
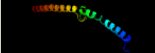


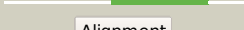


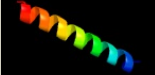

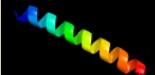









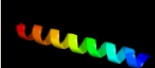




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3769_(-)_4214793_4215065
Date	Fri Aug 9 18:20:47 BST 2019
Unique Job ID	f626008e8ad40063

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5appB_</a>	 Alignment		91.3	31	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> general control protein gcn4, outer membrane protein 100; <b>PDBTitle:</b> actinobacillus actinomycetemcomitans omp100 residues 133-198 fused to2 gcn4 adaptors
2	<a href="#">c3pltB_</a>	 Alignment		52.8	15	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> sphingolipid long chain base-responsive protein lsp1; <b>PDBTitle:</b> crystal structure of lsp1 from saccharomyces cerevisiae
3	<a href="#">c3bj4B_</a>	 Alignment		51.3	48	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> potassium voltage-gated channel subfamily kqt <b>PDBTitle:</b> the kcnq1 (kv7.1) c-terminus, a multi-tiered scaffold for2 subunit assembly and protein interaction
4	<a href="#">c1unuB_</a>	 Alignment		40.1	33	<b>PDB header:</b> four helix bundle <b>Chain:</b> B; <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces of four2 helix bundles
5	<a href="#">c1unuA_</a>	 Alignment		40.1	33	<b>PDB header:</b> four helix bundle <b>Chain:</b> A; <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces of four2 helix bundles
6	<a href="#">c1ij1B_</a>	 Alignment		31.5	37	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvlt coiled-coil trimer with threonine at the d(12) position
7	<a href="#">c1ij1C_</a>	 Alignment		31.5	37	<b>PDB header:</b> transcription <b>Chain:</b> C; <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvlt coiled-coil trimer with threonine at the d(12) position
8	<a href="#">c1ij1A_</a>	 Alignment		31.5	37	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvlt coiled-coil trimer with threonine at the d(12) position
9	<a href="#">c3hfeC_</a>	 Alignment		30.2	57	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> potassium voltage-gated channel subfamily kqt member 1; <b>PDBTitle:</b> a trimeric form of the kv7.1 a domain tail
10	<a href="#">c1uo5A_</a>	 Alignment		27.8	30	<b>PDB header:</b> four helix bundle <b>Chain:</b> A; <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces of four2 helix bundles
11	<a href="#">c1uo5B_</a>	 Alignment		27.8	30	<b>PDB header:</b> four helix bundle <b>Chain:</b> B; <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces of four2 helix bundles

12	<a href="#">c1untA_</a>	Alignment		26.9	30	<b>PDB header:</b> four helix bundle <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces of four2 helix bundles
13	<a href="#">c1untB_</a>	Alignment		26.1	30	<b>PDB header:</b> four helix bundle <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces of four2 helix bundles
14	<a href="#">c1ij0C_</a>	Alignment		21.5	33	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> coiled coil trimer gcn4-pvls ser at buried d position
15	<a href="#">c1ij0A_</a>	Alignment		21.5	33	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> coiled coil trimer gcn4-pvls ser at buried d position
16	<a href="#">c1ij0B_</a>	Alignment		21.5	33	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> coiled coil trimer gcn4-pvls ser at buried d position
17	<a href="#">c6fiaB_</a>	Alignment		21.4	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> line-1 retrotransposable element orf1 protein; <b>PDBTitle:</b> structure of the human line-1 orf1p coiled coil domain
18	<a href="#">c1junB_</a>	Alignment		21.2	31	<b>PDB header:</b> transcription regulation <b>Chain:</b> B: <b>PDB Molecule:</b> c-jun homodimer; <b>PDBTitle:</b> nmr study of c-jun homodimer
19	<a href="#">c1uo3B_</a>	Alignment		20.4	30	<b>PDB header:</b> four helix bundle <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces of four2 helix bundles
20	<a href="#">d2o3la1</a>	Alignment		18.5	45	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> BH3980-like <b>Family:</b> BH3980-like
21	<a href="#">c2yonA_</a>	Alignment	not modelled	17.8	50	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sensory box protein; <b>PDBTitle:</b> solution nmr structure of the c-terminal extension of two bacterial2 light, oxygen, voltage (lov) photoreceptor proteins from3 pseudomonas putida
22	<a href="#">d2hh6a1</a>	Alignment	not modelled	17.0	32	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> BH3980-like <b>Family:</b> BH3980-like
23	<a href="#">c1gclC_</a>	Alignment	not modelled	16.9	30	<b>PDB header:</b> leucine zipper <b>Chain:</b> C: <b>PDB Molecule:</b> gcn4; <b>PDBTitle:</b> gcn4 leucine zipper core mutant p-li
24	<a href="#">c1gclD_</a>	Alignment	not modelled	16.9	30	<b>PDB header:</b> leucine zipper <b>Chain:</b> D: <b>PDB Molecule:</b> gcn4; <b>PDBTitle:</b> gcn4 leucine zipper core mutant p-li
25	<a href="#">c1gclB_</a>	Alignment	not modelled	16.9	30	<b>PDB header:</b> leucine zipper <b>Chain:</b> B: <b>PDB Molecule:</b> gcn4; <b>PDBTitle:</b> gcn4 leucine zipper core mutant p-li
26	<a href="#">c1gclA_</a>	Alignment	not modelled	16.9	30	<b>PDB header:</b> leucine zipper <b>Chain:</b> A: <b>PDB Molecule:</b> gcn4; <b>PDBTitle:</b> gcn4 leucine zipper core mutant p-li
27	<a href="#">c1w5iA_</a>	Alignment	not modelled	15.5	30	<b>PDB header:</b> four helix bundle <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> aba does not affect topology of pli.
28	<a href="#">c1uo2A_</a>	Alignment	not modelled	15.5	30	<b>PDB header:</b> four helix bundle <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces of four2 helix bundles
						<b>PDB header:</b> four helix bundle

29	<a href="#">c1uo2B_</a>	Alignment	not modelled	15.0	30	<b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces of four2 helix bundles
30	<a href="#">c1w5iB_</a>	Alignment	not modelled	15.0	30	<b>PDB header:</b> four helix bundle <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> aba does not affect topology of pli.
31	<a href="#">c4v1au_</a>	Alignment	not modelled	14.6	17	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 22 of 2
32	<a href="#">d1tc3c_</a>	Alignment	not modelled	14.5	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
33	<a href="#">c1unvB_</a>	Alignment	not modelled	14.5	29	<b>PDB header:</b> four helix bundle <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces of four2 helix bundles
34	<a href="#">c1gcmA_</a>	Alignment	not modelled	14.0	26	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> gcn4p-ii; <b>PDBTitle:</b> gcn4 leucine zipper core mutant p-li
35	<a href="#">c1bb1A_</a>	Alignment	not modelled	13.0	38	<b>PDB header:</b> de novo protein design <b>Chain:</b> A: <b>PDB Molecule:</b> designed, thermostable heterotrimeric coiled <b>PDBTitle:</b> crystal structure of a designed, thermostable2 heterotrimeric coiled coil
36	<a href="#">c5u0pU_</a>	Alignment	not modelled	13.0	10	<b>PDB header:</b> transcription <b>Chain:</b> U: <b>PDB Molecule:</b> mediator complex subunit 21; <b>PDBTitle:</b> cryo-em structure of the transcriptional mediator
37	<a href="#">c1gcmB_</a>	Alignment	not modelled	12.8	26	<b>PDB header:</b> transcription regulation <b>Chain:</b> B: <b>PDB Molecule:</b> gcn4p-ii; <b>PDBTitle:</b> gcn4 leucine zipper core mutant p-li
38	<a href="#">c1gcmC_</a>	Alignment	not modelled	12.3	26	<b>PDB header:</b> transcription regulation <b>Chain:</b> C: <b>PDB Molecule:</b> gcn4p-ii; <b>PDBTitle:</b> gcn4 leucine zipper core mutant p-li
39	<a href="#">c2ccfA_</a>	Alignment	not modelled	12.0	26	<b>PDB header:</b> four helix bundle <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> antiparallel configuration of pli e20s
40	<a href="#">c5fv8B_</a>	Alignment	not modelled	11.7	60	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> fosw; <b>PDBTitle:</b> structure of cjun-fosw coiled coil complex.
41	<a href="#">c5fv8A_</a>	Alignment	not modelled	11.5	60	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> fosw; <b>PDBTitle:</b> structure of cjun-fosw coiled coil complex.
42	<a href="#">c2cceB_</a>	Alignment	not modelled	11.4	26	<b>PDB header:</b> four helix bundle <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> parallel configuration of pli e20s
43	<a href="#">c2cceA_</a>	Alignment	not modelled	11.4	26	<b>PDB header:</b> four helix bundle <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> parallel configuration of pli e20s
44	<a href="#">c1unxA_</a>	Alignment	not modelled	11.0	30	<b>PDB header:</b> four helix bundle <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces2 of four helix bundles
45	<a href="#">c1unwB_</a>	Alignment	not modelled	10.4	30	<b>PDB header:</b> four helix bundle <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces2 of four helix bundles
46	<a href="#">c1unxB_</a>	Alignment	not modelled	9.7	30	<b>PDB header:</b> four helix bundle <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces2 of four helix bundles
47	<a href="#">c4j4aK_</a>	Alignment	not modelled	9.6	43	<b>PDB header:</b> de novo protein <b>Chain:</b> K: <b>PDB Molecule:</b> cortexillin-1; <b>PDBTitle:</b> crystal structure of engineered trimeric cortexillin-1 coiled-coil2 variant
48	<a href="#">c4j4aG_</a>	Alignment	not modelled	9.6	43	<b>PDB header:</b> de novo protein <b>Chain:</b> G: <b>PDB Molecule:</b> cortexillin-1; <b>PDBTitle:</b> crystal structure of engineered trimeric cortexillin-1 coiled-coil2 variant
49	<a href="#">c3l34H_</a>	Alignment	not modelled	9.5	62	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> the crystal structure of a two-component sensor domain (2nd2 form) from pseudomonas aeruginosa pa01
50	<a href="#">c1n54A_</a>	Alignment	not modelled	9.5	20	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> 80 kda nuclear cap binding protein; <b>PDBTitle:</b> cap binding complex m7gpppg free
51	<a href="#">c1abzA_</a>	Alignment	not modelled	9.4	40	<b>PDB header:</b> de novo design <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-t-alpha; <b>PDBTitle:</b> alpha-t-alpha, a de novo designed peptide, nmr, 232 structures
52	<a href="#">c2q7cC_</a>	Alignment	not modelled	9.4	30	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> fusion protein between yeast variant gcn4 and hivgp41; <b>PDBTitle:</b> crystal structure of iqn17
53	<a href="#">c3ci9B_</a>	Alignment	not modelled	9.0	31	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> heat shock factor-binding protein 1; <b>PDBTitle:</b> crystal structure of the human hsbp1
54	<a href="#">c4j4aD_</a>	Alignment	not modelled	9.0	43	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> cortexillin-1; <b>PDBTitle:</b> crystal structure of engineered trimeric cortexillin-1 coiled-coil2 variant
55	<a href="#">c4j4aA_</a>	Alignment	not modelled	9.0	43	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> cortexillin-1; <b>PDBTitle:</b> crystal structure of engineered trimeric cortexillin-1

