Phyre^2

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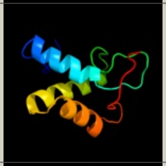
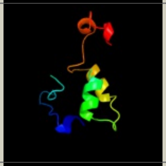
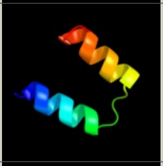
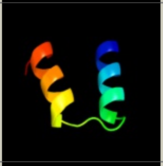
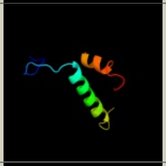
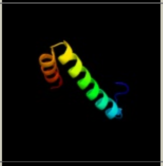
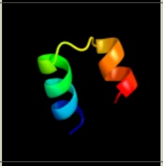
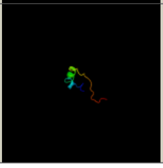
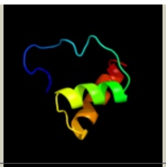
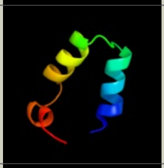
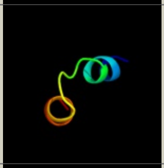
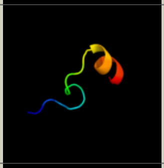
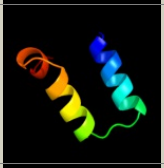
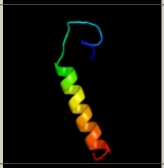
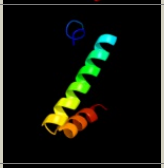
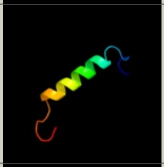
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hl7A_	Alignment		100.0	44	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccmh; **PDBTitle:** crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
2	c2kw0A_	Alignment		100.0	43	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ccmh protein; **PDBTitle:** solution structure of n-terminal domain of ccmh from escherichia.coli
3	d1pbya1	Alignment		73.5	15	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
4	c2qsrA_	Alignment		66.4	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of c-terminal domain of transcription-repair2 coupling factor
5	d2eyqa6	Alignment		62.8	37	**Fold:**TRCF domain-like **Superfamily:**TRCF domain-like **Family:**TRCF domain
6	c3omdB_	Alignment		62.2	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of unknown function protein from leptospirillum2 rubarum
7	c2c4rL_	Alignment		61.0	18	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**ribonuclease e; **PDBTitle:** catalytic domain of e. coli rnase e
8	d1r5ya_	Alignment		59.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**tRNA-guanine transglycosylase **Family:**tRNA-guanine transglycosylase
9	c2x48B_	Alignment		54.4	9	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
10	c2bpbB_	Alignment		54.1	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sulfite\:cytochrome c oxidoreductase subunit b; **PDBTitle:** sulfite dehydrogenase from starkeya novella
11	c3lm3A_	Alignment		52.1	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative glycoside hydrolase/deacetylase2 (bdi_3119) from parabacteroides distasonis at 1.44 a resolution

12	d1jmxa1	Alignment		46.9	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
13	c3d3mB_	Alignment		46.4	6	**PDB header:**translation **Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 4 gamma **PDBTitle:** the crystal structure of the c-terminal region of death2 associated protein 5(dap5)
14	d1fs1b1	Alignment		42.6	32	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
15	d1fs2b1	Alignment		40.6	32	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
16	d1ug3a2	Alignment		39.1	11	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**MIF4G domain-like
17	c1iq8B_	Alignment		38.6	38	**PDB header:**transferase **Chain:** B: **PDB Molecule:**archaeosine trna-guanine transglycosylase; **PDBTitle:** crystal structure of archaeosine trna-guanine2 transglycosylase from pyrococcus horikoshii
18	d1iq8a1	Alignment		38.2	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**tRNA-guanine transglycosylase **Family:**tRNA-guanine transglycosylase
19	d1jm7a_	Alignment		37.1	21	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
20	d1nexa1	Alignment		35.8	21	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
21	c2ashB_	Alignment	not modelled	35.5	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**queuine trna-ribosyltransferase; **PDBTitle:** crystal structure of queuine trna-ribosyltransferase (ec 2.4.2.29)2 (trna-guanine (tm1561) from thermotoga maritima at 1.90 a resolution
22	d1ef4a_	Alignment	not modelled	35.4	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**RNA polymerase subunit RPB10 **Family:**RNA polymerase subunit RPB10
23	c2jq5A_	Alignment	not modelled	35.1	14	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**sec-c motif; **PDBTitle:** solution structure of rpa3114, a sec-c motif containing2 protein from rhodopseudomonas palustris; northeast3 structural genomics consortium target rpt5 / ontario4 center for structural proteomics target rp3097
24	d6paxa1	Alignment	not modelled	33.7	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
25	c2eyqA_	Alignment	not modelled	32.9	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of escherichia coli transcription-repair2 coupling factor
26	c1u78A_	Alignment	not modelled	30.8	14	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element tc3 transposase; **PDBTitle:** structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
27	c3floD_	Alignment	not modelled	29.1	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna polymerase alpha catalytic subunit a; **PDBTitle:** crystal structure of the carboxyl-terminal domain of yeast2 dna polymerase alpha in complex with its b subunit
						Fold:DNA/RNA-binding 3-helical bundle

28	d2gmga1	Alignment	not modelled	28.6	42	**Superfamily:**"Winged helix" DNA-binding domain **Family:**PF0610-like
29	d1wgna_	Alignment	not modelled	27.0	22	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
30	c2opfA_	Alignment	not modelled	26.3	67	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**endonuclease viii; **PDBTitle:** crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
31	c3b40A_	Alignment	not modelled	25.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable dipeptidase; **PDBTitle:** crystal structure of the probable dipeptidase pvdm from2 pseudomonas aeruginosa
32	d1k78a1	Alignment	not modelled	24.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
33	d1p7ia_	Alignment	not modelled	23.9	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
34	c3hosA_	Alignment	not modelled	23.3	21	**PDB header:**transferase, dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element mariner, complete cds; **PDBTitle:** crystal structure of the mariner mos1 paired end complex with mg
35	c2qeuA_	Alignment	not modelled	22.7	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative carboxymuconolactone decarboxylase; **PDBTitle:** crystal structure of putative carboxymuconolactone decarboxylase2 (yp_555818.1) from burkholderia xenovorans lb400 at 1.65 a resolution
36	c3llkA_	Alignment	not modelled	22.7	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfhydryl oxidase 1; **PDBTitle:** sulfhydryl oxidase fragment of human qsox1
37	c3iz6X_	Alignment	not modelled	22.7	24	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**40s ribosomal protein s27 (s27e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
38	c3g2bA_	Alignment	not modelled	21.9	8	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**coenzyme pqq synthesis protein d; **PDBTitle:** crystal structure of pqqd from xanthomonas campestris
39	d1od6a_	Alignment	not modelled	21.0	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
40	d2ovra1	Alignment	not modelled	20.9	32	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
41	d1qxfa_	Alignment	not modelled	20.5	18	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27e
42	c2ragB_	Alignment	not modelled	20.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dipeptidase; **PDBTitle:** crystal structure of aminohydrolase from caulobacter crescentus
43	c3b9bA_	Alignment	not modelled	20.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
44	d1eb7a2	Alignment	not modelled	20.0	22	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
45	c1ug3A_	Alignment	not modelled	19.8	13	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic protein synthesis initiation factor **PDBTitle:** c-terminal portion of human eif4gi
46	c2jnhA_	Alignment	not modelled	19.7	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of the uba domain from cbl-b
47	d1p91a_	Alignment	not modelled	19.4	31	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase RlmA
48	d1odfa_	Alignment	not modelled	19.3	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
49	d2ga1a1	Alignment	not modelled	18.9	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Alr1493-like
50	c1nexC_	Alignment	not modelled	18.7	21	**PDB header:**ligase, cell cycle **Chain:** C: **PDB Molecule:**centromere dna-binding protein complex cbf3 **PDBTitle:** crystal structure of scskp1-sccdc4-cpd peptide complex
51	c1ztbA_	Alignment	not modelled	18.7	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**chorismate synthase; **PDBTitle:** crystal structure of chorismate synthase from mycobacterium2 tuberculosis
52	c3o0rC_	Alignment	not modelled	18.6	13	**PDB header:**immune system/oxidoreductase **Chain:** C: **PDB Molecule:**nitric oxide reductase subunit c; **PDBTitle:** crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
53	c2pmzN_	Alignment	not modelled	18.2	18	**PDB header:**translation, transferase **Chain:** N: **PDB Molecule:**dna-directed rna polymerase subunit n;

						PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
54	c2jr6A_	Alignment	not modelled	18.0	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein nma0874; **PDBTitle:** solution structure of upf0434 protein nma0874. northeast structural2 genomics target mr32
55	c3lrqB_	Alignment	not modelled	18.0	30	**PDB header:**ligase **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase trim37; **PDBTitle:** crystal structure of the u-box domain of human ubiquitin-2 protein ligase (e3), northeast structural genomics3 consortium target hr4604d.
56	c2js4A_	Alignment	not modelled	17.9	44	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein bb2007; **PDBTitle:** solution nmr structure of bordetella bronchiseptica protein2 bb2007. northeast structural genomics consortium target3 bor54
57	c2jvwA_	Alignment	not modelled	17.4	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of uncharacterized protein q5e7h1 from vibrio2 fischeri. northeast structural genomics target vfr117
58	c2xzmO_	Alignment	not modelled	17.2	10	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**rps13e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
59	d1y0ua_	Alignment	not modelled	17.1	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
60	d2cwqa1	Alignment	not modelled	17.0	13	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**TTHA0727-like
61	c3axjB_	Alignment	not modelled	16.9	7	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**translin associated factor x, isoform b; **PDBTitle:** high resolution crystal structure of c3po
62	c2p1nD_	Alignment	not modelled	16.3	32	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**skp1-like protein 1a; **PDBTitle:** mechanism of auxin perception by the tir1 ubiqutin ligase
63	d1lv3a_	Alignment	not modelled	16.1	22	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Hypothetical zinc finger protein YacG
64	c2ecgA_	Alignment	not modelled	16.0	9	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 4; **PDBTitle:** solution structure of the ring domain of the baculoviral2 iap repeat-containing protein 4 from homo sapiens
65	d2lfba_	Alignment	not modelled	16.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
66	d1sxjd1	Alignment	not modelled	15.3	14	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
67	c3itcA_	Alignment	not modelled	15.2	4	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**renal dipeptidase; **PDBTitle:** crystal structure of sco3058 with bound citrate and glycerol
68	d2gmya1	Alignment	not modelled	15.2	14	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
69	d2c0sa1	Alignment	not modelled	14.9	43	**Fold:**ROP-like **Superfamily:**BAS1536-like **Family:**BAS1536-like
70	c3s93B_	Alignment	not modelled	14.5	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tudor domain-containing protein 5; **PDBTitle:** crystal structure of conserved motif in tdrd5
71	d1itua_	Alignment	not modelled	14.5	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Renal dipeptidase
72	c3a44D_	Alignment	not modelled	14.5	36	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
73	c2d9sA_	Alignment	not modelled	14.4	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cbl e3 ubiquitin protein ligase; **PDBTitle:** solution structure of rsgi ruh-049, a uba domain from mouse2 cdna
74	d1dl6a_	Alignment	not modelled	14.4	25	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
75	c3izbX_	Alignment	not modelled	14.3	33	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**40s ribosomal protein rps27 (s27e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
76	c3lpeF_	Alignment	not modelled	14.3	24	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit e''; **PDBTitle:** crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
77	c1b6aA_	Alignment	not modelled	14.3	21	**PDB header:**angiogenesis inhibitor **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** human methionine aminopeptidase 2 complexed with tnp-470
78	d2c2vv1	Alignment	not modelled	14.2	13	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box

79	c3pjaK_	Alignment	not modelled	13.9	13	**PDB header:**hydrolase **Chain:** K: **PDB Molecule:**translin-associated protein x; **PDBTitle:** crystal structure of human c3po complex
80	d2cqxa1	Alignment	not modelled	13.8	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
81	c3qw4B_	Alignment	not modelled	13.8	15	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**ump synthase; **PDBTitle:** structure of leishmania donovani ump synthase
82	c1dl0A_	Alignment	not modelled	13.7	46	**PDB header:**toxin **Chain:** A: **PDB Molecule:**j-atracotoxin-hv1c; **PDBTitle:** solution structure of the insecticidal neurotoxin j-2 atracotoxin-hv1c
83	d1dl0a_	Alignment	not modelled	13.7	46	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
84	d2jnya1	Alignment	not modelled	13.6	33	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
85	c2xzm6_	Alignment	not modelled	13.4	47	**PDB header:**ribosome **Chain:** 6: **PDB Molecule:**rps27e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
86	c1nl0G_	Alignment	not modelled	13.3	50	**PDB header:**immune system **Chain:** G: **PDB Molecule:**factor ix; **PDBTitle:** crystal structure of human factor ix gla domain in complex2 of an inhibitory antibody, 10c12
87	d1jgga_	Alignment	not modelled	13.1	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
88	c3l6aA_	Alignment	not modelled	13.0	5	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 4 gamma 2; **PDBTitle:** crystal structure of the c-terminal region of human p97
89	d1o6ba_	Alignment	not modelled	12.9	8	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
90	c3fdgA_	Alignment	not modelled	12.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidase ac. metallo peptidase. merops family m19; **PDBTitle:** the crystal structure of the dipeptidase ac, metallo peptidase. merops2 family m19
91	d1xkpa1	Alignment	not modelled	12.3	14	**Fold:**Type III secretion system domain **Superfamily:**Type III secretion system domain **Family:**LcrE-like
92	c2ao9H_	Alignment	not modelled	12.2	13	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**phage protein; **PDBTitle:** structural genomics, the crystal structure of a phage protein2 (phbc6a51) from bacillus cereus atcc 14579
93	c2kpiA_	Alignment	not modelled	12.1	44	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sco3027; **PDBTitle:** solution nmr structure of streptomyces coelicolor sco30272 modeled with zn+2 bound, northeast structural genomics3 consortium target rr58
94	d2ao9a1	Alignment	not modelled	12.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Nanomeric phage protein-like
95	c1ee8A_	Alignment	not modelled	11.9	57	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
96	d1d8ja_	Alignment	not modelled	11.9	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**The central core domain of TFIIE beta
97	c3bg3B_	Alignment	not modelled	11.9	10	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase, mitochondrial; **PDBTitle:** crystal structure of human pyruvate carboxylase (missing2 the biotin carboxylase domain at the n-terminus)
98	c2do6A_	Alignment	not modelled	11.9	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of rsgi ruh-065, a uba domain from human2 cdna
99	d1vnda_	Alignment	not modelled	11.8	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain