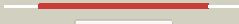


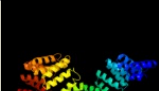
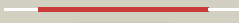
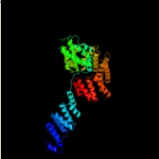


















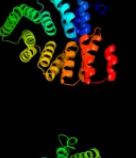

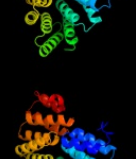
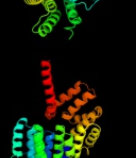

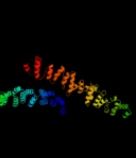
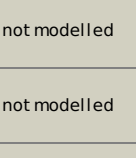


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	A0AVF1
Date	Sat Jun 16 10:27:57 BST 2012
Unique Job ID	a988f912b3359d4b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xpiA_	 Alignment		100.0	13	PDB header: cell cycle Chain: A; PDB Molecule: anaphase-promoting complex subunit cut9; PDBTitle: crystal structure of apc/c hetero-tetramer cut9-hcn1
2	d1w3ba_	 Alignment		100.0	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
3	c3fp4A_	 Alignment		100.0	13	PDB header: transport protein Chain: A; PDB Molecule: tpr repeat-containing protein yhr117w; PDBTitle: crystal structure of tom71 complexed with ssa1 c-terminal2 fragment
4	c2y4tA_	 Alignment		100.0	13	PDB header: chaperone Chain: A; PDB Molecule: dnaj homolog subfamily c member 3; PDBTitle: crystal structure of the human co-chaperone p58(ipk)
5	d2o0ea1	 Alignment		100.0	10	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: HAT/Suf repeat
6	c3iegB_	 Alignment		100.0	13	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
7	c2gw1A_	 Alignment		100.0	12	PDB header: protein transport Chain: A; PDB Molecule: mitochondrial precursor proteins import receptor; PDBTitle: crystal structure of the yeast tom70
8	c4e85B_	 Alignment		100.0	7	PDB header: structural protein Chain: B; PDB Molecule: mrna 3'-end-processing protein rna14; PDBTitle: crystal structure of hat domain of rna14
9	c4ebaC_	 Alignment		100.0	9	PDB header: structural protein/rna binding protein Chain: C; PDB Molecule: mrna 3'-end-processing protein rna14; PDBTitle: crystal structure of the rna14-rna15 complex
10	c3v6pA_	 Alignment		100.0	10	PDB header: dna binding protein Chain: A; PDB Molecule: dhax3; PDBTitle: crystal structure of the dna-binding domain of dhax3, a tal effector
11	d1qsaa1	 Alignment		100.0	9	Fold: alpha-alpha superhelix Superfamily: Bacterial muramidases Family: Bacterial muramidases

12	c2uy1A_	Alignment		100.0	10	PDB header: rna-binding protein Chain: A: PDB Molecule: cleavage stimulation factor 77; PDBTitle: crystal structure of cstf-77
13	c3hymB_	Alignment		100.0	12	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
14	c1fchB_	Alignment		100.0	10	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
15	d1fcha_	Alignment		100.0	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
16	c3cypA_	Alignment		99.9	11	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)
17	c4eqfA_	Alignment		99.9	14	PDB header: protein binding/transport protein Chain: A: PDB Molecule: pex5-related protein; PDBTitle: trip8b-1a#206-567 interacting with the carboxy-terminal seven residues2 of hcn2
18	c3mkrA_	Alignment		99.9	18	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
19	d1dcea1	Alignment		99.9	10	Fold: alpha-alpha superhelix Superfamily: Protein prenylyltransferase Family: Protein prenylyltransferase
20	c1xi4D_	Alignment		99.9	12	PDB header: endocytosis/exocytosis Chain: D: PDB Molecule: clathrin heavy chain; PDBTitle: clathrin d6 coat
21	d1hz4a_	Alignment	not modelled	99.9	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Transcription factor MalT domain III
22	c4abnA_	Alignment	not modelled	99.9	15	PDB header: gene regulation Chain: A: PDB Molecule: tetratricopeptide repeat protein 5; PDBTitle: crystal structure of full length mouse strap (ttc5)
23	c3q75A_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: farnesyltransferase alpha subunit; PDBTitle: cryptococcus neoformans protein farnesyltransferase in complex with2 fpt-ii and tkcvvm peptide
24	c3pe3D_	Alignment	not modelled	99.9	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
25	d1d8da_	Alignment	not modelled	99.9	10	Fold: alpha-alpha superhelix Superfamily: Protein prenylyltransferase Family: Protein prenylyltransferase
26	c3q15A_	Alignment	not modelled	99.9	15	PDB header: hydrolase/kinase Chain: A: PDB Molecule: response regulator aspartate phosphatase h; PDBTitle: crystal structure of raph complexed with spo0f
27	d2h6fa1	Alignment	not modelled	99.9	10	Fold: alpha-alpha superhelix Superfamily: Protein prenylyltransferase Family: Protein prenylyltransferase
28	c2q7fa_	Alignment	not modelled	99.9	17	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 PDB header: protein binding

29	c2ho1B_	Alignment	not modelled	99.9	16	Chain: B: PDB Molecule: type 4 fimbrial biogenesis protein pilf; PDBTitle: functional characterization of pseudomonas aeruginosa pilf
30	c1tno_	Alignment	not modelled	99.9	10	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 kkkstkcvm peptide derived from k-3 ras4b
31	c3uq3A_	Alignment	not modelled	99.9	14	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein sti1; PDBTitle: tpr2ab-domain:phsp90-complex of yeast sti1
32	c3draA_	Alignment	not modelled	99.9	10	PDB header: transferase Chain: A: PDB Molecule: protein PDBTitle: candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp
33	c3mv3B_	Alignment	not modelled	99.9	9	PDB header: protein transport Chain: B: PDB Molecule: coatomer subunit epsilon; PDBTitle: crystal structure of a-cop in complex with e-cop
34	d1xnfa_	Alignment	not modelled	99.9	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
35	c2vq2A_	Alignment	not modelled	99.9	19	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
36	c3ro2A_	Alignment	not modelled	99.9	14	PDB header: protein binding Chain: A: PDB Molecule: g-protein-signaling modulator 2; PDBTitle: structures of the lgn/numa complex
37	c4a1sB_	Alignment	not modelled	99.9	14	PDB header: cell cycle Chain: B: PDB Molecule: partner of inscuteable; PDBTitle: crystallographic structure of the pins:insc complex
38	c3sf4B_	Alignment	not modelled	99.9	15	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
39	c3v6tA_	Alignment	not modelled	99.9	10	PDB header: dna binding protein/dna Chain: A: PDB Molecule: dhax3; PDBTitle: crystal structure of the dna-bound dhax3, a tal effector, at 1.852 angstrom
40	c3as5A_	Alignment	not modelled	99.8	12	PDB header: protein binding Chain: A: PDB Molecule: mama; PDBTitle: mama amb-1 p212121
41	c3ulqA_	Alignment	not modelled	99.8	13	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
42	c2pl2A_	Alignment	not modelled	99.8	19	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
43	c2r5sB_	Alignment	not modelled	99.8	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	c1slyA_	Alignment	not modelled	99.8	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
45	c4f3vB_	Alignment	not modelled	99.8	11	PDB header: protein transport Chain: B: PDB Molecule: esx-1 secretion system protein eccA1; PDBTitle: crystal structure of n-terminal domain of eccA1 atpase from esx-12 secretion system of mycobacterium tuberculosis
46	c3urzB_	Alignment	not modelled	99.8	8	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	d1hh8a_	Alignment	not modelled	99.8	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
48	c1wao4_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: 4: PDB Molecule: serine/threonine protein phosphatase 5; PDBTitle: pp5 structure
49	d2c2la1	Alignment	not modelled	99.8	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
50	c2c2lD_	Alignment	not modelled	99.7	11	PDB header: chaperone Chain: D: PDB Molecule: carboxy terminus of hsp70-interacting protein; PDBTitle: crystal structure of the chip u-box e3 ubiquitin ligase
51	c2e2eA_	Alignment	not modelled	99.7	20	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
52	c2xcba_	Alignment	not modelled	99.7	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
53	c2hyzA_	Alignment	not modelled	99.7	16	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)

