Phyre^2

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Description	P38394
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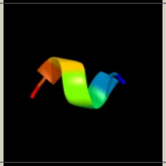
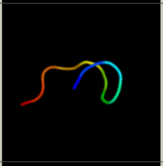
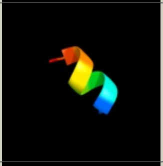
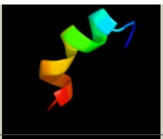
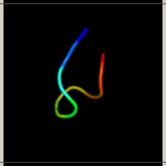
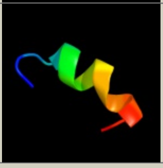
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jjda_	Alignment		33.3	47	**Fold:**Metallothionein **Superfamily:**Metallothionein **Family:**Metallothionein
2	c2jz3A_	Alignment		29.1	71	**PDB header:**transcription inhibitor/transcription **Chain:** A: **PDB Molecule:**suppressor of cytokine signaling 3; **PDBTitle:** socs box elonginbc ternary complex
3	d1lv3a_	Alignment		27.5	40	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Hypothetical zinc finger protein YacG
4	d1u5sb1	Alignment		19.9	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
5	c1c94B_	Alignment		11.4	44	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**retro-gcn4 leucine zipper; **PDBTitle:** reversing the sequence of the gcn4 leucine zipper does not2 affect its fold.
6	c2w0tA_	Alignment		9.6	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lethal(3)malignant brain tumor-like 2 protein; **PDBTitle:** solution structure of the fcs zinc finger domain of human2 lmbl2
7	c2oddA_	Alignment		8.5	43	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**protein cbfa2t1; **PDBTitle:** solution structure of the mynd domain from aml1-eto2 complexed with smrt, a corepressor
8	c1qcrD_	Alignment		8.3	30	**PDB header:** **PDB COMPND:**
9	d2dj8a1	Alignment		8.2	43	**Fold:**HIT/MYND zinc finger-like **Superfamily:**HIT/MYND zinc finger-like **Family:**MYND zinc finger
10	d1pg5b2	Alignment		7.8	29	**Fold:**Rubredoxin-like **Superfamily:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain **Family:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain
11	c2dj8A_	Alignment		7.5	43	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**protein cbfa2t1; **PDBTitle:** solution structure of zf-mynd domain of protein cbfa2ti2 (protein mtg8)

12	c3qwvA_	Alignment		6.7	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**set and mynd domain-containing protein 2; **PDBTitle:** crystal structure of histone lysine methyltransferase smyd2 in complex2 with the cofactor product adohcy
13	c2jw6A_	Alignment		6.7	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**deformed epidermal autoregulatory factor 1 homolog; **PDBTitle:** solution structure of the deaf1 mynd domain
14	d2d8qa1	Alignment		6.6	36	**Fold:**HIT/MYND zinc finger-like **Superfamily:**HIT/MYND zinc finger-like **Family:**MYND zinc finger
15	d1u6pa_	Alignment		6.4	71	**Fold:**Retrovirus zinc finger-like domains **Superfamily:**Retrovirus zinc finger-like domains **Family:**Retrovirus zinc finger-like domains
16	c1mv4B_	Alignment		6.4	29	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**tropomyosin 1 alpha chain; **PDBTitle:** tm9a251-284: a peptide model of the c-terminus of a rat2 striated alpha tropomyosin
17	d1ppjd1	Alignment		6.2	30	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Cytochrome bc1 domain
18	d2jw6a1	Alignment		6.1	50	**Fold:**HIT/MYND zinc finger-like **Superfamily:**HIT/MYND zinc finger-like **Family:**MYND zinc finger
19	d1a6sa_	Alignment		5.9	37	**Fold:**Retroviral matrix proteins **Superfamily:**Retroviral matrix proteins **Family:**GAG polyprotein M-domain
20	c2danA_	Alignment		5.6	36	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**zinc finger mynd domain containing protein 10; **PDBTitle:** the solution structure of the mynd domain (leu384-cys430)2 of human zinc finger mynd domain containing protein 10
21	c3iz5w_	Alignment	not modelled	5.6	21	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**60s ribosomal protein l22 (l22e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
22	c2yiuE_	Alignment	not modelled	5.6	50	**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
23	d1ubdc2	Alignment	not modelled	5.5	44	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
24	d2dana1	Alignment	not modelled	5.5	36	**Fold:**HIT/MYND zinc finger-like **Superfamily:**HIT/MYND zinc finger-like **Family:**MYND zinc finger
25	d3cx5d1	Alignment	not modelled	5.4	40	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Cytochrome bc1 domain