Phyre2

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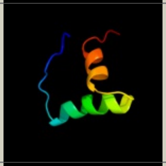
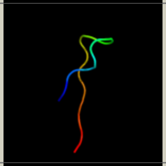
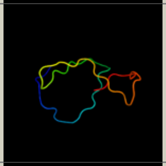
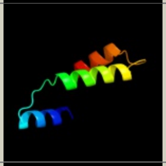
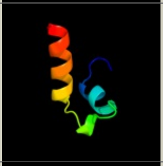
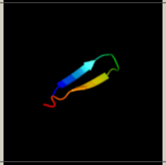
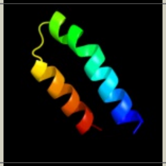
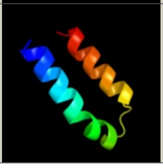
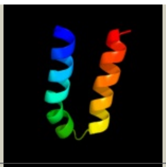
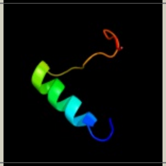
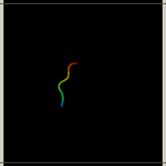
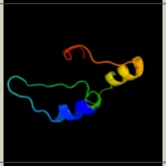
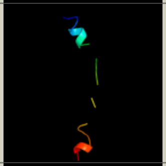
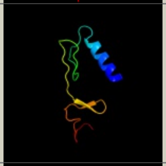
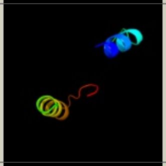
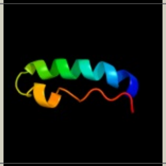
Description	P11071
Date	Thu Jan 5 11:32:28 GMT 2012
Unique Job ID	6c4c1230b88a96be

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3epsB_	Alignment		100.0	99	**PDB header:**transferase, hydrolase **Chain:** B: **PDB Molecule:**isocitrate dehydrogenase kinase/phosphatase; **PDBTitle:** the crystal structure of isocitrate dehydrogenase kinase/phosphatase2 from e. coli
2	c2an7A_	Alignment		60.7	33	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein pard; **PDBTitle:** solution structure of the bacterial antidote pard
3	d1o5ua_	Alignment		49.4	22	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Hypothetical protein TM1112
4	c3pcsB_	Alignment		47.3	35	**PDB header:**protein transport/transferase **Chain:** B: **PDB Molecule:**espg; **PDBTitle:** structure of espg-pak2 autoinhibitory ialpha3 helix complex
5	c3es4B_	Alignment		46.9	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein duf861 with a rmlc-like cupin fold; **PDBTitle:** crystal structure of protein of unknown function (duf861) with a rmlc-2 like cupin fold (17741406) from agrobacterium tumefaciens str. c583 (dupont) at 1.64 a resolution
6	c3myxA_	Alignment		40.7	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pspto_0244; **PDBTitle:** crystal structure of a pspto_0244 (protein with unknown function which2 belongs to pfam duf861 family) from pseudomonas syringae pv. tomato3 str. dc3000 at 1.30 a resolution
7	c3rmiA_	Alignment		39.2	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**chorismate mutase protein; **PDBTitle:** crystal structure of chorismate mutase from bartonella henselae str.2 houston-1 in complex with malate
8	c3hm5A_	Alignment		38.0	36	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna methyltransferase 1-associated protein 1; **PDBTitle:** sant domain of human dna methyltransferase 1 associated2 protein 1
9	c3hzpA_	Alignment		36.5	53	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ntf2-like protein of unknown function; **PDBTitle:** crystal structure of ntf2-like protein of unknown function mn2a_05052 from prochlorococcus marinus (yp_291699.1) from prochlorococcus sp.3 natl2a at 1.40 a resolution
10	c1nvpB_	Alignment		35.0	23	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcription initiation factor iia alpha chain; **PDBTitle:** human tfiia/tbp/dna complex
11	d1nvpb_	Alignment		35.0	23	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain

12	d1nh2b_	Alignment		34.3	22	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
13	d1dwka2	Alignment		32.7	19	**Fold:**Cyanase C-terminal domain **Superfamily:**Cyanase C-terminal domain **Family:**Cyanase C-terminal domain
14	d2pyta1	Alignment		30.1	45	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**EutQ-like
15	d1oe4a_	Alignment		29.8	17	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Single-strand selective monofunctional uracil-DNA glycosylase SMUG1
16	c3ff6D_	Alignment		27.7	28	**PDB header:**ligase **Chain:** D: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** human acc2 ct domain with cp-640186
17	c2wk1A_	Alignment		26.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**novp; **PDBTitle:** structure of the o-methyltransferase novp
18	c2b3fD_	Alignment		26.0	14	**PDB header:**sugar binding protein **Chain:** D: **PDB Molecule:**glucose-binding protein; **PDBTitle:** thermus thermophilus glucose/galactose binding protein2 bound with galactose
19	d1zl8a1	Alignment		25.2	29	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
20	c3fewX_	Alignment		24.2	42	**PDB header:**immune system **Chain:** X: **PDB Molecule:**colicin s4; **PDBTitle:** structure and function of colicin s4, a colicin with a2 duplicated receptor binding domain
21	c3ic7A_	Alignment	not modelled	22.8	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator of gntr family2 from bacteroides thetaiotaomicron
22	c2w7yA_	Alignment	not modelled	22.7	22	**PDB header:**sugar-binding protein **Chain:** A: **PDB Molecule:**probable sugar abc transporter, sugar-binding **PDBTitle:** structure of a streptococcus pneumoniae solute-binding2 protein in complex with the blood group a-trisaccharide.
23	c2og5A_	Alignment	not modelled	22.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxygenase; **PDBTitle:** crystal structure of asparagine oxygenase (asno)
24	c3kpaB_	Alignment	not modelled	22.2	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**probable ubiquitin fold modifier conjugating enzyme; **PDBTitle:** ubiquitin fold modifier conjugating enzyme from leishmania major2 (probable)
25	d1f3va_	Alignment	not modelled	21.5	19	**Fold:**Ferredoxin-like **Superfamily:**TRADD, N-terminal domain **Family:**TRADD, N-terminal domain
26	c3ckxA_	Alignment	not modelled	21.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase 24; **PDBTitle:** crystal structure of sterile 20-like kinase 3 (mst3, stk24)2 in complex with staurosporine
27	c3nquA_	Alignment	not modelled	20.8	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**histone h3-like centromeric protein a; **PDBTitle:** crystal structure of partially trypsinized (cenp-a/h4)2 heterotetramer
28	d2gtvx1	Alignment	not modelled	20.6	10	**Fold:**Chorismate mutase II **Superfamily:**Chorismate mutase II **Family:**monomeric chorismate mutase

29	c1rm1C_	Alignment	not modelled	20.3	23	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**transcription initiation factor iia large chain; **PDBTitle:** structure of a yeast tfiia/tbp/tata-box dna complex
30	c2z8fB_	Alignment	not modelled	20.0	19	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**galacto-n-biose/lacto-n-biose i transporter substrate- **PDBTitle:** the galacto-n-biose-/lacto-n-biose i-binding protein (gl-bp) of the2 abc transporter from bifidobacterium longum in complex with lacto-n-3 tetraose
31	c3i3vC_	Alignment	not modelled	19.8	14	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**probable secreted solute-binding lipoprotein; **PDBTitle:** crystal structure of probable secreted solute-binding2 lipoprotein from streptomyces coelicolor
32	c2l0rA_	Alignment	not modelled	19.4	21	**PDB header:**hydrolase,toxin **Chain:** A: **PDB Molecule:**lethal factor; **PDBTitle:** conformational dynamics of the anthrax lethal factor catalytic center
33	d1ppjw_	Alignment	not modelled	18.8	7	**Fold:**Single transmembrane helix **Superfamily:**Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
34	c2hjvB_	Alignment	not modelled	18.7	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase dbpa; **PDBTitle:** structure of the second domain (residues 207-368) of the2 bacillus subtilis yxin protein
35	c3koxA_	Alignment	not modelled	18.1	50	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**d-ornithine aminomutase e component; **PDBTitle:** crystal structure of ornithine 4,5 aminomutase in complex with 2,4-2 diaminobutyrate (anaerobic)
36	c3lj4i_	Alignment	not modelled	17.3	20	**PDB header:**viral protein **Chain:** I: **PDB Molecule:**portal protein; **PDBTitle:** bacteriophage p22 portal protein bound to middle tail factor gp4. this2 file contain the first biological assembly
37	d1p3ie_	Alignment	not modelled	17.3	13	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
38	d1miua1	Alignment	not modelled	17.2	33	**Fold:**BRCA2 helical domain **Superfamily:**BRCA2 helical domain **Family:**BRCA2 helical domain
39	c2iv1J_	Alignment	not modelled	16.7	19	**PDB header:**lyase **Chain:** J: **PDB Molecule:**cyanate hydratase; **PDBTitle:** site directed mutagenesis of key residues involved in the2 catalytic mechanism of cyanase
40	d1ckma2	Alignment	not modelled	16.6	23	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**mRNA capping enzyme
41	d2ihoa2	Alignment	not modelled	16.4	26	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**MOA C-terminal domain-like
42	d2ff4a2	Alignment	not modelled	16.2	5	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**BTAD-like
43	c3bcwB_	Alignment	not modelled	16.1	31	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a duf861 family protein with a rmlc-like cupin2 fold (bb1179) from bordetella bronchiseptica rb50 at 1.60 a3 resolution
44	d1pc2a_	Alignment	not modelled	15.5	22	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
45	d1t5ia_	Alignment	not modelled	15.3	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
46	c3oqhB_	Alignment	not modelled	15.2	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein yvmc; **PDBTitle:** crystal structure of b. licheniformis cdps yvmc-blic
47	c2dnrA_	Alignment	not modelled	15.2	35	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**synaptojanin-1; **PDBTitle:** solution structure of rna binding domain in synaptojanin 1
48	d2h9ec1	Alignment	not modelled	15.1	33	**Fold:**Serine protease inhibitors **Superfamily:**Serine protease inhibitors **Family:**ATI-like
49	d1mvfd_	Alignment	not modelled	14.5	21	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote
50	c3ls1A_	Alignment	not modelled	14.3	15	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**sll1638 protein; **PDBTitle:** crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
51	c2ihoA_	Alignment	not modelled	14.3	26	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**lectin; **PDBTitle:** crystal structure of moa, a lectin from the mushroom marasmius oreades2 in complex with the trisaccharide gal(1,3)gal(1,4)glcnac
52	c2a8vA_	Alignment	not modelled	14.1	24	**PDB header:**protein/rna **Chain:** A: **PDB Molecule:**rna binding domain of rho transcription **PDBTitle:** rho transcription termination factor/rna complex
53	d2e29a1	Alignment	not modelled	13.8	38	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**GUCT domain

54	c2vwiC_	Alignment	not modelled	13.6	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**serine/threonine-protein kinase osr1; **PDBTitle:** structure of the osr1 kinase, a hypertension drug target
55	d1a62a2	Alignment	not modelled	13.4	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
56	d2enda_	Alignment	not modelled	13.2	15	**Fold:**T4 endonuclease V **Superfamily:**T4 endonuclease V **Family:**T4 endonuclease V
57	c2qbvA_	Alignment	not modelled	13.1	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**chorismate mutase; **PDBTitle:** crystal structure of intracellular chorismate mutase from2 mycobacterium tuberculosis
58	c3dkqB_	Alignment	not modelled	12.9	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pkhd-type hydroxylase sbal_3634; **PDBTitle:** crystal structure of putative oxygenase (yp_001051978.1) from2 shewanella baltica os155 at 2.26 a resolution
59	c2q6tB_	Alignment	not modelled	12.9	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dnab replication fork helicase; **PDBTitle:** crystal structure of the thermus aquaticus dnab monomer
60	d1k28d2	Alignment	not modelled	12.9	36	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
61	d1ht6a2	Alignment	not modelled	12.8	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
62	c1yt8A_	Alignment	not modelled	12.6	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of thiosulfate sulfurtransferase from pseudomonas2 aeruginosa
63	c3fgrA_	Alignment	not modelled	12.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phospholipase b-like 2 28 kda form; **PDBTitle:** two chain form of the 66.3 kda protein at 1.8 angstroem
64	d1z84a1	Alignment	not modelled	12.5	26	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
65	c3qufB_	Alignment	not modelled	12.4	28	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**extracellular solute-binding protein, family 1; **PDBTitle:** the structure of a family 1 extracellular solute-binding protein from2 bifidobacterium longum subsp. infantis
66	c3iz5G_	Alignment	not modelled	12.3	38	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**60s ribosomal protein l6 (l6e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
67	c1tqmA_	Alignment	not modelled	12.3	13	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of a. fulgidus rio2 serine protein kinase bound to2 amppnp
68	d2fp1a1	Alignment	not modelled	12.0	8	**Fold:**Chorismate mutase II **Superfamily:**Chorismate mutase II **Family:**Secreted chorismate mutase-like
69	d2d8da1	Alignment	not modelled	11.9	12	**Fold:**Chorismate mutase II **Superfamily:**Chorismate mutase II **Family:**Dimeric chorismate mutase
70	d1t56a2	Alignment	not modelled	11.9	10	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
71	d3dwya1	Alignment	not modelled	11.8	9	**Fold:**Bromodomain-like **Superfamily:**Bromodomain **Family:**Bromodomain
72	c2gbbA_	Alignment	not modelled	11.7	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative chorismate mutase; **PDBTitle:** crystal structure of secreted chorismate mutase from2 yersinia pestis
73	d1ecma_	Alignment	not modelled	11.5	9	**Fold:**Chorismate mutase II **Superfamily:**Chorismate mutase II **Family:**Dimeric chorismate mutase
74	c2xvtC_	Alignment	not modelled	11.5	15	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**receptor activity-modifying protein 2; **PDBTitle:** structure of the extracellular domain of human ramp2
75	d2ok5a4	Alignment	not modelled	11.4	27	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
76	c3olhA_	Alignment	not modelled	11.3	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-mercaptopyruvate sulfurtransferase; **PDBTitle:** human 3-mercaptopyruvate sulfurtransferase
77	d1j03a_	Alignment	not modelled	11.1	23	**Fold:**Cytochrome b5-like heme/steroid binding domain **Superfamily:**Cytochrome b5-like heme/steroid binding domain **Family:**Steroid-binding domain
78	d1nz6a_	Alignment	not modelled	11.1	22	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
79	c2i58B_	Alignment	not modelled	11.0	25	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**sugar abc transporter, sugar-binding protein; **PDBTitle:** crystal structure of rafe from streptococcus pneumoniae complexed with2 raffinose
80	d1cz5a1	Alignment	not modelled	10.9	12	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like

						Family: Cdc48 N-terminal domain-like
81	c1x58A_	Alignment	not modelled	10.9	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein 4930532d21rik; **PDBTitle:** solution structures of the myb-like dna binding domain of2 4930532d21rik protein
82	d1y74a1	Alignment	not modelled	10.8	19	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
83	c3r9jD_	Alignment	not modelled	10.7	12	**PDB header:**cell cycle,hydrolase/cell cycle **Chain:** D: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** 4.3a resolution structure of a mind-mine(i24n) protein complex
84	d1njha_	Alignment	not modelled	10.7	20	**Fold:**Hypothetical protein YojF **Superfamily:**Hypothetical protein YojF **Family:**Hypothetical protein YojF
85	d1w07a2	Alignment	not modelled	10.7	2	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**acyl-CoA oxidase C-terminal domains
86	c1qrjB_	Alignment	not modelled	10.7	9	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**htlv-i capsid protein; **PDBTitle:** solution structure of htlv-i capsid protein
87	c2r5uD_	Alignment	not modelled	10.6	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**replicative dna helicase; **PDBTitle:** crystal structure of the n-terminal domain of dnab helicase from2 mycobacterium tuberculosis
88	c3kvpB_	Alignment	not modelled	10.6	33	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ymzc; **PDBTitle:** crystal structure of uncharacterized protein ymzc precursor2 from bacillus subtilis, northeast structural genomics3 consortium target sr378a
89	d1f35a_	Alignment	not modelled	10.6	21	**Fold:**Olfactory marker protein **Superfamily:**Olfactory marker protein **Family:**Olfactory marker protein
90	d1wb8a1	Alignment	not modelled	10.5	15	**Fold:**Long alpha-hairpin **Superfamily:**Fe,Mn superoxide dismutase (SOD), N-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), N-terminal domain
91	c2uvgA_	Alignment	not modelled	10.4	19	**PDB header:**sugar-binding protein **Chain:** A: **PDB Molecule:**abc type periplasmic sugar-binding protein; **PDBTitle:** structure of a periplasmic oligogalacturonide binding2 protein from yersinia enterocolitica
92	d1hv8a2	Alignment	not modelled	10.4	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
93	d1xr7a_	Alignment	not modelled	10.3	14	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
94	d1jwea_	Alignment	not modelled	10.3	13	**Fold:**N-terminal domain of DnaB helicase **Superfamily:**N-terminal domain of DnaB helicase **Family:**N-terminal domain of DnaB helicase
95	d2in1a1	Alignment	not modelled	10.3	33	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UFC1-like
96	d1ufwa_	Alignment	not modelled	10.1	17	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
97	c3i1lC_	Alignment	not modelled	10.1	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**hemagglutinin-esterase protein; **PDBTitle:** structure of porcine torovirus hemagglutinin-esterase in complex with2 its receptor
98	c1fi8E_	Alignment	not modelled	9.9	36	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** E: **PDB Molecule:**ecotin; **PDBTitle:** rat granzyme b [n66q] complexed to ecotin [81-84 iepd]
99	d1ub4c_	Alignment	not modelled	9.9	15	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote