Phyre^2

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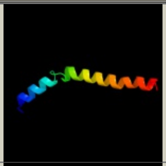
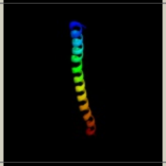
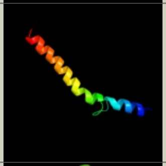
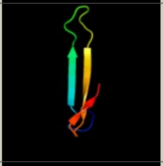
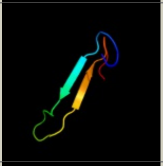
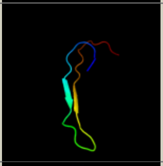
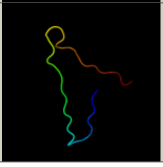
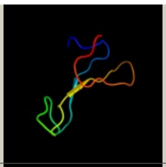
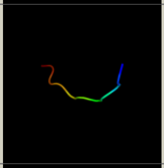
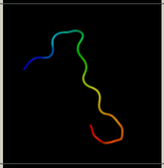
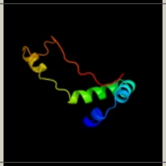
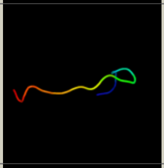
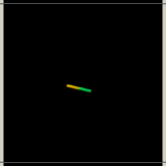
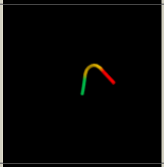
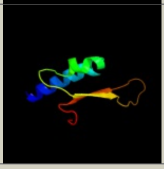
Description	P08372
Date	Thu Jan 5 11:01:22 GMT 2012
Unique Job ID	1cbe3cb0e5e204c6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sokB_	Alignment		95.6	24	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**fimbrial protein; **PDBTitle:** dichelobacter nodosus pilin fima
2	d1oqwa_	Alignment		94.5	8	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
3	d2pila_	Alignment		91.6	17	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
4	c2ky8A_	Alignment		62.2	17	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**methyl-cpg-binding domain protein 2; **PDBTitle:** solution structure and dynamic analysis of chicken mbd2 methyl binding2 domain bound to a target methylated dna sequence
5	d1ig4a_	Alignment		55.0	12	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**Methyl-CpG-binding domain, MBD
6	d1qk9a_	Alignment		44.7	21	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**Methyl-CpG-binding domain, MBD
7	d1ub1a_	Alignment		34.0	21	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**Methyl-CpG-binding domain, MBD
8	d1w8oa1	Alignment		28.3	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
9	d3ci0i1	Alignment		25.6	7	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**GSPII I/J protein-like
10	d2reta1	Alignment		18.9	10	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**GSPII I/J protein-like
11	d1yfua1	Alignment		15.7	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like

12	c2jv4A_	Alignment		13.4	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis/trans isomerase; **PDBTitle:** structure characterisation of pina ww domain and comparison2 with other group iv ww domains, pin1 and ess1
13	d2uuyb1	Alignment		11.4	27	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Tick tryptase inhibitor-like
14	c1ymzA_	Alignment		10.2	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cc45; **PDBTitle:** cc45, an artificial ww domain designed using statistical2 coupling analysis
15	c3nctC_	Alignment		9.7	20	**PDB header:**dna binding protein, chaperone **Chain:** C: **PDB Molecule:**protein psib; **PDBTitle:** x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca
16	c1e0mA_	Alignment		9.7	14	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**wwprototype; **PDBTitle:** prototype ww domain
17	c1wr4A_	Alignment		9.7	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin-protein ligase nedd4-2; **PDBTitle:** solution structure of the second ww domain of nedd4-2
18	c1dvaY_	Alignment		9.3	50	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** Y: **PDB Molecule:**peptide e-76; **PDBTitle:** crystal structure of the complex between the peptide exosite inhibitor2 e-76 and coagulation factor viia
19	c1dvaX_	Alignment		9.3	50	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** X: **PDB Molecule:**peptide e-76; **PDBTitle:** crystal structure of the complex between the peptide exosite inhibitor2 e-76 and coagulation factor viia
20	c2retE_	Alignment		8.9	15	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**pseudopilin epsi; **PDBTitle:** the crystal structure of a binary complex of two pseudopilins: epsi2 and epsj from the type 2 secretion system of vibrio vulnificus
21	c2ysbA_	Alignment	not modelled	8.1	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**salvador homolog 1 protein; **PDBTitle:** solution structure of the first ww domain from the mouse2 salvador homolog 1 protein (sav1)
22	d1tk7a2	Alignment	not modelled	7.6	13	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
23	d2jmfa1	Alignment	not modelled	7.5	15	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
24	d1is3a_	Alignment	not modelled	7.5	8	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Galectin (animal S-lectin)
25	c1yiuA_	Alignment	not modelled	7.3	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**itchy e3 ubiquitin protein ligase; **PDBTitle:** itch e3 ubiquitin ligase ww3 domain
26	d1k9ra_	Alignment	not modelled	7.1	20	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
27	d2e9ia1	Alignment	not modelled	7.0	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
28	d2cs3a1	Alignment	not modelled	6.8	20	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**Variant RING domain
29	c2yshA	Alignment	not modelled	6.5	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**growth-arrest-specific protein 7;

29	c2yshA_	Alignment	not modelled	6.5	18	**PDBTitle:** solution structure of the ww domain from the human growth-2 arrest-specific protein 7, gas-7
30	c2y69Z_	Alignment	not modelled	6.3	8	**PDB header:**electron transport **Chain:** Z: **PDB Molecule:**cytochrome c oxidase polypeptide 8h; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
31	c3a0hl_	Alignment	not modelled	6.3	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
32	c3a0hL_	Alignment	not modelled	6.3	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
33	c1wr7A_	Alignment	not modelled	6.3	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nedd4-2; **PDBTitle:** solution structure of the third ww domain of nedd4-2
34	c3a0bl_	Alignment	not modelled	6.2	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
35	c3a0bL_	Alignment	not modelled	6.2	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
36	c2lawA_	Alignment	not modelled	6.0	23	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**yorkie homolog; **PDBTitle:** structure of the second ww domain from human yap in complex with a2 human smad1 derived peptide
37	d2axtl1	Alignment	not modelled	6.0	30	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein L, PsbL **Family:**PsbL-like
38	c1s5lL_	Alignment	not modelled	6.0	30	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
39	c1s5ll_	Alignment	not modelled	6.0	30	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
40	c2axtL_	Alignment	not modelled	6.0	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
41	c2axtl_	Alignment	not modelled	6.0	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
42	c3bz1L_	Alignment	not modelled	6.0	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer
43	c3arcL_	Alignment	not modelled	6.0	30	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
44	c3prqL_	Alignment	not modelled	6.0	30	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
45	c3kziL_	Alignment	not modelled	6.0	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of monomeric form of cyanobacterial photosystem ii
46	c3prrL_	Alignment	not modelled	6.0	30	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
47	c3bz2L_	Alignment	not modelled	6.0	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 22 of 2). this file contains second monomer of psii dimer
48	d2ysca1	Alignment	not modelled	6.0	15	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
49	c3u5eL_	Alignment	not modelled	5.9	35	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**60s ribosomal protein l13-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 resolution
50	c3arcl_	Alignment	not modelled	5.6	30	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
51	c2dmvA_	Alignment	not modelled	5.6	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**itchy homolog e3 ubiquitin protein ligase; **PDBTitle:** solution structure of the second ww domain of itchy homolog2 e3 ubiquitin protein ligase (itch)
52	c2ez5W_	Alignment	not modelled	5.5	13	**PDB header:**signalling protein,ligase **Chain:** W: **PDB Molecule:**e3 ubiquitin-protein ligase nedd4; **PDBTitle:** solution structure of the dnedd4 ww3* domain- comm lpsy2 peptide complex
53	c2djyA_	Alignment	not modelled	5.4	20	**PDB header:**ligase/signaling protein **Chain:** A: **PDB Molecule:**smad ubiquitination regulatory factor 2; **PDBTitle:** solution structure of smurf2 ww3 domain-smad7 py peptide2 complex
54	c2wsfG_	Alignment	not modelled	5.4	25	**PDB header:**photosynthesis **Chain:** G: **PDB Molecule:**photosystem i reaction center subunit v; **PDBTitle:** improved model of plant photosystem i
						PDB header:protein binding

55	c2yscA_	Alignment	not modelled	5.3	15	**Chain:** A: **PDB Molecule:**amyloid beta a4 precursor protein-binding family **PDBTitle:** solution structure of the ww domain from the human amyloid2 beta a4 precursor protein-binding family b member 3, apbb3