Phyre^2

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Description	P15286
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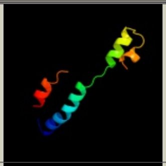
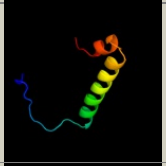
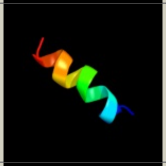
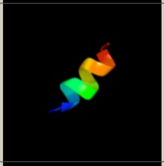
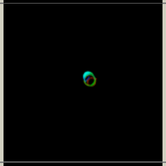
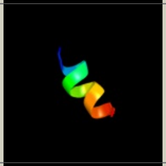
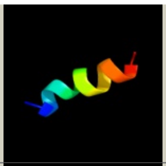
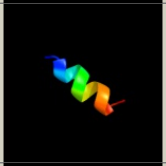
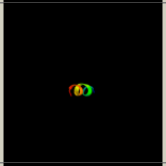
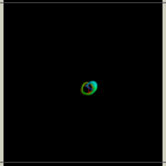
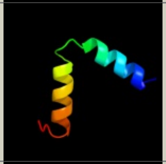
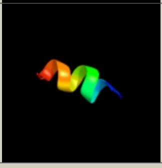
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3chtA_	Alignment		48.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**p-aminobenzoate n-oxygenase; **PDBTitle:** crystal structure of di-iron aurf with partially bound ligand
2	c3gzxB_	Alignment		47.9	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**biphenyl dioxygenase subunit beta; **PDBTitle:** crystal structure of the biphenyl dioxygenase in complex with biphenyl2 from comamonas testosteroni sp. strain b-356
3	d1ktdb2	Alignment		41.7	31	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
4	d1i3rb2	Alignment		40.0	38	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
5	d1klub2	Alignment		38.4	62	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
6	d2pxyd2	Alignment		38.4	23	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
7	d2iadb2	Alignment		37.2	38	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
8	d1d5mb2	Alignment		36.7	50	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
9	d1iakb2	Alignment		36.4	31	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
10	d1bx2b2	Alignment		36.1	62	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
11	d1fv1b2	Alignment		34.2	62	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain

12	d1s9vb2	Alignment		33.8	38	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
13	d1uvqb2	Alignment		32.8	31	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
14	d3c5zd2	Alignment		32.7	31	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
15	d1mujb2	Alignment		32.7	31	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
16	d2nnab2	Alignment		32.4	31	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
17	d1es0b2	Alignment		32.1	31	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
18	d1fngb2	Alignment		32.0	38	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
19	d1dd4c_	Alignment		30.1	18	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain
20	d1a6ab2	Alignment		28.8	54	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
21	d1w7ca2	Alignment	not modelled	27.4	17	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
22	d1ulib_	Alignment	not modelled	23.6	14	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Ring hydroxylating beta subunit
23	d1z3xa1	Alignment	not modelled	22.5	19	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**GUN4-associated domain
24	c2gbxF_	Alignment	not modelled	21.5	14	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**biphenyl 2,3-dioxygenase beta subunit; **PDBTitle:** crystal structure of biphenyl 2,3-dioxygenase from sphingomonas2 yanoikuyae b1 bound to biphenyl
25	d1kkxa_	Alignment	not modelled	20.4	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**ARID-like **Family:**ARID domain
26	c1dd3C_	Alignment	not modelled	19.7	19	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** crystal structure of ribosomal protein l12 from thermotoga maritima
27	c1dd3D_	Alignment	not modelled	19.7	19	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** crystal structure of ribosomal protein l12 from thermotoga maritima
28	d1dd4d_	Alignment	not modelled	19.0	19	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain

29	d1g4ma1	Alignment	not modelled	18.8	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Arrestin/Vps26-like
30	c2ib1A_	Alignment	not modelled	18.7	15	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**death domain containing membrane protein nradd; **PDBTitle:** solution structure of p45 death domain
31	c2kkvA_	Alignment	not modelled	17.9	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution nmr structure of an integrase domain from protein2 spa4288 from salmonella enterica, northeast structural3 genomics consortium target slr105h
32	c2hl7A_	Alignment	not modelled	17.7	21	**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
33	c2k9sA_	Alignment	not modelled	17.2	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arabinose operon regulatory protein; **PDBTitle:** solution structure of dna binding domain of e. coli arac
34	c2kj8A_	Alignment	not modelled	16.9	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative prophage cps-53 integrase; **PDBTitle:** nmr structure of fragment 87-196 from the putative phage2 integrase ints of e. coli: northeast structural genomics3 consortium target er652a, psi-2
35	c1nohB_	Alignment	not modelled	16.5	27	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**head morphogenesis protein; **PDBTitle:** the structure of bacteriophage phi29 scaffolding protein2 gp7 after prohead assembly
36	d2coba1	Alignment	not modelled	16.5	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
37	c1bl0A_	Alignment	not modelled	16.4	14	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (multiple antibiotic resistance protein); **PDBTitle:** multiple antibiotic resistance protein (mara)/dna complex
38	c2lboA_	Alignment	not modelled	16.1	25	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**microneme protein 3; **PDBTitle:** eimeria tenella microneme protein 3 mar_b domain
39	c2kkpA_	Alignment	not modelled	15.5	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of the phage integrase sam-like2 domain from moth 1796 from moorella thermoacetica.3 northeast structural genomics consortium target mtr39k4 (residues 64-171).
40	c2wx3A_	Alignment	not modelled	14.8	46	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**mrna-decapping enzyme 1a; **PDBTitle:** asymmetric trimer of the human dcp1a c-terminal domain
41	c3lysC_	Alignment	not modelled	13.7	8	**PDB header:**recombination **Chain:** C: **PDB Molecule:**prophage pi2 protein 01, integrase; **PDBTitle:** crystal structure of the n-terminal domain of the prophage2 pi2 protein 01 (integrase) from lactococcus lactis,3 northeast structural genomics consortium target kr124f
42	d2g2ub1	Alignment	not modelled	13.7	25	**Fold:**BLIP-like **Superfamily:**beta-lactamase-inhibitor protein, BLIP **Family:**beta-lactamase-inhibitor protein, BLIP
43	c2kw0A_	Alignment	not modelled	13.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ccmh protein; **PDBTitle:** solution structure of n-terminal domain of ccmh from escherichia.coli
44	c1giyJ_	Alignment	not modelled	13.2	20	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** crystal structure of the ribosome at 5.5 a resolution. this2 file, 1giy, contains the 50s ribosome subunit. the 30s3 ribosome subunit, three trna, and mrna molecules are in the4 file 1gix
45	c3ahrA_	Alignment	not modelled	13.2	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ero1-like protein alpha; **PDBTitle:** inactive human ero1
46	c2khqA_	Alignment	not modelled	12.8	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution nmr structure of a phage integrase ssp19472 fragment 59-159 from staphylococcus saprophyticus,3 northeast structural genomics consortium target syr103b
47	c3oa8B_	Alignment	not modelled	12.7	19	**PDB header:**heme-binding protein/heme-binding protei **Chain:** B: **PDB Molecule:**soxx; **PDBTitle:** diheme soxax
48	c3ol4B_	Alignment	not modelled	12.6	27	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
49	c3btpA_	Alignment	not modelled	12.5	25	**PDB header:**dna binding protein, chaperone **Chain:** A: **PDB Molecule:**single-strand dna-binding protein; **PDBTitle:** crystal structure of agrobacterium tumefaciens vire2 in complex with2 its chaperone vire1: a novel fold and implications for dna binding
50	d1usta_	Alignment	not modelled	12.0	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Linker histone H1/H5
51	c2kj5A_	Alignment	not modelled	11.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of a domain from a putative phage2 integrase protein nmul_a0064 from nitrosospira multiformis,3 northeast structural genomics consortium target nmr46c
						PDB header:dna binding protein **Chain:** A: **PDB Molecule:**integrase;

52	c2kj9A_	Alignment	not modelled	11.9	11	**PDBTitle:** nmr structure of intb phage-integrase-like protein fragment2 90-199 from erwinia carotova subsp. atroseptica: northeast3 structural genomics consortium target ewr217e
53	c2nyxB_	Alignment	not modelled	11.7	36	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulatory protein, rv1404; **PDBTitle:** crystal structure of rv1404 from mycobacterium tuberculosis
54	c2noxP_	Alignment	not modelled	11.7	19	**PDB header:**oxidoreductase **Chain:** P: **PDB Molecule:**tryptophan 2,3-dioxygenase; **PDBTitle:** crystal structure of tryptophan 2,3-dioxygenase from ralstonia2 metallidurans
55	d3ebya1	Alignment	not modelled	11.6	14	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Ring hydroxylating beta subunit
56	c2dxbR_	Alignment	not modelled	11.5	26	**PDB header:**hydrolase **Chain:** R: **PDB Molecule:**thiocyanate hydrolase subunit gamma; **PDBTitle:** recombinant thiocyanate hydrolase comprising partially-modified cobalt2 centers
57	c3pstA_	Alignment	not modelled	11.4	27	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**protein doa1; **PDBTitle:** crystal structure of pul and pfu(mutate) domain
58	c2ee7A_	Alignment	not modelled	11.0	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**sperm flagellar protein 1; **PDBTitle:** solution structure of the ch domain from human sperm2 flagellar protein 1
59	c2d96A_	Alignment	not modelled	10.8	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nuclear factor nf-kappa-b p100 subunit; **PDBTitle:** solution structure of the death domain of nuclear factor nf-2 kappa-b p100
60	d1uzxa_	Alignment	not modelled	10.8	25	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UEV domain
61	c3m5bA_	Alignment	not modelled	10.7	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger and btb domain-containing protein 32; **PDBTitle:** crystal structure of the btb domain from fazf/zbtb32
62	c2z3xC_	Alignment	not modelled	10.4	29	**PDB header:**dna binding protein/dna **Chain:** C: **PDB Molecule:**small, acid-soluble spore protein c; **PDBTitle:** structure of a protein-dna complex essential for dna2 protection in spore of bacillus species
63	d1dd3a1	Alignment	not modelled	10.3	20	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain
64	c2ld7A_	Alignment	not modelled	10.0	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**histone deacetylase complex subunit sap30; **PDBTitle:** solution structure of the msin3a pah3-sap30 sid complex
65	d1iufa1	Alignment	not modelled	9.9	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
66	d1ig6a_	Alignment	not modelled	9.9	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**ARID-like **Family:**ARID domain
67	c2jhdA_	Alignment	not modelled	9.7	11	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**micronemal protein 1; **PDBTitle:** crystal structure of toxoplasma gondii micronemal protein 12 bound to 3'-sialyl-n-acetyllactosamine
68	d1s7oa_	Alignment	not modelled	9.3	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
69	c2jxjA_	Alignment	not modelled	9.2	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**histone demethylase jarid1a; **PDBTitle:** nmr structure of the arid domain from the histone h3k42 demethylase rbp2
70	c2khvA_	Alignment	not modelled	8.9	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of protein nmul_a0922 from2 nitrosospira multiformis. northeast structural genomics3 consortium target nmr38b.
71	d1h9xa1	Alignment	not modelled	8.7	28	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
72	c3lsgD_	Alignment	not modelled	8.6	14	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**two-component response regulator yesn; **PDBTitle:** the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
73	c3oioA_	Alignment	not modelled	8.6	21	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (arac-type dna-binding domain- **PDBTitle:** crystal structure of transcriptional regulator (arac-type dna-binding2 domain-containing proteins) from chromobacterium violaceum
74	c2krfB_	Alignment	not modelled	8.5	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
75	d1zu1a1	Alignment	not modelled	8.5	14	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**HkH motif-containing C2H2 finger
76	d2b1xb1	Alignment	not modelled	8.5	7	**Fold:**Cystatin-like **Superfamily:**NTF2-like

						Family: Ring hydroxylating beta subunit
77	d1hlma_	Alignment	not modelled	8.4	14	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
78	c2ou2A_	Alignment	not modelled	8.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone acetyltransferase htatip; **PDBTitle:** acetyltransferase domain of human hiv-1 tat interacting2 protein, 60kda, isoform 3
79	c2jnsA_	Alignment	not modelled	8.4	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**bromodomain-containing protein 4; **PDBTitle:** solution structure of the bromodomain-containing protein 42 et domain
80	d1dzfa1	Alignment	not modelled	8.4	9	**Fold:**Restriction endonuclease-like **Superfamily:**Eukaryotic RPB5 N-terminal domain **Family:**Eukaryotic RPB5 N-terminal domain
81	d1wqlb1	Alignment	not modelled	8.3	18	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Ring hydroxylating beta subunit
82	d2ozua1	Alignment	not modelled	8.2	21	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
83	c2ys9A_	Alignment	not modelled	8.2	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox and leucine zipper protein homez; **PDBTitle:** structure of the third homeodomain from the human homeobox2 and leucine zipper protein, homez
84	d1yqaa1	Alignment	not modelled	8.1	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Linker histone H1/H5
85	d1kv9a1	Alignment	not modelled	8.1	20	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinoprotein alcohol dehydrogenase, C-terminal domain
86	d1ijwc_	Alignment	not modelled	8.1	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
87	c3h9xB_	Alignment	not modelled	8.0	29	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein pspto_3016; **PDBTitle:** crystal structure of the pspto_3016 protein from2 pseudomonas syringae, northeast structural genomics3 consortium target psr293
88	c2obuA_	Alignment	not modelled	7.8	28	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**gastric inhibitory polypeptide; **PDBTitle:** solution structure of gip in tfe/water
89	c3ixzA_	Alignment	not modelled	7.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**potassium-transporting atpase alpha; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
90	c3l3fX_	Alignment	not modelled	7.8	39	**PDB header:**protein binding **Chain:** X: **PDB Molecule:**protein doa1; **PDBTitle:** crystal structure of a pfu-pul domain pair of saccharomyces cerevisiae2 doa1/ufd3
91	d3ejva1	Alignment	not modelled	7.7	9	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**BaiE/LinA-like
92	c1iijA_	Alignment	not modelled	7.7	33	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**erbb-2 receptor protein-tyrosine kinase; **PDBTitle:** solution structure of the neu/erbb-2 membrane spanning2 segment
93	d1eb7a2	Alignment	not modelled	7.5	15	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
94	d1wmga_	Alignment	not modelled	7.4	11	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
95	c2kw7A_	Alignment	not modelled	7.3	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** solution nmr structure of the n-terminal domain of protein pg_03612 from p.gingivalis, northeast structural genomics consortium target3 pgr37a
96	c2c1dB_	Alignment	not modelled	7.3	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**soxx; **PDBTitle:** crystal structure of soxxa from p. pantotrophus
97	d3e99a1	Alignment	not modelled	7.2	7	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Ring hydroxylating beta subunit
98	c2eqxA_	Alignment	not modelled	7.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**kelch repeat and btb domain-containing protein 4; **PDBTitle:** solution structure of the back domain of kelch repeat and2 btb domain-containing protein 4
99	d1hcra_	Alignment	not modelled	7.0	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain