Phyre^2

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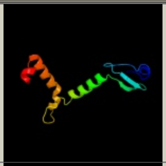
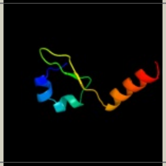
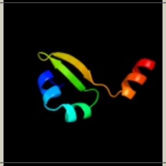
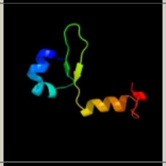
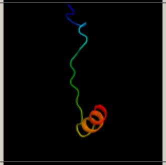
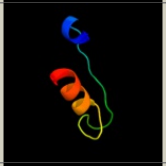
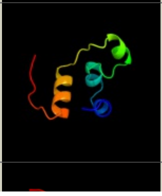
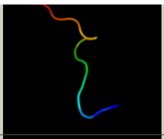
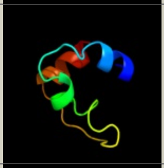
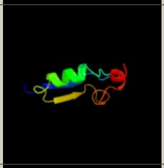
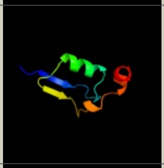
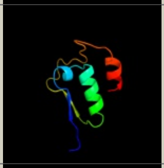
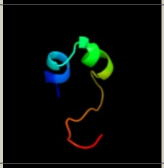
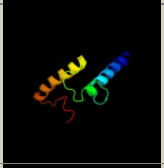
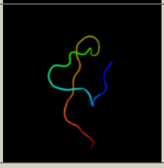
Description	Q47156
Date	Thu Jan 5 12:36:32 GMT 2012
Unique Job ID	7485cc4082b0980f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3g5oA_	Alignment		97.9	17	**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
2	c3hs2H_	Alignment		97.8	22	**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
3	d2a6qa1	Alignment		97.4	20	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
4	c2odkD_	Alignment		97.2	11	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative prevent-host-death protein from nitrosomonas europaea
5	d2odka1	Alignment		97.2	11	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
6	d2a6qb1	Alignment		97.2	20	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
7	c3hryA_	Alignment		97.1	20	**PDB header:**antitoxin **Chain:** A: **PDB Molecule:**prevent host death protein; **PDBTitle:** crystal structure of phd in a trigonal space group and partially2 disordered
8	c1f3mB_	Alignment		22.2	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak-alpha; **PDBTitle:** crystal structure of human serine/threonine kinase pak1
9	c2k9iB_	Alignment		17.2	17	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**plasmid prn1, complete sequence; **PDBTitle:** nmr structure of plasmid copy control protein orf56 from2 sulfolobus islandicus
10	c3nutC_	Alignment		16.3	25	**PDB header:**transferase **Chain:** C: **PDB Molecule:**precorrin-3 methylase; **PDBTitle:** crystal structure of the methyltransferase cobj
11	d1zcea1	Alignment		14.6	15	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like

12	c3owvA_	Alignment		14.2	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna-entry nuclease; **PDBTitle:** structural insights into catalytic and substrate binding mechanisms of2 the strategic enda nuclease from streptococcus pneumoniae
13	d3kvta_	Alignment		12.4	10	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
14	d2gbsa1	Alignment		11.7	18	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
15	c3trrA_	Alignment		11.4	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
16	c3swxB_	Alignment		11.2	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**probable enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
17	c3he2C_	Alignment		11.1	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**enoyl-coa hydratase echa6; **PDBTitle:** crystal structure of enoyl-coa hydratase from mycobacterium2 tuberculosis
18	c3gqcB_	Alignment		9.8	41	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** structure of human rev1-dna-dntp ternary complex
19	c2o18A_	Alignment		9.4	7	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**thiamine biosynthesis lipoprotein apbe; **PDBTitle:** crystal structure of a thiamine biosynthesis lipoprotein2 apbe, northeast strcutural genomics target er559
20	c3a5zF_	Alignment		9.4	18	**PDB header:**ligase **Chain:** F: **PDB Molecule:**elongation factor p; **PDBTitle:** crystal structure of escherichia coli genx in complex with elongation2 factor p
21	c1vdbA_	Alignment	not modelled	9.3	41	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fibroin-modulator-binding-protein-1; **PDBTitle:** nmr structure of fmbp-1 tandem repeat 1 in 30%(v/v) tfe2 solution
22	c3eopB_	Alignment	not modelled	9.1	16	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**thymocyte nuclear protein 1; **PDBTitle:** crystal structure of the duf55 domain of human thymocyte nuclear2 protein 1
23	d2ar1a1	Alignment	not modelled	8.7	25	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
24	c2e0kA_	Alignment	not modelled	8.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**precorrin-2 c20-methyltransferase; **PDBTitle:** crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
25	c2wjeA_	Alignment	not modelled	8.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase cpsb; **PDBTitle:** crystal structure of the tyrosine phosphatase cps4b from2 steptococcus pneumoniae tigr4.
26	c3d89A_	Alignment	not modelled	8.2	13	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rieske domain-containing protein; **PDBTitle:** crystal structure of a soluble rieske ferredoxin from mus musculus
27	c2x5fB_	Alignment	not modelled	8.1	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartate_tyrosine_phenylalanine pyridoxal-5' **PDBTitle:** crystal structure of the methicillin-resistant2 staphylococcus aureus sar2028, an3 aspartate_tyrosine_phenylalanine pyridoxal-5'-phosphate4 dependent aminotransferase
28	d2evea1	Alignment	not modelled	8.0	10	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like

29	c2fllA_	Alignment	not modelled	7.6	26	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**dna polymerase iota; **PDBTitle:** ternary complex of human dna polymerase iota with dna and dttp
30	d2o16a3	Alignment	not modelled	7.2	19	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
31	d1uiya_	Alignment	not modelled	7.2	25	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
32	c2ngrB_	Alignment	not modelled	7.2	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (gtpase activating protein (rhg)); **PDBTitle:** transition state complex for gtp hydrolysis by cdc42:2 comparisons of the high resolution structures for cdc423 bound to the active and catalytically compromised forms of4 the cdc42-gap.
33	c2kc8B_	Alignment	not modelled	7.0	29	**PDB header:**toxin/toxin repressor **Chain:** B: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of e. coli toxin rele (r81a/r83a) mutant in2 complex with antitoxin relbc (k47-l79) peptide
34	c1t3nB_	Alignment	not modelled	7.0	26	**PDB header:**replication/dna **Chain:** B: **PDB Molecule:**polymerase (dna directed) iota; **PDBTitle:** structure of the catalytic core of dna polymerase iota in2 complex with dna and dttp
35	d1qkia1	Alignment	not modelled	6.9	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
36	c2fwtA_	Alignment	not modelled	6.7	41	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**dhc, diheme cytochrome c; **PDBTitle:** crystal structure of dhc purified from rhodobacter2 sphaeroides
37	c2bb3B_	Alignment	not modelled	6.7	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cobalamin biosynthesis precorrin-6y methylase (cbie); **PDBTitle:** crystal structure of cobalamin biosynthesis precorrin-6y methylase2 (cbie) from archaeoglobus fulgidus
38	d1uxda_	Alignment	not modelled	6.6	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
39	c3lkeA_	Alignment	not modelled	6.5	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydratase from bacillus2 halodurans
40	d1t94a2	Alignment	not modelled	6.3	30	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
41	c1s97D_	Alignment	not modelled	6.3	15	**PDB header:**transferase/dna **Chain:** D: **PDB Molecule:**dna polymerase iv; **PDBTitle:** dpo4 with gt mismatch
42	c2i2rK_	Alignment	not modelled	6.2	9	**PDB header:**transport protein **Chain:** K: **PDB Molecule:**potassium voltage-gated channel subfamily d member 3; **PDBTitle:** crystal structure of the kchip1/kv4.3 t1 complex
43	d1vrma1	Alignment	not modelled	5.9	12	**Fold:**T-fold **Superfamily:**ApbE-like **Family:**ApbE-like
44	c2l7kA_	Alignment	not modelled	5.9	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein cd1104.2 from clostridium difficile,2 northeast structural genomics consortium target cfr130
45	c2q35A_	Alignment	not modelled	5.9	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**curf; **PDBTitle:** crystal structure of the y82f variant of ech2 decarboxylase domain of2 curf from lyngbya majuscula
46	c2ahpB_	Alignment	not modelled	5.9	20	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper, mutation of lys15 to epsilon-azido-lys
47	d1exbe_	Alignment	not modelled	5.8	9	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
48	c1untA_	Alignment	not modelled	5.8	38	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
49	d1xn7a_	Alignment	not modelled	5.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Hypothetical protein YhgG
50	c2ahpA_	Alignment	not modelled	5.6	20	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper, mutation of lys15 to epsilon-azido-lys
51	c3eevC_	Alignment	not modelled	5.6	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**chloramphenicol acetyltransferase; **PDBTitle:** crystal structure of chloramphenicol acetyltransferase vca0300 from2 vibrio cholerae o1 biovar eltor
52	c1ciyA_	Alignment	not modelled	5.5	14	**PDB header:**toxin **Chain:** A: **PDB Molecule:**cryia(a); **PDBTitle:** insecticidal toxin: structure and channel formation
53	c2oh2B_	Alignment	not modelled	5.4	39	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase kappa; **PDBTitle:** ternary complex of human dna polymerase
54	d1t1da_	Alignment	not modelled	5.4	9	**Fold:**POZ domain **Superfamily:**POZ domain

						Family: Tetramerization domain of potassium channels
55	c1untB_	Alignment	not modelled	5.3	38	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
56	d1zeta2	Alignment	not modelled	5.3	26	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
57	d1xata_	Alignment	not modelled	5.3	13	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
58	c1t94B_	Alignment	not modelled	5.3	39	**PDB header:**replication **Chain:** B: **PDB Molecule:**polymerase (dna directed) kappa; **PDBTitle:** crystal structure of the catalytic core of human dna2 polymerase kappa