						coiled-coil2 variant
56	<a href="#">d1wgnA_</a>	Alignment	not modelled	8.9	32	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
57	<a href="#">c4j4aB_</a>	Alignment	not modelled	8.9	43	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> cortexillin-1; <b>PDBTitle:</b> crystal structure of engineered trimeric cortexillin-1 coiled-coil2 variant
58	<a href="#">c6qbrA_</a>	Alignment	not modelled	8.4	18	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> polymerase cofactor vp35; <b>PDBTitle:</b> crystal structure of the oligomerization domain of vp35 from reston2 virus, mercury derivative
59	<a href="#">c4j4aJ_</a>	Alignment	not modelled	8.4	43	<b>PDB header:</b> de novo protein <b>Chain:</b> J: <b>PDB Molecule:</b> cortexillin-1; <b>PDBTitle:</b> crystal structure of engineered trimeric cortexillin-1 coiled-coil2 variant
60	<a href="#">c4j4aC_</a>	Alignment	not modelled	8.4	43	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> cortexillin-1; <b>PDBTitle:</b> crystal structure of engineered trimeric cortexillin-1 coiled-coil2 variant
61	<a href="#">c6gboG_</a>	Alignment	not modelled	7.1	31	<b>PDB header:</b> viral protein <b>Chain:</b> G: <b>PDB Molecule:</b> polymerase cofactor vp35; <b>PDBTitle:</b> crystal structure of the oligomerization domain of vp35 from ebola2 virus
62	<a href="#">c3onjA_</a>	Alignment	not modelled	6.9	23	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> t-snare vti1; <b>PDBTitle:</b> crystal structure of yeast vti1p_habc domain
63	<a href="#">c1piqA_</a>	Alignment	not modelled	6.8	26	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (general control protein gcn4-piq); <b>PDBTitle:</b> crystal structure of gcn4-piq, a trimeric coiled coil with buried2 polar residues
64	<a href="#">c1unvA_</a>	Alignment	not modelled	6.7	30	<b>PDB header:</b> four helix bundle <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces of four2 helix bundles
65	<a href="#">d1ykhb1</a>	Alignment	not modelled	6.5	12	<b>Fold:</b> Mediator hinge subcomplex-like <b>Superfamily:</b> Mediator hinge subcomplex-like <b>Family:</b> CSE2-like
66	<a href="#">c4wy4D_</a>	Alignment	not modelled	6.0	27	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> synaptosomal-associated protein 29; <b>PDBTitle:</b> crystal structure of autophagic snare complex
67	<a href="#">c2xzrA_</a>	Alignment	not modelled	5.9	14	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> immunoglobulin-binding protein eibd; <b>PDBTitle:</b> escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
68	<a href="#">c2gl2B_</a>	Alignment	not modelled	5.9	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> adhesion a; <b>PDBTitle:</b> crystal structure of the tetra mutant (t66g,r67g,f68g,y69g) of2 bacterial adhesin fada
69	<a href="#">c3nzza_</a>	Alignment	not modelled	5.7	23	<b>PDB header:</b> cell invasion <b>Chain:</b> A: <b>PDB Molecule:</b> cell invasion protein sipd; <b>PDBTitle:</b> crystal structure of the salmonella type iii secretion system tip2 protein sipd
70	<a href="#">d2csua3</a>	Alignment	not modelled	5.6	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
71	<a href="#">c3thfA_</a>	Alignment	not modelled	5.6	15	<b>PDB header:</b> actin-binding protein/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein shroom; <b>PDBTitle:</b> crystal structure of the sd2 domain from drosophila shroom
72	<a href="#">c3u0cA_</a>	Alignment	not modelled	5.6	17	<b>PDB header:</b> cell invasion <b>Chain:</b> A: <b>PDB Molecule:</b> invasin ipab; <b>PDBTitle:</b> crystal structure of n-terminal region of type iii secretion first2 translocator ipab (residues 74-224)
73	<a href="#">c4bxtH_</a>	Alignment	not modelled	5.6	47	<b>PDB header:</b> viral protein <b>Chain:</b> H: <b>PDB Molecule:</b> phosphoprotein p; <b>PDBTitle:</b> crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
74	<a href="#">c5oiyF_</a>	Alignment	not modelled	5.4	47	<b>PDB header:</b> viral protein <b>Chain:</b> F: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> structure of the hmpv p oligomerization domain at 2.2 a
75	<a href="#">c5oixD_</a>	Alignment	not modelled	5.4	47	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> structure of the hmpv p oligomerization domain at 1.6 a
76	<a href="#">c4bxtA_</a>	Alignment	not modelled	5.4	47	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoprotein p; <b>PDBTitle:</b> crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
77	<a href="#">c5oixH_</a>	Alignment	not modelled	5.4	47	<b>PDB header:</b> viral protein <b>Chain:</b> H: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> structure of the hmpv p oligomerization domain at 1.6 a
78	<a href="#">c5oiyD_</a>	Alignment	not modelled	5.4	47	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> structure of the hmpv p oligomerization domain at 2.2 a
79	<a href="#">c6j5id_</a>	Alignment	not modelled	5.3	21	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> atp synthase subunit beta; <b>PDBTitle:</b> cryo-em structure of the mammalian dp-state atp synthase
80	<a href="#">c4hjdB_</a>	Alignment	not modelled	5.3	38	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> gcn4pli(alpha/beta/acyclic gamma); <b>PDBTitle:</b> gcn4pli derivative with alpha/beta/acyclic-gamma amino acid2 substitution pattern
81	<a href="#">c4hjdA_</a>	Alignment	not modelled	5.3	38	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> gcn4pli(alpha/beta/acyclic gamma); <b>PDBTitle:</b> gcn4pli derivative with alpha/beta/acyclic-gamma amino acid2 substitution pattern

82	<a href="#">d1j26a_</a>	Alignment	not modelled	5.3	24	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> Peptidyl-tRNA hydrolase domain-like <b>Family:</b> Peptidyl-tRNA hydrolase domain
83	<a href="#">c3mxzA_</a>	Alignment	not modelled	5.2	13	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> tubulin-specific chaperone a; <b>PDBTitle:</b> crystal structure of tubulin folding cofactor a from arabidopsis2 thaliana
84	<a href="#">c4bxtC_</a>	Alignment	not modelled	5.2	47	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoprotein p; <b>PDBTitle:</b> crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
85	<a href="#">d1uhma_</a>	Alignment	not modelled	5.2	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Linker histone H1/H5
86	<a href="#">c4g1aB_</a>	Alignment	not modelled	5.1	36	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> aq-c16c19 peptide; <b>PDBTitle:</b> metal-binding properties of a self-assembled coiled coil: formation of2 a polynuclear cd-thiolated cluster
87	<a href="#">c5oiyC_</a>	Alignment	not modelled	5.1	47	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> structure of the hmpv p oligomerization domain at 2.2 a
88	<a href="#">c5oiyE_</a>	Alignment	not modelled	5.0	47	<b>PDB header:</b> viral protein <b>Chain:</b> E: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> structure of the hmpv p oligomerization domain at 2.2 a
89	<a href="#">c4bxtD_</a>	Alignment	not modelled	5.0	47	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoprotein p; <b>PDBTitle:</b> crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
90	<a href="#">c5oiyG_</a>	Alignment	not modelled	5.0	47	<b>PDB header:</b> viral protein <b>Chain:</b> G: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> structure of the hmpv p oligomerization domain at 2.2 a
91	<a href="#">c5oixE_</a>	Alignment	not modelled	5.0	47	<b>PDB header:</b> viral protein <b>Chain:</b> E: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> structure of the hmpv p oligomerization domain at 1.6 a