54	c3gyzB_	Alignment	not modelled	99.7	10	PDB header: chaperone Chain: B: PDB Molecule: chaperone protein ipgc; PDBTitle: crystal structure of ipgc from shigella flexneri
55	d1bxia_	Alignment	not modelled	99.7	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
56	c3upvA_	Alignment	not modelled	99.7	13	PDB header: peptide binding protein Chain: A: PDB Molecule: heat shock protein sti1; PDBTitle: tpr2b-domain:phsp70-complex of yeast sti1
57	c2yhCA_	Alignment	not modelled	99.7	15	PDB header: membrane protein Chain: A: PDB Molecule: upf0169 lipoprotein yfio; PDBTitle: structure of bamd from e. coli
58	d1elwa_	Alignment	not modelled	99.7	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
59	c2ifua_	Alignment	not modelled	99.7	11	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: gamma-snap; PDBTitle: crystal structure of a gamma-snap from danio rerio
60	c3sz7A_	Alignment	not modelled	99.7	14	PDB header: chaperone regulator Chain: A: PDB Molecule: hsc70 cochaperone (sgt); PDBTitle: crystal structure of the sgt2 tpr domain from aspergillus fumigatus
61	c3qkyA_	Alignment	not modelled	99.6	13	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane assembly lipoprotein yfio; PDBTitle: crystal structure of rhodothermus marinus bamd
62	c2kckA_	Alignment	not modelled	99.6	17	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
63	c2vviA_	Alignment	not modelled	99.6	14	PDB header: chaperone Chain: A: PDB Molecule: sgta protein; PDBTitle: crystal structure of the tpr domain of human sgt
64	c3gw4B_	Alignment	not modelled	99.6	12	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.
65	c3u64A_	Alignment	not modelled	99.6	10	PDB header: transport protein Chain: A: PDB Molecule: protein tp_0956; PDBTitle: the crystal structure of ta-t (tp0956)
66	d1a17a_	Alignment	not modelled	99.6	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
67	c3q49B_	Alignment	not modelled	99.6	12	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
68	c1kt0A_	Alignment	not modelled	99.6	15	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
69	c3qdnA_	Alignment	not modelled	99.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin protein; PDBTitle: putative thioredoxin protein from salmonella typhimurium
70	c2dbaA_	Alignment	not modelled	99.6	15	PDB header: structural protein Chain: A: PDB Molecule: smooth muscle cell associated protein-1, isoform PDBTitle: the solution structure of the tetratricopeptide repeat of2 human smooth muscle cell associated protein-1, isoform 2
71	c2katA_	Alignment	not modelled	99.6	17	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
72	d2buga1	Alignment	not modelled	99.6	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
73	d1zu2a1	Alignment	not modelled	99.6	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
74	d1qqea_	Alignment	not modelled	99.6	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
75	c2lniA_	Alignment	not modelled	99.6	17	PDB header: chaperone Chain: A: PDB Molecule: stress-induced-phosphoprotein 1; PDBTitle: solution nmr structure of stress-induced-phosphoprotein 1 sti1 from2 homo sapiens, northeast structural genomics consortium target hr4403e
76	d2onda1	Alignment	not modelled	99.6	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: HAT/Suf repeat
77	c3k9iA_	Alignment	not modelled	99.6	21	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
78	c3ly8A_	Alignment	not modelled	99.6	13	PDB header: signaling protein Chain: A: PDB Molecule: transcriptional activator cadc; PDBTitle: crystal structure of mutant d471e of the periplasmic domain of cadc
79	d1nznA_	Alignment	not modelled	99.6	17	Fold: alpha-alpha superhelix Superfamily: TPR-like

