















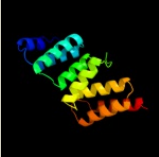


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ly8A_	 Alignment		100.0	11	PDB header: signaling protein Chain: A: PDB Molecule: transcriptional activator cadc; PDBTitle: crystal structure of mutant d471e of the periplasmic domain of cadc
2	c3pe3D_	 Alignment		99.9	11	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
3	c2hqnA_	 Alignment		99.9	18	PDB header: signaling protein Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
4	c2jzyA_	 Alignment		99.9	16	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein pcor; PDBTitle: solution structure of c-terminal effector domain of2 putative two-component-system response regulator involved3 in copper resistance from klebsiella pneumoniae
5	d1p2fa1	 Alignment		99.9	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
6	d1gxqa_	 Alignment		99.9	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
7	c2pmuD_	 Alignment		99.9	19	PDB header: transcription regulation Chain: D: PDB Molecule: response regulator phop; PDBTitle: crystal structure of the dna-binding domain of phop
8	c2hvwA_	 Alignment		99.9	14	PDB header: transcription Chain: A: PDB Molecule: dna-binding response regulator vicr; PDBTitle: crystal structure of an essential response regulator dna binding2 domain, vicrc in enterococcus faecalis, a member of the yycf3 subfamily.
9	c3q9vB_	 Alignment		99.9	17	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of rra c-terminal domain(123-221) from deinococcus2 radiodurans
10	d1ys7a1	 Alignment		99.9	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
11	d1opca_	 Alignment		99.8	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like

12	c2xpiA_	Alignment		99.8	11	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit cut9; PDBTitle: crystal structure of apc/c hetero-tetramer cut9-hcn1
13	c2zxiB_	Alignment		99.8	16	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein walr; PDBTitle: crystal structure of yycf dna-binding domain from staphylococcus2 aureus
14	d1d8da_	Alignment		99.8	9	Fold: alpha-alpha superhelix Superfamily: Protein prenyltransferase Family: Protein prenyltransferase
15	c2k4jA_	Alignment		99.8	18	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: arsr dna binding domain
16	d1kgsa1	Alignment		99.8	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
17	d2h6fa1	Alignment		99.8	10	Fold: alpha-alpha superhelix Superfamily: Protein prenyltransferase Family: Protein prenyltransferase
18	c1tnol_	Alignment		99.8	9	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 kkskstkcvim peptide derived from k-3 ras4b
19	c2y4tA_	Alignment		99.8	27	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 3; PDBTitle: crystal structure of the human co-chaperone p58(ipk)
20	c2oqrA_	Alignment		99.8	18	PDB header: transcription,signaling protein Chain: A: PDB Molecule: sensory transduction protein regx3; PDBTitle: the structure of the response regulator regx3 from mycobacterium2 tuberculosis
21	c1ys7B_	Alignment	not modelled	99.8	19	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed with2 mg2+
22	d1dcea1	Alignment	not modelled	99.7	8	Fold: alpha-alpha superhelix Superfamily: Protein prenyltransferase Family: Protein prenyltransferase
23	c2hqrA_	Alignment	not modelled	99.7	18	PDB header: signaling protein Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
24	c3iegB_	Alignment	not modelled	99.7	27	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
25	c3q75A_	Alignment	not modelled	99.7	8	PDB header: transferase Chain: A: PDB Molecule: farnesyltransferase alpha subunit; PDBTitle: cryptococcus neoformans protein farnesyltransferase in complex with2 fpt-ii and tkcvvm peptide
26	d1w3ba_	Alignment	not modelled	99.7	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
27	c1fchB_	Alignment	not modelled	99.7	11	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
28	c3as5A_	Alignment	not modelled	99.7	11	PDB header: protein binding Chain: A: PDB Molecule: mama; PDBTitle: mama amb-1 p212121

29	c3hymB_	Alignment	not modelled	99.7	14	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
30	c2r5sB_	Alignment	not modelled	99.7	15	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
31	c1wao4_	Alignment	not modelled	99.7	11	PDB header: hydrolase Chain: 4: PDB Molecule: serine/threonine protein phosphatase 5; PDBTitle: pp5 structure
32	c3fp4A_	Alignment	not modelled	99.7	14	PDB header: transport protein Chain: A: PDB Molecule: tpr repeat-containing protein yhr117w; PDBTitle: crystal structure of tom71 complexed with ssa1 c-terminal2 fragment
33	c3urzB_	Alignment	not modelled	99.7	10	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
34	c2e2eA_	Alignment		99.7	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
35	c3gyzB_	Alignment	not modelled	99.7	8	PDB header: chaperone Chain: B: PDB Molecule: chaperone protein ipgc; PDBTitle: crystal structure of ipgc from shigella flexneri
36	d2c2la1	Alignment	not modelled	99.7	9	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
37	c2gwrA_	Alignment	not modelled	99.7	19	PDB header: signaling protein Chain: A: PDB Molecule: dna-binding response regulator mtra; PDBTitle: crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
38	c2xcbA_	Alignment	not modelled	99.7	7	PDB header: protein binding Chain: A: PDB Molecule: regulatory protein pcrr; PDBTitle: crystal structure of pcrr in complex with the chaperone2 binding region of popd
39	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)
40	c3cvpA_	Alignment	not modelled	99.7	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)
41	c2ho1B_	Alignment	not modelled	99.7	12	PDB header: protein binding Chain: B: PDB Molecule: type 4 fimbrial biogenesis protein pilf; PDBTitle: functional characterization of pseudomonas aeruginosa pilf
42	c2vq2A_	Alignment	not modelled	99.7	9	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
43	d1fcha_	Alignment	not modelled	99.7	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
44	d1zu2a1	Alignment	not modelled	99.7	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
45	c2q7fA_	Alignment	not modelled	99.7	10	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
46	d1hh8a_	Alignment	not modelled	99.6	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
47	c2vsnB_	Alignment	not modelled	99.6	14	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
48	d1xnfa_	Alignment	not modelled	99.6	10	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
49	c2c21D_	Alignment	not modelled	99.6	15	PDB header: chaperone Chain: D: PDB Molecule: carboxy terminus of hsp70-interacting protein; PDBTitle: crystal structure of the chip u-box e3 ubiquitin ligase
50	c3sz7A_	Alignment	not modelled	99.6	14	PDB header: chaperone regulator Chain: A: PDB Molecule: hsc70 cochaperone (sgt); PDBTitle: crystal structure of the sgt2 tpr domain from aspergillus fumigatus
51	c3draA_	Alignment	not modelled	99.6	6	PDB header: transferase Chain: A: PDB Molecule: protein PDBTitle: candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp
52	c1p2fA_	Alignment	not modelled	99.6	29	PDB header: transcription Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure analysis of response regulator drrb, a2 thermotoga maritima omp/pr/phob homolog

53	c2katA		Alignment	not modelled	99.6	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
54	d1elwa		Alignment	not modelled	99.6	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
55	d2ff4a1		Alignment	not modelled	99.6	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
56	c3mkrA		Alignment	not modelled	99.6	10	PDB header: transport protein Chain: A: PDB Molecule: coatomer subunit epsilon; PDBTitle: crystal structure of yeast alpha/epsilon-cop subcomplex of the cop2 vesicular coat
57	c2kckA		Alignment	not modelled	99.6	13	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
58	c3r0jA		Alignment	not modelled	99.6	19	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
59	c2gw1A		Alignment	not modelled	99.6	9	PDB header: protein transport Chain: A: PDB Molecule: mitochondrial precursor proteins import receptor; PDBTitle: crystal structure of the yeast tom70
60	c3k9iA		Alignment	not modelled	99.6	10	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
61	d1a17a		Alignment	not modelled	99.6	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
62	c3mv3B		Alignment	not modelled	99.6	12	PDB header: protein transport Chain: B: PDB Molecule: coatomer subunit epsilon; PDBTitle: crystal structure of a-cop in complex with e-cop
63	c2vyiA		Alignment	not modelled	99.5	14	PDB header: chaperone Chain: A: PDB Molecule: sgta protein; PDBTitle: crystal structure of the tpr domain of human sgt
64	c1ltxA		Alignment	not modelled	99.5	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
65	c2pl2A		Alignment	not modelled	99.5	18	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
66	d2hqsa2		Alignment	not modelled	99.5	14	Fold: Anticodon-binding domain-like Superfamily: TolB, N-terminal domain Family: TolB, N-terminal domain
67	d1elra		Alignment	not modelled	99.5	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
68	c2vgxA		Alignment	not modelled	99.5	8	PDB header: chaperone Chain: A: PDB Molecule: chaperone sycd; PDBTitle: structure of the yersinia enterocolitica type iii secretion2 translocator chaperone sycd
69	d1hxia		Alignment	not modelled	99.5	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
70	c3q49B		Alignment	not modelled	99.5	16	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
71	d2buga1		Alignment	not modelled	99.5	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
72	d2o0ea1		Alignment	not modelled	99.5	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: HAT/Suf repeat
73	c1kgsA		Alignment	not modelled	99.4	23	PDB header: dna binding protein Chain: A: PDB Molecule: dna binding response regulator d; PDBTitle: crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
74	c1na3A		Alignment	not modelled	99.4	14	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	c2dbaA		Alignment	not modelled	99.4	15	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
76	c3qdnA		Alignment	not modelled	99.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin protein; PDBTitle: putative thioredoxin protein from salmonella typhimurium
77	d1nzna		Alignment	not modelled	99.4	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
78	d1iyga		Alignment	not modelled	99.4	14	Fold: alpha-alpha superhelix Superfamily: TPR-like

					Family: Tetratricopeptide repeat (TPR)
79	c1ihgA_	Alignment	not modelled	99.4	11 PDB header: isomerase Chain: A: PDB Molecule: cyclophilin 40; PDBTitle: bovine cyclophilin 40, monoclinic form
80	d1zbpa1	Alignment	not modelled	99.4	11 Fold: ImpE-like Superfamily: ImpE-like Family: ImpE-like
81	d1pc2a_	Alignment	not modelled	99.4	15 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
82	c1kt0A_	Alignment	not modelled	99.4	16 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
83	c2uy1A_	Alignment	not modelled	99.4	12 PDB header: rna-binding protein Chain: A: PDB Molecule: cleavage stimulation factor 77; PDBTitle: crystal structure of cstf-77
84	c3gw4B_	Alignment	not modelled	99.4	13 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.
85	c2kcvA_	Alignment	not modelled	99.4	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 (nesg) target srr115c
86	d1kt1a1	Alignment	not modelled	99.4	12 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
87	c2xevB_	Alignment	not modelled	99.4	11 PDB header: metal binding Chain: B: PDB Molecule: ybgf; PDBTitle: crystal structure of the tpr domain of xanthomonas2 campestris ybgf
88	d1p5qa1	Alignment	not modelled	99.3	13 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
89	c3rkva_	Alignment	not modelled	99.3	13 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	d1ihga1	Alignment	not modelled	99.3	13 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
91	d1hz4a_	Alignment	not modelled	99.3	15 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Transcription factor MalT domain III
92	c2ff4B_	Alignment	not modelled	99.3	20 PDB header: transcription Chain: B: PDB Molecule: probable regulatory protein embr; PDBTitle: mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide
93	c2l6jA_	Alignment	not modelled	99.3	8 PDB header: protein binding Chain: A: PDB Molecule: tpr repeat-containing protein associated with hsp90; PDBTitle: tah1 complexed by meevd
94	c3q15A_	Alignment	not modelled	99.3	8 PDB header: hydrolase/kinase Chain: A: PDB Molecule: response regulator aspartate phosphatase h; PDBTitle: crystal structure of raph complexed with spoOf
95	c1qz2B_	Alignment	not modelled	99.3	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
96	d2hr2a1	Alignment	not modelled	99.3	16 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: CT2138-like
97	c2fbaA_	Alignment	not modelled	99.3	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
98	d2fbna1	Alignment	not modelled	99.3	16 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
99	d1qsaa1	Alignment	not modelled	99.3	8 Fold: alpha-alpha superhelix Superfamily: Bacterial muramidases Family: Bacterial muramidases
100	c2avpA_	Alignment	not modelled	99.3	18 PDB header: de novo protein Chain: A: PDB Molecule: synthetic consensus tpr protein; PDBTitle: crystal structure of an 8 repeat consensus tpr superhelix
101	c2if4A_	Alignment	not modelled	99.2	12 PDB header: signaling protein Chain: A: PDB Molecule: atfkbp42; PDBTitle: crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana
102	c2yhca_	Alignment	not modelled	99.2	13 PDB header: membrane protein Chain: A: PDB Molecule: upf0169 lipoprotein yfio; PDBTitle: structure of bamd from e. coli
103	c2ifuA_	Alignment	not modelled	99.2	13 PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: gamma-snap; PDBTitle: crystal structure of a gamma-snap from danio rerio
104	d2onda1	Alignment	not modelled	99.2	9 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: HAT/Suf repeat

105	d1y8ma1	Alignment	not modelled	99.2	8	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
106	c3q9sa_	Alignment	not modelled	99.2	15	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of rra(1-215) from deinococcus radiodurans
107	c3qkyA_	Alignment	not modelled	99.1	13	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane assembly lipoprotein yfio; PDBTitle: crystal structure of rhodothermus marinus bamd
108	c2kc7A_	Alignment	not modelled	99.1	11	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
109	c3ulqA_	Alignment	not modelled	99.1	9	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
110	d1tjca_	Alignment	not modelled	99.1	17	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
111	d1qqea_	Alignment	not modelled	99.0	10	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
112	c3beeB_	Alignment	not modelled	99.0	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative yfre protein; PDBTitle: crystal structure of putative yfre protein from vibrio2 parahaemolyticus
113	c3sf4B_	Alignment	not modelled	98.9	18	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
114	c3fflC_	Alignment	not modelled	98.9	17	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
115	d2pqrbl	Alignment	not modelled	98.8	9	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
116	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
117	d2ff4a2	Alignment	not modelled	98.7	10	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: BTAD-like
118	c3nf1A_	Alignment	not modelled	98.6	11	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
119	c3q3ha_	Alignment	not modelled	98.5	6	PDB header: transferase Chain: A: PDB Molecule: hmw1c-like glycosyltransferase; PDBTitle: crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
120	c1slvA_	Alignment	not modelled	98.4	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