

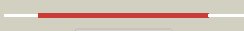
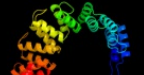





























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xm6A_	 Alignment		100.0	34	PDB header: unknown function Chain: A: PDB Molecule: protein corresponding to locus c5321 from cft073 e.coli PDBTitle: crystal structure of the protein corresponding to locus c5321 from2 cft073 e.coli strain
2	dlouva_	 Alignment		100.0	22	Fold: alpha-alpha superhelix Superfamily: HCP-like Family: HCP-like
3	c3e4bD_	 Alignment		100.0	34	PDB header: protein binding Chain: D: PDB Molecule: algk; PDBTitle: crystal structure of algk from pseudomonas fluorescens wcs374r
4	c3rjvA_	 Alignment		99.9	30	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
5	d1klxa_	 Alignment		99.8	24	Fold: alpha-alpha superhelix Superfamily: HCP-like Family: HCP-like
6	c3hymB_	 Alignment		98.9	8	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
7	c2v4tA_	 Alignment		98.8	10	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 3; PDBTitle: crystal structure of the human co-chaperone p58(ipk)
8	c3iegB_	 Alignment		98.8	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
9	d1w3ba_	 Alignment		98.6	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
10	c2xpiA_	 Alignment		98.4	19	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit cut9; PDBTitle: crystal structure of apc/c hetero-tetramer cut9-hcn1
11	c2gw1A_	 Alignment		98.4	16	PDB header: protein transport Chain: A: PDB Molecule: mitochondrial precursor proteins import receptor; PDBTitle: crystal structure of the yeast tom70

12	c1fchB_	Alignment		98.4	17	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
13	c3pe3D_	Alignment		98.1	19	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
14	c2ho1B_	Alignment		98.1	16	PDB header: protein binding Chain: B: PDB Molecule: type 4 fimbrial biogenesis protein pilf; PDBTitle: functional characterization of pseudomonas aeruginosa pilf
15	d1xnfa_	Alignment		98.1	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
16	c2q7fA_	Alignment		98.0	18	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
17	c3sf4B_	Alignment		98.0	11	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
18	c2vq2A_	Alignment		97.9	12	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	c2pl2A_	Alignment		97.9	23	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
20	d1fcha_	Alignment		97.9	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
21	c3as5A_	Alignment	not modelled	97.8	20	PDB header: protein binding Chain: A: PDB Molecule: mama; PDBTitle: mama amb-1 p212121
22	c3cvpA_	Alignment	not modelled	97.8	15	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)
23	c3urzB_	Alignment	not modelled	97.7	12	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
24	d1tjca_	Alignment	not modelled	97.7	20	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
25	c2ifuA_	Alignment	not modelled	97.5	13	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: gamma-snap; PDBTitle: crystal structure of a gamma-snap from danio rerio
26	d1y8ma1	Alignment	not modelled	97.4	9	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
27	d1hxia_	Alignment	not modelled	97.4	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
28	c3draA_	Alignment	not modelled	97.4	7	PDB header: transferase Chain: A: PDB Molecule: protein PDBTitle: candida albicans protein geranylgeranyltransferase-i2

