






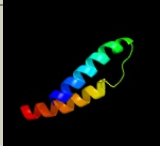



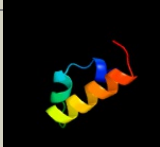

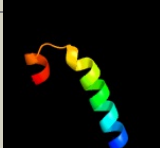





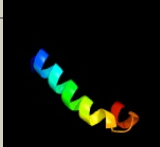

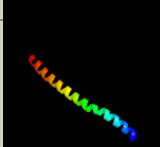







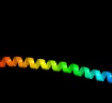
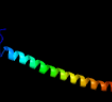


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3850 (- )_4324193_4324849
Date	Sat Aug 10 22:05:03 BST 2019
Unique Job ID	bfb71124eda092bb

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4dndA_</a>	 Alignment		71.1	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> syntaxin-10; <b>PDBTitle:</b> crystal structure of syntaxin 10 from homo sapiens
2	<a href="#">c5frgA_</a>	 Alignment		68.8	24	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> formin-binding protein 1-like; <b>PDBTitle:</b> the nmr structure of the cdc42-interacting region of toca1
3	<a href="#">c2ke4A_</a>	 Alignment		66.6	24	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cdc42-interacting protein 4; <b>PDBTitle:</b> the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
4	<a href="#">d1lvfa_</a>	 Alignment		65.5	17	<b>Fold:</b> STAT-like <b>Superfamily:</b> t-snare proteins <b>Family:</b> t-snare proteins
5	<a href="#">c1f4jC_</a>	 Alignment		39.2	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> catalase; <b>PDBTitle:</b> structure of tetragonal crystals of human erythrocyte catalase
6	<a href="#">d1szpa1</a>	 Alignment		36.3	31	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Rad51 N-terminal domain-like <b>Family:</b> DNA repair protein Rad51, N-terminal domain
7	<a href="#">d4blca_</a>	 Alignment		34.5	11	<b>Fold:</b> Heme-dependent catalase-like <b>Superfamily:</b> Heme-dependent catalase-like <b>Family:</b> Heme-dependent catalases
8	<a href="#">c4cabA_</a>	 Alignment		34.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> catalase; <b>PDBTitle:</b> the refined structure of catalase dr1998 from deinococcus radiodurans2 at 2.6 a resolution
9	<a href="#">d1e93a_</a>	 Alignment		31.7	14	<b>Fold:</b> Heme-dependent catalase-like <b>Superfamily:</b> Heme-dependent catalase-like <b>Family:</b> Heme-dependent catalases
10	<a href="#">d1dgfa_</a>	 Alignment		31.5	11	<b>Fold:</b> Heme-dependent catalase-like <b>Superfamily:</b> Heme-dependent catalase-like <b>Family:</b> Heme-dependent catalases
11	<a href="#">c6fiaB_</a>	 Alignment		29.2	27	<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

12	<a href="#">c1u9pA</a>	Alignment		29.0	7	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> parc; <b>PDBTitle:</b> permuted single-chain arc
13	<a href="#">d1mnta</a>	Alignment		27.9	14	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
14	<a href="#">d1m7sa</a>	Alignment		27.9	10	<b>Fold:</b> Heme-dependent catalase-like <b>Superfamily:</b> Heme-dependent catalase-like <b>Family:</b> Heme-dependent catalases
15	<a href="#">c3geiB</a>	Alignment		27.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> trna modification gtpase mme; <b>PDBTitle:</b> crystal structure of mme from chlorobium tepidum in complex2 with gcp
16	<a href="#">c1ye9E</a>	Alignment		26.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> catalase hpii; <b>PDBTitle:</b> crystal structure of proteolytically truncated catalase2 hpii from e. coli
17	<a href="#">d1gwea</a>	Alignment		26.0	24	<b>Fold:</b> Heme-dependent catalase-like <b>Superfamily:</b> Heme-dependent catalase-like <b>Family:</b> Heme-dependent catalases
18	<a href="#">c4qoqC</a>	Alignment		24.7	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> catalase; <b>PDBTitle:</b> structure of bacillus pumilus catalase with guaiacol bound
19	<a href="#">c6g18t</a>	Alignment		23.2	24	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 40s ribosomal protein s19; <b>PDBTitle:</b> cryo-em structure of a late human pre-40s ribosomal subunit - state c
20	<a href="#">c6g53t</a>	Alignment		23.1	24	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 40s ribosomal protein s19; <b>PDBTitle:</b> cryo-em structure of a late human pre-40s ribosomal subunit - state e
21	<a href="#">c2lswA</a>	Alignment	not modelled	21.9	33	<b>PDB header:</b> blood clotting <b>Chain:</b> A: <b>PDB Molecule:</b> disabled homolog 2; <b>PDBTitle:</b> structure, sulfatide-binding properties, and inhibition of platelet2 aggregation by a disabled-2-derived peptide
22	<a href="#">c4b7hB</a>	Alignment	not modelled	21.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> catalase; <b>PDBTitle:</b> structure of a highdose liganded bacterial catalase
23	<a href="#">c3us6A</a>	Alignment	not modelled	17.3	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine-containing phosphotransfer protein type 1, <b>PDBTitle:</b> crystal structure of histidine-containing phosphotransfer protein2 mthpt1 from medicago truncatula
24	<a href="#">c2xq1M</a>	Alignment	not modelled	16.9	4	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> peroxisomal catalase; <b>PDBTitle:</b> crystal structure of peroxisomal catalase from the yeast hansenula2 polymorpha
25	<a href="#">c1xzqA</a>	Alignment	not modelled	16.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable trna modification gtpase trme; <b>PDBTitle:</b> structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
26	<a href="#">d1iwga6</a>	Alignment	not modelled	16.8	39	<b>Fold:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains <b>Superfamily:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains <b>Family:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
27	<a href="#">d1qwla</a>	Alignment	not modelled	16.6	17	<b>Fold:</b> Heme-dependent catalase-like <b>Superfamily:</b> Heme-dependent catalase-like <b>Family:</b> Heme-dependent catalases
28	<a href="#">c3gocC</a>	Alignment	not modelled	16.1	21	<b>PDB header:</b> transcription/dna <b>Chain:</b> C: <b>PDB Molecule:</b> alginate and motility regulator z;

28	<a href="#">c3qbc</a>	Alignment	not modelled	10.1	41	<b>PDBTitle:</b> crystal structure of the transcription factor amrz in complex with the 2 18 base pair amrz1 binding site <b>PDB header:</b> hydrolase
29	<a href="#">c3gehA</a>	Alignment	not modelled	15.7	15	<b>Chain:</b> A: <b>PDB Molecule:</b> trna modification gtpase mnme; <b>PDBTitle:</b> crystal structure of mnme from nostoc in complex with gdp, folinic2 acid and zn
30	<a href="#">d2eyqa6</a>	Alignment	not modelled	12.5	28	<b>Fold:</b> TRCF domain-like <b>Superfamily:</b> TRCF domain-like <b>Family:</b> TRCF domain
31	<a href="#">d1wn0a1</a>	Alignment	not modelled	12.3	15	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Histidine-containing phosphotransfer domain, HPT domain <b>Family:</b> Phosphorelay protein-like
32	<a href="#">d1e0ga</a>	Alignment	not modelled	11.8	25	<b>Fold:</b> LysM domain <b>Superfamily:</b> LysM domain <b>Family:</b> LysM domain
33	<a href="#">d1si8a</a>	Alignment	not modelled	11.6	18	<b>Fold:</b> Heme-dependent catalase-like <b>Superfamily:</b> Heme-dependent catalase-like <b>Family:</b> Heme-dependent catalases
34	<a href="#">c1ydiB</a>	Alignment	not modelled	11.6	15	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-actinin 4; <b>PDBTitle:</b> human vinculin head domain (vh1, 1-258) in complex with2 human alpha-actinin's vinculin-binding site (residues 731-3 760)
35	<a href="#">d2ilqa1</a>	Alignment	not modelled	11.0	17	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Rad51 N-terminal domain-like <b>Family:</b> DNA repair protein Rad51, N-terminal domain
36	<a href="#">d1szpb1</a>	Alignment	not modelled	10.4	31	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Rad51 N-terminal domain-like <b>Family:</b> DNA repair protein Rad51, N-terminal domain
37	<a href="#">c4g78A</a>	Alignment	not modelled	10.1	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine phosphotransfer protein; <b>PDBTitle:</b> subatomic resolution crystal structure of histidine-containing2 phosphotransfer protein mthpt2 from medicago truncatula
38	<a href="#">c2qsrA</a>	Alignment	not modelled	9.8	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription-repair coupling factor; <b>PDBTitle:</b> crystal structure of c-terminal domain of transcription-repair2 coupling factor
39	<a href="#">c3ci9B</a>	Alignment	not modelled	9.8	20	<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
40	<a href="#">d2ao9a1</a>	Alignment	not modelled	9.1	30	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Nanomeric phage protein-like
41	<a href="#">c5tmxA</a>	Alignment	not modelled	8.9	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> protein sini; <b>PDBTitle:</b> solution structure of sini, antagonist to the master biofilm-regulator2 sinr in bacillus subtilis
42	<a href="#">d1pzqa</a>	Alignment	not modelled	7.9	33	<b>Fold:</b> Dimerisation interlock <b>Superfamily:</b> Docking domain A of the erythromycin polyketide synthase (DEBS) <b>Family:</b> Docking domain A of the erythromycin polyketide synthase (DEBS)
43	<a href="#">c4huqT</a>	Alignment	not modelled	7.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> T: <b>PDB Molecule:</b> energy-coupling factor transporter transmembrane protein <b>PDBTitle:</b> crystal structure of a transporter
44	<a href="#">c4b9hA</a>	Alignment	not modelled	7.8	21	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular protein 6; <b>PDBTitle:</b> cladosporium fulvum lysm effector ecp6 in complex with a2 beta-1,4-linked n-acetyl-d-glucosamine tetramer: i3c heavy3 atom derivative
45	<a href="#">c3cqxD</a>	Alignment	not modelled	7.7	15	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> bag family molecular chaperone regulator 2; <b>PDBTitle:</b> chaperone complex
46	<a href="#">c4rfsT</a>	Alignment	not modelled	7.6	17	<b>PDB header:</b> hydrolase, transport protein <b>Chain:</b> T: <b>PDB Molecule:</b> energy-coupling factor transporter transmembrane protein <b>PDBTitle:</b> structure of a pantothenate energy coupling factor transporter
47	<a href="#">d1rioA</a>	Alignment	not modelled	7.6	21	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
48	<a href="#">c6j5id</a>	Alignment	not modelled	7.4	12	<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
49	<a href="#">c2cpmA</a>	Alignment	not modelled	7.3	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sperm-associated antigen 7; <b>PDBTitle:</b> solution structure of the r3h domain of human sperm-2 associated antigen 7
50	<a href="#">c5t0fB</a>	Alignment	not modelled	7.2	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> protein tify 9; <b>PDBTitle:</b> crystal structure of the myc3 n-terminal domain [44-242] in complex2 with jaz10 cmid domain [16-58] from arabidopsis
51	<a href="#">d1pzna1</a>	Alignment	not modelled	7.2	17	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Rad51 N-terminal domain-like <b>Family:</b> DNA repair protein Rad51, N-terminal domain
52	<a href="#">d1vcsa1</a>	Alignment	not modelled	7.0	10	<b>Fold:</b> STAT-like <b>Superfamily:</b> t-snare proteins <b>Family:</b> t-snare proteins
53	<a href="#">c2mkxA</a>	Alignment	not modelled	7.0	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> autolysin; <b>PDBTitle:</b> solution structure of lysm the peptidoglycan binding

						domain of2 autolysin atla from enterococcus faecalis
54	<a href="#">d1y7ma2</a>	Alignment	not modelled	7.0	13	<b>Fold:</b> LysM domain <b>Superfamily:</b> LysM domain <b>Family:</b> LysM domain
55	<a href="#">c4uetA</a>	Alignment	not modelled	6.8	11	<b>PDB header:</b> retinol-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nematode fatty acid retinoid binding protein; <b>PDBTitle:</b> diversity in the structures and ligand binding sites among2 the fatty acid and retinol binding proteins of nematodes3 revealed by na-far-1 from necator americanus
56	<a href="#">d2h9da1</a>	Alignment	not modelled	6.7	25	<b>Fold:</b> Chorismate mutase II <b>Superfamily:</b> Chorismate mutase II <b>Family:</b> Dimeric chorismate mutase
57	<a href="#">c6hwB</a>	Alignment	not modelled	6.6	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glucosamine kinase; <b>PDBTitle:</b> glucosamine kinase in complex with glucosamine, adp and inorganic2 phosphate
58	<a href="#">d1yvia1</a>	Alignment	not modelled	6.6	9	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Histidine-containing phosphotransfer domain, HPT domain <b>Family:</b> Phosphorelay protein-like
59	<a href="#">c2dnxA</a>	Alignment	not modelled	6.3	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> syntaxin-12; <b>PDBTitle:</b> solution structure of rsg1 ruh-063, an n-terminal domain of2 syntaxin 12 from human cdna
60	<a href="#">c4awaA</a>	Alignment	not modelled	6.3	43	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> legumain; <b>PDBTitle:</b> crystal structure of active legumain in complex with yvad-cmk2 at ph 5.0
61	<a href="#">c2ao9H</a>	Alignment	not modelled	6.2	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> H: <b>PDB Molecule:</b> phage protein; <b>PDBTitle:</b> structural genomics, the crystal structure of a phage protein2 (phbc6a51) from bacillus cereus atcc 14579
62	<a href="#">c4bgoA</a>	Alignment	not modelled	6.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> efem m75 peptidase; <b>PDBTitle:</b> structural and functional role of the imelysin-like protein2 efem from pseudomonas syringae pv. syringae and3 implications in bacterial iron transport
63	<a href="#">c3kxyW</a>	Alignment	not modelled	6.1	60	<b>PDB header:</b> chaperone/transcription inhibitor <b>Chain:</b> W: <b>PDB Molecule:</b> exse; <b>PDBTitle:</b> crystal structure of the excsc-exse complex
64	<a href="#">c5tw7E</a>	Alignment	not modelled	6.0	24	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae
65	<a href="#">c5k2IA</a>	Alignment	not modelled	5.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitinase, lysozyme; <b>PDBTitle:</b> crystal structure of lysm domain from volvox carteri chitinase
66	<a href="#">c5jceA</a>	Alignment	not modelled	5.7	19	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> chitin elicitor-binding protein; <b>PDBTitle:</b> crystal structure of oscebip complex
67	<a href="#">c2j2mD</a>	Alignment	not modelled	5.7	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> catalase; <b>PDBTitle:</b> crystal structure analysis of catalase from exiguobacterium2 oxidotolerans
68	<a href="#">d1p80a2</a>	Alignment	not modelled	5.7	14	<b>Fold:</b> Heme-dependent catalase-like <b>Superfamily:</b> Heme-dependent catalase-like <b>Family:</b> Heme-dependent catalases
69	<a href="#">d1b22a</a>	Alignment	not modelled	5.7	27	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Rad51 N-terminal domain-like <b>Family:</b> DNA repair protein Rad51, N-terminal domain
70	<a href="#">c1b22A</a>	Alignment	not modelled	5.7	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rad51; <b>PDBTitle:</b> rad51 (n-terminal domain)
71	<a href="#">c3hrdF</a>	Alignment	not modelled	5.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> nicotinate dehydrogenase medium molybdopterin <b>PDBTitle:</b> crystal structure of nicotinate dehydrogenase
72	<a href="#">c5zyvB</a>	Alignment	not modelled	5.5	15	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> flagellar hook-associated protein 3; <b>PDBTitle:</b> crystal structure of bacillus cereus flgI
73	<a href="#">c2msvA</a>	Alignment	not modelled	5.5	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> mixed lineage kinase domain-like protein; <b>PDBTitle:</b> solution structure of the mkl1 n-terminal domain
74	<a href="#">c3bijC</a>	Alignment	not modelled	5.4	80	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein gsu0716; <b>PDBTitle:</b> crystal structure of protein gsu0716 from geobacter sulfurreducens.2 northeast structural genomics target gsr13
75	<a href="#">c4afpA</a>	Alignment	not modelled	5.3	67	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metacaspase mca2; <b>PDBTitle:</b> the structure of metacaspase 2 from t. brucei determined in the2 presence of samarium
76	<a href="#">c3pf0A</a>	Alignment	not modelled	5.3	10	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> imelysin-like protein; <b>PDBTitle:</b> crystal structure of an imelysin-like protein (psyc_1802) from2 psychrobacter arcticum 273-4 at 2.15 a resolution
77	<a href="#">c4ua2B</a>	Alignment	not modelled	5.2	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> crystal structure of dual function transcriptional regulator merr from2 bacillus megaterium mb1
78	<a href="#">c5o34C</a>	Alignment	not modelled	5.2	16	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> enoyl-coa hydratase carb homologue; <b>PDBTitle:</b> thne from s.clavuligerus
						<b>PDB header:</b> hydrolase

79	<a href="#">c4ad9E_</a>	Alignment	not modelled	5.1	21	<b>Chain:</b> E: <b>PDB Molecule:</b> beta-lactamase-like protein 2; <b>PDBTitle:</b> crystal structure of human lactb2.
80	<a href="#">c3pmkP_</a>	Alignment	not modelled	5.1	44	<b>PDB header:</b> viral protein <b>Chain:</b> P: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> crystal structure of the vesicular stomatitis virus rna free2 nucleoprotein/phosphoprotein complex
81	<a href="#">c3pmkR_</a>	Alignment	not modelled	5.1	44	<b>PDB header:</b> viral protein <b>Chain:</b> R: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> crystal structure of the vesicular stomatitis virus rna free2 nucleoprotein/phosphoprotein complex
82	<a href="#">c4f6oA_</a>	Alignment	not modelled	5.1	80	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metacaspase-1; <b>PDBTitle:</b> crystal structure of the yeast metacaspase yca1
83	<a href="#">c5bumA_</a>	Alignment	not modelled	5.1	19	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> chitinase a; <b>PDBTitle:</b> crystal structure of lysm domain from equisetum arvense chitinase a
84	<a href="#">c3pmkO_</a>	Alignment	not modelled	5.0	44	<b>PDB header:</b> viral protein <b>Chain:</b> Q: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> crystal structure of the vesicular stomatitis virus rna free2 nucleoprotein/phosphoprotein complex
85	<a href="#">c3pmkN_</a>	Alignment	not modelled	5.0	44	<b>PDB header:</b> viral protein <b>Chain:</b> N: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> crystal structure of the vesicular stomatitis virus rna free2 nucleoprotein/phosphoprotein complex