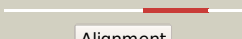






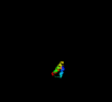








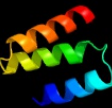
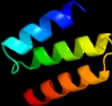


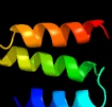


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2772c (-)_3081129_3081602
Date	Wed Aug 7 12:50:43 BST 2019
Unique Job ID	57331da38e544989

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2katA_	 Alignment		95.3	29	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
2	c4uqzA_	 Alignment		95.3	17	PDB header: protein transport Chain: A: PDB Molecule: hsie1; PDBTitle: coevolution of the atpase clpv, the tssb-tssc sheath and2 the accessory hsie protein distinguishes two type vi3 secretion classes
3	c2vgxA_	 Alignment		94.7	14	PDB header: chaperone Chain: A: PDB Molecule: chaperone sycd; PDBTitle: structure of the yersinia enterocolitica type iii secretion2 translocator chaperone sycd
4	c6g70A_	 Alignment		94.6	17	PDB header: splicing Chain: A: PDB Molecule: pre-mrna-processing factor 39; PDBTitle: structure of murine prpf39
5	c5fzqB_	 Alignment		94.6	19	PDB header: unknown function Chain: B: PDB Molecule: designed tpr protein; PDBTitle: designed tpr protein m4n
6	d1zbpA1	 Alignment		93.9	15	Fold: ImpE-like Superfamily: ImpE-like Family: ImpE-like
7	d1hxia_	 Alignment		93.6	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
8	c5dseC_	 Alignment		93.6	23	PDB header: protein binding Chain: C: PDB Molecule: tetratricopeptide repeat protein 7b; PDBTitle: crystal structure of the ttc7b/hyccin complex
9	c5dseA_	 Alignment		93.5	23	PDB header: protein binding Chain: A: PDB Molecule: tetratricopeptide repeat protein 7b; PDBTitle: crystal structure of the ttc7b/hyccin complex
10	c6bqsA_	 Alignment		93.0	17	PDB header: heme binding protein Chain: A: PDB Molecule: hypothetical protein pg_2227; PDBTitle: husa haemophore from porphyromonas gingivalis
11	c2kcvA_	 Alignment		93.0	15	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

12	c6b85J_	Alignment		92.8	29	PDB header: membrane protein Chain: J; PDB Molecule: tmhc4_r; PDBTitle: crystal structure of transmembrane protein tmhc4_r
13	c4aifA_	Alignment		92.4	13	PDB header: signaling protein/peptide Chain: A; PDB Molecule: ah receptor-interacting protein; PDBTitle: aip tpr domain in complex with human hsp90 peptide
14	c3upvA_	Alignment		92.3	21	PDB header: peptide binding protein Chain: A; PDB Molecule: heat shock protein sti1; PDBTitle: tpr2b-domain:phsp70-complex of yeast sti1
15	c2if4A_	Alignment		92.1	17	PDB header: signaling protein Chain: A; PDB Molecule: atfkbp42; PDBTitle: crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana
16	c4j8dC_	Alignment		91.6	17	PDB header: chaperone Chain: C; PDB Molecule: hsc70-interacting protein; PDBTitle: middle domain of hsc70-interacting protein, crystal form ii
17	c4nrhB_	Alignment		91.4	13	PDB header: chaperone/protein binding Chain: B; PDB Molecule: chaperone sycd; PDBTitle: copn-scc3 complex
18	c2kc7A_	Alignment		91.4	21	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
19	c4f3vB_	Alignment		91.3	13	PDB header: protein transport Chain: B; PDB Molecule: esx-1 secretion system protein eccA1; PDBTitle: crystal structure of n-terminal domain of eccA1 atpase from esx-12 secretion system of mycobacterium tuberculosis
20	c1kt0A_	Alignment		91.3	15	PDB header: isomerase Chain: A; PDB Molecule: 51 kda fkbp-like protein; PDBTitle: structure of the large fkbp-like protein, fkbp51, involved in steroid2 receptor complexes
21	c3as5A_	Alignment	not modelled	91.2	19	PDB header: protein binding Chain: A; PDB Molecule: mama; PDBTitle: mama amb-1 p212121
22	c5jitA_	Alignment	not modelled	91.1	19	PDB header: hydrolase Chain: A; PDB Molecule: serine/threonine-protein phosphatase 5; PDBTitle: crystal structure of a type 5 serine/threonine protein phosphatase2 from arabidopsis thaliana
23	c5aioA_	Alignment	not modelled	91.0	13	PDB header: transcription Chain: A; PDB Molecule: transcription factor tau 131 kda subunit; PDBTitle: crystal structure of t131 n-terminal tpr array
24	c1qz2B_	Alignment	not modelled	90.9	25	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
25	c4zlhB_	Alignment	not modelled	90.9	15	PDB header: metal binding protein Chain: B; PDB Molecule: lipopolysaccharide assembly protein b; PDBTitle: structure of the lapb cytoplasmic domain at 2 angstroms
26	c4e85B_	Alignment	not modelled	90.8	9	PDB header: structural protein Chain: B; PDB Molecule: mrna 3'-end-processing protein rna14; PDBTitle: crystal structure of hat domain of rna14
27	c3urzB_	Alignment	not modelled	90.5	10	PDB header: protein binding Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative protein binding protein (bacova_03105)2 from bacteroides ovatus atcc 8483 at 2.19 a resolution
28	c2xcbA_	Alignment	not modelled	90.5	17	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

29	c2hyzA	Alignment	not modelled	90.5	33	PDB header: de novo protein Chain: A: PDB Molecule: synthetic consensus tpr protein; PDBTitle: crystal structure of an 8 repeat consensus tpr superhelix (orthorhombic2 crystal form)
30	c5djsA	Alignment	not modelled	90.5	19	PDB header: transferase Chain: A: PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcnae transferase mutant - k341m
31	c5ctqD	Alignment	not modelled	90.5	15	PDB header: immune system, nuclear protein, rna bind Chain: D: PDB Molecule: squamous cell carcinoma antigen recognized by t-cells 3; PDBTitle: crystal structure of human sart3/tip110 half-a tpr (hat) domain
32	c5mgxG	Alignment	not modelled	90.4	23	PDB header: isomerase Chain: G: PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp8; PDBTitle: the structure of fkbp38 in complex with the meevd tetratricopeptide2 binding-motif of hsp90
33	c3sz7A	Alignment	not modelled	90.2	21	PDB header: chaperone regulator Chain: A: PDB Molecule: hsc70 cochaperone (sgt); PDBTitle: crystal structure of the sgt2 tpr domain from aspergillus fumigatus
34	c2e2eA	Alignment	not modelled	90.1	23	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	c3uq3A	Alignment	not modelled	90.1	21	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein sti1; PDBTitle: tpr2ab-domain:phsp90-complex of yeast sti1
36	c2dbaA	Alignment	not modelled	90.0	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
37	c3u64A	Alignment	not modelled	89.9	16	PDB header: transport protein Chain: A: PDB Molecule: protein tp_0956; PDBTitle: the crystal structure of tat-t (tp0956)
38	d1y8ma1	Alignment	not modelled	89.2	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
39	c6n3qF	Alignment	not modelled	89.0	15	PDB header: transport protein Chain: F: PDB Molecule: translocation protein sec72; PDBTitle: cryo-em structure of the yeast sec complex
40	c5waqA	Alignment	not modelled	88.9	11	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein assembly factor bamd; PDBTitle: structure of bamd from neisseria gonorrhoeae
41	c1fchB	Alignment	not modelled	88.9	29	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
42	c4cgwA	Alignment	not modelled	88.9	19	PDB header: chaperone Chain: A: PDB Molecule: rna polymerase ii-associated protein 3; PDBTitle: second tpr of spaghetti (rpap3) bound to hsp90 peptide srmeevd
43	c6aitD	Alignment	not modelled	88.9	20	PDB header: hydrolase Chain: D: PDB Molecule: beta-barrel assembly-enhancing protease; PDBTitle: crystal structure of e. coli bepa
44	c6i57A	Alignment	not modelled	88.8	13	PDB header: chaperone Chain: A: PDB Molecule: sperm-associated antigen 1; PDBTitle: nmr structure of the third tpr domain of the human spag1 protein
45	d1nzna	Alignment	not modelled	88.8	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
46	c4xi0E	Alignment	not modelled	88.5	17	PDB header: protein binding Chain: E: PDB Molecule: magnetosome protein mama; PDBTitle: mama 41-end from desulfovibrio magneticus rs-1
47	c5ompA	Alignment	not modelled	88.3	15	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp5; PDBTitle: human fkbp5 protein
48	c3rkvA	Alignment	not modelled	88.1	19	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
49	c5udjA	Alignment	not modelled	88.1	26	PDB header: rna binding protein Chain: A: PDB Molecule: interferon-induced protein with tetratricopeptide repeats PDBTitle: ifit1 monomeric mutant (l457e/l464e) with gppp-aaaa
50	c4rg6B	Alignment	not modelled	88.0	10	PDB header: protein binding Chain: B: PDB Molecule: cell division cycle protein 27 homolog; PDBTitle: crystal structure of apc3-apc16 complex
51	c5xi8A	Alignment	not modelled	87.9	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-barrel assembly-enhancing protease; PDBTitle: structure and function of the tpr domain
52	c2lniA	Alignment	not modelled	87.9	17	PDB header: chaperone Chain: A: PDB Molecule: stress-induced-phosphoprotein 1; PDBTitle: solution nmr structure of stress-induced-phosphoprotein 1 sti1 from2 homo sapiens, northeast structural genomics consortium target hr4403e
53	c1na3A	Alignment	not modelled	87.6	33	PDB header: de novo protein Chain: A: PDB Molecule: designed protein ctp2; PDBTitle: design of stable alpha-helical arrays from an idealized tpr2 motif PDB header: structural genomics, unknown function

54	c4w9rA	Alignment	not modelled	87.5	21	Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterised protein coch_1243 from2 capnocytophaga ochracea dsm 7271
55	c3iegB	Alignment	not modelled	87.4	17	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
56	c3fp4A	Alignment	not modelled	87.4	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
57	c3beeB	Alignment	not modelled	87.1	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative yfre protein; PDBTitle: crystal structure of putative yfre protein from vibrio2 parahaemolyticus
58	c5ic8A	Alignment	not modelled	86.7	17	PDB header: structural protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of utp6
59	c4hotA	Alignment	not modelled	86.6	25	PDB header: rna binding protein/rna Chain: A: PDB Molecule: interferon-induced protein with tetratricopeptide repeats PDBTitle: crystal structure of full-length human ifit5 with 5'-triphosphate2 oligoadenine
60	c3vtxB	Alignment	not modelled	86.5	25	PDB header: protein binding Chain: B: PDB Molecule: mama; PDBTitle: crystal structure of mama protein
61	c2l6jA	Alignment	not modelled	86.4	11	PDB header: protein binding Chain: A: PDB Molecule: tpr repeat-containing protein associated with hsp90; PDBTitle: tah1 complexed by meevd
62	d1zu2a1	Alignment	not modelled	86.2	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
63	c6gxzA	Alignment	not modelled	86.1	19	PDB header: chaperone Chain: A: PDB Molecule: rna polymerase ii-associated protein 3; PDBTitle: crystal structure of the human rpap3(tpr2)-pih1d1(cs) complex
64	c2avpA	Alignment	not modelled	85.8	33	PDB header: de novo protein Chain: A: PDB Molecule: synthetic consensus tpr protein; PDBTitle: crystal structure of an 8 repeat consensus tpr superhelix
65	c4i2wA	Alignment	not modelled	85.8	25	PDB header: chaperone/protein binding Chain: A: PDB Molecule: protein unc-45; PDBTitle: crystal structure of the myosin chaperone unc-45 from c.elegans in2 complex with a hsp70 peptide
66	c3pe3D	Alignment	not modelled	85.6	17	PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcna3 transferase and its complex with a peptide2 substrate
67	c5aplA	Alignment	not modelled	85.6	28	PDB header: transferase Chain: A: PDB Molecule: adenylation domain; PDBTitle: structure of the adenylation domain thr1 involved in the biosynthesis2 of 4-chlorothreonine in streptomyces sp. oh-5093, apo structure
68	c5xw7B	Alignment	not modelled	85.5	19	PDB header: biosynthetic protein Chain: B: PDB Molecule: cellulose synthase subunit c; PDBTitle: crystal structure of the flexible tandem repeat domain of bacterial2 cellulose synthase subunit c
69	c5nnd	Alignment	not modelled	85.2	27	PDB header: transferase Chain: D: PDB Molecule: n-terminal acetyltransferase-like protein; PDBTitle: structure of naa15/naa10 bound to hypk-thb
70	c3ly8A	Alignment	not modelled	85.0	30	PDB header: signaling protein Chain: A: PDB Molecule: transcriptional activator cadc; PDBTitle: crystal structure of mutant d471e of the periplasmic domain of cadc
71	c4u0zH	Alignment	not modelled	84.8	15	PDB header: transferase Chain: H: PDB Molecule: adenosine monophosphate-protein transferase ficd; PDBTitle: eukaryotic fic domain containing protein with bound apcpp
72	c4eqfA	Alignment	not modelled	84.7	27	PDB header: protein binding/transport protein Chain: A: PDB Molecule: pex5-related protein; PDBTitle: trip8b-1a#206-567 interacting with the carboxy-terminal seven residues2 of hcn2
73	c2yhCA	Alignment	not modelled	84.7	11	PDB header: membrane protein Chain: A: PDB Molecule: upf0169 lipoprotein yfio; PDBTitle: structure of bamd from e. coli
74	c3v6pA	Alignment	not modelled	84.0	8	PDB header: dna binding protein Chain: A: PDB Molecule: dhax3; PDBTitle: crystal structure of the dna-binding domain of dhax3, a tal effector
75	d1iyga	Alignment	not modelled	83.9	17	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
76	c3hymB	Alignment	not modelled	83.9	17	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
77	c4gcoA	Alignment	not modelled	83.8	19	PDB header: protein binding Chain: A: PDB Molecule: protein sti-1; PDBTitle: central domain of stress-induced protein-1 (sti-1) from c.elegans
78	c5lynA	Alignment	not modelled	83.8	27	PDB header: chaperone Chain: A: PDB Molecule: small glutamine-rich tetratricopeptide repeat-containing PDBTitle: structure of the tpr domain of sgt2 in complex with yeast ssa1 peptide2 fragment
79	c4u9K	Alignment	not modelled	83.7	17	PDB header: cell cycle Chain: K: PDB Molecule: cell division cycle protein 16 homolog;

79	c4uizK	Alignment	not modelled	83.7	17	PDBTitle: atomic structure of the human anaphase-promoting complex PDB header: transport protein Chain: A; PDB Molecule: peroxisome targeting signal 1 receptor pex5;
80	c3cvpA	Alignment	not modelled	83.6	15	PDBTitle: structure of peroxisomal targeting signal 1 (pts1) binding domain of2 trypanosoma brucei peroxin 5 (tbpex5)complexed to pts1 peptide (10-3 skl)
81	c1wao4	Alignment	not modelled	83.5	19	PDB header: hydrolase Chain: 4; PDB Molecule: serine/threonine protein phosphatase 5; PDBTitle: pp5 structure
82	d1w3ba	Alignment	not modelled	83.5	19	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
83	c5jqvA	Alignment	not modelled	83.2	19	PDB header: oxidoreductase Chain: A; PDB Molecule: aspartyl/asparaginyl beta-hydroxylase; PDBTitle: aspartyl/asparaginyl beta-hydroxylase (asph)oxygenase and tpr domains2 in complex with manganese, n-oxalyglycine and factor x substrate3 peptide fragment(39mer-4ser)
84	c2vviA	Alignment	not modelled	83.1	17	PDB header: chaperone Chain: A; PDB Molecule: sgta protein; PDBTitle: crystal structure of the tpr domain of human sgt
85	c2q7fA	Alignment	not modelled	83.0	21	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
86	c3q49B	Alignment	not modelled	82.7	19	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
87	d1fcha	Alignment	not modelled	82.7	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
88	c1ihgA	Alignment	not modelled	82.7	19	PDB header: isomerase Chain: A; PDB Molecule: cyclophilin 40; PDBTitle: bovine cyclophilin 40, monoclinic form
89	c4gnsB	Alignment	not modelled	82.6	23	PDB header: transport protein Chain: B; PDB Molecule: chitin biosynthesis protein chs6; PDBTitle: crystal structure of the chs5-chs6 exomer cargo adaptor complex
90	c4cgvA	Alignment	not modelled	82.4	13	PDB header: chaperone Chain: A; PDB Molecule: rna polymerase ii-associated protein 3; PDBTitle: first tpr of spaghetti (rpap3) bound to hsp90 peptide srmeevd
91	c2xevB	Alignment	not modelled	82.3	12	PDB header: metal binding Chain: B; PDB Molecule: ybgf; PDBTitle: crystal structure of the tpr domain of xanthomonas2 campestris ybgf
92	c2y4tA	Alignment	not modelled	82.2	19	PDB header: chaperone Chain: A; PDB Molecule: dnaj homolog subfamily c member 3; PDBTitle: crystal structure of the human co-chaperone p58(ipk)
93	c5c9sB	Alignment	not modelled	82.1	18	PDB header: gene regulation Chain: B; PDB Molecule: rrna biogenesis protein rrp5; PDBTitle: crystal structure of the c-terminal domain of rrp5
94	d2c2la1	Alignment	not modelled	81.6	19	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
95	c4a1sB	Alignment	not modelled	81.6	25	PDB header: cell cycle Chain: B; PDB Molecule: partner of inscuteable; PDBTitle: crystallographic structure of the pins:insc complex
96	c6hpgA	Alignment	not modelled	81.5	17	PDB header: plant protein Chain: A; PDB Molecule: outer envelope protein 64, mitochondrial; PDBTitle: arabidopsis om64 tpr domain
97	c2vsnB	Alignment	not modelled	81.4	19	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
98	c3gyzB	Alignment	not modelled	81.3	8	PDB header: chaperone Chain: B; PDB Molecule: chaperone protein ipgc; PDBTitle: crystal structure of ipgc from shigella flexneri
99	c4in3D	Alignment	not modelled	81.1	21	PDB header: protein transport Chain: D; PDB Molecule: protein bch1; PDBTitle: crystal structure of the chs5-bch1 exomer cargo adaptor complex
100	c5ganJ	Alignment	not modelled	80.9	17	PDB header: transcription Chain: J; PDB Molecule: pre-mrna-splicing factor 6; PDBTitle: the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom
101	c4j8fA	Alignment	not modelled	80.7	17	PDB header: chaperone Chain: A; PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein; PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip
102	c3k9iA	Alignment	not modelled	80.7	8	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
103	d1xnfa	Alignment	not modelled	80.7	19	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
104	c2gw1A	Alignment	not modelled	80.6	12	PDB header: protein transport Chain: A; PDB Molecule: mitochondrial precursor proteins import receptor;

						PDBTitle: crystal structure of the yeast tom70
105	c5y88I_	Alignment	not modelled	80.4	27	PDB header: splicing Chain: I; PDB Molecule: pre-mrna-splicing factor clf1; PDBTitle: cryo-em structure of the intron-lariat spliceosome ready for2 disassembly from s.cerevisiae at 3.5 angstrom
106	c5gmkd_	Alignment	not modelled	80.1	25	PDB header: rna binding protein/rna Chain: D; PDB Molecule: u5 snrna; PDBTitle: cryo-em structure of the catalytic step i spliceosome (c complex) at2 3.4 angstrom resolution
107	c5ey8D_	Alignment	not modelled	79.5	43	PDB header: ligase Chain: D; PDB Molecule: acyl-coa synthase; PDBTitle: structure of fadd32 from mycobacterium smegmatis complexed to ampc20
108	c4ynvA_	Alignment	not modelled	78.2	15	PDB header: chaperone Chain: A; PDB Molecule: acl4; PDBTitle: assembly chaperone of rpl4 (acl4) (residues 28-338)
109	c3gqwB_	Alignment	not modelled	77.7	21	PDB header: ligase Chain: B; PDB Molecule: fatty acid amp ligase; PDBTitle: crystal structure of a fatty acid amp ligase from e. coli with an acyl2 adenylate product bound
110	c4hnxA_	Alignment	not modelled	77.7	13	PDB header: transferase Chain: A; PDB Molecule: n-terminal acetyltransferase a complex subunit nat1; PDBTitle: the nata acetyltransferase complex bound to ppppp
111	c4r0mB_	Alignment	not modelled	77.5	16	PDB header: ligase Chain: B; PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
112	c4kvmA_	Alignment	not modelled	77.4	21	PDB header: transferase/transferase inhibitor Chain: A; PDB Molecule: n-terminal acetyltransferase a complex subunit nat1; PDBTitle: the nata (naa10p/naa15p) amino-terminal acetyltransferase complex2 bound to a bisubstrate analog
113	d2buga1	Alignment	not modelled	77.4	19	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
114	c4bt8B_	Alignment	not modelled	77.3	19	PDB header: oxidoreductase Chain: B; PDB Molecule: prolyl 4-hydroxylase subunit alpha-1; PDBTitle: crystal structure of the apo form of n-terminal domain and2 peptide substrate binding domain of prolyl-4 hydroxylase3 type i from human
115	c4ebaC_	Alignment	not modelled	76.7	9	PDB header: structural protein/rna binding protein Chain: C; PDB Molecule: mrna 3'-end-processing protein rna14; PDBTitle: crystal structure of the rna14-rna15 complex
116	c4r7sA_	Alignment	not modelled	76.7	11	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: tetratricopeptide repeat protein; PDBTitle: crystal structure of a tetratricopeptide repeat protein (parmer_03812)2 from parabacteroides merdae atcc 43184 at 2.39 a resolution
117	c4ga0A_	Alignment	not modelled	76.5	17	PDB header: transport protein Chain: A; PDB Molecule: e3 sumo-protein ligase ranbp2; PDBTitle: structure of the n-terminal domain of nup358
118	c3ro2A_	Alignment	not modelled	76.4	21	PDB header: protein binding Chain: A; PDB Molecule: g-protein-signaling modulator 2; PDBTitle: structures of the lgn/numa complex
119	c2r5sB_	Alignment	not modelled	75.9	22	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
120	c6c95A_	Alignment	not modelled	75.2	17	PDB header: transferase Chain: A; PDB Molecule: n-alpha-acetyltransferase 15, nata auxiliary subunit; PDBTitle: the human nata (naa10/naa15) amino-terminal acetyltransferase complex2 bound to hypk