












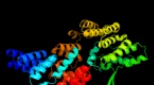
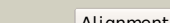











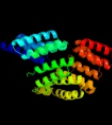









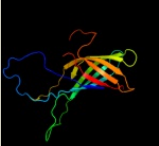


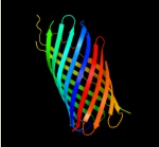
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xpiA_	 Alignment		100.0	12	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit cut9; PDBTitle: crystal structure of apc/c hetero-tetramer cut9-hcn1
2	d1w3ba_	 Alignment		100.0	14	Fold: alpha-alpha 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	d2o0ea1	 Alignment		100.0	10	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: HAT/Suf repeat
5	c3iegB_	 Alignment		100.0	14	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
6	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)
7	c2gw1A_	 Alignment		100.0	10	PDB header: protein transport Chain: A: PDB Molecule: mitochondrial precursor proteins import receptor; PDBTitle: crystal structure of the yeast tom70
8	d1qsaal	 Alignment		99.9	12	Fold: alpha-alpha superhelix Superfamily: Bacterial muramidases Family: Bacterial muramidases
9	c3hymB_	 Alignment		99.9	10	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	c2uy1A_	 Alignment		99.9	9	PDB header: rna-binding protein Chain: A: PDB Molecule: cleavage stimulation factor 77; PDBTitle: crystal structure of cstf-77
11	c1fchB_	 Alignment		99.9	16	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

12	c3cvpA_	Alignment		99.9	16	PDB header: transport protein Chain: A: PDB Molecule: peroxisome targeting signal 1 receptor pex5; PDBTitle: structure of peroxisomal targeting signal 1 (pts1) binding2 domain of trypanosoma brucei peroxin 5 (tbpex5)complexed3 to pts1 peptide (10-skl)
13	d1fcha_	Alignment		99.9	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
14	c3mkrA_	Alignment		99.9	14	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
15	c2ho1B_	Alignment		99.9	21	PDB header: protein binding Chain: B: PDB Molecule: type 4 fimbrial biogenesis protein pilf; PDBTitle: functional characterization of pseudomonas aeruginosa pilf
16	d1hz4a_	Alignment		99.9	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Transcription factor MalT domain III
17	c3pe3D_	Alignment		99.8	16	PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcna transferase and its complex with a peptide2 substrate
18	c2vq2A_	Alignment		99.8	25	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
19	d1dcea1	Alignment		99.8	13	Fold: alpha-alpha superhelix Superfamily: Protein prenylyltransferase Family: Protein prenylyltransferase
20	c1xi4D_	Alignment		99.8	11	PDB header: endocytosis/exocytosis Chain: D: PDB Molecule: clathrin heavy chain; PDBTitle: clathrin d6 coat
21	c3q75A_	Alignment	not modelled	99.8	8	PDB header: transferase Chain: A: PDB Molecule: farnesyltransferase alpha subunit; PDBTitle: cryptococcus neoformans protein farnesyltransferase in complex with2 fpt-ii and tkcvvm peptide
22	c3draA_	Alignment	not modelled	99.8	9	PDB header: transferase Chain: A: PDB Molecule: protein PDBTitle: candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp
23	d1d8da_	Alignment	not modelled	99.8	9	Fold: alpha-alpha superhelix Superfamily: Protein prenylyltransferase Family: Protein prenylyltransferase
24	c2q7fA_	Alignment	not modelled	99.8	14	PDB header: protein binding Chain: A: PDB Molecule: yrrb protein; PDBTitle: crystal structure of yrrb: a tpr protein with an unusual peptide-2 binding site
25	d1xnfa_	Alignment	not modelled	99.8	17	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
26	c3mv3B_	Alignment	not modelled	99.7	13	PDB header: protein transport Chain: B: PDB Molecule: coatomer subunit epsilon; PDBTitle: crystal structure of a-cop in complex with e-cop
27	d2h6fa1	Alignment	not modelled	99.7	9	Fold: alpha-alpha superhelix Superfamily: Protein prenylyltransferase Family: Protein prenylyltransferase
28	c1slyA_	Alignment	not modelled	99.7	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
						PDB header: transferase

29	c1tnol_	Alignment	not modelled	99.7	12	Chain: I: PDB Molecule: geranylgeranyltransferase type i alpha subunit; PDBTitle: rat protein geranylgeranyltransferase type-i complexed with2 a ggpp analog and a kksktkcvm peptide derived from k-3 ras4b
30	c3sf4B_	Alignment	not modelled	99.7	12	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
31	c3urzB_	Alignment	not modelled	99.7	16	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
32	c2pl2A_	Alignment	not modelled	99.7	31	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
33	c2hyzA_	Alignment	not modelled	99.6	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)
34	c3q15A_	Alignment	not modelled	99.6	9	PDB header: hydrolase/kinase Chain: A: PDB Molecule: response regulator aspartate phosphatase h; PDBTitle: crystal structure of raph complexed with spo0f
35	c2r5sB_	Alignment	not modelled	99.6	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
36	c1wao4_	Alignment	not modelled	99.5	12	PDB header: hydrolase Chain: 4: PDB Molecule: serine/threonine protein phosphatase 5; PDBTitle: pp5 structure
37	c2e2eA_	Alignment	not modelled	99.5	19	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
38	c3gyzB_	Alignment	not modelled	99.5	12	PDB header: chaperone Chain: B: PDB Molecule: chaperone protein ipgc; PDBTitle: crystal structure of ipgc from shigella flexneri
39	c2xcba_	Alignment	not modelled	99.5	11	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
40	d1hh8a_	Alignment	not modelled	99.5	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
41	c3as5A_	Alignment	not modelled	99.5	13	PDB header: protein binding Chain: A: PDB Molecule: mama; PDBTitle: mama amb-1 p212121
42	d1kt1a1	Alignment	not modelled	99.5	8	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
43	d2onda1	Alignment	not modelled	99.5	9	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: HAT/Suf repeat
44	d2c21a1	Alignment	not modelled	99.5	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
45	c2vyia_	Alignment	not modelled	99.5	16	PDB header: chaperone Chain: A: PDB Molecule: sgta protein; PDBTitle: crystal structure of the tpr domain of human sgt
46	d1elwa_	Alignment	not modelled	99.5	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
47	c3qdnA_	Alignment	not modelled	99.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin protein; PDBTitle: putative thioredoxin protein from salmonella typhimurium
48	d1p5qa1	Alignment	not modelled	99.4	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
49	c3ulqa_	Alignment	not modelled	99.4	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
50	c2c21D_	Alignment	not modelled	99.4	10	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	d1hxia_	Alignment	not modelled	99.4	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
52	c3sz7A_	Alignment	not modelled	99.4	14	PDB header: chaperone regulator Chain: A: PDB Molecule: hsc70 cochaperone (sgt); PDBTitle: crystal structure of the sgt2 tpr domain from aspergillus fumigatus
53	d1a17a_	Alignment	not modelled	99.4	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
						PDB header: structural protein Chain: A: PDB Molecule: smooth muscle cell associated protein-1,

54	c2dbaA	Alignment	not modelled	99.4	16	isoform PDBTitle: the solution structure of the tetratrico peptide repeat of2 human smooth muscle cell associated protein-1, isoform 2 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 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 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
55	c3rkvA	Alignment	not modelled	99.4	15	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 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 PDB header: ligase/chaperone Chain: B: PDB Molecule: stip1 homology and u box-containing protein 1; PDBTitle: crystal structure of the tpr domain of chip complexed with hsp70-c2 peptide
56	c2kckA	Alignment	not modelled	99.4	9	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 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 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
57	c3q49B	Alignment	not modelled	99.4	13	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
58	c2vsnB	Alignment	not modelled	99.3	13	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
59	c1ihgA	Alignment	not modelled	99.3	15	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin 40; PDBTitle: bovine cyclophilin 40, monoclinic form
60	d1ihga1	Alignment	not modelled	99.3	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
61	d1zu2a1	Alignment	not modelled	99.3	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
62	c2ifuA	Alignment	not modelled	99.3	10	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: gamma-snap; PDBTitle: crystal structure of a gamma-snap from danio rerio
63	c3k9iA	Alignment	not modelled	99.3	18	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
64	c1kt0A	Alignment	not modelled	99.3	8	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
65	d2buga1	Alignment	not modelled	99.3	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
66	c1qz2B	Alignment	not modelled	99.3	10	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
67	c2yhca	Alignment	not modelled	99.3	16	PDB header: membrane protein Chain: A: PDB Molecule: upf0169 lipoprotein yfio; PDBTitle: structure of bamd from e. coli
68	c3qkyA	Alignment	not modelled	99.3	11	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane assembly lipoprotein yfio; PDBTitle: crystal structure of rhodothermus marinus bamd
69	c3ly8A	Alignment	not modelled	99.3	8	PDB header: signaling protein Chain: A: PDB Molecule: transcriptional activator cadc; PDBTitle: crystal structure of mutant d471e of the periplasmic domain of cadc
70	c2fbaA	Alignment	not modelled	99.3	13	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
71	d2fba1	Alignment	not modelled	99.3	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
72	d1qqea	Alignment	not modelled	99.3	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
73	c2katA	Alignment	not modelled	99.3	12	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
74	c1na3A	Alignment	not modelled	99.3	13	PDB header: de novo protein Chain: A: PDB Molecule: designed protein ctrp2; PDBTitle: design of stable alpha-helical arrays from an idealized tpr2 motif
75	c3nf1A	Alignment	not modelled	99.2	20	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
76	c2xeVB	Alignment	not modelled	99.2	9	PDB header: metal binding Chain: B: PDB Molecule: ybgf; PDBTitle: crystal structure of the tpr domain of xanthomonas2 campestris ybgf
77	d1nzna	Alignment	not modelled	99.2	17	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
78	c3gw4B	Alignment	not modelled	99.2	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.
						Fold: alpha-alpha superhelix

79	d1elra_	Alignment	not modelled	99.2	13	Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
80	c2l6jA_	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
81	d1zbpa1	Alignment	not modelled	99.1	15	Fold: ImpE-like Superfamily: ImpE-like Family: ImpE-like
82	c2vgxA_	Alignment	not modelled	99.1	13	PDB header: chaperone Chain: A: PDB Molecule: chaperone sycd; PDBTitle: structure of the yersinia enterocolitica type iii secretion2 translocator chaperone sycd
83	d1iyga_	Alignment	not modelled	99.1	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
84	d1pc2a_	Alignment	not modelled	99.1	17	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
85	c3cegB_	Alignment	not modelled	99.1	18	PDB header: motor protein, transport protein Chain: B: PDB Molecule: kinesin light chain 2; PDBTitle: the tpr domain of human kinesin light chain 2 (hklc2)
86	c2avpA_	Alignment	not modelled	99.0	21	PDB header: de novo protein Chain: A: PDB Molecule: synthetic consensus tpr protein; PDBTitle: crystal structure of an 8 repeat consensus tpr superhelix
87	c2kcvA_	Alignment	not modelled	99.0	11	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 (nsg) target srr115c
88	c1lxA_	Alignment	not modelled	99.0	9	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
89	c2kc7A_	Alignment	not modelled	99.0	17	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
90	d2hr2a1	Alignment	not modelled	98.9	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: CT2138-like
91	c2if4A_	Alignment	not modelled	98.9	11	PDB header: signaling protein Chain: A: PDB Molecule: atfkbp42; PDBTitle: crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana
92	c3beeB_	Alignment	not modelled	98.8	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative yfre protein; PDBTitle: crystal structure of putative yfre protein from vibrio2 parahaemolyticus
93	d1tjca_	Alignment	not modelled	98.8	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
94	c3fflC_	Alignment	not modelled	98.8	8	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
95	d1y8ma1	Alignment	not modelled	98.7	6	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
96	c3n71A_	Alignment	not modelled	98.7	17	PDB header: transcription Chain: A: PDB Molecule: histone lysine methyltransferase smyd1; PDBTitle: crystal structure of cardiac specific histone methyltransferase smyd1
97	d2ff4a2	Alignment	not modelled	98.6	9	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: BTAD-like
98	d2pqrbl	Alignment	not modelled	98.5	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
99	c3q3hA_	Alignment	not modelled	98.3	4	PDB header: transferase Chain: A: PDB Molecule: hmw1c-like glycosyltransferase; PDBTitle: crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
100	c2xm6A_	Alignment	not modelled	98.1	9	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
101	c3qvwA_	Alignment	not modelled	97.8	9	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
102	c3mekA_	Alignment	not modelled	97.8	10	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
103	c3oxgA_	Alignment	not modelled	97.6	10	PDB header: transferase Chain: A: PDB Molecule: set and mynd domain-containing protein 3; PDBTitle: human lysine methyltransferase smyd3 in complex with adohcy (form iii)
						PDB header: transcription

104	c2ff4B_	Alignment	not modelled	97.5	5	Chain: B: PDB Molecule: probable regulatory protein embr; PDBTitle: mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide
105	c3aehB_	Alignment		97.5	10	PDB header: hydrolase Chain: B: PDB Molecule: hemoglobin-binding protease hbp PDBTitle: integral membrane domain of autotransporter hbp
106	c3qq2C_	Alignment		97.4	12	PDB header: membrane protein/protein transport Chain: C: PDB Molecule: brka autotransporter; PDBTitle: crystal structure of the beta domain of the bordetella autotransporter2 brka
107	c3txmA_	Alignment	not modelled	97.3	7	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
108	c3mkqA_	Alignment	not modelled	97.3	12	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
109	d1qjpa_	Alignment		97.3	17	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
110	d1ouva_	Alignment	not modelled	97.3	11	Fold: alpha-alpha superhelix Superfamily: HCP-like Family: HCP-like
111	c2qfcB_	Alignment	not modelled	97.3	12	PDB header: transcription regulation Chain: B: PDB Molecule: plcr protein; PDBTitle: crystal structure of bacillus thuringiensis plcr complexed with papr
112	c2k0lA_	Alignment		97.2	14	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein a; PDBTitle: nmr structure of the transmembrane domain of the outer2 membrane protein a from klebsiella pneumoniae in dhpc3 micelles.
113	c2lahA_	Alignment	not modelled	97.1	15	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)
114	c2x4mD_	Alignment		96.8	10	PDB header: hydrolase Chain: D: PDB Molecule: coagulase/fibrinolysin; PDBTitle: yersinia pestis plasminogen activator pla
115	c3lvhA_	Alignment	not modelled	96.8	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
116	c3nb3C_	Alignment		96.8	17	PDB header: virus Chain: C: PDB Molecule: outer membrane protein a; PDBTitle: the host outer membrane proteins ompa and ompc are packed at specific2 sites in the shigella phage sf6 virion as structural components
117	d1t16a_	Alignment	not modelled	96.7	11	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Outer membrane protein transport protein
118	c3dwoX_	Alignment	not modelled	96.7	13	PDB header: membrane protein Chain: X: PDB Molecule: probable outer membrane protein; PDBTitle: crystal structure of a pseudomonas aeruginosa fadl homologue
119	d1uynx_	Alignment		96.6	13	Fold: Transmembrane beta-barrels Superfamily: Autotransporter Family: Autotransporter
120	c3brzA_	Alignment	not modelled	96.5	13	PDB header: transport protein Chain: A: PDB Molecule: todx; PDBTitle: crystal structure of the pseudomonas putida toluene2 transporter todx