Phyre²

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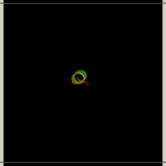
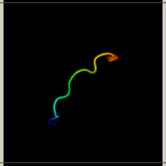
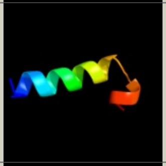
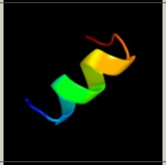
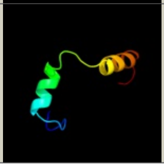
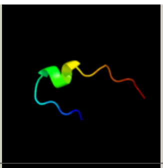
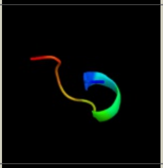
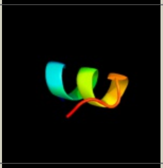
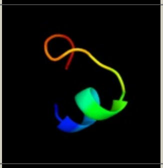
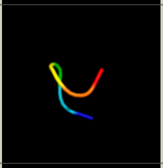
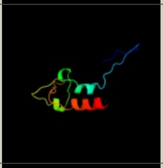
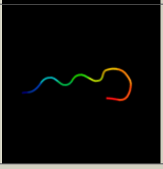
Description	P0AF61
Date	Wed Jan 25 15:20:33 GMT 2012
Unique Job ID	0f5c145a1d7702fa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2rk5a1	 Alignment		18.6	15	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
2	d1t2sa_	 Alignment		12.7	27	**Fold:**SH3-like barrel **Superfamily:**PAZ domain **Family:**PAZ domain
3	d1r6za1	 Alignment		11.2	25	**Fold:**SH3-like barrel **Superfamily:**PAZ domain **Family:**PAZ domain
4	c2be6F_	 Alignment		9.8	50	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**voltage-dependent l-type calcium channel alpha-1c subunit; **PDBTitle:** 2.0 a crystal structure of the cav1.2 iq domain-ca/cam complex
5	c3fqiA_	 Alignment		9.6	40	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein dom3z; **PDBTitle:** crystal structure of the mouse dom3z
6	d1nw3a_	 Alignment		9.0	43	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Catalytic, N-terminal domain of histone methyltransferase Dot1l
7	c1nw3A_	 Alignment		9.0	43	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone methyltransferase dot1l; **PDBTitle:** structure of the catalytic domain of human dot1l, a non-set2 domain nucleosomal histone methyltransferase
8	d1si2a_	 Alignment		8.1	50	**Fold:**SH3-like barrel **Superfamily:**PAZ domain **Family:**PAZ domain
9	d1h6za2	 Alignment		7.8	21	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
10	d2b0la1	 Alignment		7.5	50	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CodY HTH domain
11	c2k9qB_	 Alignment		7.5	34	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of hth_xre family transcriptional2 regulator bt_p548217 from bacteroides thetaiotaomicron.3 northeast structural genomics consortium target btr244.

12	c3m1cB_	Alignment		7.5	37	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**envelope glycoprotein l; **PDBTitle:** crystal structure of the conserved herpesvirus fusion regulator2 complex gh-gl
13	d1bw6a_	Alignment		7.3	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
14	d1hlva1	Alignment		7.3	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
15	d1kbla2	Alignment		7.3	21	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
16	d2fc7a1	Alignment		7.3	33	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**ZZ domain
17	c3kowH_	Alignment		7.3	50	**PDB header:**metal binding protein **Chain:** H: **PDB Molecule:**d-ornithine aminomutase s component; **PDBTitle:** crystal structure of ornithine 4,5 aminomutase backsoaked complex
18	c3zrgB_	Alignment		7.3	100	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**pexrd2 family secreted rxlr effector peptide, putative; **PDBTitle:** crystal structure of rxlr effector pexrd2 from phytophthora infestans
19	d1q8ia2	Alignment		7.1	13	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**DNA polymerase I
20	d1kkea2	Alignment		7.0	50	**Fold:**Virus attachment protein globular domain **Superfamily:**Virus attachment protein globular domain **Family:**Reovirus attachment protein sigma 1 head domain
21	d2ghvc1	Alignment	not modelled	6.9	25	**Fold:**SARS receptor-binding domain-like **Superfamily:**SARS receptor-binding domain-like **Family:**SARS receptor-binding domain-like
22	c2elhA_	Alignment	not modelled	6.4	33	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cg11849-pa; **PDBTitle:** solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
23	d2coba1	Alignment	not modelled	6.1	44	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
24	d2dloa2	Alignment	not modelled	5.9	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
25	d1s5ja2	Alignment	not modelled	5.7	15	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**DNA polymerase I
26	d1vbga2	Alignment	not modelled	5.7	25	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
27	c1kkeA_	Alignment	not modelled	5.3	50	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**sigma 1 protein; **PDBTitle:** crystal structure of reovirus attachment protein sigma12 trimer
28	c3o7vX_	Alignment	not modelled	5.1	25	**PDB header:**rna binding protein/rna **Chain:** X: **PDB Molecule:**piwi-like protein 1; **PDBTitle:** crystal structure of human hiwi1 (v361m) paz domain (residues 277-399)2 in complex with 14-mer rna (12-bp + 2-nt overhang) containing 2'-och33 at its 3'-end