


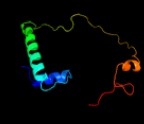

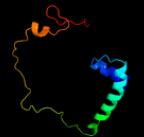





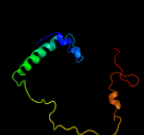



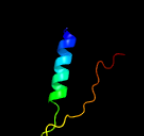





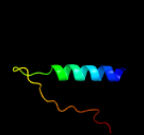


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3012c\_gatC\_3371441\_3371740  
 Date Thu Aug 8 16:20:18 BST 2019  
 Unique Job ID b53a16ded8092473

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4wj3F_</a>	 Alignment		100.0	31	<b>PDB header:</b> ligase/rna <b>Chain:</b> F: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit c; <b>PDBTitle:</b> crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
2	<a href="#">d2f2ac1</a>	 Alignment		100.0	36	<b>Fold:</b> Non-globular all-alpha subunits of globular proteins <b>Superfamily:</b> Glu-tRNA <sup>Gln</sup> amidotransferase C subunit <b>Family:</b> Glu-tRNA <sup>Gln</sup> amidotransferase C subunit
3	<a href="#">c3h0mU_</a>	 Alignment		100.0	34	<b>PDB header:</b> ligase <b>Chain:</b> U: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit c; <b>PDBTitle:</b> structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
4	<a href="#">c3kfuJ_</a>	 Alignment		99.9	31	<b>PDB header:</b> ligase/rna <b>Chain:</b> J: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit c; <b>PDBTitle:</b> crystal structure of the transamidosome
5	<a href="#">c4n0hF_</a>	 Alignment		99.9	17	<b>PDB header:</b> ligase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit f, <b>PDBTitle:</b> crystal structure of s. cerevisiae mitochondrial gatfab
6	<a href="#">c3a10C_</a>	 Alignment		99.3	30	<b>PDB header:</b> ligase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit c,linker, <b>PDBTitle:</b> crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
7	<a href="#">c3o0rC_</a>	 Alignment		53.3	17	<b>PDB header:</b> immune system/oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nitric oxide reductase subunit c; <b>PDBTitle:</b> crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
8	<a href="#">c2bvtB_</a>	 Alignment		27.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-1,4-mannanase; <b>PDBTitle:</b> the structure of a modular endo-beta-1,4-mannanase from cellulomonas2 fimi explains the product specificity of glycoside hydrolase family3 26 mannanases.
9	<a href="#">c2lycA_</a>	 Alignment		27.0	22	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> spindle and kinetochore-associated protein 1 homolog; <b>PDBTitle:</b> structure of c-terminal domain of ska1
10	<a href="#">c4xydB_</a>	 Alignment		25.1	4	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> norc-like protein; <b>PDBTitle:</b> nitric oxide reductase from roseobacter denitrificans (rdnor)
11	<a href="#">d1odza_</a>	 Alignment		20.2	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases

12	<a href="#">c6ct6B_</a>	Alignment		19.2	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of lactate dehydrogenase from eimeria maxima with2 nadh and oxamate
13	<a href="#">d1tuza_</a>	Alignment		16.3	13	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> EF-hand modules in multidomain proteins
14	<a href="#">c2aucC_</a>	Alignment		15.2	20	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> myosin a tail interacting protein; <b>PDBTitle:</b> structure of the plasmodium mtip-myoa complex, a key component of the2 parasite invasion motor
15	<a href="#">c4c9yB_</a>	Alignment		14.6	14	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> spindle and kinetochore-associated protein 1; <b>PDBTitle:</b> structural basis for the microtubule binding of the human2 kinetochore ska complex
16	<a href="#">c5g3qA_</a>	Alignment		13.9	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> wnk1; <b>PDBTitle:</b> crystal structure of a hypothetical domain in wnk1
17	<a href="#">c3nepX_</a>	Alignment		13.1	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> 1.55a resolution structure of malate dehydrogenase from salinibacter2 ruber
18	<a href="#">d1yira2</a>	Alignment		11.8	15	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Nicotinate/Quinolinate PRTase N-terminal domain-like <b>Family:</b> Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
19	<a href="#">c5tdyD_</a>	Alignment		11.1	11	<b>PDB header:</b> motor protein <b>Chain:</b> D: <b>PDB Molecule:</b> flagellar motor switch protein flig; <b>PDBTitle:</b> structure of cofolded flifc:flign complex from thermotoga maritima
20	<a href="#">d1y7ta2</a>	Alignment		11.0	17	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
21	<a href="#">d2fcea1</a>	Alignment	not modelled	10.7	19	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
22	<a href="#">c5cuvB_</a>	Alignment	not modelled	10.6	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> acidocalcisomal pyrophosphatase; <b>PDBTitle:</b> crystal structure of trypanosoma cruzi vacuolar soluble2 pyrophosphatases in apo form
23	<a href="#">c5vt9A_</a>	Alignment	not modelled	10.3	17	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin light chain tgmlc1; <b>PDBTitle:</b> myosin light chain 1 and myoa complex
24	<a href="#">d1izma_</a>	Alignment	not modelled	10.3	22	<b>Fold:</b> Ygfb-like <b>Superfamily:</b> Ygfb-like <b>Family:</b> Ygfb-like
25	<a href="#">c2amiA_</a>	Alignment	not modelled	10.0	14	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> caltractin; <b>PDBTitle:</b> solution structure of the calcium-loaded n-terminal sensor domain of2 centrin
26	<a href="#">d1wrka1</a>	Alignment	not modelled	9.6	23	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
27	<a href="#">c5wlmC_</a>	Alignment	not modelled	9.1	46	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> helical bundle 4dh2; <b>PDBTitle:</b> de novo design of polynuclear transition metal clusters in helix2 bundles-4dh2
28	<a href="#">c5wlmD_</a>	Alignment	not modelled	9.1	46	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> helical bundle 4dh2; <b>PDBTitle:</b> de novo design of polynuclear transition metal clusters in helix2 bundles-4dh2
						<b>PDB header:</b> de novo protein

29	<a href="#">c5wlmB_</a>	Alignment	not modelled	9.1	46	<b>Chain:</b> B: <b>PDB Molecule:</b> helical bundle 4dh2; <b>PDBTitle:</b> de novo design of polynuclear transition metal clusters in helix2 bundles-4dh2
30	<a href="#">c5wlmA_</a>	Alignment	not modelled	9.1	46	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> helical bundle 4dh2; <b>PDBTitle:</b> de novo design of polynuclear transition metal clusters in helix2 bundles-4dh2
31	<a href="#">c5wlkC_</a>	Alignment	not modelled	8.9	54	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> helical bundle 4eh2; <b>PDBTitle:</b> de novo design of polynuclear transition metal clusters in helix2 bundles-4eh2
32	<a href="#">c5wlkB_</a>	Alignment	not modelled	8.9	54	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> helical bundle 4eh2; <b>PDBTitle:</b> de novo design of polynuclear transition metal clusters in helix2 bundles-4eh2
33	<a href="#">c5wlkA_</a>	Alignment	not modelled	8.9	54	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> helical bundle 4eh2; <b>PDBTitle:</b> de novo design of polynuclear transition metal clusters in helix2 bundles-4eh2
34	<a href="#">c5wlkD_</a>	Alignment	not modelled	8.9	54	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> helical bundle 4eh2; <b>PDBTitle:</b> de novo design of polynuclear transition metal clusters in helix2 bundles-4eh2
35	<a href="#">c3korD_</a>	Alignment	not modelled	8.9	13	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> possible trp repressor; <b>PDBTitle:</b> crystal structure of a putative trp repressor from staphylococcus2 aureus
36	<a href="#">c2fcdA_</a>	Alignment	not modelled	8.7	15	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> myosin light chain 1; <b>PDBTitle:</b> solution structure of n-lobe myosin light chain from2 saccharomices cerevisiae
37	<a href="#">d1s6ja_</a>	Alignment	not modelled	8.6	20	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
38	<a href="#">d2bvya2</a>	Alignment	not modelled	8.3	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
39	<a href="#">c3jbhl_</a>	Alignment	not modelled	8.3	13	<b>PDB header:</b> contractile protein <b>Chain:</b> I: <b>PDB Molecule:</b> myosin 2 essential light chain striated muscle; <b>PDBTitle:</b> two heavy meromyosin interacting-heads motifs flexible docked into2 tarantula thick filament 3d-map allows in depth study of intra- and3 intermolecular interactions
40	<a href="#">d1wlza1</a>	Alignment	not modelled	8.1	26	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> EF-hand modules in multidomain proteins
41	<a href="#">d1f54a_</a>	Alignment	not modelled	8.1	28	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
42	<a href="#">d1jc2a_</a>	Alignment	not modelled	7.9	13	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
43	<a href="#">c1jc2A_</a>	Alignment	not modelled	7.9	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> troponin c, skeletal muscle; <b>PDBTitle:</b> complex of the c-domain of troponin c with residues 1-40 of2 troponin i
44	<a href="#">c1wlzD_</a>	Alignment	not modelled	7.9	27	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> cap-binding protein complex interacting protein <b>PDBTitle:</b> crystal structure of djbp fragment which was obtained by2 limited proteolysis
45	<a href="#">c4cvoA_</a>	Alignment	not modelled	7.5	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna excision repair protein ercc-6; <b>PDBTitle:</b> crystal structure of the n-terminal colled-coil domain of human dna2 excision repair protein ercc-6
46	<a href="#">d1sbqa_</a>	Alignment	not modelled	7.1	16	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> Methenyltetrahydrofolate synthetase
47	<a href="#">c1u3fA_</a>	Alignment	not modelled	7.1	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> 5,10-methenyltetrahydrofolate synthetase; <b>PDBTitle:</b> structural and functional characterization of a 5,10-2 methenyltetrahydrofolate synthetase from mycoplasma3 pneumoniae (gi: 13508087)
48	<a href="#">c2vx6A_</a>	Alignment	not modelled	7.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellvibrio japonicus mannanase cjman26c; <b>PDBTitle:</b> cellvibrio japonicus mannanase cjman26c gal1man4-bound form
49	<a href="#">c1zmzA_</a>	Alignment	not modelled	7.0	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> centrin-2; <b>PDBTitle:</b> solution structure of the n-terminal domain (m1-s98) of2 human centrin 2
50	<a href="#">d1lavsa_</a>	Alignment	not modelled	6.8	27	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
51	<a href="#">d1cmga_</a>	Alignment	not modelled	6.7	27	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
52	<a href="#">d3e9va1</a>	Alignment	not modelled	6.6	32	<b>Fold:</b> BTG domain-like <b>Superfamily:</b> BTG domain-like <b>Family:</b> BTG domain-like
53	<a href="#">c5i2oA_</a>	Alignment	not modelled	6.5	10	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ef-hand domain-containing protein d2; <b>PDBTitle:</b> structure of ef-hand containing protein
54	<a href="#">c2k7bA_</a>	Alignment	not modelled	6.5	23	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> calcium-binding protein 1;

						<b>PDBTitle:</b> nmr structure of mg2+-bound cabp1 n-domain
55	<a href="#">c2l2eA_</a>	Alignment	not modelled	6.5	25	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> calcium-binding protein ncs-1; <b>PDBTitle:</b> solution nmr structure of myristoylated ncs1p in apo form
56	<a href="#">c4wjbb_</a>	Alignment	not modelled	6.4	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative amidohydrolase/peptidase; <b>PDBTitle:</b> x-ray crystal structure of a putative amidohydrolase/peptidase from2 burkholderia cenocepacia
57	<a href="#">d1fw4a_</a>	Alignment	not modelled	6.3	27	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
58	<a href="#">d1id3b_</a>	Alignment	not modelled	6.2	18	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
59	<a href="#">c3izcw_</a>	Alignment	not modelled	6.2	7	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> 60s ribosomal protein rpl22 (l22e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
60	<a href="#">d1n0yb_</a>	Alignment	not modelled	6.2	27	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
61	<a href="#">c3zm8A_</a>	Alignment	not modelled	6.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gh26 endo-beta-1,4-mannanase; <b>PDBTitle:</b> crystal structure of podospira anserina gh26-cbm352 beta-(1,4)-mannanase
62	<a href="#">d1wdcc_</a>	Alignment	not modelled	6.1	23	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
63	<a href="#">c5ve9B_</a>	Alignment	not modelled	6.0	21	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> microtubule-actin cross-linking factor 1, isoforms 1/2/3/5; <b>PDBTitle:</b> structure of hacf7 ef1-ef2-gar domains
64	<a href="#">d1tiza_</a>	Alignment	not modelled	5.9	20	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
65	<a href="#">c2b1uA_</a>	Alignment	not modelled	5.9	24	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> calmodulin-like protein 5; <b>PDBTitle:</b> solution structure of calmodulin-like skin protein c2 terminal domain
66	<a href="#">c3iz5w_</a>	Alignment	not modelled	5.9	7	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> 60s ribosomal protein l22 (l22e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
67	<a href="#">c4xpmA_</a>	Alignment	not modelled	5.9	27	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein meh1; <b>PDBTitle:</b> crystal structure of ego-tc
68	<a href="#">c3wdrA_</a>	Alignment	not modelled	5.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-mannanase; <b>PDBTitle:</b> crystal structure of beta-mannanase from a symbiotic protist of the2 termite reticulitermes speratus complexed with gluco-manno-3 oligosaccharide
69	<a href="#">c2oltB_</a>	Alignment	not modelled	5.8	19	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a phou-like protein (so_3770) from shewanella2 oneidensis mr-1 at 2.00 a resolution
70	<a href="#">c4okhC_</a>	Alignment	not modelled	5.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> calpain-3; <b>PDBTitle:</b> crystal structure of calpain-3 penta-ef-hand domain
71	<a href="#">c2k2aA_</a>	Alignment	not modelled	5.7	20	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> troponin c; <b>PDBTitle:</b> solution structure of the apo c terminal domain of lethocerus troponin2 c isoform f1
72	<a href="#">c6jxbB_</a>	Alignment	not modelled	5.6	12	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid biosynthesis transcriptional regulator; <b>PDBTitle:</b> crystal structure of streptococcus pneumoniae fabt in complex with dna
73	<a href="#">c2m29A_</a>	Alignment	not modelled	5.5	23	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> calcium-binding protein 4; <b>PDBTitle:</b> nmr structure of ca2+ bound cabp4 n-domain
74	<a href="#">d1pzga2</a>	Alignment	not modelled	5.4	24	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
75	<a href="#">c6e0oA_</a>	Alignment	not modelled	5.3	19	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> cgas/dncv-like nucleotidyltransferase in e. coli homolog; <b>PDBTitle:</b> structure of elizabethkingia meningoseptica cdne cyclic dinucleotide2 synthase with pppa[3'-5']pa
76	<a href="#">d1lcda_</a>	Alignment	not modelled	5.2	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
77	<a href="#">d1g8ia_</a>	Alignment	not modelled	5.2	22	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
78	<a href="#">d1m39a_</a>	Alignment	not modelled	5.2	23	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
79	<a href="#">d1b8pa2</a>	Alignment	not modelled	5.1	14	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
						<b>PDB header:</b> metal binding protein

80	<a href="#">c2d58A_</a>	Alignment	not modelled	5.1	17	<b>Chain:</b> A; <b>PDB Molecule:</b> allograft inflammatory factor 1; <b>PDBTitle:</b> human microglia-specific protein iba1
81	<a href="#">c4pkfC_</a>	Alignment	not modelled	5.1	43	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> tutf; <b>PDBTitle:</b> benzylsuccinate synthase alpha-beta-gamma complex
82	<a href="#">c3sluB_</a>	Alignment	not modelled	5.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> m23 peptidase domain protein; <b>PDBTitle:</b> crystal structure of nmb0315
83	<a href="#">c6bp6A_</a>	Alignment	not modelled	5.0	22	<b>PDB header:</b> endocytosis <b>Chain:</b> A; <b>PDB Molecule:</b> comm domain-containing protein 9; <b>PDBTitle:</b> crystal structure of commd9 comm domain