Phyre^2

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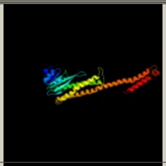
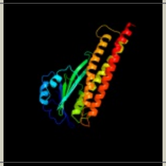
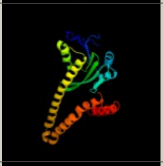
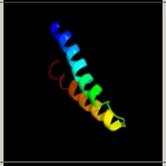
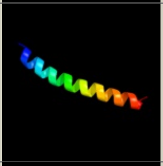
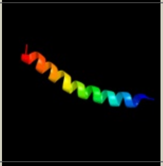
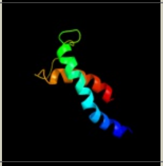
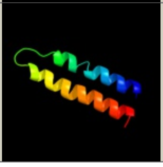
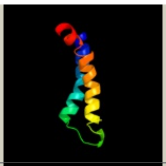
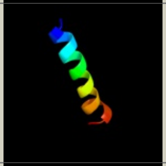
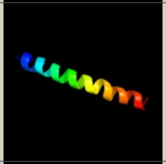
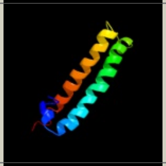
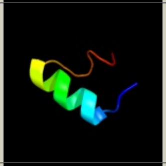
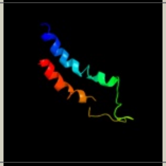
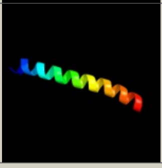
Description	P0ABI4
Date	Thu Jan 5 11:15:33 GMT 2012
Unique Job ID	84d26ae60415d8b0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2bbjB_	Alignment		100.0	17	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
2	d2iuba1	Alignment		100.0	13	**Fold:**CorA soluble domain-like **Superfamily:**CorA soluble domain-like **Family:**CorA soluble domain-like
3	c3nwiC_	Alignment		100.0	13	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**zinc transport protein zntb; **PDBTitle:** the soluble domain structure of the zntb zn2+ efflux system
4	c2hn1A_	Alignment		100.0	15	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**magnesium and cobalt transporter; **PDBTitle:** crystal structure of a cora soluble domain from a. fulgidus in complex2 with co2+
5	c3ck6E_	Alignment		100.0	13	**PDB header:**structural protein **Chain:** E: **PDB Molecule:**putative membrane transport protein; **PDBTitle:** crystal structure of zntb cytoplasmic domain from vibrio2 parahaemolyticus rimd 2210633
6	d2bbha1	Alignment		100.0	13	**Fold:**CorA soluble domain-like **Superfamily:**CorA soluble domain-like **Family:**CorA soluble domain-like
7	d2iuba2	Alignment		99.5	26	**Fold:**Transmembrane helix hairpin **Superfamily:**Magnesium transport protein CorA, transmembrane region **Family:**Magnesium transport protein CorA, transmembrane region
8	d3cx5d2	Alignment		55.8	13	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor **Family:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor
9	d1ppjd2	Alignment		54.8	22	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor **Family:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor
10	c3j01A_	Alignment		28.4	8	**PDB header:**ribosome/ribosomal protein **Chain:** A: **PDB Molecule:**preprotein translocase secy subunit; **PDBTitle:** structure of the ribosome-secye complex in the membrane environment
11	c1oy8A_	Alignment		28.4	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump

12	c3rfuC_	Alignment		27.2	8	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
13	c1zrtD_	Alignment		26.7	23	**PDB header:**oxidoreductase/metal transport **Chain:** D: **PDB Molecule:**cytochrome c1; **PDBTitle:** rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
14	c3dl8H_	Alignment		25.6	8	**PDB header:**protein transport **Chain:** H: **PDB Molecule:**preprotein translocase subunit secy; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
15	c1qcrD_	Alignment		23.3	22	**PDB header:** **PDB COMPND:**
16	c3mkuA_	Alignment		21.3	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**multi antimicrobial extrusion protein (na(+)/drug **PDBTitle:** structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
17	c3r1fO_	Alignment		19.7	9	**PDB header:**transcription **Chain:** O: **PDB Molecule:**esx-1 secretion-associated regulator espr; **PDBTitle:** crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
18	c2akiY_	Alignment		19.6	8	**PDB header:**protein transport **Chain:** Y: **PDB Molecule:**preprotein translocase secy subunit; **PDBTitle:** normal mode-based flexible fitted coordinates of a2 translocating secyeg protein-conducting channel into the3 cryo-em map of a secyeg-nascent chain-70s ribosome complex4 from e. coli
19	d1xuba1	Alignment		19.3	14	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
20	c1p84D_	Alignment		18.9	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
21	d1lnga_	Alignment	not modelled	18.4	10	**Fold:**SRP19 **Superfamily:**SRP19 **Family:**SRP19
22	c3cwbQ_	Alignment	not modelled	17.2	19	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**mitochondrial cytochrome c1, heme protein; **PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
23	c2yiuE_	Alignment	not modelled	16.9	13	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
24	d1e3oc1	Alignment	not modelled	16.5	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
25	d1o4xa1	Alignment	not modelled	15.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
26	c3ktwA_	Alignment	not modelled	15.3	13	**PDB header:**rna/rna binding protein **Chain:** A: **PDB Molecule:**signal recognition particle 19 kda protein; **PDBTitle:** crystal structure of the srp19/s-domain srp rna complex of sulfolobus2 solfataricus
27	c2fynH_	Alignment	not modelled	14.8	9	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c1; **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
28	d1mh3a1	Alignment	not modelled	14.7	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like

						Family: Homeodomain
29	c1s1iJ_	Alignment	not modelled	14.6	38	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**60s ribosomal protein l11; **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, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
30	d1x2na1	Alignment	not modelled	14.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
31	c2ks1B_	Alignment	not modelled	14.5	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
32	d1au7a1	Alignment	not modelled	14.1	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
33	c2da1A_	Alignment	not modelled	13.6	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**alpha-fetoprotein enhancer binding protein; **PDBTitle:** solution structure of the first homeobox domain of at-2 binding transcription factor 1 (atbf1)
34	d1jida_	Alignment	not modelled	13.5	18	**Fold:**SRP19 **Superfamily:**SRP19 **Family:**SRP19
35	d2r5yb1	Alignment	not modelled	13.3	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
36	c2fz0A_	Alignment	not modelled	12.9	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**v-snare component of the vacuolar snare complex **PDBTitle:** identification of yeast r-snare nyv1p as a novel longin2 domain protein
37	d9anta_	Alignment	not modelled	12.9	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
38	d1hx1b_	Alignment	not modelled	12.8	14	**Fold:**Spectrin repeat-like **Superfamily:**BAG domain **Family:**BAG domain
39	d1du0a_	Alignment	not modelled	12.6	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
40	d1k61a_	Alignment	not modelled	12.6	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
41	d1wh5a_	Alignment	not modelled	12.5	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
42	d1dzfa2	Alignment	not modelled	11.8	13	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
43	d1uhsa_	Alignment	not modelled	11.7	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
44	d1fjlb_	Alignment	not modelled	11.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
45	d1z3ea1	Alignment	not modelled	11.5	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
46	d1ig7a_	Alignment	not modelled	11.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
47	c3nauA_	Alignment	not modelled	11.4	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 2; **PDBTitle:** crystal structure of zhx2 hd2 (zinc-fingers and homeoboxes protein 2,2 homeodomain 2)
48	d1le8a_	Alignment	not modelled	11.3	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
49	d1gjja2	Alignment	not modelled	11.3	19	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
50	c4a1cD_	Alignment	not modelled	11.2	43	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**60s ribosomal protein l11; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
51	c2vi6F_	Alignment	not modelled	11.2	14	**PDB header:**transcription **Chain:** F: **PDB Molecule:**homeobox protein nanog; **PDBTitle:** crystal structure of the nanog homeodomain
52	d2p81a1	Alignment	not modelled	11.2	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
53	d1du6a_	Alignment	not modelled	11.0	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
54	c2oszA_	Alignment	not modelled	11.0	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**nucleoporin p58/p45;

		Alignment	not modelled			**PDBTitle:** structure of nup58/45 suggests flexible nuclear pore diameter by2 intermolecular sliding
55	d1s7ea1	Alignment	not modelled	10.9	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
56	d2craa1	Alignment	not modelled	10.9	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
57	c3a03A_	Alignment	not modelled	10.9	19	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**t-cell leukemia homeobox protein 2; **PDBTitle:** crystal structure of hox11l1 homeodomain
58	d2cuea1	Alignment	not modelled	10.8	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
59	c3ednB_	Alignment	not modelled	10.7	16	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**phenazine biosynthesis protein, phzf family; **PDBTitle:** crystal structure of the bacillus anthracis phenazine2 biosynthesis protein, phzf family
60	c3ci9B_	Alignment	not modelled	10.7	27	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat shock factor-binding protein 1; **PDBTitle:** crystal structure of the human hsbp1
61	c2pmzV_	Alignment	not modelled	10.7	26	**PDB header:**translation, transferase **Chain:** V: **PDB Molecule:**dna-directed rna polymerase subunit h; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
62	d1eika_	Alignment	not modelled	10.6	23	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
63	d1hdpa_	Alignment	not modelled	10.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
64	d2hddb_	Alignment	not modelled	10.2	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
65	d1iwga8	Alignment	not modelled	10.1	7	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
66	c2dn0A_	Alignment	not modelled	10.0	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 3; **PDBTitle:** solution structure of the second homeobox domain of human2 zinc fingers and homeoboxes protein 3
67	d1f43a_	Alignment	not modelled	9.9	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
68	c2da2A_	Alignment	not modelled	9.9	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**alpha-fetoprotein enhancer binding protein; **PDBTitle:** solution structure of the second homeobox domain of at-2 binding transcription factor 1 (atbf1)
69	c3l09B_	Alignment	not modelled	9.6	18	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator2 (jann_22dec04_contig27_revised_gene3569) from jannaschia sp. ccs1 at3 2.81 a resolution
70	d1bw5a_	Alignment	not modelled	9.5	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
71	d1qusa_	Alignment	not modelled	9.3	27	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
72	d1b72a_	Alignment	not modelled	9.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
73	d1p7jb_	Alignment	not modelled	9.1	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
74	d1jgga_	Alignment	not modelled	9.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
75	d1p7ia_	Alignment	not modelled	9.0	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
76	c2e19A_	Alignment	not modelled	8.9	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor 8; **PDBTitle:** solution structure of the homeobox domain from human nil-2-2 a zinc finger protein, transcription factor 8
77	d1x2ma1	Alignment	not modelled	8.7	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
78	c3narA_	Alignment	not modelled	8.6	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 1; **PDBTitle:** crystal structure of zhx1 hd4 (zinc-fingers and homeoboxes protein 1,2 homeodomain 4)
79	c2da4A_	Alignment	not modelled	8.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dkfzp686k21156; **PDBTitle:** solution structure of the homeobox domain of the2 hypothetical protein, dkfzp686k21156
80	d1hmja_	Alignment	not modelled	8.5	6	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5

81	d1ftta_	Alignment	not modelled	8.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
82	c3l78A_	Alignment	not modelled	8.4	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein spx; **PDBTitle:** the crystal structure of smu.1142c from streptococcus mutans ua159
83	d2cqxa1	Alignment	not modelled	8.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
84	d1sana_	Alignment	not modelled	8.3	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
85	c3dluA_	Alignment	not modelled	8.2	25	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**signal recognition particle 19 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
86	d1akha_	Alignment	not modelled	8.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
87	d1fjla_	Alignment	not modelled	8.2	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
88	c2yvxD_	Alignment	not modelled	8.1	8	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
89	c2w9pC_	Alignment	not modelled	8.1	6	**PDB header:**hydrolase inhibitor **Chain:** C: **PDB Molecule:**multicystatin; **PDBTitle:** crystal structure of potato multicystatin
90	d1wi3a_	Alignment	not modelled	8.1	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
91	d1jeia_	Alignment	not modelled	8.0	10	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
92	d2e1oa1	Alignment	not modelled	8.0	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
93	c1s7eA_	Alignment	not modelled	7.8	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 6; **PDBTitle:** solution structure of hnf-6
94	d1gt0c1	Alignment	not modelled	7.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
95	c3ixzA_	Alignment	not modelled	7.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**potassium-transporting atpase alpha; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
96	d1octc1	Alignment	not modelled	7.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
97	d1b8ia_	Alignment	not modelled	7.8	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
98	c2dmuA_	Alignment	not modelled	7.6	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein goosecoid; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein goosecoid
99	d1yrnb_	Alignment	not modelled	7.6	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain