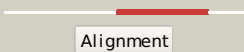
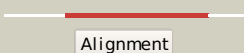
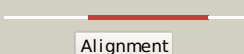
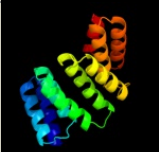
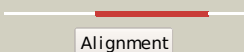
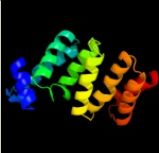
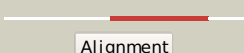
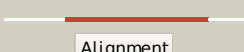
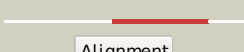
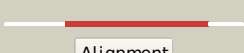
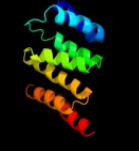


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P45955
Date	Thu Jan 5 12:03:52 GMT 2012
Unique Job ID	72f9ad17c2495245

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xevB_	 Alignment		99.8	34	PDB header: metal binding Chain: B: PDB Molecule: ybgf; PDBTitle: crystal structure of the tpr domain of xanthomonas2 campestris ybgf
2	c2xpiA_	 Alignment		99.8	12	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit cut9; PDBTitle: crystal structure of apc/c hetero-tetramer cut9-hcn1
3	c3pe3D_	 Alignment		99.7	14	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
4	c1wao4_	 Alignment		99.7	11	PDB header: hydrolase Chain: 4: PDB Molecule: serine/threonine protein phosphatase 5; PDBTitle: pp5 structure
5	c3gyzB_	 Alignment		99.7	16	PDB header: chaperone Chain: B: PDB Molecule: chaperone protein ipgc; PDBTitle: crystal structure of ipgc from shigella flexneri
6	c2dbaA_	 Alignment		99.7	9	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
7	c2xcbA_	 Alignment		99.6	15	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
8	d1w3ba_	 Alignment		99.6	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratrico peptide repeat (TPR)
9	d1elwa_	 Alignment		99.6	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratrico peptide repeat (TPR)
10	c3fp4A_	 Alignment		99.6	10	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	c2c2ID_	 Alignment		99.6	12	PDB header: chaperone Chain: D: PDB Molecule: carboxy terminus of hsp70-interacting protein; PDBTitle: crystal structure of the chip u-box e3 ubiquitin ligase

12	d2c2la1	Alignment		99.6	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
13	d1nzna_	Alignment		99.6	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
14	c1kt0A_	Alignment		99.6	9	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
15	c2e2eA_	Alignment		99.6	10	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
16	c2gw1A_	Alignment		99.6	11	PDB header: protein transport Chain: A: PDB Molecule: mitochondrial precursor proteins import receptor; PDBTitle: crystal structure of the yeast tom70
17	c2y4tA_	Alignment		99.6	19	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 3; PDBTitle: crystal structure of the human co-chaperone p58(ipk)
18	d2buga1	Alignment		99.6	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
19	c2vviA_	Alignment		99.6	13	PDB header: chaperone Chain: A: PDB Molecule: sgta protein; PDBTitle: crystal structure of the tpr domain of human sgt
20	c3k9iA_	Alignment		99.6	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
21	d1iyga_	Alignment	not modelled	99.6	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
22	c2pl2A_	Alignment	not modelled	99.5	28	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
23	d1p5qa1	Alignment	not modelled	99.5	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
24	c3hymB_	Alignment	not modelled	99.5	13	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
25	d1a17a_	Alignment	not modelled	99.5	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
26	c3qkyA_	Alignment	not modelled	99.5	17	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane assembly lipoprotein yfio; PDBTitle: crystal structure of rhodothermus marinus bamd
27	c2kckA_	Alignment	not modelled	99.5	11	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
28	clihgA_	Alignment	not modelled	99.5	10	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin 40; PDBTitle: bovine cyclophilin 40, monoclinic form
						Fold: alpha-alpha superhelix

