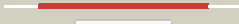



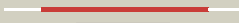






















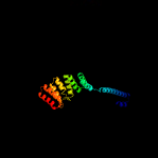

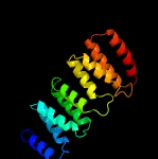
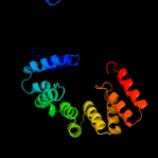


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1691 (-) _1915956_1916708
Date	Fri Aug 2 13:30:29 BST 2019
Unique Job ID	d19ad44d14769ec9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5dseC_</a>	 Alignment		99.9	15	<b>PDB header:</b> protein binding <b>Chain:</b> C; <b>PDB Molecule:</b> tetratricopeptide repeat protein 7b; <b>PDBTitle:</b> crystal structure of the ttc7b/hyccin complex
2	<a href="#">c3pe3D_</a>	 Alignment		99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> udp-n-acetylglucosamine--peptide n- <b>PDBTitle:</b> structure of human o-glcnae transferase and its complex with a peptide2 substrate
3	<a href="#">c5ganJ_</a>	 Alignment		99.9	11	<b>PDB header:</b> transcription <b>Chain:</b> J; <b>PDB Molecule:</b> pre-mrna-splicing factor 6; <b>PDBTitle:</b> the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom
4	<a href="#">c6c95A_</a>	 Alignment		99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> n-alpha-acetyltransferase 15, nata auxiliary subunit; <b>PDBTitle:</b> the human nata (naa10/naa15) amino-terminal acetyltransferase complex2 bound to hypk
5	<a href="#">c4abnA_</a>	 Alignment		99.9	16	<b>PDB header:</b> gene regulation <b>Chain:</b> A; <b>PDB Molecule:</b> tetratricopeptide repeat protein 5; <b>PDBTitle:</b> crystal structure of full length mouse strap (ttc5)
6	<a href="#">c2xpiA_</a>	 Alignment		99.9	14	<b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> anaphase-promoting complex subunit cut9; <b>PDBTitle:</b> crystal structure of apc/c hetero-tetramer cut9-hcn1
7	<a href="#">c4kvmA_</a>	 Alignment		99.9	12	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> n-terminal acetyltransferase a complex subunit nat1; <b>PDBTitle:</b> the nata (naa10p/naa15p) amino-terminal acetyltransferase complex2 bound to a bisubstrate analog
8	<a href="#">c4bujF_</a>	 Alignment		99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> superkiller protein 3; <b>PDBTitle:</b> crystal structure of the s. cerevisiae ski2-3-8 complex
9	<a href="#">c5nnrD_</a>	 Alignment		99.9	9	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> n-terminal acetyltransferase-like protein; <b>PDBTitle:</b> structure of naa15/naa10 bound to hypk-thb
10	<a href="#">c2y4tA_</a>	 Alignment		99.9	23	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> dnaj homolog subfamily c member 3; <b>PDBTitle:</b> crystal structure of the human co-chaperone p58(ipk)
11	<a href="#">c4hnxA_</a>	 Alignment		99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> n-terminal acetyltransferase a complex subunit nat1; <b>PDBTitle:</b> the nata acetyltransferase complex bound to ppgpp

12	<a href="#">c4ui9K_</a>	Alignment		99.9	11	<b>PDB header:</b> cell cycle <b>Chain:</b> K: <b>PDB Molecule:</b> cell division cycle protein 16 homolog; <b>PDBTitle:</b> atomic structure of the human anaphase-promoting complex
13	<a href="#">c5dseA_</a>	Alignment		99.9	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> tetra-tricopeptide repeat protein 7b; <b>PDBTitle:</b> crystal structure of the ttc7b/hyccin complex
14	<a href="#">c3iegB_</a>	Alignment		99.9	23	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> dnaj homolog subfamily c member 3; <b>PDBTitle:</b> crystal structure of p58(ipk) tpr domain at 2.5 a
15	<a href="#">c4ui9C_</a>	Alignment		99.9	17	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> cell division cycle protein 23 homolog; <b>PDBTitle:</b> atomic structure of the human anaphase-promoting complex
16	<a href="#">c5jqvA_</a>	Alignment		99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl/asparaginyl beta-hydroxylase; <b>PDBTitle:</b> aspartyl/asparaginyl beta-hydroxylase (asph) oxygenase and tpr domains2 in complex with manganese, n-oxalylglycine and factor x substrate3 peptide fragment(39mer-4ser)
17	<a href="#">c6b85J_</a>	Alignment		99.9	17	<b>PDB header:</b> membrane protein <b>Chain:</b> J: <b>PDB Molecule:</b> tmhc4_r; <b>PDBTitle:</b> crystal structure of transmembrane protein tmhc4_r
