Phyre^2

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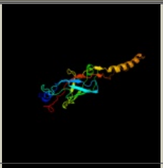
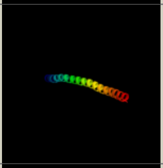
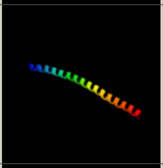
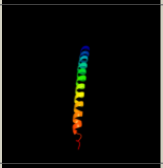
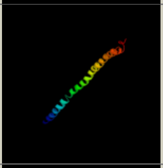
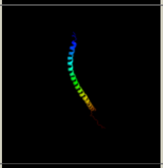
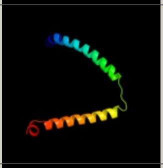
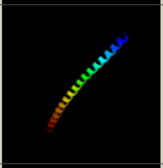
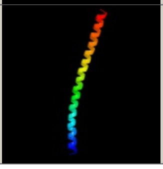
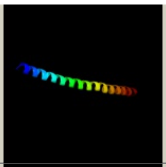
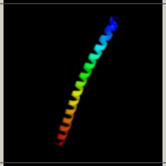
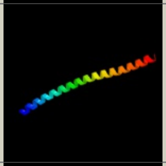
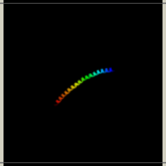
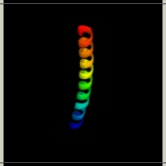
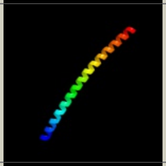
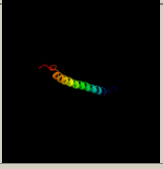
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3jqoV_	Alignment		99.9	15	**PDB header:**transport protein **Chain:** V: **PDB Molecule:**traf protein; **PDBTitle:** crystal structure of the outer membrane complex of a type iv2 secretion system
2	c2bhvC_	Alignment		99.8	19	**PDB header:**bacterial protein **Chain:** C: **PDB Molecule:**comb10; **PDBTitle:** structure of comb10 of the com type iv secretion system of2 helicobacter pylori
3	c3ghgK_	Alignment		63.9	5	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
4	c1ei3E_	Alignment		52.3	5	**PDB header:** **PDB COMPND:**
5	c3n4xB_	Alignment		46.4	13	**PDB header:**replication **Chain:** B: **PDB Molecule:**monopolin complex subunit csm1; **PDBTitle:** structure of csm1 full-length
6	c3m9bK_	Alignment		43.6	22	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
7	c1deqO_	Alignment		41.4	5	**PDB header:** **PDB COMPND:**
8	c1deqF_	Alignment		39.1	11	**PDB header:** **PDB COMPND:**
9	c3l9oA_	Alignment		38.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** crystal structure of mtr4, a co-factor of the nuclear exosome
10	c3ojaB_	Alignment		38.3	24	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
11	c3hnwB_	Alignment		36.0	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750

12	c2jeeA_	Alignment		25.4	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**yiiu; **PDBTitle:** xray structure of e. coli yiiu
13	d1d0gr1	Alignment		22.9	55	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**TNF receptor-like
14	c2x7aB_	Alignment		22.8	26	**PDB header:**immune system **Chain:** B: **PDB Molecule:**bone marrow stromal antigen 2; **PDBTitle:** structural basis of hiv-1 tethering to membranes by the2 bst2-tetherin ectodomain
15	c3a7pB_	Alignment		22.3	10	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg16
16	c3dtpA_	Alignment		21.7	11	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**myosin 2 heavy chain chimera of smooth and **PDBTitle:** tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map
17	c2oqqB_	Alignment		20.8	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor hy5; **PDBTitle:** crystal structure of hy5 leucine zipper homodimer from2 arabidopsis thaliana
18	c2xzrA_	Alignment		19.6	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**immunoglobulin-binding protein eibd; **PDBTitle:** escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
19	d2fd6u3	Alignment		19.5	26	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Extracellular domain of cell surface receptors
20	c2hpcF_	Alignment		19.5	14	**PDB header:**blood clotting **Chain:** F: **PDB Molecule:**fibrinogen, gamma polypeptide; **PDBTitle:** crystal structure of fragment d from human fibrinogen complexed with2 gly-pro-arg-pro-amide.
21	c1cz7C_	Alignment	not modelled	18.7	13	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**microtubule motor protein ncd; **PDBTitle:** the crystal structure of a minus-end directed microtubule2 motor protein ncd reveals variable dimer conformations
22	c2xgjA_	Alignment	not modelled	18.5	13	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** structure of mtr4, a dexh helicase involved in nuclear rna2 processing and surveillance
23	c2w6aB_	Alignment	not modelled	18.3	22	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**arf gtpase-activating protein git1; **PDBTitle:** x-ray structure of the dimeric git1 coiled-coil domain
24	c3oa7A_	Alignment	not modelled	18.2	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**head morphogenesis protein, chaotic nuclear migration **PDBTitle:** structure of the c-terminal domain of cnm67, a core component of the2 spindle pole body of saccharomyces cerevisiae
25	c1junB_	Alignment	not modelled	17.5	11	**PDB header:**transcription regulation **Chain:** B: **PDB Molecule:**c-jun homodimer; **PDBTitle:** nmr study of c-jun homodimer
26	c2yy0D_	Alignment	not modelled	15.6	3	**PDB header:**transcription **Chain:** D: **PDB Molecule:**c-myc-binding protein; **PDBTitle:** crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
27	c1n73C_	Alignment	not modelled	15.4	8	**PDB header:**blood clotting **Chain:** C: **PDB Molecule:**fibrin gamma chain; **PDBTitle:** fibrin d-dimer, lamprey complexed with the peptide ligand: gly-his-2 arg-pro-amide
28	c2z0fA_	Alignment	not modelled	15.3	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphoglucomutase; **PDBTitle:** crystal structure of putative phosphoglucomutase from

						thermus2 thermophilus hb8
29	c2jo1A_	Alignment	not modelled	14.4	17	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
30	d1gpia_	Alignment	not modelled	13.2	19	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolase family 7 catalytic core
31	c1dipA_	Alignment	not modelled	13.0	18	**PDB header:**acetylation **Chain:** A: **PDB Molecule:**delta-sleep-inducing peptide immunoreactive **PDBTitle:** the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
32	d1ogda_	Alignment	not modelled	12.9	16	**Fold:**RbsD-like **Superfamily:**RbsD-like **Family:**RbsD-like
33	d2ncda_	Alignment	not modelled	12.7	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Motor proteins
34	d1fxkc_	Alignment	not modelled	12.7	11	**Fold:**Long alpha-hairpin **Superfamily:**Prefoldin **Family:**Prefoldin
35	c1jocA_	Alignment	not modelled	12.7	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**early endosomal autoantigen 1; **PDBTitle:** eea1 homodimer of c-terminal fyve domain bound to inositol2 1,3-diphosphate
36	c3he5D_	Alignment	not modelled	12.7	18	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**synzip2; **PDBTitle:** heterospecific coiled-coil pair synzip2:synzip1
37	c2wl2B_	Alignment	not modelled	12.0	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** crystal structure of n-terminal domain of gyra with the2 antibiotic simocyclinone d8
38	c3hizB_	Alignment	not modelled	11.8	9	**PDB header:**transferase/oncoprotein **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit **PDBTitle:** crystal structure of p110alpha h1047r mutant in complex with2 nish2 of p85alpha
39	c3cvfA_	Alignment	not modelled	11.3	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**homer protein homolog 3; **PDBTitle:** crystal structure of the carboxy terminus of homer3
40	c3h9mA_	Alignment	not modelled	11.2	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**p-aminobenzoate synthetase, component i; **PDBTitle:** crystal structure of para-aminobenzoate synthetase,2 component i from cytophaga hutchinsonii
41	d1ykhb1	Alignment	not modelled	11.2	20	**Fold:**Mediator hinge subcomplex-like **Superfamily:**Mediator hinge subcomplex-like **Family:**CSE2-like
42	c3hd7A_	Alignment	not modelled	11.2	13	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
43	c3ni0A_	Alignment	not modelled	11.1	17	**PDB header:**immune system **Chain:** A: **PDB Molecule:**bone marrow stromal antigen 2; **PDBTitle:** crystal structure of mouse bst-2/tetherin ectodomain
44	c2wukD_	Alignment	not modelled	10.6	8	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**septum site-determining protein diviva; **PDBTitle:** diviva n-terminal domain, f17a mutant
45	c2x5qA_	Alignment	not modelled	10.6	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**sso1986; **PDBTitle:** crystal structure of hypothetical protein sso1986 from2 sulfolobus solfataricus p2
46	d1ivsa1	Alignment	not modelled	10.4	10	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Valyl-tRNA synthetase (ValRS) C-terminal domain
47	c3q0xA_	Alignment	not modelled	10.3	12	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**centriole protein; **PDBTitle:** n-terminal coiled-coil dimer domain of c. reinhardtii sas-6 homolog2 bld12p
48	c2gl2B_	Alignment	not modelled	9.9	10	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**adhesion a; **PDBTitle:** crystal structure of the tetra muntant (t66g,r67g,f68g,2 y69g) of bacterial adhesin fada
49	c3i3wB_	Alignment	not modelled	9.6	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucosamine mutase; **PDBTitle:** structure of a phosphoglucosamine mutase from francisella tularensis
50	d2ga1a1	Alignment	not modelled	9.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Alr1493-like
51	c2aanA_	Alignment	not modelled	9.4	31	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**auracyanin a; **PDBTitle:** auracyanin a: a "blue" copper protein from the green thermophilic2 photosynthetic bacterium,chloroflexus aurantiacus
52	c2fuvB_	Alignment	not modelled	9.4	8	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucomutase; **PDBTitle:** phosphoglucomutase from salmonella typhimurium.
53	d1e30a_	Alignment	not modelled	9.2	33	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
54	d2ob5a1	Alignment	not modelled	9.1	24	**Fold:**RbsD-like **Superfamily:**RbsD-like

						Family: RbsD-like
55	c1ci6A_	Alignment	not modelled	9.1	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor atf-4; **PDBTitle:** transcription factor atf4-c/ebp beta bzip heterodimer
56	c2ykqC_	Alignment	not modelled	9.0	13	**PDB header:**rna-binding protein **Chain:** C: **PDB Molecule:**line-1 orf1p; **PDBTitle:** structure of the human line-1 orf1p trimer
57	c3ol1A_	Alignment	not modelled	8.9	8	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** crystal structure of vimentin (fragment 144-251) from homo sapiens,2 northeast structural genomics consortium target hr4796b
58	c1cosC_	Alignment	not modelled	8.5	16	**PDB header:**alpha-helical bundle **Chain:** C: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
59	c1cosB_	Alignment	not modelled	8.5	16	**PDB header:**alpha-helical bundle **Chain:** B: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
60	c1cosA_	Alignment	not modelled	8.5	16	**PDB header:**alpha-helical bundle **Chain:** A: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
61	c2zdiC_	Alignment	not modelled	8.4	13	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**prefoldin subunit alpha; **PDBTitle:** crystal structure of prefoldin from pyrococcus horikoshii2 ot3
62	c1l4aD_	Alignment	not modelled	8.4	11	**PDB header:**endocytosis/exocytosis **Chain:** D: **PDB Molecule:**s-snap25 fusion protein; **PDBTitle:** x-ray structure of the neuronal complexin/snare complex2 from the squid loligo pealei
63	c1debA_	Alignment	not modelled	8.2	26	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**adenomatous polyposis coli protein; **PDBTitle:** crystal structure of the n-terminal coiled coil domain from2 apc
64	d2axtj1	Alignment	not modelled	8.2	25	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein J, PsbJ **Family:**PsbJ-like
65	c3iv1F_	Alignment	not modelled	8.0	15	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**tumor susceptibility gene 101 protein; **PDBTitle:** coiled-coil domain of tumor susceptibility gene 101
66	d2rkya2	Alignment	not modelled	8.0	27	**Fold:**FnI-like domain **Superfamily:**FnI-like domain **Family:**Fibronectin type I module
67	c3u59C_	Alignment	not modelled	7.7	8	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**tropomyosin beta chain; **PDBTitle:** n-terminal 98-aa fragment of smooth muscle tropomyosin beta
68	c1tuoA_	Alignment	not modelled	7.5	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative phosphomannomutase; **PDBTitle:** crystal structure of putative phosphomannomutase from2 thermus thermophilus hb8
69	c1jccC_	Alignment	not modelled	7.3	7	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**major outer membrane lipoprotein; **PDBTitle:** crystal structure of a novel alanine-zipper trimer at 1.7 a2 resolution, v13a,l16a,v20a,l23a,v27a,m30a,v34a mutations
70	d1sdda1	Alignment	not modelled	7.3	25	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
71	c2js5B_	Alignment	not modelled	7.3	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of protein q60c73_metca. northeast structural2 genomics consortium target mcr1
72	d2phcb1	Alignment	not modelled	7.3	21	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**PH0987 C-terminal domain-like
73	c3bvhC_	Alignment	not modelled	7.2	9	**PDB header:**blood clotting **Chain:** C: **PDB Molecule:**fibrinogen gamma chain; **PDBTitle:** crystal structure of recombinant gammad364a fibrinogen fragment d with2 the peptide ligand gly-pro-arg-pro-amide
74	c2kg4A_	Alignment	not modelled	7.1	26	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**growth arrest and dna-damage-inducible protein **PDBTitle:** three-dimensional structure of human gadd45alpha in2 solution by nmr
75	d1tsfa_	Alignment	not modelled	7.1	13	**Fold:**Rof/RNase P subunit-like **Superfamily:**Rof/RNase P subunit-like **Family:**RNase P subunit p29-like
76	d1qhqa_	Alignment	not modelled	7.0	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
77	d2cpta1	Alignment	not modelled	6.9	24	**Fold:**Spectrin repeat-like **Superfamily:**MIT domain **Family:**MIT domain
78	c2phcB_	Alignment	not modelled	6.7	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ph0987; **PDBTitle:** crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
79	c1fosF_	Alignment	not modelled	6.7	12	**PDB header:**transcription/dna **Chain:** F: **PDB Molecule:**c-jun proto-oncogene protein; **PDBTitle:** two human c-fos:c-jun:dna complexes
80	c3hvzB_	Alignment	not modelled	6.7	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the tgs domain of the clolep_03100

						protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
81	c3iynR_	Alignment	not modelled	6.6	21	**PDB header:**virus **Chain:** R: **PDB Molecule:**hexon-associated protein; **PDBTitle:** 3.6-angstrom cryoem structure of human adenovirus type 5
82	c3lqiA_	Alignment	not modelled	6.5	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mll1 phd3-bromo; **PDBTitle:** crystal structure of mll1 phd3-bromo complexed with h3(1-9)k4me22 peptide
83	c3qo8A_	Alignment	not modelled	6.5	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase, cytoplasmic; **PDBTitle:** crystal structure of seryl-trna synthetase from candida albicans
84	d1wr0a1	Alignment	not modelled	6.5	18	**Fold:**Spectrin repeat-like **Superfamily:**MIT domain **Family:**MIT domain
85	d1hfua1	Alignment	not modelled	6.4	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
86	c2xgfA_	Alignment	not modelled	6.3	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**long tail fiber protein p37; **PDBTitle:** structure of the bacteriophage t4 long tail fibre needle-2 shaped receptor-binding tip
87	d1an2a_	Alignment	not modelled	6.3	11	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
88	c1bf5A_	Alignment	not modelled	6.1	13	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** tyrosine phosphorylated stat-1/dna complex
89	d1l8na2	Alignment	not modelled	6.1	13	**Fold:**Zincin-like **Superfamily:**beta-N-acetylhexosaminidase-like domain **Family:**alpha-D-glucuronidase, N-terminal domain
90	c3b5nC_	Alignment	not modelled	6.1	3	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**protein transport protein sec9; **PDBTitle:** structure of the yeast plasma membrane snare complex
91	d1nkpa_	Alignment	not modelled	6.0	20	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
92	c3demB_	Alignment	not modelled	6.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**complement factor masp-3; **PDBTitle:** cub1-egf-cub2 domain of human masp-1/3
93	c2eqbC_	Alignment	not modelled	5.9	12	**PDB header:**endocytosis/exocytosis **Chain:** C: **PDB Molecule:**rab guanine nucleotide exchange factor sec2; **PDBTitle:** crystal structure of the rab gtpase sec4p, the sec2p gef2 domain, and phosphate complex
94	c2rfyB_	Alignment	not modelled	5.9	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cellulose 1,4-beta-cellobiosidase; **PDBTitle:** crystal structure of cellobiohydrolase from melanocarpus2 albomyces complexed with cellobiose
95	c1coiA_	Alignment	not modelled	5.8	12	**PDB header:**alpha-helical bundle **Chain:** A: **PDB Molecule:**coil-vald; **PDBTitle:** designed trimeric coiled coil-vald
96	c1zbtA_	Alignment	not modelled	5.7	12	**PDB header:**translation **Chain:** A: **PDB Molecule:**peptide chain release factor 1; **PDBTitle:** crystal structure of peptide chain release factor 1 (rf-1) (smu.1085)2 from streptococcus mutans at 2.34 a resolution
97	d2h8pc1	Alignment	not modelled	5.7	11	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
98	d1gyca1	Alignment	not modelled	5.7	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
99	c3bg4D_	Alignment	not modelled	5.7	45	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** D: **PDB Molecule:**guamerin; **PDBTitle:** the crystal structure of guamerin in complex with2 chymotrypsin and the development of an elastase-specific3 inhibitor