						complexed with ggpp
29	d1dcea1	Alignment	not modelled	97.4	5	Fold: alpha-alpha superhelix Superfamily: Protein prenyltransferase Family: Protein prenyltransferase
30	c3q15A	Alignment	not modelled	97.3	12	PDB header: hydrolase/kinase Chain: A: PDB Molecule: response regulator aspartate phosphatase h; PDBTitle: crystal structure of raph complexed with spo0f
31	c2katA	Alignment	not modelled	97.3	13	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
32	c3nf1A	Alignment	not modelled	97.2	12	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
33	c2e2eA	Alignment	not modelled	97.0	21	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
34	d1iyga	Alignment	not modelled	96.9	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
35	c2xcba	Alignment	not modelled	96.9	8	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
36	c2c21D	Alignment	not modelled	96.9	14	PDB header: chaperone Chain: D: PDB Molecule: carboxy terminus of hsp70-interacting protein; PDBTitle: crystal structure of the chip u-box e3 ubiquitin ligase
37	c1wao4	Alignment	not modelled	96.9	12	PDB header: hydrolase Chain: 4: PDB Molecule: serine/threonine protein phosphatase 5; PDBTitle: pp5 structure
38	c3k9iA	Alignment	not modelled	96.8	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
39	c3ulqA	Alignment	not modelled	96.8	13	PDB header: gene regulation/transcription activator Chain: A: PDB Molecule: response regulator aspartate phosphatase f; PDBTitle: crystal structure of the anti-activator rapf complexed with the2 response regulator coma dna binding domain
40	c3fp4A	Alignment	not modelled	96.8	17	PDB header: transport protein Chain: A: PDB Molecule: tpr repeat-containing protein yhr117w; PDBTitle: crystal structure of tom71 complexed with ssa1 c-terminal2 fragment
41	d2buga1	Alignment	not modelled	96.8	25	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
42	c1ihgA	Alignment	not modelled	96.7	25	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin 40; PDBTitle: bovine cyclophilin 40, monoclinic form
43	d1elwa	Alignment	not modelled	96.7	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
44	d1pc2a	Alignment	not modelled	96.6	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
45	c2dbaA	Alignment	not modelled	96.6	23	PDB header: structural protein Chain: A: PDB Molecule: smooth muscle cell associated protein-1, isoform PDBTitle: the solution structure of the tetratricopeptide repeat of2 human smooth muscle cell associated protein-1, isoform 2
46	c3gyzB	Alignment	not modelled	96.6	11	PDB header: chaperone Chain: B: PDB Molecule: chaperone protein ipgc; PDBTitle: crystal structure of ipgc from shigella flexneri
47	c2kckA	Alignment	not modelled	96.6	12	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
48	d1nzna	Alignment	not modelled	96.5	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
49	c3beeB	Alignment	not modelled	96.5	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative yfre protein; PDBTitle: crystal structure of putative yfre protein from vibrio2 parahaemolyticus
50	c2kc7A	Alignment	not modelled	96.5	19	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
51	c1na3A	Alignment	not modelled	96.4	25	PDB header: de novo protein Chain: A: PDB Molecule: designed protein ctp2; PDBTitle: design of stable alpha-helical arrays from an idealized tpr2 motif
52	c2kcvA	Alignment	not modelled	96.4	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
53	c2vsnB	Alignment	not modelled	96.1	9	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
54	d1zu2a1	Alignment	not modelled	96.1	17	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
55	c1kt0A_	Alignment	not modelled	96.1	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
56	d1p5qa1	Alignment	not modelled	96.0	17	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
57	c3fflC_	Alignment	not modelled	96.0	14	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
58	c3q75A_	Alignment	not modelled	95.9	7	PDB header: transferase Chain: A: PDB Molecule: farnesyltransferase alpha subunit; PDBTitle: cryptococcus neoformans protein farnesyltransferase in complex with2 fpt-ii and tkcvvm peptide
59	d2pqrbl	Alignment	not modelled	95.9	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
60	c2xeVB_	Alignment	not modelled	95.8	16	PDB header: metal binding Chain: B: PDB Molecule: ybgf; PDBTitle: crystal structure of the tpr domain of xanthomonas2 campestris ybgf
61	c2avpA_	Alignment	not modelled	95.7	38	PDB header: de novo protein Chain: A: PDB Molecule: synthetic consensus tpr protein; PDBTitle: crystal structure of an 8 repeat consensus tpr superhelix
62	c2if4A_	Alignment	not modelled	95.7	24	PDB header: signaling protein Chain: A: PDB Molecule: atfkbp42; PDBTitle: crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana
63	d1hh8a_	Alignment	not modelled	95.7	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
64	c1qz2B_	Alignment	not modelled	95.6	17	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
65	d1kt1a1	Alignment	not modelled	95.5	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
66	d2c2la1	Alignment	not modelled	95.2	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
67	c2l6jA_	Alignment	not modelled	95.1	12	PDB header: protein binding Chain: A: PDB Molecule: tpr repeat-containing protein associated with hsp90; PDBTitle: tah1 complexed by meevd
68	c3ceqB_	Alignment	not modelled	95.0	22	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)
69	c3qkyA_	Alignment	not modelled	94.7	15	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane assembly lipoprotein yfio; PDBTitle: crystal structure of rhodothermus marinus bamd
70	d1elra_	Alignment	not modelled	94.6	25	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
71	d2fbna1	Alignment	not modelled	94.6	25	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
72	c2fbaA_	Alignment	not modelled	94.6	25	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
73	c3ly8A_	Alignment	not modelled	94.4	10	PDB header: signaling protein Chain: A: PDB Molecule: transcriptional activator cadc; PDBTitle: crystal structure of mutant d471e of the periplasmic domain of cadc
74	d1ihga1	Alignment	not modelled	94.3	25	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
75	c2vyiaA_	Alignment	not modelled	94.3	12	PDB header: chaperone Chain: A: PDB Molecule: sgta protein; PDBTitle: crystal structure of the tpr domain of human sgt
76	c2r5sB_	Alignment	not modelled	94.0	11	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
77	c3mkrA_	Alignment	not modelled	93.5	16	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
78	c2vgxA_	Alignment	not modelled	93.3	8	PDB header: chaperone Chain: A: PDB Molecule: chaperone sycd; PDBTitle: structure of the yersinia enterocolitica type iii secretion2 translocator chaperone sycd
79	d1qsaa1	Alignment	not modelled	92.9	10	Fold: alpha-alpha superhelix Superfamily: Bacterial muramidases Family: Bacterial muramidases

80	d1a17a_	Alignment	not modelled	92.2	22	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
81	c3rkvA_	Alignment	not modelled	90.9	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
82	c3gw4B_	Alignment	not modelled	90.2	17	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.
83	c2hyzA_	Alignment	not modelled	89.3	38	PDB header: de novo protein Chain: A: PDB Molecule: synthetic consensus tpr protein; PDBTitle: crystal structure of an 8 repeat consensus tpr superhelix2 (orthorombic crystal form)
84	d1d8da_	Alignment	not modelled	88.3	12	Fold: alpha-alpha superhelix Superfamily: Protein prenyltransferase Family: Protein prenyltransferase
85	d2hr2a1	Alignment	not modelled	86.9	22	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: CT2138-like
86	c3sz7A_	Alignment	not modelled	85.1	18	PDB header: chaperone regulator Chain: A: PDB Molecule: hsc70 cochaperone (sgt); PDBTitle: crystal structure of the sgt2 tpr domain from aspergillus fumigatus
87	d2o0ea1	Alignment	not modelled	85.0	5	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: HAT/Suf repeat
88	c3oxgA_	Alignment	not modelled	84.6	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)
89	d1zbpa1	Alignment	not modelled	84.1	16	Fold: ImpE-like Superfamily: ImpE-like Family: ImpE-like
90	d1hz4a_	Alignment	not modelled	84.0	19	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Transcription factor MalT domain III
91	d1qqea_	Alignment	not modelled	83.7	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
92	c2uy1A_	Alignment	not modelled	83.5	12	PDB header: rna-binding protein Chain: A: PDB Molecule: cleavage stimulation factor 77; PDBTitle: crystal structure of cstf-77
93	c3q49B_	Alignment	not modelled	83.4	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
94	c3mv3B_	Alignment	not modelled	83.0	8	PDB header: protein transport Chain: B: PDB Molecule: coatomer subunit epsilon; PDBTitle: crystal structure of a-cop in complex with e-cop
95	c1slyA_	Alignment	not modelled	77.9	10	PDB header: glycosyltransferase Chain: A: PDB Molecule: 70-kda soluble lytic transglycosylase; PDBTitle: complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
96	c1tnol_	Alignment	not modelled	76.8	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 kkskstkcvim peptide derived from k-3 ras4b
97	c3mekA_	Alignment	not modelled	74.7	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
98	c2yhca_	Alignment	not modelled	70.0	10	PDB header: membrane protein Chain: A: PDB Molecule: upf0169 lipoprotein yfio; PDBTitle: structure of bamd from e. coli
99	c3qwvA_	Alignment	not modelled	69.6	23	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
100	c1xi4D_	Alignment	not modelled	66.6	8	PDB header: endocytosis/exocytosis Chain: D: PDB Molecule: clathrin heavy chain; PDBTitle: clathrin d6 coat
101	c3n71A_	Alignment	not modelled	64.0	10	PDB header: transcription Chain: A: PDB Molecule: histone lysine methyltransferase smyd1; PDBTitle: crystal structure of cardiac specific histone methyltransferase smyd1
102	d1ya0a1	Alignment	not modelled	62.0	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
103	c3qtmB_	Alignment	not modelled	52.4	14	PDB header: translation Chain: B: PDB Molecule: uncharacterized protein c4b3.07; PDBTitle: structure of a yeast protein
104	c3qdnA_	Alignment	not modelled	51.8	9	PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin protein; PDBTitle: putative thioredoxin protein from salmonella

					typhimurium
105	d1wy6a1	Alignment	not modelled	48.3	19 Fold: alpha-alpha superhelix Superfamily: Hypothetical protein ST1625 Family: Hypothetical protein ST1625
106	c2hz8A	Alignment	not modelled	39.9	32 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
107	d2ff4a2	Alignment	not modelled	32.9	19 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: BTAD-like
108	d1wfda	Alignment	not modelled	31.0	35 Fold: Spectrin repeat-like Superfamily: MIT domain Family: MIT domain
109	d1wr0a1	Alignment	not modelled	29.2	26 Fold: Spectrin repeat-like Superfamily: MIT domain Family: MIT domain
110	d2jq9a1	Alignment	not modelled	21.4	30 Fold: Spectrin repeat-like Superfamily: MIT domain Family: MIT domain
111	c2w2uA	Alignment	not modelled	20.7	19 PDB header: hydrolase/transport Chain: A: PDB Molecule: hypothetical p60 katanin; PDBTitle: structural insight into the interaction between archaeal2 esct-iii and aaa-atpase