Phyre2

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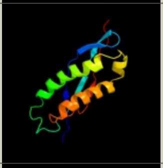
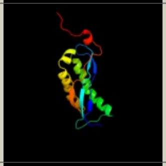
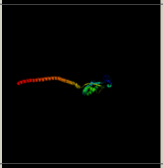
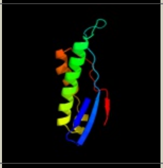
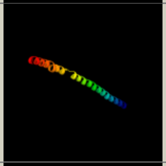
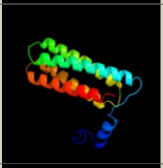
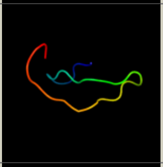
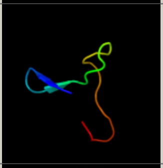
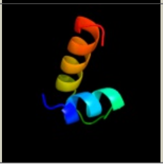
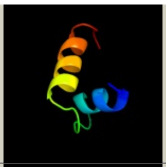
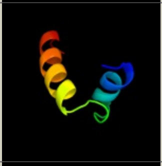
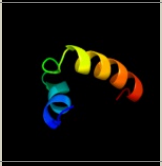
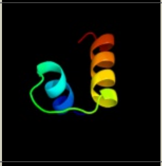
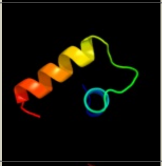
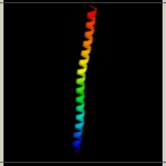
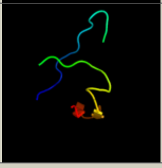
Description	P0AA53
Date	Thu Jan 5 11:11:56 GMT 2012
Unique Job ID	59470f5144a0aa4c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bk6C_	Alignment		99.9	42	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**ph stomatin; **PDBTitle:** crystal structure of a core domain of stomatin from2 pyrococcus horikoshii
2	c2rpbA_	Alignment		99.8	50	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical membrane protein; **PDBTitle:** the solution structure of membrane protein
3	d1wina_	Alignment		99.8	15	**Fold:**EF-Ts domain-like **Superfamily:**Band 7/SPFH domain **Family:**Band 7/SPFH domain
4	c2zv4O_	Alignment		98.4	16	**PDB header:**structural protein **Chain:** O: **PDB Molecule:**major vault protein; **PDBTitle:** the structure of rat liver vault at 3.5 angstrom resolution
5	c3u5gB_	Alignment		58.4	19	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**40s ribosomal protein s1-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
6	c2xzm4_	Alignment		43.2	11	**PDB header:**ribosome **Chain:** 4: **PDB Molecule:**40s ribosomal protein s3a; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
7	c3k5bB_	Alignment		42.1	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**v-type atp synthase, subunit (vapc-therm); **PDBTitle:** crystal structure of the peripheral stalk of thermus thermophilus h+-2 atpase/synthase
8	c1y4cA_	Alignment		23.5	16	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
9	d1nkta1	Alignment		21.3	31	**Fold:**Pre-protein crosslinking domain of SecA **Superfamily:**Pre-protein crosslinking domain of SecA **Family:**Pre-protein crosslinking domain of SecA
10	d1tf5a1	Alignment		18.9	31	**Fold:**Pre-protein crosslinking domain of SecA **Superfamily:**Pre-protein crosslinking domain of SecA **Family:**Pre-protein crosslinking domain of SecA
11	d2hsga1	Alignment		12.8	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator

12	d1lcda_	Alignment		11.8	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
13	d2bjca1	Alignment		10.8	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
14	c2lcvA_	Alignment		10.8	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional repressor cytr; **PDBTitle:** structure of the cytidine repressor dna-binding domain; an alternate2 calculation
15	c2k88A_	Alignment		10.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**vacuolar proton pump subunit g; **PDBTitle:** association of subunit d (vma6p) and e (vma4p) with g2 (vma10p) and the nmr solution structure of subunit g (g1-3 59) of the saccharomyces cerevisiae v1vo atpase
16	c2l8nA_	Alignment		9.6	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional repressor cytr; **PDBTitle:** nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
17	d1qpza1	Alignment		9.2	6	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
18	d1efaa1	Alignment		8.7	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
19	d1l2pa_	Alignment		8.4	31	**Fold:**Single transmembrane helix **Superfamily:**F1F0 ATP synthase subunit B, membrane domain **Family:**F1F0 ATP synthase subunit B, membrane domain
20	d2f1la1	Alignment		8.1	17	**Fold:**PRC-barrel domain **Superfamily:**PRC-barrel domain **Family:**RimM C-terminal domain-like
21	c1wd6B_	Alignment	not modelled	7.9	38	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydhr; **PDBTitle:** crystal structure of jw1657 from escherichia coli
22	c2kk7A_	Alignment	not modelled	7.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**v-type atp synthase subunit e; **PDBTitle:** nmr solution structure of the n terminal domain of subunit e2 (e1-52) of a1ao atp synthase from methanocaldococcus3 jannaschii
23	c3lj5H_	Alignment	not modelled	7.6	15	**PDB header:**viral protein **Chain:** H: **PDB Molecule:**portal protein; **PDBTitle:** full length bacteriophage p22 portal protein
24	c3sbtB_	Alignment	not modelled	7.1	8	**PDB header:**splicing **Chain:** B: **PDB Molecule:**a1 cistron-splicing factor aar2; **PDBTitle:** crystal structure of a aar2-prp8 complex
25	c2ptmA_	Alignment	not modelled	6.9	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hyperpolarization-activated (ih) channel; **PDBTitle:** structure and rearrangements in the carboxy-terminal region of spih2 channels
26	c1o7fA_	Alignment	not modelled	6.8	21	**PDB header:**regulation **Chain:** A: **PDB Molecule:**camp-dependent rap1 guanine-nucleotide exchange **PDBTitle:** crystal structure of the regulatory domain of epac2
27	c1wrgA_	Alignment	not modelled	6.8	22	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**light-harvesting protein b-880, beta chain; **PDBTitle:** light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum
28	c3sokB_	Alignment	not modelled	6.6	22	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**fimbrial protein; **PDBTitle:** dichelobacter nodosus pilin fima

29	c3h5tA_	Alignment	not modelled	6.5	6	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from corynebacterium glutamicum
30	c2jp3A_	Alignment	not modelled	6.4	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4; **PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles
31	c3arcl_	Alignment	not modelled	6.3	12	**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
32	c3arcL_	Alignment	not modelled	6.2	12	**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
33	c1s5lL_	Alignment	not modelled	6.2	12	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
34	c3kziL_	Alignment	not modelled	6.2	12	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of monomeric form of cyanobacterial photosystem ii
35	c2axtl_	Alignment	not modelled	6.2	12	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
36	c3bz1L_	Alignment	not modelled	6.2	12	**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
37	c3a0hl_	Alignment	not modelled	6.2	12	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
38	c3a0bl_	Alignment	not modelled	6.2	12	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
39	c3a0hL_	Alignment	not modelled	6.2	12	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
40	c3prqL_	Alignment	not modelled	6.2	12	**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
41	c3prrL_	Alignment	not modelled	6.2	12	**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
42	c1s5ll_	Alignment	not modelled	6.2	12	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
43	d2axtl1	Alignment	not modelled	6.2	12	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein L, PsbL **Family:**PsbL-like
44	c3bz2L_	Alignment	not modelled	6.2	12	**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
45	c3a0bL_	Alignment	not modelled	6.2	12	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
46	c2axtL_	Alignment	not modelled	6.2	12	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
47	c2jo1A_	Alignment	not modelled	6.1	28	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
48	d1uxda_	Alignment	not modelled	6.0	3	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
49	d2pila_	Alignment	not modelled	5.9	33	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
50	d2ix0a1	Alignment	not modelled	5.9	28	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
51	d2h8pc1	Alignment	not modelled	5.8	12	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
52	c3f6sI_	Alignment	not modelled	5.6	13	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**flavodoxin; **PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
53	d1qd1a2	Alignment	not modelled	5.6	9	**Fold:**Ferredoxin-like **Superfamily:**Formiminotransferase domain of formiminotransferase-cyclodeaminase. **Family:**Formiminotransferase domain of formiminotransferase-cyclodeaminase.
54	d2ha9a1	Alignment	not modelled	5.4	14	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes

						Family:SP0239-like
55	d1oqwa_	Alignment	not modelled	5.4	17	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
56	c2opkC_	Alignment	not modelled	5.3	23	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
57	d1i9za_	Alignment	not modelled	5.3	13	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**Inositol polyphosphate 5-phosphatase (IPP5)
58	c2f1lA_	Alignment	not modelled	5.2	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**16s rrna processing protein; **PDBTitle:** crystal structure of a putative 16s ribosomal rna processing protein2 rimm (pa3744) from pseudomonas aeruginosa at 2.46 a resolution
59	d1jeya1	Alignment	not modelled	5.1	41	**Fold:**SPOC domain-like **Superfamily:**SPOC domain-like **Family:**Ku70 subunit middle domain
60	c1zvvA_	Alignment	not modelled	5.1	9	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**glucose-resistance amylase regulator; **PDBTitle:** crystal structure of a ccpa-crh-dna complex