PDB header:</b> hydrolase/kinase <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator aspartate phosphatase h; <b>PDBTitle:</b> crystal structure of raph complexed with spo0f
86	<a href="#">c1ltxA_</a>	Alignment	not modelled	99.3	9 <b>PDB header:</b> transferase/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> rab geranylgeranyltransferase alpha subunit; <b>PDBTitle:</b> structure of rab escort protein-1 in complex with rab2 geranylgeranyl transferase and isoprenoid
87	<a href="#">c2ifuA_</a>	Alignment	not modelled	99.3	8 <b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-snap; <b>PDBTitle:</b> crystal structure of a gamma-snap from danio rerio
88	<a href="#">c3nf1A_</a>	Alignment	not modelled	99.3	9 <b>PDB header:</b> motor protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> kinesin light chain 1; <b>PDBTitle:</b> crystal structure of the tpr domain of kinesin light chain 1
89	<a href="#">c3ulqA_</a>	Alignment	not modelled	99.3	6 <b>PDB header:</b> gene regulation/transcription activator <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator aspartate phosphatase f; <b>PDBTitle:</b> crystal structure of the anti-activator rapf complexed with the2 response regulator coma dna binding domain
90	<a href="#">c3qdnA_</a>	Alignment	not modelled	99.2	11 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioredoxin protein; <b>PDBTitle:</b> putative thioredoxin protein from salmonella typhimurium
91	<a href="#">dlqqea_</a>	Alignment	not modelled	99.2	5 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
92	<a href="#">dlzbpa1</a>	Alignment	not modelled	99.1	15 <b>Fold:</b> ImpE-like <b>Superfamily:</b> ImpE-like <b>Family:</b> ImpE-like
93	<a href="#">c3ceqB_</a>	Alignment	not modelled	99.0	13 <b>PDB header:</b> motor protein, transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> kinesin light chain 2; <b>PDBTitle:</b> the tpr domain of human kinesin light chain 2 (hklc2)
94	<a href="#">d2onda1</a>	Alignment	not modelled	98.9	9 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> HAT/Suf repeat
95	<a href="#">c1xi4D_</a>	Alignment	not modelled	98.8	9 <b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> D: <b>PDB Molecule:</b> clathrin heavy chain; <b>PDBTitle:</b> clathrin d6 coat
96	<a href="#">c3n71A_</a>	Alignment	not modelled	98.8	15 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> histone lysine methyltransferase smyd1; <b>PDBTitle:</b> crystal structure of cardiac specific histone methyltransferase smyd1
97	<a href="#">d2ff4a2</a>	Alignment	not modelled	98.7	11 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> BTAD-like
98	<a href="#">c3q3hA_</a>	Alignment	not modelled	98.7	6 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hmw1c-like glycosyltransferase; <b>PDBTitle:</b> crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
99	<a href="#">c1slyA_</a>	Alignment	not modelled	98.7	8 <b>PDB header:</b> glycosyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> 70-kda soluble lytic transglycosylase; <b>PDBTitle:</b> complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
100	<a href="#">c3qwwA_</a>	Alignment	not modelled	98.7	12 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> set and mynd domain-containing protein 2; <b>PDBTitle:</b> crystal structure of histone lysine methyltransferase smyd2 in complex2 with the cofactor product adohcy
101	<a href="#">c3mekA_</a>	Alignment	not modelled	98.5	12 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> set and mynd domain-containing protein 3; <b>PDBTitle:</b> crystal structure of human histone-lysine n-2 methyltransferase smyd3 in complex with s-adenosyl-l-3 methionine
102	<a href="#">c2qfcB_</a>	Alignment	not modelled	98.4	11 <b>PDB header:</b> transcription regulation <b>Chain:</b> B: <b>PDB Molecule:</b> plcr protein; <b>PDBTitle:</b> crystal structure of bacillus thuringiensis plcr complexed with papr
103	<a href="#">c3oxga_</a>	Alignment	not modelled	98.3	13 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> set and mynd domain-containing protein 3; <b>PDBTitle:</b> human lysine methyltransferase smyd3 in complex with adohcy (form iii)
104	<a href="#">dliipa1</a>	Alignment	not modelled	98.2	13 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like

					<b>Family:</b> Tetratricopeptide repeat (TPR)
105	<a href="#">c2xm6A_</a>	Alignment	not modelled	98.1	12 <b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein corresponding to locus c5321 from cft073 e.coli <b>PDBTitle:</b> crystal structure of the protein corresponding to locus c5321 from2 cft073 e.coli strain
106	<a href="#">d1louva_</a>	Alignment	not modelled	97.5	17 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> HCP-like <b>Family:</b> HCP-like
107	<a href="#">c2ff4B_</a>	Alignment	not modelled	97.1	12 <b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> probable regulatory protein embr; <b>PDBTitle:</b> mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide
108	<a href="#">c2lahA_</a>	Alignment	not modelled	96.8	8 <b>PDB header:</b> cell cycle, apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> mitotic checkpoint serine/threonine-protein kinase bub1; <b>PDBTitle:</b> 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)
109	<a href="#">d1ya0a1</a>	Alignment	not modelled	95.8	10 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
110	<a href="#">c2wviA_</a>	Alignment	not modelled	95.6	9 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mitotic checkpoint serine/threonine-protein <b>PDBTitle:</b> crystal structure of the n-terminal domain of bubr1
111	<a href="#">c3rvjA_</a>	Alignment	not modelled	95.6	7 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> putative sel1 repeat protein; <b>PDBTitle:</b> crystal structure of a putative sel1 repeat protein (kpn_04481) from2 klebsiella pneumoniae subsp. pneumoniae at 1.65 a resolution
112	<a href="#">c3e4bD_</a>	Alignment	not modelled	94.9	9 <b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> algk; <b>PDBTitle:</b> crystal structure of algk from pseudomonas fluorescens wcs374r
113	<a href="#">c2w2uA_</a>	Alignment	not modelled	94.2	14 <b>PDB header:</b> hydrolase/transport <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical p60 katanin; <b>PDBTitle:</b> structural insight into the interaction between archaeal2 escrt-iii and aaa-atpase
114	<a href="#">c3eslA_</a>	Alignment	not modelled	94.0	13 <b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> checkpoint serine/threonine-protein kinase bub1; <b>PDBTitle:</b> crystal structure of the conserved n-terminal domain of the2 mitotic checkpoint component bub1
115	<a href="#">c2v6yA_</a>	Alignment	not modelled	93.2	16 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aaa family atpase, p60 katanin; <b>PDBTitle:</b> structure of the mit domain from a s. solfataricus vps4-2 like atpase
116	<a href="#">c3kaeC_</a>	Alignment	not modelled	93.0	11 <b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> possible protein of nuclear scaffold; <b>PDBTitle:</b> cdc27 n-terminus
117	<a href="#">c3mkqB_</a>	Alignment	not modelled	90.9	15 <b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> coatomer subunit alpha; <b>PDBTitle:</b> crystal structure of yeast alpha/betaprime-cop subcomplex of the cop12 vesicular coat
118	<a href="#">c3txmA_</a>	Alignment	not modelled	90.4	12 <b>PDB header:</b> hydrolase, protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> 26s proteasome regulatory complex subunit p42b; <b>PDBTitle:</b> crystal structure of rp6 from drosophila melanogaster, gd(3+) complex
119	<a href="#">d2crba1</a>	Alignment	not modelled	88.3	7 <b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> MIT domain-like <b>Family:</b> MIT domain
120	<a href="#">d2jq9a1</a>	Alignment	not modelled	83.4	13 <b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> MIT domain <b>Family:</b> MIT domain