29	d1elra_	Alignment	not modelled	99.5	12	Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
30	c3rkvA_	Alignment	not modelled	99.5	12	PDB header: isomerase Chain: A: PDB Molecule: putative peptidylprolyl isomerase; PDBTitle: c-terminal domain of protein c56c10.10, a putative peptidylprolyl isomerase, from caenorhabditis elegans
31	c3sz7A_	Alignment	not modelled	99.5	14	PDB header: chaperone regulator Chain: A: PDB Molecule: hsc70 cochaperone (sgt); PDBTitle: crystal structure of the sgt2 tpr domain from aspergillus fumigatus
32	d1kt1a1	Alignment	not modelled	99.5	10	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
33	d1hh8a_	Alignment	not modelled	99.5	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
34	c1qz2B_	Alignment	not modelled	99.5	13	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
35	d1pc2a_	Alignment	not modelled	99.5	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
36	c2ho1B_	Alignment		99.5	12	PDB header: protein binding Chain: B: PDB Molecule: type 4 fimbrial biogenesis protein pilf; PDBTitle: functional characterization of pseudomonas aeruginosa pilf
37	c2fbnA_	Alignment	not modelled	99.5	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
38	d2fba1	Alignment	not modelled	99.5	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
39	d2hr2a1	Alignment	not modelled	99.5	10	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: CT2138-like
40	d1d8da_	Alignment	not modelled	99.5	10	Fold: alpha-alpha superhelix Superfamily: Protein prenyltransferase Family: Protein prenyltransferase
41	c3iegB_	Alignment	not modelled	99.5	18	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
42	c3q49B_	Alignment	not modelled	99.5	11	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
43	d1xnfa_	Alignment	not modelled	99.5	18	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
44	d2h6fa1	Alignment	not modelled	99.5	10	Fold: alpha-alpha superhelix Superfamily: Protein prenyltransferase Family: Protein prenyltransferase
45	c2vq2A_	Alignment	not modelled	99.5	13	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
46	c3urzB_	Alignment	not modelled	99.5	12	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
47	c3as5A_	Alignment	not modelled	99.5	12	PDB header: protein binding Chain: A: PDB Molecule: mama; PDBTitle: mama amb-1 p212121
48	d1hxia_	Alignment	not modelled	99.5	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
49	c2q7fA_	Alignment	not modelled	99.5	19	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
50	c2yhca_	Alignment	not modelled	99.4	22	PDB header: membrane protein Chain: A: PDB Molecule: upf0169 lipoprotein yfio; PDBTitle: structure of bamd from e. coli
51	c2hyzA_	Alignment	not modelled	99.4	21	PDB header: de novo protein Chain: A: PDB Molecule: synthetic consensus tpr protein; PDBTitle: crystal structure of an 8 repeat consensus tpr superhelix2 (orthorhombic crystal form)
52	c3gw4B_	Alignment	not modelled	99.4	18	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.
53	c1hol	Alignment	not modelled	99.4	10	PDB header: transferase Chain: I: PDB Molecule: geranylgeranyltransferase type i alpha subunit;

53	c1uho1	Alignment	not modelled	99.4	10	PDBTitle: rat protein geranylgeranyltransferase type-i complexed with2 a ggpp analog and a kkkstktcvim peptide derived from k-3 ras4b
54	d1ihga1	Alignment	not modelled	99.4	10	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
55	d1zu2a1	Alignment	not modelled	99.4	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
56	c3mv3B	Alignment	not modelled	99.4	13	PDB header: protein transport Chain: B: PDB Molecule: coatomer subunit epsilon; PDBTitle: crystal structure of a-cop in complex with e-cop
57	c2katA	Alignment	not modelled	99.4	14	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
58	c3cvpA	Alignment	not modelled	99.4	10	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)
59	c2r5sB	Alignment	not modelled	99.4	9	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
60	c3mkrA	Alignment	not modelled	99.4	11	PDB header: transport protein Chain: A: PDB Molecule: coatomer subunit epsilon; PDBTitle: crystal structure of yeast alpha/epsilon-cop subcomplex of the cop12 vesicular coat
61	d1tjca	Alignment	not modelled	99.4	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
62	c1fchB	Alignment	not modelled	99.4	13	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
63	c3q75A	Alignment	not modelled	99.4	10	PDB header: transferase Chain: A: PDB Molecule: farnesyltransferase alpha subunit; PDBTitle: cryptococcus neoformans protein farnesyltransferase in complex with2 fpt-ii and tkcvvm peptide
64	c3fflC	Alignment	not modelled	99.4	10	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
65	c2if4A	Alignment	not modelled	99.3	15	PDB header: signaling protein Chain: A: PDB Molecule: atfkbp42; PDBTitle: crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana
66	c2vsnB	Alignment	not modelled	99.3	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
67	c2vgxA	Alignment	not modelled	99.3	13	PDB header: chaperone Chain: A: PDB Molecule: chaperone sycd; PDBTitle: structure of the yersinia enterocolitica type iii secretion2 translocator chaperone sycd
68	c3ly8A	Alignment	not modelled	99.3	13	PDB header: signaling protein Chain: A: PDB Molecule: transcriptional activator cadc; PDBTitle: crystal structure of mutant d471e of the periplasmic domain of cadc
69	d1fcha	Alignment	not modelled	99.3	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
70	c2avpA	Alignment	not modelled	99.3	29	PDB header: de novo protein Chain: A: PDB Molecule: synthetic consensus tpr protein; PDBTitle: crystal structure of an 8 repeat consensus tpr superhelix
71	c2kcvA	Alignment	not modelled	99.2	19	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
72	c1na3A	Alignment	not modelled	99.2	28	PDB header: de novo protein Chain: A: PDB Molecule: designed protein ctrp2; PDBTitle: design of stable alpha-helical arrays from an idealized tpr2 motif
73	d1dcea1	Alignment	not modelled	99.2	9	Fold: alpha-alpha superhelix Superfamily: Protein prenilyltransferase Family: Protein prenilyltransferase
74	c3qdnA	Alignment	not modelled	99.2	10	PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin protein; PDBTitle: putative thioredoxin protein from salmonella typhimurium
75	d1qsaa1	Alignment	not modelled	99.2	10	Fold: alpha-alpha superhelix Superfamily: Bacterial muramidases Family: Bacterial muramidases
76	d1y8ma1	Alignment	not modelled	99.2	5	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
77	c2kc7A	Alignment	not modelled	99.2	19	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
78	c3nflA	Alignment	not modelled	99.2	10	PDB header: motor protein, transport protein Chain: A: PDB Molecule: kinesin light chain 1;

78	c3n1A_	Alignment	not modelled	99.2	19	PDBTitle: crystal structure of the tpr domain of kinesin light chain 1 PDB header: transcription Chain: A: PDB Molecule: histone lysine methyltransferase smyd1; PDBTitle: crystal structure of cardiac specific histone methyltransferase smyd1
79	c3n71A_	Alignment	not modelled	99.2	10	PDB header: protein binding Chain: A: PDB Molecule: tpr repeat-containing protein associated with hsp90; PDBTitle: tah1 complexed by meevd
80	c2l6jA_	Alignment	not modelled	99.2	9	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: gamma-snap; PDBTitle: crystal structure of a gamma-snap from danio rerio
81	c2ifuA_	Alignment	not modelled	99.1	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: HAT/Suf repeat
82	d2o0ea1	Alignment	not modelled	99.1	11	PDB header: transferase Chain: A: PDB Molecule: protein PDBTitle: candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp
83	c3draA_	Alignment	not modelled	99.1	10	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Transcription factor MalT domain III
84	d1hz4a_	Alignment	not modelled	99.1	10	PDB header: rna-binding protein Chain: A: PDB Molecule: cleavage stimulation factor 77; PDBTitle: crystal structure of cstf-77
85	c2uy1A_	Alignment	not modelled	99.1	9	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
86	d2pqrbl	Alignment	not modelled	99.1	6	PDB header: hydrolase/kinase Chain: A: PDB Molecule: response regulator aspartate phosphatase h; PDBTitle: crystal structure of raph complexed with spo0f
87	c3q15A_	Alignment	not modelled	99.0	10	PDB header: transferase Chain: A: PDB Molecule: set and mynd domain-containing protein 2; PDBTitle: crystal structure of histone lysine methyltransferase smyd2 in complex2 with the cofactor product adohcy
88	c3qwvA_	Alignment	not modelled	99.0	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
89	d1qqea_	Alignment	not modelled	99.0	8	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
90	c3ulqA_	Alignment	not modelled	98.9	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative yfre protein; PDBTitle: crystal structure of putative yfre protein from vibrio2 parahaemolyticus
91	c3beeB_	Alignment	not modelled	98.9	8	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
92	c3sf4B_	Alignment	not modelled	98.9	11	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
93	c3mekA_	Alignment	not modelled	98.9	14	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)
94	c3ceqB_	Alignment	not modelled	98.9	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)
95	c3oxgA_	Alignment	not modelled	98.8	13	Fold: ImpE-like Superfamily: ImpE-like Family: ImpE-like
96	d1zbpa1	Alignment	not modelled	98.8	14	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
97	c1ltxA_	Alignment	not modelled	98.7	9	PDB header: transcription regulation Chain: B: PDB Molecule: plcr protein; PDBTitle: crystal structure of bacillus thuringiensis plcr complexed with papr
98	c2qfcB_	Alignment	not modelled	98.6	8	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: BTAD-like
99	d2ff4a2	Alignment	not modelled	98.5	10	PDB header: glycosyltransferase Chain: A: PDB Molecule: 70-kda soluble lytic transglycosylase; PDBTitle: complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
100	c1slvA_	Alignment	not modelled	98.5	12	PDB header: transferase Chain: A: PDB Molecule: hmw1c-like glycosyltransferase; PDBTitle: crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
101	c3q3hA_	Alignment	not modelled	98.3	5	PDB header: endocytosis/exocytosis Chain: D: PDB Molecule: clathrin heavy chain; PDBTitle: clathrin d6 coat
102	c1xi4D_	Alignment	not modelled	98.3	13	Fold: alpha-alpha superhelix Superfamily: TPR-like
103	d2onda1	Alignment	not modelled	98.2	7	

						Family: HAT/Suf repeat
104	c2xm6A_	Alignment	not modelled	97.7	16	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
105	d1louva_	Alignment	not modelled	97.6	22	Fold: alpha-alpha superhelix Superfamily: HCP-like Family: HCP-like
106	c3bxmA_	Alignment	not modelled	97.5	6	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
107	d1iipa1	Alignment	not modelled	97.2	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
108	c2xdjF_	Alignment	not modelled	97.1	100	PDB header: unknown function Chain: F: PDB Molecule: uncharacterized protein ybgf; PDBTitle: crystal structure of the n-terminal domain of e.coli ybgf
109	c2lahA_	Alignment	not modelled	96.3	12	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)
110	c2ff4B_	Alignment	not modelled	95.8	9	PDB header: transcription Chain: B: PDB Molecule: probable regulatory protein embr; PDBTitle: mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide
111	c2wviA_	Alignment	not modelled	95.8	8	PDB header: transferase Chain: A: PDB Molecule: mitotic checkpoint serine/threonine-protein PDBTitle: crystal structure of the n-terminal domain of bubr1
112	c3e4bD_	Alignment	not modelled	95.6	19	PDB header: protein binding Chain: D: PDB Molecule: algk; PDBTitle: crystal structure of algk from pseudomonas fluorescens wcs374r
113	c2v6yA_	Alignment	not modelled	94.6	21	PDB header: hydrolase Chain: A: PDB Molecule: aaa family atpase, p60 katanin; PDBTitle: structure of the mit domain from a s. solfataricus vps4-2 like atpase
114	c3rjvA_	Alignment	not modelled	94.5	18	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
115	c2w2uA_	Alignment	not modelled	94.4	21	PDB header: hydrolase/transport Chain: A: PDB Molecule: hypothetical p60 katanin; PDBTitle: structural insight into the interaction between archaeal2 escrt-iii and aaa-atpase
116	c3lvhA_	Alignment	not modelled	93.3	13	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
117	d1ya0a1	Alignment	not modelled	90.5	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
118	c3kaeC_	Alignment	not modelled	90.1	12	PDB header: protein binding Chain: C: PDB Molecule: possible protein of nuclear scaffold; PDBTitle: cdc27 n-terminus
119	c3eslA_	Alignment	not modelled	88.1	8	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
120	c3mkqA_	Alignment	not modelled	82.2	13	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