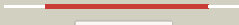
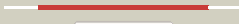
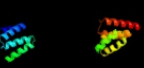
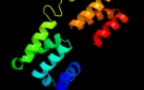
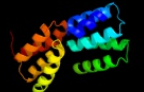
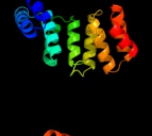
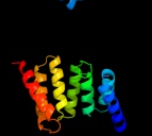
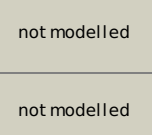


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2e2eA_	 Alignment		99.9	97	PDB header: lyase Chain: A: PDB Molecule: formate-dependent nitrite reductase complex nrfg subunit; PDBTitle: tpr domain of nrfg mediates the complex formation between heme lyase2 and formate-dependent nitrite reductase in escherichia coli o157:h7
2	c3pe3D_	 Alignment		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
3	c2y4tA_	 Alignment		99.8	23	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 3; PDBTitle: crystal structure of the human co-chaperone p58(ipk)
4	c2xpiA_	 Alignment		99.8	14	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit cut9; PDBTitle: crystal structure of apc/c hetero-tetramer cut9-hcn1
5	c1fchB_	 Alignment		99.8	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
6	c3iegB_	 Alignment		99.8	25	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	c2r5sB_	 Alignment		99.8	12	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
8	c3urzB_	 Alignment		99.8	20	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
9	c3hymB_	 Alignment		99.8	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
10	d1fcha_	 Alignment		99.8	18	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
11	d1d8da_	 Alignment		99.8	9	Fold: alpha-alpha superhelix Superfamily: Protein prenyltransferase Family: Protein prenyltransferase

12	c3q75A_	Alignment		99.8	13 PDB header: transferase Chain: A: PDB Molecule: farnesyltransferase alpha subunit; PDBTitle: cryptococcus neoformans protein farnesyltransferase in complex with2 fpt-ii and tkcvvm peptide
13	c3cvpA_	Alignment		99.8	19 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)
14	d1w3ba_	Alignment		99.8	16 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
15	c2hyzA_	Alignment		99.8	27 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)
16	d2h6fa1	Alignment		99.8	12 Fold: alpha-alpha superhelix Superfamily: Protein prenyltransferase Family: Protein prenyltransferase
17	c1wao4_	Alignment		99.8	16 PDB header: hydrolase Chain: 4: PDB Molecule: serine/threonine protein phosphatase 5; PDBTitle: pp5 structure
18	c2q7fA_	Alignment		99.8	16 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
19	d1xnfa_	Alignment		99.7	13 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
20	c2xcba_	Alignment		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
21	c3fp4A_	Alignment	not modelled	99.7	16 PDB header: transport protein Chain: A: PDB Molecule: tpr repeat-containing protein yhr117w; PDBTitle: crystal structure of tom71 complexed with ssa1 c-terminal2 fragment
22	c3gyzB_	Alignment	not modelled	99.7	13 PDB header: chaperone Chain: B: PDB Molecule: chaperone protein ipgc; PDBTitle: crystal structure of ipgc from shigella flexneri
23	c1tnol_	Alignment	not modelled	99.7	12 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 kkskktkvim peptide derived from k-3 ras4b
24	d1hh8a_	Alignment	not modelled	99.7	14 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
25	c2pl2A_	Alignment	not modelled	99.7	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
26	d1dcea1	Alignment	not modelled	99.7	13 Fold: alpha-alpha superhelix Superfamily: Protein prenyltransferase Family: Protein prenyltransferase
27	d1elwa_	Alignment	not modelled	99.7	12 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
28	c3as5A_	Alignment	not modelled	99.7	17 PDB header: protein binding Chain: A: PDB Molecule: mama; PDBTitle: mama amb-1 p212121

29	c2ho1B_	Alignment	not modelled	99.7	17	PDB header: protein binding Chain: B: PDB Molecule: type 4 fimbrial biogenesis protein pilf; PDBTitle: functional characterization of pseudomonas aeruginosa pilf
30	d2c2la1	Alignment	not modelled	99.7	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
31	d1zu2a1	Alignment	not modelled	99.7	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
32	c2dbaA_	Alignment	not modelled	99.7	18	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
33	c2vq2A_	Alignment	not modelled	99.7	20	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
34	c3qdnA_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin protein; PDBTitle: putative thioredoxin protein from salmonella typhimurium
35	c2vviA_	Alignment	not modelled	99.7	13	PDB header: chaperone Chain: A: PDB Molecule: sgta protein; PDBTitle: crystal structure of the tpr domain of human sgt
36	d2buga1	Alignment	not modelled	99.7	18	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
37	c3ly8A_	Alignment	not modelled	99.7	14	PDB header: signaling protein Chain: A: PDB Molecule: transcriptional activator cadc; PDBTitle: crystal structure of mutant d471e of the periplasmic domain of cadc
38	d1nzna_	Alignment	not modelled	99.7	10	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
39	c2c21D_	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
40	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
41	c3sz7A_	Alignment	not modelled	99.6	17	PDB header: chaperone regulator Chain: A: PDB Molecule: hsc70 cochaperone (sgt); PDBTitle: crystal structure of the sgt2 tpr domain from aspergillus fumigatus
42	d1a17a_	Alignment	not modelled	99.6	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
43	c3draA_	Alignment	not modelled	99.6	10	PDB header: transferase Chain: A: PDB Molecule: protein PDBTitle: candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp
44	d1zbpa1	Alignment	not modelled	99.6	15	Fold: ImpE-like Superfamily: ImpE-like Family: ImpE-like
45	c3beeB_	Alignment	not modelled	99.6	38	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative yfre protein; PDBTitle: crystal structure of putative yfre protein from vibrio2 parahaemolyticus
46	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
47	d1iyga_	Alignment	not modelled	99.6	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
48	c2gw1A_	Alignment	not modelled	99.6	20	PDB header: protein transport Chain: A: PDB Molecule: mitochondrial precursor proteins import receptor; PDBTitle: crystal structure of the yeast tom70
49	d1pc2a_	Alignment	not modelled	99.6	9	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
50	d1hxia_	Alignment	not modelled	99.6	18	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
51	c3q49B_	Alignment	not modelled	99.5	14	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
52	d1elra_	Alignment	not modelled	99.5	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
53	c2vsnb_	Alignment	not modelled	99.5	19	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
54	d2ooea1	Alignment	not modelled	99.5	9	Fold: alpha-alpha superhelix Superfamily: TPR-like

					Family: HAT/Suf repeat
55	c3mv3B_	Alignment	not modelled	99.5	11 PDB header: protein transport Chain: B: PDB Molecule: coatomer subunit epsilon; PDBTitle: crystal structure of a-cop in complex with e-cop
56	c3qkyA_	Alignment	not modelled	99.5	14 PDB header: membrane protein Chain: A: PDB Molecule: outer membrane assembly lipoprotein yfio; PDBTitle: crystal structure of rhodothermus marinus bamd
57	dlihga1	Alignment	not modelled	99.5	13 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
58	c2xevB_	Alignment	not modelled	99.5	11 PDB header: metal binding Chain: B: PDB Molecule: ybgf; PDBTitle: crystal structure of the tpr domain of xanthomonas2 campestris ybgf
59	c3gw4B_	Alignment	not modelled	99.5	19 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.
60	c2katA_	Alignment	not modelled	99.5	18 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
61	c3sf4B_	Alignment	not modelled	99.5	25 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
62	c1kt0A_	Alignment	not modelled	99.5	20 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
63	c1ihgA_	Alignment	not modelled	99.5	14 PDB header: isomerase Chain: A: PDB Molecule: cyclophilin 40; PDBTitle: bovine cyclophilin 40, monoclinic form
64	d1p5qa1	Alignment	not modelled	99.5	21 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
65	c3mkrA_	Alignment	not modelled	99.5	8 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
66	c2vgxA_	Alignment	not modelled	99.5	12 PDB header: chaperone Chain: A: PDB Molecule: chaperone sycd; PDBTitle: structure of the yersinia enterocolitica type iii secretion2 translocator chaperone sycd
67	c2fbaA_	Alignment	not modelled	99.5	17 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
68	d2fba1	Alignment	not modelled	99.5	17 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
69	d1kt1a1	Alignment	not modelled	99.4	8 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
70	c1qz2B_	Alignment	not modelled	99.4	21 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
71	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
72	d1hz4a_	Alignment	not modelled	99.4	14 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Transcription factor MalT domain III
73	c1lxA_	Alignment	not modelled	99.4	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
74	c2kcvA_	Alignment	not modelled	99.4	16 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tetratricopeptide repeat domain protein; PDBTitle: solution nmr structure of tetratricopeptide repeat domain2 protein sru_0103 from salinibacter ruber, northeast3 structural genomics consortium (nesg) target srr115c
75	c1na3A_	Alignment	not modelled	99.4	33 PDB header: de novo protein Chain: A: PDB Molecule: designed protein ctrp2; PDBTitle: design of stable alpha-helical arrays from an idealized tpr2 motif
76	c2uy1A_	Alignment	not modelled	99.4	9 PDB header: rna-binding protein Chain: A: PDB Molecule: cleavage stimulation factor 77; PDBTitle: crystal structure of cstf-77
77	d2hr2a1	Alignment	not modelled	99.4	15 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: CT2138-like
78	c3nf1A_	Alignment	not modelled	99.3	24 PDB header: motor protein, transport protein Chain: A: PDB Molecule: kinesin light chain 1; PDBTitle: crystal structure of the tpr domain of kinesin light chain 1
79	c2yhCA_	Alignment	not modelled	99.3	8 PDB header: membrane protein Chain: A: PDB Molecule: upf0169 lipoprotein yfio; PDBTitle: structure of bamd from e. coli

80	c2l6jA_	Alignment	not modelled	99.3	10	PDB header: protein binding Chain: A: PDB Molecule: tpr repeat-containing protein associated with hsp90; PDBTitle: tah1 complexed by meevd
81	dlqsaa1	Alignment	not modelled	99.3	8	Fold: alpha-alpha superhelix Superfamily: Bacterial muramidases Family: Bacterial muramidases
82	c2if4A_	Alignment	not modelled	99.3	11	PDB header: signaling protein Chain: A: PDB Molecule: atfkbp42; PDBTitle: crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana
83	dly8ma1	Alignment	not modelled	99.3	7	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
84	c3cegB_	Alignment	not modelled	99.3	24	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)
85	d1tjca_	Alignment	not modelled	99.2	20	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
86	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 bfr1650. northeast structural genomics consortium target3 bfr218
87	c2ifuA_	Alignment	not modelled	99.2	10	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: gamma-snap; PDBTitle: crystal structure of a gamma-snap from danio rerio
88	c3ulqA_	Alignment	not modelled	99.2	18	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
89	dlqqea_	Alignment	not modelled	99.2	10	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
90	c3q15A_	Alignment	not modelled	99.2	15	PDB header: hydrolase/kinase Chain: A: PDB Molecule: response regulator aspartate phosphatase h; PDBTitle: crystal structure of raph complexed with spo0f
91	d2pqrbl	Alignment	not modelled	99.1	7	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
