Phyre^2

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Description	P0A7V8
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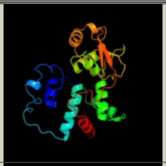
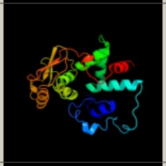
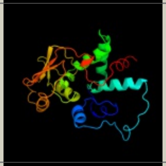
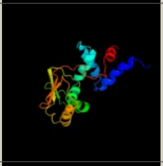
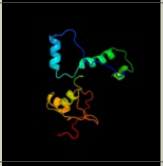
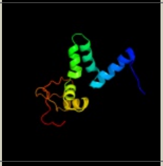
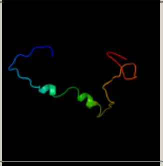
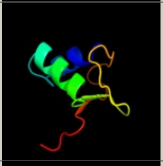
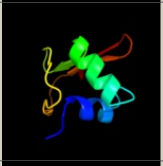
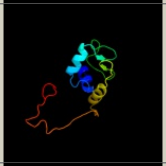
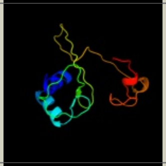
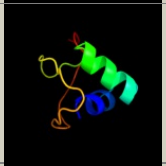
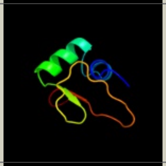
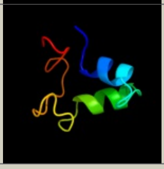
Unique Job ID	5ca1368638c01950

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gy9d1	Alignment		100.0	100	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
2	d2uubd1	Alignment		100.0	48	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
3	c3bbnD_	Alignment		100.0	38	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**ribosomal protein s4; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
4	d1c06a_	Alignment		100.0	54	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
5	c2xzmD_	Alignment		99.8	26	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**ribosomal protein s4 containing protein; **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
6	c1s1hD_	Alignment		99.8	22	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**40s ribosomal protein s9-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
7	c3iz6C_	Alignment		99.6	26	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**40s ribosomal protein s9 (s4p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
8	c2cqjA_	Alignment		99.5	22	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u3 small nucleolar ribonucleoprotein protein **PDBTitle:** solution structure of the s4 domain of u3 small nucleolar2 ribonucleoprotein protein imp3 homolog
9	d1dm9a_	Alignment		99.4	27	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Heat shock protein 15 kD
10	c1dm9A_	Alignment		99.4	27	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka **PDBTitle:** heat shock protein 15 kd
11	d1p9ka_	Alignment		99.3	17	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like

12	c2k6pA_	Alignment		99.2	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein hp_1423; **PDBTitle:** solution structure of hypothetical protein, hp1423
13	d1vioa2	Alignment		99.2	27	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
14	c3dh3C_	Alignment		99.0	23	**PDB header:**isomerase/rna **Chain:** C: **PDB Molecule:**ribosomal large subunit pseudouridine synthase f; **PDBTitle:** crystal structure of rluf in complex with a 22 nucleotide2 rna substrate
15	c1kskA_	Alignment		99.0	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a; **PDBTitle:** structure of rsua
16	c1vioA_	Alignment		99.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a; **PDBTitle:** crystal structure of pseudouridylate synthase
17	c3hp7A_	Alignment		98.9	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hemolysin, putative; **PDBTitle:** putative hemolysin from streptococcus thermophilus.
18	d1h3fa2	Alignment		97.8	18	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
19	c1h3eA_	Alignment		97.7	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl-trna synthetase from thermus thermophilus complexed2 with wild-type trnatyr(gua) and with atp and tyrosinol
20	d1jh3a_	Alignment		97.6	19	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
21	c2janD_	Alignment	not modelled	97.6	15	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
22	c3kbgA_	Alignment	not modelled	96.5	21	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s4e; **PDBTitle:** crystal structure of the 30s ribosomal protein s4e from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar28.
23	c3iz6D_	Alignment	not modelled	96.3	26	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**40s ribosomal protein s4 (s4e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
24	c2xzmW_	Alignment	not modelled	96.0	21	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**40s ribosomal protein s4; **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
25	c3izbD_	Alignment	not modelled	95.8	19	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**40s ribosomal protein rps4 (s4e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
26	d1kska3	Alignment	not modelled	92.7	25	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
27	d2g1la1	Alignment	not modelled	80.0	15	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
28	c2eh0A_	Alignment	not modelled	78.4	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**kinesin-like protein kif1b;

28	c2eh0A_	Alignment	not modelled	78.4	21	**PDBTitle:** solution structure of the fha domain from human kinesin-2 like protein kif1b
29	c2jqlA_	Alignment	not modelled	72.3	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna damage response protein kinase dun1; **PDBTitle:** nmr structure of the yeast dun1 fha domain in complex with2 a doubly phosphorylated (pt) peptide derived from rad533 scd1
30	d1fm0d_	Alignment	not modelled	70.7	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
31	c3fm8A_	Alignment	not modelled	69.3	23	**PDB header:**transport protein/hydrolase activator **Chain:** A: **PDB Molecule:**kinesin-like protein kif13b; **PDBTitle:** crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target)
32	d1xo3a_	Alignment	not modelled	69.0	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
33	c3rpfC_	Alignment	not modelled	67.7	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**molybdopterin converting factor, subunit 1 (moad); **PDBTitle:** protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
34	d1zud21	Alignment	not modelled	67.6	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
35	c3hvzB_	Alignment	not modelled	66.6	27	**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
36	d1vjka_	Alignment	not modelled	65.4	30	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
37	c2kmmA_	Alignment	not modelled	64.2	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**guanosine-3',5'-bis(diphosphate) 3'- **PDBTitle:** solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481)
38	c3po0A_	Alignment	not modelled	64.2	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**small archaeal modifier protein 1; **PDBTitle:** crystal structure of samp1 from haloferax volcanii
39	c3dwmA_	Alignment	not modelled	62.1	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**9.5 kda culture filtrate antigen cfp10a; **PDBTitle:** crystal structure of mycobacterium tuberculosis cyso, an antigen
40	c2ktlA_	Alignment	not modelled	62.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** structure of c-terminal domain from mttyrrs of a. nidulans
41	c2qjlA_	Alignment	not modelled	60.3	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin-related modifier 1; **PDBTitle:** crystal structure of urm1
42	c3poaA_	Alignment	not modelled	55.1	29	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein tb39.8; **PDBTitle:** structural and functional analysis of phosphothreonine-dependent fha2 domain interactions
43	c1v8cA_	Alignment	not modelled	54.8	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**moad related protein; **PDBTitle:** crystal structure of moad related protein from thermus2 thermophilus hb8
44	d1v8ca1	Alignment	not modelled	53.4	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
45	d2cu3a1	Alignment	not modelled	53.3	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
46	c2g1eA_	Alignment	not modelled	53.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ta0895; **PDBTitle:** solution structure of ta0895
47	d1gxca_	Alignment	not modelled	53.0	19	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
48	c1gxcA_	Alignment	not modelled	53.0	19	**PDB header:**phosphoprotein-binding domain **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase chk2; **PDBTitle:** fha domain from human chk2 kinase in complex with a2 synthetic phosphopeptide
49	d1g3ga_	Alignment	not modelled	51.4	26	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
50	d2piea1	Alignment	not modelled	50.7	15	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
51	d1g6ga_	Alignment	not modelled	50.4	22	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
52	c2k9xA_	Alignment	not modelled	50.4	28	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of urm1 from trypanosoma brucei
53	c2qieB_	Alignment	not modelled	50.1	32	**PDB header:**transferase **Chain:** B: **PDB Molecule:**molybdopterin synthase small subunit; **PDBTitle:** staphylococcus aureus molybdopterin synthase in complex2 with precursor z

54	c3ixzA_	Alignment	not modelled	50.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**potassium-transporting atpase alpha; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
55	d2affa1	Alignment	not modelled	49.4	31	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
56	c3hx1B_	Alignment	not modelled	49.1	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**slr1951 protein; **PDBTitle:** crystal structure of the slr1951 protein from synechocystis sp.2 northeast structural genomics consortium target sgr167a
57	c1r21A_	Alignment	not modelled	48.8	29	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**antigen ki-67; **PDBTitle:** solution structure of human ki67 fha domain
58	d1wgka_	Alignment	not modelled	48.4	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
59	c3gqsB_	Alignment	not modelled	48.3	31	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**adenylate cyclase-like protein; **PDBTitle:** crystal structure of the fha domain of ct664 protein from chlamydia2 trachomatis
60	d1tkea1	Alignment	not modelled	47.9	32	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
61	c3j08A_	Alignment	not modelled	47.7	21	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
62	d1wxqa2	Alignment	not modelled	47.6	32	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain
63	d1yjma1	Alignment	not modelled	47.5	23	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
64	c3kt9A_	Alignment	not modelled	47.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aprataxin; **PDBTitle:** aprataxin fha domain
65	c3cwiA_	Alignment	not modelled	47.1	26	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**thiamine-biosynthesis protein this; **PDBTitle:** crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
66	c2zxeA_	Alignment	not modelled	46.6	17	**PDB header:**hydrolase/transport protein **Chain:** A: **PDB Molecule:**na, k-atpase alpha subunit; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
67	c2l52A_	Alignment	not modelled	46.5	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**methanosarcina acetivorans samp1 homolog; **PDBTitle:** solution structure of the small archaeal modifier protein 1 (samp1)2 from methanosarcina acetivorans
68	d2ff4a3	Alignment	not modelled	46.1	15	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
69	d1tygb_	Alignment	not modelled	45.6	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
70	d1wlna1	Alignment	not modelled	44.8	8	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
71	c2hc8A_	Alignment	not modelled	44.4	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
72	c3j09A_	Alignment	not modelled	44.4	15	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
73	c1yj5C_	Alignment	not modelled	44.1	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**5' polynucleotide kinase-3' phosphatase fha domain; **PDBTitle:** molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
74	d1lgpa_	Alignment	not modelled	43.4	19	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
75	c3elsA_	Alignment	not modelled	42.0	18	**PDB header:**splicing **Chain:** A: **PDB Molecule:**pre-mrna leakage protein 1; **PDBTitle:** crystal structure of yeast pml1p, residues 51-204
76	c2kklA_	Alignment	not modelled	41.6	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mb1858; **PDBTitle:** solution nmr structure of fha domain of mb1858 from2 mycobacterium bovis. northeast structural genomics3 consortium target mbr243c (24-155).
77	c1mhsA_	Alignment	not modelled	40.2	21	**PDB header:**membrane protein, proton transport **Chain:** A: **PDB Molecule:**plasma membrane atpase; **PDBTitle:** model of neurospora crassa proton atpase
78	c2kl0A_	Alignment	not modelled	38.8	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thiamin biosynthesis this; **PDBTitle:** solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
						PDB header:hydrolase/transport protein

79	c3b8eC_	Alignment	not modelled	34.6	21	**Chain:** C: **PDB Molecule:**sodium/potassium-transporting atpase subunit **PDBTitle:** crystal structure of the sodium-potassium pump
80	c3b8cB_	Alignment	not modelled	34.1	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atpase 2, plasma membrane-type; **PDBTitle:** crystal structure of a plasma membrane proton pump
81	d2r5yb1	Alignment	not modelled	33.1	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
82	d1mzka_	Alignment	not modelled	33.0	19	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
83	c2jkdB_	Alignment	not modelled	32.8	24	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**pre-mrna leakage protein 1; **PDBTitle:** structure of the yeast pml1 splicing factor and its2 integration into the res complex
84	c3b9bA_	Alignment	not modelled	32.5	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
85	d1xnea_	Alignment	not modelled	32.2	12	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
86	d1nyra2	Alignment	not modelled	31.4	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
87	c2zagB_	Alignment	not modelled	30.1	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**oligosaccharyl transferase stt3 subunit related protein; **PDBTitle:** crystal structure of the semet-substituted soluble domain of stt3 from2 p. furiosus
88	c3pp5A_	Alignment	not modelled	28.8	23	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**brk1; **PDBTitle:** high-resolution structure of the trimeric scar/wave complex precursor2 brk1
89	c1tygG_	Alignment	not modelled	28.6	17	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
90	d1rwsa_	Alignment	not modelled	26.6	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
91	d1dmza_	Alignment	not modelled	26.4	13	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
92	c2ekiA_	Alignment	not modelled	26.3	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**developmentally-regulated gtp-binding protein 1; **PDBTitle:** solution structures of the tgs domain of human2 developmentally-regulated gtp-binding protein 1
93	d1mnmc_	Alignment	not modelled	26.1	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
94	c3rfuC_	Alignment	not modelled	25.6	21	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
95	d1k61a_	Alignment	not modelled	25.6	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
96	d1i6za_	Alignment	not modelled	24.9	25	**Fold:**Spectrin repeat-like **Superfamily:**BAG domain **Family:**BAG domain
97	d1wh5a_	Alignment	not modelled	23.8	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
98	c3p8cE_	Alignment	not modelled	22.4	28	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**probable protein brick1; **PDBTitle:** structure and control of the actin regulatory wave complex
99	d1qu5a_	Alignment	not modelled	21.9	14	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
100	d1x2na1	Alignment	not modelled	21.4	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain