Phyre2

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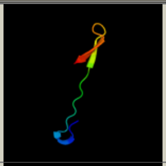
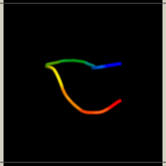
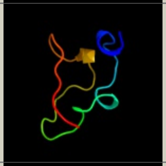
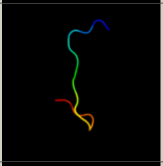
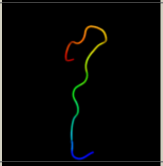
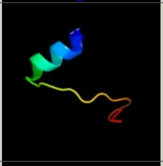
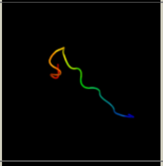
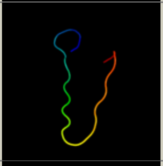
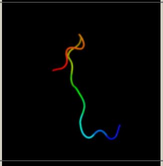
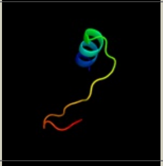
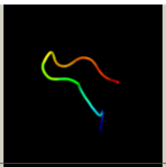
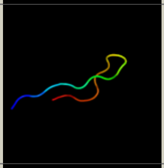
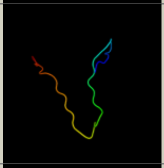
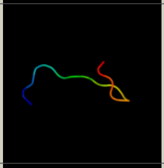
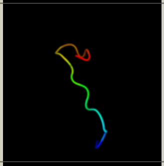
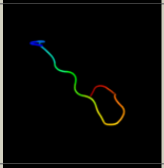
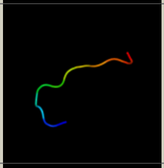
Description	P64622
Date	Thu Jan 5 12:09:59 GMT 2012
Unique Job ID	191042b61964e377

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mswA_	Alignment		29.2	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein with unknown function (bf3112) from2 bacteroides fragilis nctc 9343 at 1.90 a resolution
2	d1s6la1	Alignment		17.4	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MerB N-terminal domain-like
3	c3m3gA_	Alignment		17.3	44	**PDB header:**polysaccharide-binding protein **Chain:** A: **PDB Molecule:**epl1 protein; **PDBTitle:** crystal structure of sm1, an elicitor of plant defence responses from2 trichoderma virens.
4	c2yvzA_	Alignment		14.3	50	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form
5	c3kxrA_	Alignment		13.5	38	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**magnesium transporter, putative; **PDBTitle:** structure of the cystathionine beta-synthase pair domain of the2 putative mg2+ transporter so5017 from shewanella oneidensis mr-1.
6	d2yzqa1	Alignment		13.2	19	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
7	d2yzqa2	Alignment		12.2	38	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
8	c3gvzB_	Alignment		12.1	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein cv2077; **PDBTitle:** crystal structure of the protein cv2077 from2 chromobacterium violaceum. northeast structural genomics3 consortium target cvr62
9	c2ouxB_	Alignment		12.0	38	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**magnesium transporter; **PDBTitle:** crystal structure of the soluble part of a magnesium transporter
10	d2ooxe1	Alignment		11.0	15	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
11	c2pdtD_	Alignment		10.8	36	**PDB header:**circadian clock protein **Chain:** D: **PDB Molecule:**vivid pas protein vvd; **PDBTitle:** 2.3 angstrom structure of phosphodiesterase treated vivid

12	d1p0za_	Alignment		10.5	27	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**Sensory domain of two-component sensor kinase
13	d1e6yb2	Alignment		10.0	47	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase alpha and beta chain N-terminal domain
14	d2bbaa1	Alignment		9.8	22	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Ephrin receptor ligand binding domain
15	c2yvxD_	Alignment		9.4	50	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
16	c1vr9B_	Alignment		8.3	44	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cbs domain protein/act domain protein; **PDBTitle:** crystal structure of a cbs domain pair/act domain protein (tm0892)2 from thermotoga maritima at 1.70 a resolution
17	d1vr9a3	Alignment		8.3	44	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
18	c3fnaA_	Alignment		7.9	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**possible arabinose 5-phosphate isomerase; **PDBTitle:** crystal structure of the cbs pair of possible d-arabinose 5-phosphate2 isomerase yrbh from escherichia coli cft073
19	c3kpbA_	Alignment		7.5	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj0100; **PDBTitle:** crystal structure of mj01002 in complex with 5 -methylthioadenosine and s-adenosyl-l-3 methionine.
20	d2ouxa2	Alignment		7.1	23	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
21	d1bywa_	Alignment	not modelled	7.0	31	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
22	c2qbxB_	Alignment	not modelled	6.8	28	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ephrin type-b receptor 2; **PDBTitle:** ephb2/snew antagonistic peptide complex
23	c2p9mD_	Alignment	not modelled	6.7	25	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein mj0922; **PDBTitle:** crystal structure of conserved hypothetical protein mj0922 from2 methanocaldococcus jannaschii dsm 2661
24	d3ddja1	Alignment	not modelled	6.4	0	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
25	d1pvma4	Alignment	not modelled	6.0	23	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
26	d1oqva_	Alignment	not modelled	5.8	42	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**TcpA-like pilin
27	d1jnua_	Alignment	not modelled	5.6	15	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
28	d1jcna4	Alignment	not modelled	5.6	26	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
29	d2v8qe1	Alignment	not modelled	5.5	12	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair

						Family:CBS-domain pair
30	d2ef7a1	Alignment	not modelled	5.5	31	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
31	d2riha1	Alignment	not modelled	5.3	27	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
32	c2v8kA_	Alignment	not modelled	5.1	29	**PDB header:**lyase **Chain:** A: **PDB Molecule:**pectate lyase; **PDBTitle:** structure of a family 2 pectate lyase in complex with2 trigalacturonic acid