

# Phyre2

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Description	exo99
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5a1vK_</a>			100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> K: <b>PDB Molecule:</b> coatomer subunit alpha; <b>PDBTitle:</b> the structure of the copi coat linkage i
2	<a href="#">c3dm0A_</a>			100.0	16	<b>PDB header:</b> sugar binding protein,signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein fused with rack1; <b>PDBTitle:</b> maltose binding protein fusion with rack1 from a. thaliana
3	<a href="#">c4yczA_</a>			100.0	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein of sec13 and nup145c; <b>PDBTitle:</b> y-complex hub (nup85-nup120-nup145c-sec13 complex) from m. thermophila2 (a.k.a. t. heterothallica)
4	<a href="#">c4bzka_</a>			100.0	16	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein transport protein sec31; <b>PDBTitle:</b> the structure of the copii coat assembled on membranes
5	<a href="#">c2j04B_</a>			100.0	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> ydr362cp; <b>PDBTitle:</b> the tau60-tau91 subcomplex of yeast transcription factor2 iiiic
6	<a href="#">c3jroA_</a>			100.0	11	<b>PDB header:</b> transport protein, structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein of protein transport protein sec13 and <b>PDBTitle:</b> nup84-nup145c-sec13 edge element of the npc lattice
7	<a href="#">c2ymuA_</a>			100.0	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> wd-40 repeat protein; <b>PDBTitle:</b> structure of a highly repetitive propeller structure
8	<a href="#">c5juyB_</a>			100.0	12	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> apoptotic protease-activating factor 1; <b>PDBTitle:</b> active human apoptosome with procaspase-9
9	<a href="#">c6em5m_</a>			100.0	13	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 60s ribosomal protein l14-a; <b>PDBTitle:</b> state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
10	<a href="#">c5cv0D_</a>			100.0	14	<b>PDB header:</b> hydrolase/protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> wd repeat-containing protein 48; <b>PDBTitle:</b> wdr48:usp46~ubiquitin ternary complex
11	<a href="#">c5wb1A_</a>			100.0	16	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory-associated protein of tor 1; <b>PDBTitle:</b> crystal structure of the arabidopsis thaliana raptor

12	<a href="#">c5tzsT</a>	Alignment		100.0	14	<b>PDB header:</b> translation <b>Chain:</b> T; <b>PDB Molecule:</b> utp21; <b>PDBTitle:</b> architecture of the yeast small subunit processome
13	<a href="#">c4wjsA</a>	Alignment		100.0	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> rsa4; <b>PDBTitle:</b> crystal structure of rsa4 from chaetomium thermophilum
14	<a href="#">c5cvoA</a>	Alignment		100.0	13	<b>PDB header:</b> hydrolase/protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> wd repeat-containing protein 48; <b>PDBTitle:</b> wdr48:usp46~ubiquitin ternary complex
15	<a href="#">c5dfzB</a>	Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> serine/threonine-protein kinase vps15; <b>PDBTitle:</b> structure of vps34 complex ii from s. cerevisiae.
16	<a href="#">c5nzvC</a>	Alignment		100.0	18	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> coatomer subunit beta'; <b>PDBTitle:</b> the structure of the copi coat linkage iv
17	<a href="#">c5i2tA</a>	Alignment		100.0	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> periodic tryptophan protein 2; <b>PDBTitle:</b> domain characterization of the wd protein pwp2 and their relevance in2 ribosome biogenesis
18	<a href="#">c3j65q</a>	Alignment		100.0	13	<b>PDB header:</b> ribosome <b>Chain:</b> Q; <b>PDB Molecule:</b> 60s ribosomal protein l18; <b>PDBTitle:</b> arx1 pre-60s particle. this entry contains the r-proteins and2 biogenesis factors.
19	<a href="#">c5n1aB</a>	Alignment		100.0	8	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> utp4; <b>PDBTitle:</b> crystal structure of utp4 from chaetomium thermophilum
20	<a href="#">c5a1vl</a>	Alignment		100.0	18	<b>PDB header:</b> transport protein <b>Chain:</b> L; <b>PDB Molecule:</b> coatomer subunit beta'; <b>PDBTitle:</b> the structure of the copi coat linkage i
21	<a href="#">c4wjuB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B; <b>PDB Molecule:</b> ribosome assembly protein 4; <b>PDBTitle:</b> crystal structure of rsa4 from saccharomyces cerevisiae
22	<a href="#">c5cvIA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> wd repeat-containing protein 48; <b>PDBTitle:</b> wdr48 (uaf-1), residues 2-580
23	<a href="#">c3iytG</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> apoptosis <b>Chain:</b> G; <b>PDB Molecule:</b> apoptotic protease-activating factor 1; <b>PDBTitle:</b> structure of an apoptosome-procaspase-9 card complex
24	<a href="#">c1pi6A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> actin interacting protein 1; <b>PDBTitle:</b> yeast actin interacting protein 1 (aip1), orthorhombic crystal form
25	<a href="#">c5a1uC</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> coatomer subunit alpha'; <b>PDBTitle:</b> the structure of the copi coat triad
26	<a href="#">c5n4aA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> intraflagellar transport protein 80; <b>PDBTitle:</b> crystal structure of chlamydomonas ift80
27	<a href="#">c5k1bB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> protein binding/hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> wd repeat-containing protein 48; <b>PDBTitle:</b> crystal structure of the uaf1/usp12 complex in f222 space group
28	<a href="#">c3mkqA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> coatomer beta'-subunit; <b>PDBTitle:</b> crystal structure of yeast alpha/beta prime-cop subcomplex of the copi2 vesicular coat
						<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> actin interacting protein 1;

29	<a href="#">c1nr0A</a>	Alignment	not modelled	100.0	19	<b>PDBTitle:</b> two seven-bladed beta-propeller domains revealed by the2 structure of a <i>c. elegans</i> homologue of yeast actin3 interacting protein 1 (api1).
30	<a href="#">c5thaA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gem-associated protein 5; <b>PDBTitle:</b> gemin5 wd40 repeats in complex with a guanosyl moiety
31	<a href="#">c6cb1s</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> 60s ribosomal protein I20-a; <b>PDBTitle:</b> yeast nucleolar pre-60s ribosomal subunit (state 3)
32	<a href="#">c4nsxA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> u3 small nucleolar rna-associated protein 21; <b>PDBTitle:</b> crystal structure of the utp21 tandem wd domain
33	<a href="#">c6chgD</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> klla0a08800p; <b>PDBTitle:</b> crystal structure of the yeast compass catalytic module
34	<a href="#">c4xfvA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongator complex protein 2; <b>PDBTitle:</b> crystal structure of elp2
35	<a href="#">c4e54B</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna damage-binding protein 2; <b>PDBTitle:</b> damaged dna induced uv-damaged dna-binding protein (uv-ddb)2 dimerization and its roles in chromatinized dna repair
36	<a href="#">c4o9dA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> rik1-associated factor 1; <b>PDBTitle:</b> structure of dos1 propeller
37	<a href="#">c5a5uB</a>	Alignment		100.0	10	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit b; <b>PDBTitle:</b> structure of mammalian eif3 in the context of the 43S preinitiation2 complex
38	<a href="#">c2oajA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> protein sni1; <b>PDBTitle:</b> crystal structure of sro7 from <i>s. cerevisiae</i>
39	<a href="#">c6mzcG</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 5; <b>PDBTitle:</b> human tfiid bc core
40	<a href="#">c2aq5A</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> coronin-1a; <b>PDBTitle:</b> crystal structure of murine coronin-1
41	<a href="#">c2w18A</a>	Alignment	not modelled	100.0	9	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> partner and localizer of brca2; <b>PDBTitle:</b> crystal structure of the c-terminal wd40 domain of human2 palb2
42	<a href="#">c3wj9A</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 2a; <b>PDBTitle:</b> crystal structure of the eukaryotic initiation factor
43	<a href="#">c6f3tD</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 5; <b>PDBTitle:</b> crystal structure of the human taf5-taf6-taf9 complex
44	<a href="#">c5o9zF</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> splicing <b>Chain:</b> F: <b>PDB Molecule:</b> u4/u6 small nuclear ribonucleoprotein prp4; <b>PDBTitle:</b> cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
45	<a href="#">c5mzhB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> dynein assembly factor with wdr repeat domains 1; <b>PDBTitle:</b> crystal structure of oda16 from chlamydomonas reinhardtii
46	<a href="#">c5ch2A</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative polycomb protein eed; <b>PDBTitle:</b> crystal structure of an active polycomb repressive complex 2 in the basal state
47	<a href="#">c3jcmB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> u4/u6 small nuclear ribonucleoprotein prp4; <b>PDBTitle:</b> cryo-em structure of the spliceosomal u4/u6.u5 tri-snRNP
48	<a href="#">c4j0xA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna-processing protein 9; <b>PDBTitle:</b> structure of rrp9
49	<a href="#">c4ozuA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> coronin; <b>PDBTitle:</b> crystal structure of wd40 domain from toxoplasma gondii coronin
50	<a href="#">c2pm9A</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein transport protein sec31; <b>PDBTitle:</b> crystal structure of yeast sec13/31 vertex element of the copii2 vesicular coat
51	<a href="#">c4ci8B</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> echinoderm microtubule-associated protein-like 1; <b>PDBTitle:</b> crystal structure of the tandem atypical beta-propeller domain of eml1
52	<a href="#">c3lrvA</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> splicing <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mRNA-splicing factor 19; <b>PDBTitle:</b> the prp19 wd40 domain contains a conserved protein interaction region2 essential for its function.
53	<a href="#">c4pswB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> histone acetyltransferase type b subunit 2; <b>PDBTitle:</b> crystal structure of histone acetyltransferase complex

54	<a href="#">c3jrpA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transport protein, structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein of protein transport protein sec13 and <b>PDBTitle:</b> sec13 with nup145c (aa109-179) insertion blade
55	<a href="#">c4uerb</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> us2; <b>PDBTitle:</b> 40s-eif1-eif1a-eif3-eif3j translation initiation complex from2 lachancea kluyveri
56	<a href="#">c3cfvA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> histone/chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> histone-binding protein rbbp7; <b>PDBTitle:</b> structural basis of the interaction of rbap46/rbap48 with histone h4
57	<a href="#">d1sq9a</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> 7-bladed beta-propeller <b>Superfamily:</b> WD40 repeat-like <b>Family:</b> WD40-repeat
58	<a href="#">c4h5jB</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> guanine nucleotide-exchange factor sec12; <b>PDBTitle:</b> crystal structure of the guanine nucleotide exchange factor sec12 (p642 form)
59	<a href="#">c5vljB</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> nuclear distribution protein pac1; <b>PDBTitle:</b> cryo-em structure of yeast cytoplasmic dynein with walker b mutation2 at aaa3 in presence of atp-vo4
60	<a href="#">d1ospo</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> open-sided beta-meander <b>Superfamily:</b> Outer surface protein <b>Family:</b> Outer surface protein
61	<a href="#">d1tbga</a>	Alignment	not modelled	100.0	12	<b>Fold:</b> 7-bladed beta-propeller <b>Superfamily:</b> WD40 repeat-like <b>Family:</b> WD40-repeat
62	<a href="#">c4u7aA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ribosome biogenesis protein erb1; <b>PDBTitle:</b> the carboxy-terminal domain of erb1 is a seven-bladed beta-propeller2 that binds rna.
63	<a href="#">c4zoyA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> sqt1; <b>PDBTitle:</b> crystal structure of the chaetomium thermophilum sqt1
64	<a href="#">c6bx3B</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> gene regulation/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> compass component swd1; <b>PDBTitle:</b> structure of histone h3k4 methyltransferase
65	<a href="#">c3acpA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> wd repeat-containing protein ygl004c; <b>PDBTitle:</b> crystal structure of yeast rpn14, a chaperone of the 19s regulatory2 particle of the proteasome
66	<a href="#">c5o9zl</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> splicing <b>Chain:</b> L: <b>PDB Molecule:</b> wd40 repeat-containing protein smu1; <b>PDBTitle:</b> cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
67	<a href="#">c2pbIB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> guanine nucleotide-binding protein subunit beta 5; <b>PDBTitle:</b> the multifunctional nature of gbeta5/rgs9 revealed from its crystal2 structure
68	<a href="#">c6eojD</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> rna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> polyadenylation factor subunit 2,polyadenylation factor <b>PDBTitle:</b> poly-a polymerase module of the cleavage and polyadenylation factor2 (cpf) from saccharomyces cerevisiae
69	<a href="#">c3ow8A</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> wd repeat-containing protein 61; <b>PDBTitle:</b> crystal structure of the wd repeat-containing protein 61
70	<a href="#">c4a11B</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna excision repair protein ercc-8; <b>PDBTitle:</b> structure of the hsddb1-hscsa complex
71	<a href="#">c3ei4D</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> dna damage-binding protein 2; <b>PDBTitle:</b> structure of the hsddb1-hsddb2 complex
72	<a href="#">c6bm0B</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> pre-mrna 3' end processing protein wdr33; <b>PDBTitle:</b> cryo-em structure of human cpsf-160-wdr33 complex at 3.8 a resolution
73	<a href="#">c3iz6a</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> 40s ribosomal protein sa (s2p); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
74	<a href="#">c4lg9A</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> f-box-like/wd repeat-containing protein tbl1xr1; <b>PDBTitle:</b> crystal structure of tbl1xr1 wd40 repeats
75	<a href="#">c3i2nA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> wd repeat-containing protein 92; <b>PDBTitle:</b> crystal structure of wd40 repeats wdr92
76	<a href="#">c6e29C</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> swd1-like protein; <b>PDBTitle:</b> crystal structure of myceliophthora_thermophila cps50 (swd1) beta-2 propeller domain
77	<a href="#">c3ei3B</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna damage-binding protein 2; <b>PDBTitle:</b> structure of the hsddb1-drddb2 complex
78	<a href="#">c5cxca</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ribosome biogenesis protein ytm1; <b>PDBTitle:</b> structure of ytm1 bound to the c-terminal domain of erb1 in p 65 2 22 space group
79	<a href="#">c3fm0A</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein ciao1; <b>PDBTitle:</b> crystal structure of wd40 protein ciao1

80	<a href="#">c3jzhA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> polycomb protein eed; <b>PDBTitle:</b> eed-h3k79me3
81	<a href="#">c5ganH</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> u4/u6 small nuclear ribonucleoprotein prp4; <b>PDBTitle:</b> the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrrn at2 3.7 angstrom
82	<a href="#">c5nnzB</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> dynein assembly factor with wdr repeat domains 1; <b>PDBTitle:</b> crystal structure of human oda16
83	<a href="#">c4zovB</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> ribosome assembly protein sqt1; <b>PDBTitle:</b> crystal structure of the saccharomyces cerevisiae sqt1
84	<a href="#">d1gxra</a>	Alignment	not modelled	99.9	10	<b>Fold:</b> 7-bladed beta-propeller <b>Superfamily:</b> WD40 repeat-like <b>Family:</b> WD40-repeat
85	<a href="#">c3dw8B</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein phosphatase 2a 55 kda regulatory <b>PDBTitle:</b> structure of a protein phosphatase 2a holoenzyme with b55 subunit
86	<a href="#">c3mmvE</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> nuclear protein <b>Chain:</b> E: <b>PDB Molecule:</b> mRNA export factor; <b>PDBTitle:</b> structural and functional analysis of the interaction between the2 nucleoporin nup98 and the mRNA export factor rae1
87	<a href="#">c4xyhA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> kinetochore protein mis16; <b>PDBTitle:</b> wild-type full length mis16 in schizosaccharomyces japonicus
88	<a href="#">d1yfqa</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> 7-bladed beta-propeller <b>Superfamily:</b> WD40 repeat-like <b>Family:</b> Cell cycle arrest protein BUB3
89	<a href="#">c5a31R</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> cell cycle <b>Chain:</b> R: <b>PDB Molecule:</b> the anaphase-promoting complex chain r; <b>PDBTitle:</b> structure of the human apc-cdh1-hsl1-ubch10 complex.
90	<a href="#">c5wjCA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> kinetochore protein mis16; <b>PDBTitle:</b> crystal structure of schizosaccharomyces pombe mis16 in complex with2 eic1
91	<a href="#">c5cykB</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> ribosome biogenesis protein erb1; <b>PDBTitle:</b> structure of ytm1 bound to the c-terminal domain of erb1-r486e
92	<a href="#">c5mqfE</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> splicing <b>Chain:</b> E: <b>PDB Molecule:</b> pre-mRNA-processing factor 17; <b>PDBTitle:</b> cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
93	<a href="#">c5sumA</a>	Alignment	not modelled	99.9	6	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> ribosome biogenesis protein nsal; <b>PDBTitle:</b> ribosome assembly factor nsal
94	<a href="#">c2qxvA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> embryonic ectoderm development; <b>PDBTitle:</b> structural basis of ezh2 recognition by eed
95	<a href="#">c3dwiH</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> structural protein <b>Chain:</b> H: <b>PDB Molecule:</b> actin-related protein 2/3 complex subunit 1; <b>PDBTitle:</b> crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
96	<a href="#">c5gvaA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> wd repeat and hmg-box dna-binding protein 1; <b>PDBTitle:</b> wd40 domain of human and-1
97	<a href="#">c5h64b</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory-associated protein of mtor; <b>PDBTitle:</b> cryo-em structure of mtorc1
98	<a href="#">c3zwIB</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit i; <b>PDBTitle:</b> structure of eukaryotic translation initiation factor eif3i complex2 with eif3b c-terminus (655-700)
99	<a href="#">d1vyhc1</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> 7-bladed beta-propeller <b>Superfamily:</b> WD40 repeat-like <b>Family:</b> WD40-repeat
100	<a href="#">c2gnqA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> wd-repeat protein 5; <b>PDBTitle:</b> structure of wdr5
101	<a href="#">c4av9A</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> svp1-like protein 2; <b>PDBTitle:</b> kluyveromyces lactis hsv2
102	<a href="#">c2ovqB</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transcription/cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> f-box/wd repeat protein 7; <b>PDBTitle:</b> structure of the skp1-fbw7-cyclinedegc complex
103	<a href="#">c4czvB</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> pab-dependent poly(a)-specific ribonuclease subunit pan2; <b>PDBTitle:</b> structure of the neurospora crassa pan2 wd40 domain
104	<a href="#">c4noxA</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit b; <b>PDBTitle:</b> structure of the nine-bladed beta-propeller of eif3b
105	<a href="#">c2jcrD</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> splicing <b>Chain:</b> D: <b>PDB Molecule:</b> u5-40k;

105	<a href="#">c5jcrD</a>	Alignment	not modelled	99.9	13	<b>PDBTitle:</b> 3d structure determination of the human*u4/u6.u5* tri-snrrnp complex <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> tRNA (guanine-n(7)-)methyltransferase- <b>PDBTitle:</b> structure of trm8-trm82, the yeast tRNA m7g methylation2 complex
106	<a href="#">c2vdvB</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> wd repeat-containing protein 20; <b>PDBTitle:</b> crystal structure of wd repeat-containing protein 20
107	<a href="#">c5k19C</a>	Alignment	not modelled	99.9	16	
108	<a href="#">d1erja</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> 7-bladed beta-propeller <b>Superfamily:</b> WD40 repeat-like <b>Family:</b> WD40-repeat
109	<a href="#">c3w15A</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal targeting signal 2 receptor; <b>PDBTitle:</b> structure of peroxisomal targeting signal 2 (pts2) of saccharomyces cerevisiae 3-ketoacyl-coa thiolase in complex with pex7p and pex21p
110	<a href="#">c4ui9R</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> cell cycle <b>Chain:</b> R: <b>PDB Molecule:</b> fizzy-related protein homolog; <b>PDBTitle:</b> atomic structure of the human anaphase-promoting complex
111	<a href="#">c3bwSA</a>	Alignment	not modelled	99.9	8	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein Ip49; <b>PDBTitle:</b> crystal structure of the leptospiral antigen Ip49
112	<a href="#">c4yhca</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> sterol regulatory element-binding protein cleavage- <b>PDBTitle:</b> crystal structure of the wd40 domain of scap from fission yeast
113	<a href="#">c1vyhT</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> T: <b>PDB Molecule:</b> platelet-activating factor acetylhydrolase ib <b>PDBTitle:</b> paf-ah holoenzyme: lis1/alpha2
114	<a href="#">c4ggbB</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transferase/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> methylosome protein 50; <b>PDBTitle:</b> crystal structure of the human prmt5:mep50 complex
115	<a href="#">c4i79B</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoporin nup43; <b>PDBTitle:</b> crystal structure of human nup43
116	<a href="#">c5ov3B</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> retinoblastoma-binding protein 5; <b>PDBTitle:</b> structure of the rbbp5 beta-propeller domain
117	<a href="#">c4g56B</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> mgc81050 protein; <b>PDBTitle:</b> crystal structure of full length prmt5/mep50 complexes from xenopus2 laevis
118	<a href="#">c4d0ka</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> a-specific ribonuclease subunit pan2; <b>PDBTitle:</b> complex of chaetomium thermophilum pan2 (wd40-cs1) with pan3 (c-term)
119	<a href="#">c4j8bA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> coatomer alpha subunit; <b>PDBTitle:</b> crystal structure of alpha-cop/emp47p complex
120	<a href="#">c5m89B</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> splicing <b>Chain:</b> B: <b>PDB Molecule:</b> spliceosome wd40 sc; <b>PDBTitle:</b> spliceosome component