92	c3fflC_	Alignment	not modelled	99.0	21	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
93	c2avpA_	Alignment	not modelled	99.0	22	PDB header: de novo protein Chain: A: PDB Molecule: synthetic consensus tpr protein; PDBTitle: crystal structure of an 8 repeat consensus tpr superhelix
94	d2onda1	Alignment	not modelled	99.0	8	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: HAT/Suf repeat
95	c3q3hA_	Alignment	not modelled	98.9	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
96	c1xi4D_	Alignment	not modelled	98.9	11	PDB header: endocytosis/exocytosis Chain: D: PDB Molecule: clathrin heavy chain; PDBTitle: clathrin d6 coat
97	c3n71A_	Alignment	not modelled	98.8	13	PDB header: transcription Chain: A: PDB Molecule: histone lysine methyltransferase smyd1; PDBTitle: crystal structure of cardiac specific histone methyltransferase smyd1
98	d2ff4a2	Alignment	not modelled	98.8	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: BTAD-like
99	c3oxgA_	Alignment	not modelled	98.4	12	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)
100	c3mekA_	Alignment	not modelled	98.3	13	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
101	c2lahA_	Alignment	not modelled	98.3	11	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)
102	c2qfcB_	Alignment	not modelled	98.3	11	PDB header: transcription regulation Chain: B: PDB Molecule: plcr protein; PDBTitle: crystal structure of bacillus thuringiensis plcr complexed with papr
103	c3qwvA_	Alignment	not modelled	98.2	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
104	c1elva_	Alignment	not modelled	98.2	12	PDB header: glycosyltransferase Chain: A: PDB Molecule: 70-kda soluble lytic transglycosylase;

104	c13iyA_	Alignment	not modelled	98.2	12	PDBTitle: complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
105	dlouva_	Alignment	not modelled	98.1	18	Fold: alpha-alpha superhelix Superfamily: HCP-like Family: HCP-like
106	c2wviA_	Alignment	not modelled	97.8	12	PDB header: transferase Chain: A: PDB Molecule: mitotic checkpoint serine/threonine-protein PDBTitle: crystal structure of the n-terminal domain of bubr1
107	dliipa1	Alignment	not modelled	97.5	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
108	c3e4bD_	Alignment	not modelled	97.5	13	PDB header: protein binding Chain: D: PDB Molecule: algk; PDBTitle: crystal structure of algk from pseudomonas fluorescens wcs374r
109	c3rjvA_	Alignment	not modelled	97.4	15	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
110	c3txmA_	Alignment	not modelled	97.4	13	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
111	c2xm6A_	Alignment	not modelled	97.4	15	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
112	c3es1A_	Alignment	not modelled	96.8	9	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
113	c3mkqB_	Alignment	not modelled	96.4	12	PDB header: transport protein Chain: B: PDB Molecule: coatomer subunit alpha; PDBTitle: crystal structure of yeast alpha/betaprime-cop subcomplex of the cop12 vesicular coat
114	c3lvhA_	Alignment	not modelled	96.0	11	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
115	c2ff4B_	Alignment	not modelled	95.6	12	PDB header: transcription Chain: B: PDB Molecule: probable regulatory protein embr; PDBTitle: mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide
116	c3mkqA_	Alignment	not modelled	95.0	8	PDB header: transport protein Chain: A: PDB Molecule: coatomer beta'-subunit; PDBTitle: crystal structure of yeast alpha/betaprime-cop subcomplex of the cop12 vesicular coat
117	d1klxa_	Alignment	not modelled	93.7	14	Fold: alpha-alpha superhelix Superfamily: HCP-like Family: HCP-like
118	c3mkrB_	Alignment	not modelled	91.3	13	PDB header: transport protein Chain: B: PDB Molecule: coatomer subunit alpha; PDBTitle: crystal structure of yeast alpha/epsilon-cop subcomplex of the cop12 vesicular coat
119	c2pziA_	Alignment	not modelled	87.5	12	PDB header: transferase Chain: A: PDB Molecule: probable serine/threonine-protein kinase pkng; PDBTitle: crystal structure of protein kinase pkng from mycobacterium2 tuberculosis in complex with tetrahydrobenzothiophene ax20017
120	c3lpzA_	Alignment	not modelled	76.1	16	PDB header: protein transport Chain: A: PDB Molecule: get4 (yor164c homolog); PDBTitle: crystal structure of c. therm. get4