Phyre^2

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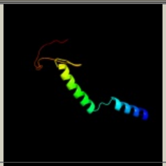
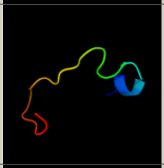
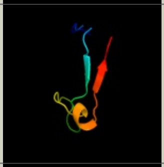
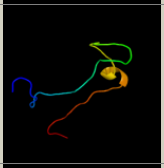
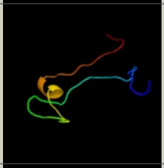
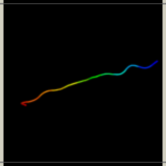
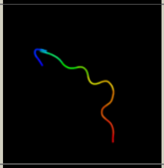
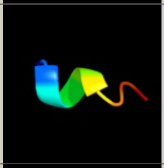
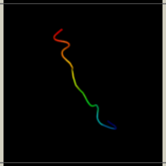
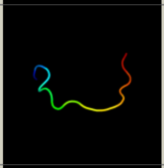
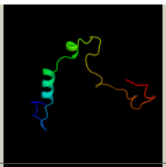
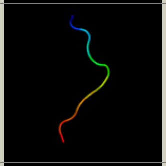
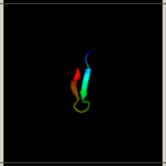
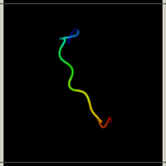
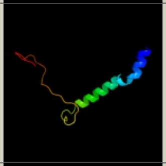
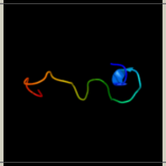
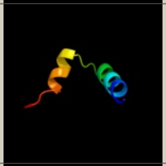
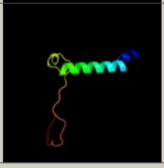
Description	O52982
Date	Thu Jan 5 10:56:32 GMT 2012
Unique Job ID	984a8762e1344498

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ig8a1	Alignment		40.6	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
2	c3fmaD_	Alignment		30.5	27	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**protein smy2; **PDBTitle:** crystal structure of the gyf domain of smy2 in complex with a proline-2 rich peptide from bbp/scsf1
3	c3d12E_	Alignment		24.5	18	**PDB header:**hydrolase/membrane protein **Chain:** E: **PDB Molecule:**ephrin-b3; **PDBTitle:** crystal structures of nipah virus g attachment glycoprotein in complex2 with its receptor ephrin-b3
4	d1ikop_	Alignment		23.4	16	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Ephrin ectodomain
5	c1ikoP_	Alignment		23.4	16	**PDB header:**signaling protein **Chain:** P: **PDB Molecule:**ephrin-b2; **PDBTitle:** crystal structure of the murine ephrin-b2 ectodomain
6	c3f1zF_	Alignment		23.1	62	**PDB header:**dna binding protein **Chain:** F: **PDB Molecule:**putative nucleic acid-binding lipoprotein; **PDBTitle:** crystal structure of putative nucleic acid-binding lipoprotein2 (yp_001337197.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 2.46 a resolution
7	d2jnaa1	Alignment		15.2	38	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
8	c2v0xB_	Alignment		14.7	56	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**lamina-associated polypeptide 2 isoforms **PDBTitle:** the dimerization domain of lap2alpha
9	d1tu2b2	Alignment		13.0	50	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
10	d1bg3a3	Alignment		11.8	47	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
11	d1j6wa_	Alignment		11.8	37	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS

12	d1qfxa_	Alignment		11.7	15	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
13	d1x9ya2	Alignment		11.4	58	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Staphopain B, prodomain
14	c2ph7B_	Alignment		10.7	33	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein af_2093; **PDBTitle:** crystal structure of af2093 from archaeoglobus fulgidus
15	d1v4sa1	Alignment		10.4	40	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
16	d1czan1	Alignment		10.2	25	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
17	d1m7ka_	Alignment		9.5	22	**Fold:**Spectrin repeat-like **Superfamily:**BAG domain **Family:**BAG domain
18	d1wh2a_	Alignment		9.2	26	**Fold:**GYF/BRK domain-like **Superfamily:**GYF domain **Family:**GYF domain
19	c3zr8X_	Alignment		8.8	25	**PDB header:**protein binding **Chain:** X: **PDB Molecule:**avr3a11; **PDBTitle:** crystal structure of rxlr effector avr3a11 from phytophthora capsici
20	d1czan3	Alignment		8.4	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
21	d1j6xa_	Alignment	not modelled	8.2	22	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
22	c2hacA_	Alignment	not modelled	7.6	36	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd3 zeta chain; **PDBTitle:** structure of zeta-zeta transmembrane dimer
23	d2nn6g2	Alignment	not modelled	7.2	35	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
24	d1xn7a_	Alignment	not modelled	7.0	53	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Hypothetical protein YhgG
25	d1wd3a1	Alignment	not modelled	6.6	33	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Alpha-L-arabinofuranosidase B, N-terminal domain
26	d3b2ua2	Alignment	not modelled	6.3	71	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Growth factor receptor domain **Family:**Growth factor receptor domain
27	d1bdga1	Alignment	not modelled	6.1	33	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
28	d1uhza_	Alignment	not modelled	5.9	17	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
29	d2hsga1	Alignment	not modelled	5.9	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains

						Family: GalR/LacI-like bacterial regulator
30	c3njqB_	Alignment	not modelled	5.6	12	**PDB header:**viral protein/inhibitor **Chain:** B: **PDB Molecule:**orf 17; **PDBTitle:** crystal structure of kaposi's sarcoma-associated herpesvirus protease2 in complex with dimer disruptor
31	d1slqa_	Alignment	not modelled	5.6	37	**Fold:**VP4 membrane interaction domain **Superfamily:**VP4 membrane interaction domain **Family:**VP4 membrane interaction domain