						Family: Tetratricopeptide repeat (TPR)
80	c1ihgA_	Alignment	not modelled	99.6	17	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin 40; PDBTitle: bovine cyclophilin 40, monoclinic form
81	d1elra_	Alignment	not modelled	99.6	18	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
82	d1pc2a_	Alignment	not modelled	99.5	17	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
83	d1iyga_	Alignment	not modelled	99.5	18	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
84	d1kt1a1	Alignment	not modelled	99.5	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
85	d1p5qa1	Alignment	not modelled	99.5	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
86	c2if4A_	Alignment	not modelled	99.5	19	PDB header: signaling protein Chain: A: PDB Molecule: atfkbp42; PDBTitle: crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana
87	c2vsnB_	Alignment	not modelled	99.5	9	PDB header: transferase Chain: B: PDB Molecule: xcogt; PDBTitle: structure and topological arrangement of an o-glcna2 transferase homolog: insight into molecular control of3 intracellular glycosylation
88	c2xevB_	Alignment	not modelled	99.5	8	PDB header: metal binding Chain: B: PDB Molecule: ybgf; PDBTitle: crystal structure of the tpr domain of xanthomonas2 campestris ybgf
89	c3rkvA_	Alignment	not modelled	99.5	19	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
90	c3nf1A_	Alignment	not modelled	99.5	15	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
91	c2kcvA_	Alignment	not modelled	99.5	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
92	c1qz2B_	Alignment	not modelled	99.5	15	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
93	c1na3A_	Alignment	not modelled	99.5	19	PDB header: de novo protein Chain: A: PDB Molecule: designed protein ctrp2; PDBTitle: design of stable alpha-helical arrays from an idealized tpr2 motif
94	d2fba1	Alignment	not modelled	99.5	18	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
95	c2fba_	Alignment	not modelled	99.5	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 70 kda peptidylprolyl isomerase, putative; PDBTitle: plasmodium falci parum putative fk506-binding protein2 pfl2275c, c-terminal tpr-containing domain
96	d1zbp1	Alignment	not modelled	99.4	15	Fold: ImpE-like Superfamily: ImpE-like Family: ImpE-like
97	c3ceqB_	Alignment	not modelled	99.4	20	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)
98	c1ltxA_	Alignment	not modelled	99.4	10	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
99	c2l6jA_	Alignment	not modelled	99.4	9	PDB header: protein binding Chain: A: PDB Molecule: tpr repeat-containing protein associated with hsp90; PDBTitle: tah1 complexed by meevd
100	c2vgxA_	Alignment	not modelled	99.4	11	PDB header: chaperone Chain: A: PDB Molecule: chaperone sycd; PDBTitle: structure of the yersinia enterocolitica type iii secretion2 translocator chaperone sycd
101	c2avpA_	Alignment	not modelled	99.4	27	PDB header: de novo protein Chain: A: PDB Molecule: synthetic consensus tpr protein; PDBTitle: crystal structure of an 8 repeat consensus tpr superhelix
102	d2hr2a1	Alignment	not modelled	99.4	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: CT2138-like
103	c3fflC_	Alignment	not modelled	99.4	17	PDB header: cell cycle Chain: C: PDB Molecule: anaphase-promoting complex subunit 7; PDBTitle: crystal structure of the n-terminal domain of anaphase-promoting2 complex subunit 7
104	d1ihga1	Alignment	not modelled	99.4	21	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
						PDB header: structural genomics, unknown function

105	c2kc7A	Alignment	not modelled	99.3	18	Chain: A; PDB Molecule: bfr218_protein; PDBTitle: solution nmr structure of bacteroides fragilis protein2 bfr1650. northeast structural genomics consortium target3 bfr218
106	d1tjca	Alignment	not modelled	99.3	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
107	d1y8ma1	Alignment	not modelled	99.2	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
108	c3ro3A	Alignment	not modelled	99.2	13	PDB header: protein binding Chain: A; PDB Molecule: g-protein-signaling modulator 2; PDBTitle: crystal structure of lgn/minscuteable complex
109	c2xm6A	Alignment	not modelled	99.2	13	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
110	c3n71A	Alignment	not modelled	99.0	8	PDB header: transcription Chain: A; PDB Molecule: histone lysine methyltransferase smyd1; PDBTitle: crystal structure of cardiac specific histone methyltransferase smyd1
111	d2pqrbl	Alignment	not modelled	99.0	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
112	c3beeB	Alignment	not modelled	99.0	15	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: putative yfre protein; PDBTitle: crystal structure of putative yfre protein from vibrio2 parahaemolyticus
113	d2ff4a2	Alignment	not modelled	98.9	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: BTAD-like
114	c3q3hA	Alignment	not modelled	98.8	10	PDB header: transferase Chain: A; PDB Molecule: hmw1c-like glycosyltransferase; PDBTitle: crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
115	c3lvhA	Alignment	not modelled	98.5	10	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
116	c3mekA	Alignment	not modelled	98.5	14	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
117	c3oxqA	Alignment	not modelled	98.5	14	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)
118	c3qwvA	Alignment	not modelled	98.5	16	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
119	c3txmA	Alignment		98.4	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
120	d1ouva	Alignment	not modelled	98.3	11	Fold: alpha-alpha superhelix Superfamily: HCP-like Family: HCP-like