Phyre^2

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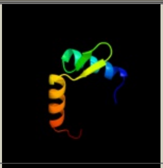
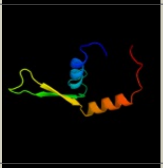
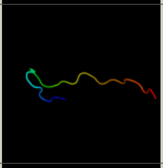
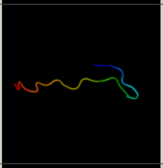
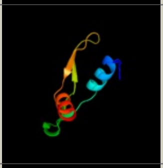
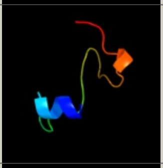
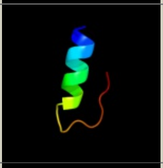
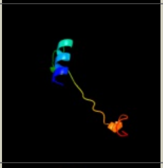
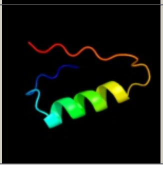
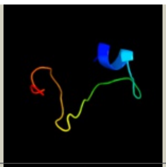
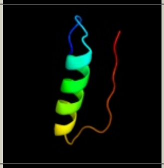
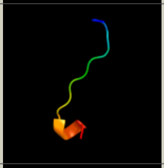
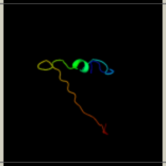
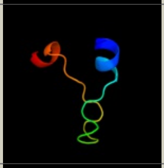
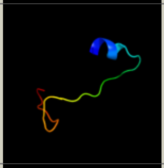
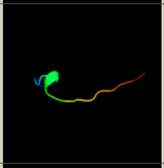
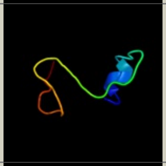
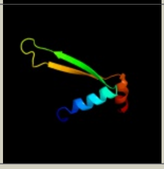
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1yg2a_	Alignment		61.0	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PadR-like
2	c3l9fD_	Alignment		55.0	15	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**putative uncharacterized protein smu.1604c; **PDBTitle:** the crystal structure of smu.1604c from streptococcus mutans ua159
3	d2gjva1	Alignment		25.8	29	**Fold:**Phage tail protein-like **Superfamily:**Phage tail protein-like **Family:**STM4215-like
4	c2gjvF_	Alignment		25.6	29	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** crystal structure of a protein of unknown function from salmonella2 typhimurium
5	d2esha1	Alignment		22.9	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PadR-like
6	d1mjda_	Alignment		19.3	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Doublecortin (DC) **Family:**Doublecortin (DC)
7	c2dt7A_	Alignment		14.9	25	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**splicing factor 3a subunit 3; **PDBTitle:** solution structure of the second surp domain of human2 splicing factor sf3a120 in complex with a fragment of3 human splicing factor sf3a60
8	d1y4oa1	Alignment		14.4	10	**Fold:**Profilin-like **Superfamily:**Roadblock/LC7 domain **Family:**Roadblock/LC7 domain
9	c3abfB_	Alignment		12.6	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
10	d1mg4a_	Alignment		11.7	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Doublecortin (DC) **Family:**Doublecortin (DC)
11	d2nu7b1	Alignment		11.1	24	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains

12	d1uf0a_	Alignment		9.7	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Doublecortin (DC) **Family:**Doublecortin (DC)
13	d1eucb1	Alignment		8.9	18	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
14	d2o3bb1	Alignment		8.5	27	**Fold:**Nuclease A inhibitor (NuiA) **Superfamily:**Nuclease A inhibitor (NuiA) **Family:**Nuclease A inhibitor (NuiA)
15	d2oqea1	Alignment		8.5	22	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain
16	d1zcca1	Alignment		7.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Glycerophosphoryl diester phosphodiesterase
17	d1tz9a_	Alignment		7.7	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**UxuA-like
18	d1o4ya_	Alignment		7.7	28	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolases family 16
19	c2dnfA_	Alignment		7.5	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**doublecortin domain-containing protein 2; **PDBTitle:** solution structure of rsgi ruh-062, a dcx domain from human
20	c3elkA_	Alignment		7.3	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcriptional regulator ta0346; **PDBTitle:** crystal structure of putative transcriptional regulator ta0346 from2 thermoplasma acidophilum
21	c2y69S_	Alignment	not modelled	6.7	30	**PDB header:**electron transport **Chain:** S: **PDB Molecule:**cytochrome c oxidase subunit 5b; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
22	c1sfeA_	Alignment	not modelled	6.5	6	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**ada o6-methylguanine-dna methyltransferase; **PDBTitle:** ada o6-methylguanine-dna methyltransferase from escherichia coli
23	c2j5gL_	Alignment	not modelled	6.4	14	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**alr4455 protein; **PDBTitle:** the native structure of a beta-diketone hydrolase from the2 cyanobacterium anabaena sp. pcc 7120
24	c3ilnB_	Alignment	not modelled	6.0	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**laminarinase; **PDBTitle:** x-ray structure of the laminarinase from rhodothermus marinus
25	d1szoa_	Alignment	not modelled	5.8	14	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
26	c2da1A_	Alignment	not modelled	5.4	29	**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)
27	c2b26A_	Alignment	not modelled	5.4	29	**PDB header:**chaperone/protein transport **Chain:** A: **PDB Molecule:**sis1 protein; **PDBTitle:** the crystal structure of the protein complex of yeast hsp402 sis1 and hsp70 ssa1
28	c2nu9E_	Alignment	not modelled	5.3	24	**PDB header:**ligase **Chain:** E: **PDB Molecule:**succinyl-coa synthetase beta chain; **PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase2

orthorhombic crystal form