18	<a href="#">c3urzB_</a>	Alignment		99.9	12	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative protein binding protein (bacova_03105)2 from bacteroides ovatus atcc 8483 at 2.19 a resolution
19	<a href="#">c4d18J_</a>	Alignment		99.9	9	<b>PDB header:</b> signaling protein <b>Chain:</b> J: <b>PDB Molecule:</b> cop9 signalosome complex subunit 2; <b>PDBTitle:</b> crystal structure of the cop9 signalosome
20	<a href="#">c5zypA_</a>	Alignment		99.9	8	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase-associated protein ctr9,rna polymerase ii- <b>PDBTitle:</b> structure of the yeast ctr9/paf1 complex
21	<a href="#">c4xi0E_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> protein binding <b>Chain:</b> E: <b>PDB Molecule:</b> magnetosome protein mama; <b>PDBTitle:</b> mama 41-end from desulfovibrio magneticus rs-1
22	<a href="#">c1fchB_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal targeting signal 1 receptor; <b>PDBTitle:</b> crystal structure of the pts1 complexed to the tpr region2 of human pex5
23	<a href="#">c4uzuA_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar associated protein; <b>PDBTitle:</b> crystal structure of the chlamydomonas ift70 and ift52 complex
24	<a href="#">c3hymB_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> cell cycle, ligase <b>Chain:</b> B: <b>PDB Molecule:</b> cell division cycle protein 16 homolog; <b>PDBTitle:</b> insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure
25	<a href="#">d1w3ba_</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetra-tricopeptide repeat (TPR)
26	<a href="#">c3as5A_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> mama; <b>PDBTitle:</b> mama amb-1 p212121
27	<a href="#">d1xnfa_</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetra-tricopeptide repeat (TPR)
28	<a href="#">c4i17A_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a tpr repeats protein (bf2334) from bacteroides2 fragilis nctc 9343 at 1.50 a resolution
						<b>Fold:</b> alpha-alpha superhelix

29	<a href="#">d1d8da_</a>	Alignment	not modelled	99.9	10	<b>Superfamily:</b> Protein prenylyltransferase <b>Family:</b> Protein prenylyltransferase
30	<a href="#">c6gmhQ_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transcription <b>Chain:</b> Q: <b>PDB Molecule:</b> ctr9,rna polymerase-associated protein ctr9 homolog,rna <b>PDBTitle:</b> structure of activated transcription complex pol ii-dsif-paf-spt6
31	<a href="#">c4r7sA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tetratricopeptide repeat protein; <b>PDBTitle:</b> crystal structure of a tetratricopeptide repeat protein (parmer_03812)2 from parabacteroides merdae atcc 43184 at 2.39 a resolution
32	<a href="#">c4eqfA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> protein binding/transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> pex5-related protein; <b>PDBTitle:</b> trip8b-1a#206-567 interacting with the carboxy-terminal seven residues2 of hcn2
33	<a href="#">c5o9zG_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> splicing <b>Chain:</b> G: <b>PDB Molecule:</b> pre-mrna-processing factor 6; <b>PDBTitle:</b> cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
34	<a href="#">c2q7fA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> yrrb protein; <b>PDBTitle:</b> crystal structure of yrrb: a tpr protein with an unusual peptide-2 binding site
35	<a href="#">c6af0A_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ctr9 protein; <b>PDBTitle:</b> structure of ctr9, paf1 and cdc73 ternary complex from myceliophthora2 thermophila
36	<a href="#">c3v6pA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dhax3; <b>PDBTitle:</b> crystal structure of the dna-binding domain of dhax3, a tal effector
37	<a href="#">c5xw7B_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> cellulose synthase subunit c; <b>PDBTitle:</b> crystal structure of the flexible tandem repeat domain of bacterial2 cellulose synthase subunit c
38	<a href="#">c1tnoI_</a>	Alignment	not modelled	99.8	9	<b>PDB header:</b> transferase <b>Chain:</b> I: <b>PDB Molecule:</b> geranylgeranyltransferase type i alpha subunit; <b>PDBTitle:</b> rat protein geranylgeranyltransferase type-i complexed with2 a ggpp analog and a kkkstkcvm peptide derived from k-3 ras4b
39	<a href="#">c3fp4A_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> tpr repeat-containing protein yhr117w; <b>PDBTitle:</b> crystal structure of tom71 complexed with ssa1 c-terminal2 fragment
40	<a href="#">d2h6fa1</a>	Alignment	not modelled	99.8	10	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Protein prenylyltransferase <b>Family:</b> Protein prenylyltransferase
41	<a href="#">c5wsgd_</a>	Alignment	not modelled	99.8	9	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> D: <b>PDB Molecule:</b> u5 snrna; <b>PDBTitle:</b> cryo-em structure of the catalytic step ii spliceosome (c* complex) at2 4.0 angstrom resolution
42	<a href="#">c4f3vB_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> esx-1 secretion system protein eccA1; <b>PDBTitle:</b> crystal structure of n-terminal domain of eccA1 atpase from esx-12 secretion system of mycobacterium tuberculosis
43	<a href="#">c3gw4B_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein from deinococcus2 radiodurans. northeast structural genomics consortium target drr162b.
44	<a href="#">c5gmkd_</a>	Alignment	not modelled	99.8	10	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> D: <b>PDB Molecule:</b> u5 snrna; <b>PDBTitle:</b> cryo-em structure of the catalytic step i spliceosome (c complex) at2 3.4 angstrom resolution
45	<a href="#">c2r5sB_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein vp0806; <b>PDBTitle:</b> the crystal structure of a domain of protein vp0806 (unknown function)2 from vibrio parahaemolyticus rimd 2210633
46	<a href="#">c3jb9R_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> R: <b>PDB Molecule:</b> pre-mrna-splicing factor cwf4; <b>PDBTitle:</b> cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
47	<a href="#">c3vtxB_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> mama; <b>PDBTitle:</b> crystal structure of mama protein
48	<a href="#">c4n5cH_</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> protein binding <b>Chain:</b> H: <b>PDB Molecule:</b> cargo-transport protein ypp1; <b>PDBTitle:</b> crystal structure of ypp1
49	<a href="#">d1fcha_</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
50	<a href="#">c4ui9Y_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> cell cycle <b>Chain:</b> Y: <b>PDB Molecule:</b> anaphase-promoting complex subunit 7; <b>PDBTitle:</b> atomic structure of the human anaphase-promoting complex
51	<a href="#">c3cvpA_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisome targeting signal 1 receptor pex5; <b>PDBTitle:</b> structure of peroxisomal targeting signal 1 (pts1) binding domain of2 trypanosoma brucei peroxin 5 (tbpex5)complexed to pts1 peptide (10-3 skl)
52	<a href="#">c3q75A_</a>	Alignment	not modelled	99.8	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> farnesyltransferase alpha subunit; <b>PDBTitle:</b> cryptococcus neoformans protein farnesyltransferase in complex with2 fpt-ii and tkcvvm peptide
53	<a href="#">c2ho1B_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> type 4 fimbrial biogenesis protein pilf; <b>PDBTitle:</b> functional characterization of pseudomonas aeruginosa

						plf
54	<a href="#">c3mv3B_</a>	Alignment	not modelled	99.8	8	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> coatomer subunit epsilon; <b>PDBTitle:</b> crystal structure of a-cop in complex with e-cop
55	<a href="#">c4nrhB_</a>	Alignment	not modelled	99.8	10	<b>PDB header:</b> chaperone/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> chaperone sycd; <b>PDBTitle:</b> copn-scc3 complex
56	<a href="#">c4i2wA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> chaperone/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein unc-45; <b>PDBTitle:</b> crystal structure of the myosin chaperone unc-45 from c.elegans in2 complex with a hsp70 peptide
57	<a href="#">c5xi8A_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-barrel assembly-enhancing protease; <b>PDBTitle:</b> structure and function of the tpr domain
58	<a href="#">c3uq3A_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein sti1; <b>PDBTitle:</b> tpr2ab-domain:phsp90-complex of yeast sti1
59	<a href="#">d1dcea1</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Protein prenyltransferase <b>Family:</b> Protein prenyltransferase
60	<a href="#">c3u4tA_</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tpr repeat-containing protein; <b>PDBTitle:</b> crystal structure of the c-terminal part of the tpr repeat-containing2 protein q11ti6_cyth3 from cytophaga hutchinsonii. northeast3 structural genomics consortium target chr11b.
61	<a href="#">c2pl2A_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical conserved protein ttc0263; <b>PDBTitle:</b> crystal structure of ttc0263: a thermophilic tpr protein in thermus2 thermophilus hb27
62	<a href="#">c6aitD_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-barrel assembly-enhancing protease; <b>PDBTitle:</b> crystal structure of e. coli bepa
63	<a href="#">c2hyzA_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> synthetic consensus tpr protein; <b>PDBTitle:</b> crystal structure of an 8 repeat consensus tpr superhelix (orthorhombic2 crystal form)
64	<a href="#">c2vq2A_</a>	Alignment	not modelled	99.8	10	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative fimbrial biogenesis and twitching motility <b>PDBTitle:</b> crystal structure of pilw, widely conserved type iv pilus biogenesis2 factor
65	<a href="#">c5zyqA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase-associated protein ctr9 homolog,rna <b>PDBTitle:</b> the structure of human paf1/ctr9 complex
66	<a href="#">c4houB_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> interferon-induced protein with tetratricopeptide repeats <b>PDBTitle:</b> crystal structure of n-terminal human ifit1
67	<a href="#">c4ynvA_</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> acl4; <b>PDBTitle:</b> assembly chaperone of rpl4 (acl4) (residues 28-338)
68	<a href="#">d1hh8a_</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
69	<a href="#">c5gjqQ_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> Q: <b>PDB Molecule:</b> 26s proteasome non-atpase regulatory subunit 11; <b>PDBTitle:</b> structure of the human 26s proteasome bound to usp14-ubal
70	<a href="#">c5efrA_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> bama-bamd fusion protein; <b>PDBTitle:</b> crystal structure of a bama-bamd fusion
71	<a href="#">c4lngA_</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> caax farnesyltransferase alpha subunit ram2; <b>PDBTitle:</b> aspergillus fumigatus protein farnesyltransferase complex with2 farnesylidiphosphate and tipifarnib
72	<a href="#">c5udjA_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> interferon-induced protein with tetratricopeptide repeats <b>PDBTitle:</b> ifit1 monomeric mutant (I457E/I464E) with gppp-aaaa
73	<a href="#">d1hz4a_</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Transcription factor MatT domain III
74	<a href="#">c5aioA_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor tau 131 kda subunit; <b>PDBTitle:</b> crystal structure of t131 n-terminal tpr array
75	<a href="#">c4uqzA_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> hsie1; <b>PDBTitle:</b> coevolution of the atpase clpv, the tssb-tssc sheath and2 the accessory hsie protein distinguishes two type vi3 secretion classes
76	<a href="#">c5tqbB_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> ribosomal protein <b>Chain:</b> B: <b>PDB Molecule:</b> assembly chaperone of ribosomal protein l4 (acl4); <b>PDBTitle:</b> crystal structure of assembly chaperone of ribosomal protein l4 (acl4)2 in complex with ribosomal protein l4 (rpl4)
77	<a href="#">c5l0wB_</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> sec72; <b>PDBTitle:</b> structure of post-translational translocation sec71/sec72 complex
78	<a href="#">c4ebaC_</a>	Alignment	not modelled	99.7	8	<b>PDB header:</b> structural protein/rna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> mrna 3'-end-processing protein rna14; <b>PDBTitle:</b> crystal structure of the rna14-rna15 complex

79	<a href="#">c3ly8A_</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> transcriptional activator cadc; <b>PDBTitle:</b> crystal structure of mutant d471e of the periplasmic domain of cadc
80	<a href="#">c4zlhB_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> lipopolysaccharide assembly protein b; <b>PDBTitle:</b> structure of the lapb cytoplasmic domain at 2 angstroms
81	<a href="#">c2e2eA_</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> formate-dependent nitrite reductase complex nrfg subunit; <b>PDBTitle:</b> tpr domain of nrfg mediates the complex formation between heme lyase2 and formate-dependent nitrite reductase in escherichia coli o157:h7
82	<a href="#">c4cr3Q_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> Q; <b>PDB Molecule:</b> 26s proteasome regulatory subunit rpn6; <b>PDBTitle:</b> deep classification of a large cryo-em dataset defines the2 conformational landscape of the 26s proteasome
83	<a href="#">c5jttA_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> serine/threonine-protein phosphatase 5; <b>PDBTitle:</b> crystal structure of a type 5 serine/threonine protein phosphatase2 from arabidopsis thaliana
84	<a href="#">c3draA_</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> protein <b>PDBTitle:</b> candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp
85	<a href="#">c6n3qF_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transport protein <b>Chain:</b> F; <b>PDB Molecule:</b> translocation protein sec72; <b>PDBTitle:</b> cryo-em structure of the yeast sec complex
86	<a href="#">c6hftA_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> hsp70/hsp90 co-chaperone cns1; <b>PDBTitle:</b> hsp90 co-chaperone cns1 from saccharomyces cerevisiae (delta69)
87	<a href="#">c5mqfO_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> splicing <b>Chain:</b> O; <b>PDB Molecule:</b> crooked neck-like protein 1; <b>PDBTitle:</b> cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
88	<a href="#">c2gw1A_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> mitochondrial precursor proteins import receptor; <b>PDBTitle:</b> crystal structure of the yeast tom70
89	<a href="#">c6g70A_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> splicing <b>Chain:</b> A; <b>PDB Molecule:</b> pre-mrna-processing factor 39; <b>PDBTitle:</b> structure of murine prpf39
90	<a href="#">c4rg6B_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> cell division cycle protein 27 homolog; <b>PDBTitle:</b> crystal structure of apc3-apc16 complex
91	<a href="#">c3mkrA_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> coatamer subunit epsilon; <b>PDBTitle:</b> crystal structure of yeast alpha/epsilon-cop subcomplex of the copi2 vesicular coat
92	<a href="#">c5fzqB_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> designed tpr protein; <b>PDBTitle:</b> designed tpr protein m4n
93	<a href="#">c3ro2A_</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> g-protein-signaling modulator 2; <b>PDBTitle:</b> structures of the lgn/numa complex
94	<a href="#">c4a1sB_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> cell cycle <b>Chain:</b> B; <b>PDB Molecule:</b> partner of inscuteable; <b>PDBTitle:</b> crystallographic structure of the pins:insc complex
95	<a href="#">c4g1tB_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> antiviral protein <b>Chain:</b> B; <b>PDB Molecule:</b> interferon-induced protein with tetratricopeptide repeats <b>PDBTitle:</b> crystal structure of interferon-stimulated gene 54
96	<a href="#">c6hpgA_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> plant protein <b>Chain:</b> A; <b>PDB Molecule:</b> outer envelope protein 64, mitochondrial; <b>PDBTitle:</b> arabidopsis om64 tpr domain
97	<a href="#">c3qdnA_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> putative thioredoxin protein; <b>PDBTitle:</b> putative thioredoxin protein from salmonella typhimurium
98	<a href="#">c4hotA_</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A; <b>PDB Molecule:</b> interferon-induced protein with tetratricopeptide repeats <b>PDBTitle:</b> crystal structure of full-length human ifit5 with 5'-triphosphate2 oligoadenine
99	<a href="#">c2c2lD_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> chaperone <b>Chain:</b> D; <b>PDB Molecule:</b> carboxy terminus of hsp70-interacting protein; <b>PDBTitle:</b> crystal structure of the chip u-box e3 ubiquitin ligase
100	<a href="#">c1wao4_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> 4; <b>PDB Molecule:</b> serine/threonine protein phosphatase 5; <b>PDBTitle:</b> pp5 structure
101	<a href="#">c5a7dB_</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> cell cycle <b>Chain:</b> B; <b>PDB Molecule:</b> pins; <b>PDBTitle:</b> tetrameric assembly of lgn with inscuteable
102	<a href="#">c2dbaA_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> smooth muscle cell associated protein-1, isoform <b>PDBTitle:</b> the solution structure of the tetratricopeptide repeat of2 human smooth muscle cell associated protein-1, isoform 2
103	<a href="#">d2c2la1</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
104	<a href="#">c5m72A_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> signal recognition particle subunit srp72; <b>PDBTitle:</b> structure of the human srp68-72 protein-binding domain

						complex
105	<a href="#">c4e85B</a>	Alignment	not modelled	99.7	8	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> mrna 3'-end-processing protein rna14; <b>PDBTitle:</b> crystal structure of hat domain of rna14
106	<a href="#">d2o0ea1</a>	Alignment	not modelled	99.7	8	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> HAT/Suf repeat
107	<a href="#">c5djsA</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> tetratricopeptide tpr_2 repeat protein; <b>PDBTitle:</b> thermobaculum terrenum o-glcnac transferase mutant - k341m
108	<a href="#">d1elwa</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
109	<a href="#">c2uy1B</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> rna-binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> cleavage stimulation factor 77; <b>PDBTitle:</b> crystal structure of cstf-77
110	<a href="#">c5wftA</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> pelb; <b>PDBTitle:</b> pelb 319-436 from pseudomonas aeruginosa pao1
111	<a href="#">d1qsaa1</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Bacterial muramidases <b>Family:</b> Bacterial muramidases
112	<a href="#">c5waqA</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> outer membrane protein assembly factor bamd; <b>PDBTitle:</b> structure of bamd from neisseria gonorrhoeae
113	<a href="#">c6i57A</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> sperm-associated antigen 1; <b>PDBTitle:</b> nmr structure of the third tpr domain of the human spag1 protein
114	<a href="#">c4aifA</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> signaling protein/peptide <b>Chain:</b> A; <b>PDB Molecule:</b> ah receptor-interacting protein; <b>PDBTitle:</b> aip tpr domain in complex with human hsp90 peptide
115	<a href="#">c2ifuA</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> A; <b>PDB Molecule:</b> gamma-snap; <b>PDBTitle:</b> crystal structure of a gamma-snap from danio rerio
116	<a href="#">c4cqva</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> rna polymerase ii-associated protein 3; <b>PDBTitle:</b> first tpr of spaghetti (rpap3) bound to hsp90 peptide srmeevd
117	<a href="#">c2kckA</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> tpr repeat; <b>PDBTitle:</b> nmr solution structure of the northeast structural genomics consortium2 (nesg) target mrr121a
118	<a href="#">c4gcoA</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> protein sti-1; <b>PDBTitle:</b> central domain of stress-induced protein-1 (sti-1) from c.elegans
119	<a href="#">c4ga0A</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> e3 sumo-protein ligase ranbp2; <b>PDBTitle:</b> structure of the n-terminal domain of nup358
120	<a href="#">c2vyiA</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> sgta protein; <b>PDBTitle:</b> crystal structure of the tpr domain of human sgt