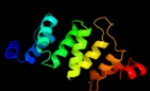
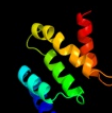


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xm6A_	 Alignment		99.9	22	PDB header: unknown function Chain: A: PDB Molecule: protein corresponding to locus c5321 from cft073 e.coli PDBTitle: crystal structure of the protein corresponding to locus c5321 from2 cft073 e.coli strain
2	c3e4bD_	 Alignment		99.9	15	PDB header: protein binding Chain: D: PDB Molecule: algk; PDBTitle: crystal structure of algk from pseudomonas fluorescens wcs374r
3	d1klxa_	 Alignment		99.8	17	Fold: alpha-alpha superhelix Superfamily: HCP-like Family: HCP-like
4	d1ouva_	 Alignment		99.7	26	Fold: alpha-alpha superhelix Superfamily: HCP-like Family: HCP-like
5	c3rjvA_	 Alignment		99.5	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
6	d1pc2a_	 Alignment		97.7	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratrico peptide repeat (TPR)
7	d1iyga_	 Alignment		97.7	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratrico peptide repeat (TPR)
8	d1tjca_	 Alignment		97.7	17	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratrico peptide repeat (TPR)
9	c2xcba_	 Alignment		97.5	12	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
10	c1wao4_	 Alignment		97.5	13	PDB header: hydrolase Chain: 4: PDB Molecule: serine/threonine protein phosphatase 5; PDBTitle: pp5 structure
11	d1nzna_	 Alignment		97.4	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratrico peptide repeat (TPR)

12	c3gyzB_	Alignment		97.3	9	PDB header: chaperone Chain: B: PDB Molecule: chaperone protein ipgc; PDBTitle: crystal structure of ipgc from shigella flexneri
13	d1w3ba_	Alignment		97.2	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
14	d1hxia_	Alignment		97.2	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
15	c2xpiA_	Alignment		97.2	10	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit cut9; PDBTitle: crystal structure of apc/c hetero-tetramer cut9-hcn1
16	c2katA_	Alignment		97.2	22	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
17	c2kcvA_	Alignment		97.1	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tetratricopeptide repeat domain protein; PDBTitle: solution nmr structure of tetratricopeptide repeat domain2 protein sru_0103 from salinibacter ruber, northeast3 structural genomics consortium (nesg) target srr115c
18	c3pe3D_	Alignment		97.0	15	PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcna2 transferase and its complex with a peptide2 substrate
19	c3iegB_	Alignment		97.0	11	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
20	c2y4tA_	Alignment		96.9	11	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 3; PDBTitle: crystal structure of the human co-chaperone p58(ipk)
21	c3fp4A_	Alignment	not modelled	96.9	12	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	c1na3A_	Alignment	not modelled	96.9	20	PDB header: de novo protein Chain: A: PDB Molecule: designed protein ctp2; PDBTitle: design of stable alpha-helical arrays from an idealized tpr2 motif
23	c2vsnB_	Alignment	not modelled	96.8	16	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
24	d1elwa_	Alignment	not modelled	96.8	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
25	c2gw1A_	Alignment	not modelled	96.8	6	PDB header: protein transport Chain: A: PDB Molecule: mitochondrial precursor proteins import receptor; PDBTitle: crystal structure of the yeast tom70
26	d2pqrbl	Alignment	not modelled	96.6	9	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
27	d2buga1	Alignment	not modelled	96.6	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
28	d1y8ma1	Alignment	not modelled	96.5	8	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)

29	c2dbaA	Alignment	not modelled	96.5	13	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
30	c3fflC	Alignment	not modelled	96.5	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
31	d1zu2a1	Alignment	not modelled	96.3	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratrico peptide repeat (TPR)
32	c2c2lD	Alignment	not modelled	96.3	16	PDB header: chaperone Chain: D: PDB Molecule: carboxy terminus of hsp70-interacting protein; PDBTitle: crystal structure of the chip u-box e3 ubiquitin ligase
33	c2kckA	Alignment	not modelled	96.2	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tptr repeat; PDBTitle: nmr solution structure of the northeast structural genomics2 consortium (nesg) target mrr121a
34	c3urzB	Alignment	not modelled	96.1	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
35	c2vyia	Alignment	not modelled	96.1	17	PDB header: chaperone Chain: A: PDB Molecule: sgta protein; PDBTitle: crystal structure of the tpr domain of human sgt
36	c3qkyA	Alignment	not modelled	96.1	11	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane assembly lipoprotein yfio; PDBTitle: crystal structure of rhodothermus marinus bamd
37	c3hymB	Alignment	not modelled	96.0	13	PDB header: cell cycle, ligase Chain: B: PDB Molecule: cell division cycle protein 16 homolog; PDBTitle: insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure
38	c3beeB	Alignment	not modelled	95.8	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative yfre protein; PDBTitle: crystal structure of putative yfre protein from vibrio2 parahaemolyticus
39	c3k9iA	Alignment	not modelled	95.7	12	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
40	d1hh8a	Alignment	not modelled	95.4	22	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratrico peptide repeat (TPR)
41	c2avpA	Alignment	not modelled	95.3	16	PDB header: de novo protein Chain: A: PDB Molecule: synthetic consensus tpr protein; PDBTitle: crystal structure of an 8 repeat consensus tpr superhelix
42	d1elra	Alignment	not modelled	95.3	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratrico peptide repeat (TPR)
43	c2e2eA	Alignment	not modelled	95.1	11	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
44	d2c2la1	Alignment	not modelled	95.1	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratrico peptide repeat (TPR)
45	c3q75A	Alignment	not modelled	94.9	12	PDB header: transferase Chain: A: PDB Molecule: farnesyltransferase alpha subunit; PDBTitle: cryptococcus neoformans protein farnesyltransferase in complex with2 fpt-ii and tkcvvm peptide
46	c2xevB	Alignment	not modelled	94.9	11	PDB header: metal binding Chain: B: PDB Molecule: ybgf; PDBTitle: crystal structure of the tpr domain of xanthomonas2 campestris ybgf
47	c1fchB	Alignment	not modelled	94.7	15	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
48	d1a17a	Alignment	not modelled	94.7	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratrico peptide repeat (TPR)
49	d1qsaal	Alignment	not modelled	94.1	9	Fold: alpha-alpha superhelix Superfamily: Bacterial muramidases Family: Bacterial muramidases
50	d1fcha	Alignment	not modelled	94.0	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratrico peptide repeat (TPR)
51	c2r5sB	Alignment	not modelled	94.0	10	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
52	c2vgxA	Alignment	not modelled	93.8	13	PDB header: chaperone Chain: A: PDB Molecule: chaperone sycd; PDBTitle: structure of the yersinia enterocolitica type iii secretion2 translocator chaperone sycd
53	c1ihgA	Alignment	not modelled	93.5	9	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin 40; PDBTitle: bovine cyclophilin 40, monoclinic form
54	c2k7A	Alignment	not modelled	93.4	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bfr218_protein;

54	c2k7A	Alignment	not modelled	93.4	10	PDBTitle: solution nmr structure of bacteroides fragilis protein2 bf1650. northeast structural genomics consortium target3 bfr218
55	d1xnfa	Alignment	not modelled	93.0	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
56	c3sz7A	Alignment	not modelled	92.9	11	PDB header: chaperone regulator Chain: A: PDB Molecule: hsc70 cochaperone (sgt); PDBTitle: crystal structure of the sgt2 tpr domain from aspergillus fumigatus
57	c2l6jA	Alignment	not modelled	92.3	9	PDB header: protein binding Chain: A: PDB Molecule: tpr repeat-containing protein associated with hsp90; PDBTitle: tah1 complexed by meevd
58	c2pl2A	Alignment	not modelled	92.2	15	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
59	c3cvpA	Alignment	not modelled	92.0	14	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)
60	c3mv3B	Alignment	not modelled	91.8	12	PDB header: protein transport Chain: B: PDB Molecule: coatomer subunit epsilon; PDBTitle: crystal structure of a-cop in complex with e-cop
61	c3sf4B	Alignment	not modelled	91.5	13	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	91.4	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
63	c2if4A	Alignment	not modelled	91.2	15	PDB header: signaling protein Chain: A: PDB Molecule: atfkbp42; PDBTitle: crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana
64	d1kt1a1	Alignment	not modelled	90.8	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
65	d1p5qa1	Alignment	not modelled	89.6	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
66	c3draA	Alignment	not modelled	89.3	14	PDB header: transferase Chain: A: PDB Molecule: protein PDBTitle: candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp
67	c3mkrA	Alignment	not modelled	89.1	7	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
68	c2vq2A	Alignment	not modelled	88.3	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
69	c1qz2B	Alignment	not modelled	87.3	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
70	c2ho1B	Alignment	not modelled	86.5	8	PDB header: protein binding Chain: B: PDB Molecule: type 4 fimbrial biogenesis protein pilf; PDBTitle: functional characterization of pseudomonas aeruginosa pilf
71	d1d8da	Alignment	not modelled	85.9	8	Fold: alpha-alpha superhelix Superfamily: Protein prenyltransferase Family: Protein prenyltransferase
72	d2hr2a1	Alignment	not modelled	85.5	7	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: CT2138-like
73	c3cegB	Alignment	not modelled	85.1	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)
74	c3rkva	Alignment	not modelled	84.2	11	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
75	c3q15A	Alignment	not modelled	83.5	10	PDB header: hydrolase/kinase Chain: A: PDB Molecule: response regulator aspartate phosphatase h; PDBTitle: crystal structure of raph complexed with spo0f
76	c1slyA	Alignment	not modelled	83.0	9	PDB header: glycosyltransferase Chain: A: PDB Molecule: 70-kda soluble lytic transglycosylase; PDBTitle: complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
77	c3q49B	Alignment	not modelled	82.5	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
78	d1ihga1	Alignment	not modelled	80.9	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
79	c2hyzA	Alignment	not modelled	79.8	15	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)
80	d2fba1	Alignment	not modelled	79.4	20 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
81	c2fbaA	Alignment	not modelled	79.4	20 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
82	c1tnoL	Alignment	not modelled	76.8	8 PDB header: transferase Chain: I: PDB Molecule: geranylgeranyltransferase type i alpha subunit; PDBTitle: rat protein geranylgeranyltransferase type-i complexed with2 a gppp analog and a kksktkcvm peptide derived from k-3 ras4b
83	d2h6fa1	Alignment	not modelled	73.5	8 Fold: alpha-alpha superhelix Superfamily: Protein prenyltransferase Family: Protein prenyltransferase
84	c3ulqA	Alignment	not modelled	69.2	10 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
85	c3ly8A	Alignment	not modelled	68.4	11 PDB header: signaling protein Chain: A: PDB Molecule: transcriptional activator cadc; PDBTitle: crystal structure of mutant d471e of the periplasmic domain of cadc
86	c3gw4B	Alignment	not modelled	67.7	14 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.
87	c3as5A	Alignment	not modelled	67.6	10 PDB header: protein binding Chain: A: PDB Molecule: mama; PDBTitle: mama amb-1 p212121
88	c2ifuA	Alignment	not modelled	66.9	4 PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: gamma-snap; PDBTitle: crystal structure of a gamma-snap from danio rerio
89	c2q7fA	Alignment	not modelled	66.3	15 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
90	d2ooea1	Alignment	not modelled	63.1	13 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: HAT/Suf repeat
91	d1zbpa1	Alignment	not modelled	61.2	14 Fold: ImpE-like Superfamily: ImpE-like Family: ImpE-like
92	d1dcea1	Alignment	not modelled	60.3	10 Fold: alpha-alpha superhelix Superfamily: Protein prenyltransferase Family: Protein prenyltransferase
93	c1xi4D	Alignment	not modelled	58.7	7 PDB header: endocytosis/exocytosis Chain: D: PDB Molecule: clathrin heavy chain; PDBTitle: clathrin d6 coat
94	c3n71A	Alignment	not modelled	56.6	9 PDB header: transcription Chain: A: PDB Molecule: histone lysine methyltransferase smyd1; PDBTitle: crystal structure of cardiac specific histone methyltransferase smyd1
95	c3oxgA	Alignment	not modelled	44.3	13 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)
96	c3qdnA	Alignment	not modelled	40.6	10 PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin protein; PDBTitle: putative thioredoxin protein from salmonella typhimurium
97	c3nf1A	Alignment	not modelled	39.6	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
98	d1hz4a	Alignment	not modelled	39.2	6 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Transcription factor Mat domain III
99	c2yhCA	Alignment	not modelled	37.1	11 PDB header: membrane protein Chain: A: PDB Molecule: upf0169 lipoprotein yfio; PDBTitle: structure of bamd from e. coli
100	c2hz8A	Alignment	not modelled	35.1	17 PDB header: de novo protein Chain: A: PDB Molecule: de novo designed diiron protein; PDBTitle: qm/mm structure refined from nmr-structure of a single2 chain diiron protein
101	c2uy1A	Alignment	not modelled	26.0	8 PDB header: rna-binding protein Chain: A: PDB Molecule: cleavage stimulation factor 77; PDBTitle: crystal structure of cstf-77