Phyre2

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Description	Q46786
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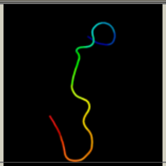
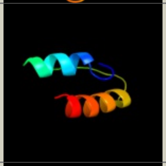
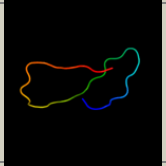
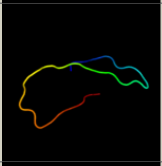
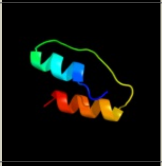
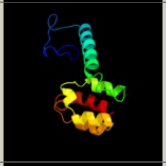
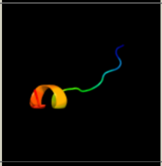
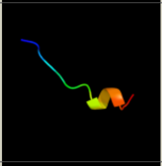
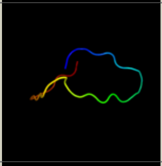
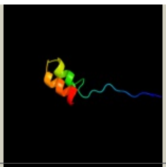
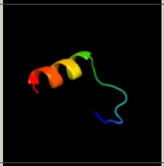
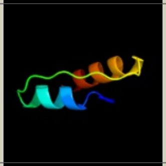
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1v1ha1	Alignment		16.3	44	**Fold:**Triple beta-spiral **Superfamily:**Fibre shaft of virus attachment proteins **Family:**Adenovirus
2	c2zifB_	Alignment		14.8	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative modification methylase; **PDBTitle:** crystal structure of ttha0409, putative dna modification2 methylase from thermus thermophilus hb8- complexed with s-3 adenosyl-l-methionine
3	d1o59a2	Alignment		13.7	24	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Allantoicase repeat
4	c1sg3A_	Alignment		11.3	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**allantoicase; **PDBTitle:** structure of allantoicase
5	d1g60a_	Alignment		10.4	25	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Type II DNA methylase
6	c1n6jG_	Alignment		10.0	73	**PDB header:**transcription/dna **Chain:** G: **PDB Molecule:**calcineurin-binding protein cabin 1; **PDBTitle:** structural basis of sequence-specific recruitment of2 histone deacetylases by myocyte enhancer factor-2
7	d191la_	Alignment		8.4	15	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
8	d1js8a2	Alignment		8.0	29	**Fold:**C-terminal domain of mollusc hemocyanin **Superfamily:**C-terminal domain of mollusc hemocyanin **Family:**C-terminal domain of mollusc hemocyanin
9	d1lnla2	Alignment		7.7	50	**Fold:**C-terminal domain of mollusc hemocyanin **Superfamily:**C-terminal domain of mollusc hemocyanin **Family:**C-terminal domain of mollusc hemocyanin
10	d1o59a1	Alignment		7.6	10	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Allantoicase repeat
11	c1r48A_	Alignment		6.9	67	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**proline/betaine transporter; **PDBTitle:** solution structure of the c-terminal cytoplasmic domain2 residues 468-497 of escherichia coli protein prop

12	c2i2xO_	Alignment		6.6	29	**PDB header:**transferase **Chain:** O: **PDB Molecule:**methyltransferase 1; **PDBTitle:** crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
13	d1e3ha6	Alignment		6.1	25	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
14	c1nw6A_	Alignment		5.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**modification methylase rsri; **PDBTitle:** structure of the beta class n6-adenine dna methyltransferase rsri2 bound to sinefungin
15	d2ieca1	Alignment		5.7	22	**Fold:**MK0786-like **Superfamily:**MK0786-like **Family:**MK0786-like

16	c2v6zM_	Alignment		5.4	17	**PDB header:**transferase **Chain:** M: **PDB Molecule:**dna polymerase epsilon subunit 2; **PDBTitle:** solution structure of amino terminal domain of human dna2 polymerase epsilon subunit b