Phyre^2

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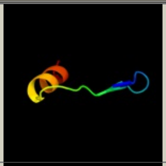
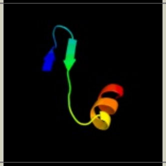
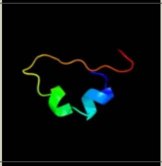
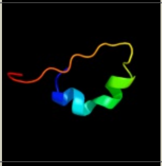
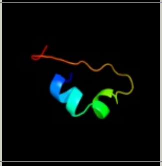
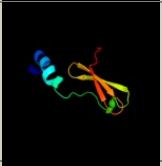
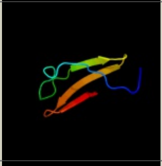
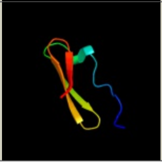
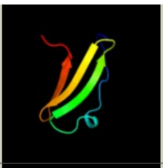
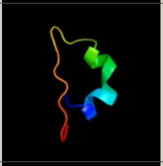
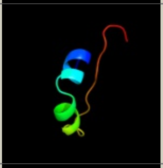
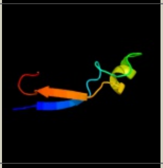
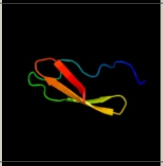
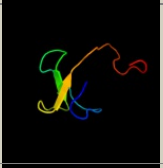
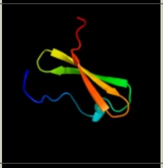
Description	P46857
Date	Thu Jan 5 12:04:29 GMT 2012
Unique Job ID	4b95b499bbdd9858

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cgiD_	Alignment		48.2	21	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**propanediol utilization protein pduu; **PDBTitle:** crystal structure of the pduu shell protein from the pdu2 microcompartment
2	c3ia0c_	Alignment		46.0	29	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**ethanolamine utilization protein euts; **PDBTitle:** ethanolamine utilization microcompartment shell subunit,2 euts-g39v mutant
3	d1ulia1	Alignment		42.1	19	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
4	c2odkD_	Alignment		35.3	25	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative prevent-host-death protein from nitrosomonas europaea
5	c3hryA_	Alignment		31.4	29	**PDB header:**antitoxin **Chain:** A: **PDB Molecule:**prevent host death protein; **PDBTitle:** crystal structure of phd in a trigonal space group and partially2 disordered
6	d2odka1	Alignment		30.5	24	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
7	d2bmoa1	Alignment		26.0	15	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
8	d1o7na1	Alignment		24.9	17	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
9	c3c5pF_	Alignment		24.6	30	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**protein bas0735 of unknown function; **PDBTitle:** crystal structure of bas0735, a protein of unknown function from2 bacillus anthracis str. sterne
10	c3gkqB_	Alignment		23.6	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**terminal oxygenase component of carbazole 1,9a- **PDBTitle:** terminal oxygenase of carbazole 1,9a-dioxygenase from2 novosphingobium sp. ka1
11	c3gcfC_	Alignment		20.9	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**terminal oxygenase component of carbazole 1,9a- **PDBTitle:** terminal oxygenase of carbazole 1,9a-dioxygenase from2 nocardioides aromaticivorans ic177

12	d2b1xa1	Alignment		20.1	32	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
13	d2a6qb1	Alignment		20.0	29	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
14	c3hs2H_	Alignment		19.3	29	**PDB header:**antitoxin **Chain:** H: **PDB Molecule:**prevent host death protein; **PDBTitle:** crystal structure of phd truncated to residue 57 in an orthorhombic2 space group
15	c2jx8A_	Alignment		18.7	39	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phosphorylated ctd-interacting factor 1; **PDBTitle:** solution structure of hpcif1 ww domain
16	d2de6a1	Alignment		17.6	17	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
17	c2jsoA_	Alignment		16.1	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**polymyxin resistance protein pmrd; **PDBTitle:** antimicrobial resistance protein
18	d1wqla1	Alignment		13.5	17	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
19	c2ckcA_	Alignment		13.3	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chromodomain-helicase-dna-binding protein 7; **PDBTitle:** solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
20	d2ckca1	Alignment		13.3	24	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
21	d2a6qa1	Alignment	not modelled	11.0	30	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
22	d2fbaa1	Alignment	not modelled	10.8	16	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glucoamylase
23	c1ncgA_	Alignment	not modelled	10.3	27	**PDB header:**cell adhesion protein **Chain:** A: **PDB Molecule:**n-cadherin; **PDBTitle:** structural basis of cell-cell adhesion by cadherins
24	d1z01a1	Alignment	not modelled	10.2	22	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
25	c1zvnA_	Alignment	not modelled	9.9	32	**PDB header:**---- **Chain:** A: **PDB Molecule:**mn-cadherin; **PDBTitle:** crystal structure of chick mn-cadherin ec1
26	d1tdha3	Alignment	not modelled	9.9	28	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
27	c2rqxA_	Alignment	not modelled	9.5	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**polymyxin b resistance protein; **PDBTitle:** solution nmr structure of pmrd from klebsiella pneumoniae
28	c2e9qA_	Alignment	not modelled	9.4	18	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**11s globulin subunit beta; **PDBTitle:** recombinant pro-11s globulin of pumpkin
29	d2idaa1	Alignment	not modelled	9.0	14	**Fold:**RING/U-box **Superfamily:**RING/U-box

						Family: Zf-UBP
30	d2pbka1	Alignment	not modelled	9.0	18	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
31	d1njha_	Alignment	not modelled	8.8	22	**Fold:**Hypothetical protein YojF **Superfamily:**Hypothetical protein YojF **Family:**Hypothetical protein YojF
32	c3ff7B_	Alignment	not modelled	8.1	27	**PDB header:**cell adhesion/immunue system **Chain:** B: **PDB Molecule:**epithelial cadherin; **PDBTitle:** structure of nk cell receptor klrg1 bound to e-cadherin
33	d1aa7a_	Alignment	not modelled	8.1	35	**Fold:**Influenza virus matrix protein M1 **Superfamily:**Influenza virus matrix protein M1 **Family:**Influenza virus matrix protein M1
34	d1o6ea_	Alignment	not modelled	8.0	13	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
35	c2b1xE_	Alignment	not modelled	7.9	26	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**naphthalene dioxygenase large subunit; **PDBTitle:** crystal structure of naphthalene 1,2-dioxygenase from rhodococcus sp.
36	c3g5oA_	Alignment	not modelled	7.4	21	**PDB header:**toxin/antitoxin **Chain:** A: **PDB Molecule:**uncharacterized protein rv2865; **PDBTitle:** the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
37	d1y0pa3	Alignment	not modelled	7.1	17	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
38	c3entB_	Alignment	not modelled	7.0	20	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of nitrollin, a betagamma-crystallin from2 nitrosospira multiformis-in alternate space group (p65)
39	d1ynha1	Alignment	not modelled	7.0	16	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Succinylarginine dihydrolase-like
40	d1r76a_	Alignment	not modelled	6.9	33	**Fold:**alpha/alpha toroid **Superfamily:**Family 10 polysaccharide lyase **Family:**Family 10 polysaccharide lyase
41	d2omzb1	Alignment	not modelled	6.9	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cadherin-like **Family:**Cadherin
42	c3jr7A_	Alignment	not modelled	6.5	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized egv family protein cog1307; **PDBTitle:** the crystal structure of the protein of degv family cog1307 with2 unknown function from ruminococcus gnavus atcc 29149
43	d1vr5a1	Alignment	not modelled	6.5	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
44	c1uljA_	Alignment	not modelled	6.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**biphenyl dioxygenase large subunit; **PDBTitle:** biphenyl dioxygenase (bpha1a2) in complex with the substrate
45	d1iega_	Alignment	not modelled	6.1	19	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
46	c3gteB_	Alignment	not modelled	6.0	21	**PDB header:**electron transport, oxidoreductase **Chain:** B: **PDB Molecule:**ddmc; **PDBTitle:** crystal structure of dicamba monooxygenase with non-heme2 iron
47	c2hjjA_	Alignment	not modelled	6.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ykff; **PDBTitle:** solution nmr structure of protein ykff from escherichia coli.2 northeast structural genomics target er397.
48	d2hjja1	Alignment	not modelled	6.0	15	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**YkfF-like
49	c2o7jA_	Alignment	not modelled	5.9	11	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**oligopeptide abc transporter, periplasmic **PDBTitle:** the x-ray crystal structure of a thermophilic cellobiose2 binding protein bound with cellopentaose
50	c2js3B_	Alignment	not modelled	5.9	28	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of protein q6n9a4_rhopa. northeast structural genomics2 consortium target rpt8
51	c2de7B_	Alignment	not modelled	5.5	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**terminal oxygenase component of carbazole; **PDBTitle:** the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
52	d1at3a_	Alignment	not modelled	5.3	16	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
53	d1smye_	Alignment	not modelled	5.3	30	**Fold:**RPB6/omega subunit-like **Superfamily:**RPB6/omega subunit-like **Family:**RNA polymerase omega subunit
54	d1vkza1	Alignment	not modelled	5.3	21	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like

55	c1nchB_	Alignment	not modelled	5.3	27	**PDB header:**cell adhesion protein **Chain:** B: **PDB Molecule:**n-cadherin; **PDBTitle:** structural basis of cell-cell adhesion by cadherins
56	c1nciB_	Alignment	not modelled	5.2	30	**PDB header:**cell adhesion protein **Chain:** B: **PDB Molecule:**n-cadherin; **PDBTitle:** structural basis of cell-cell adhesion by cadherins