Phyre2

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Description	Q47138
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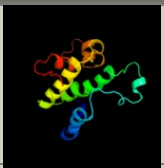
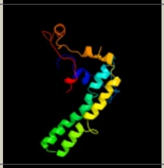
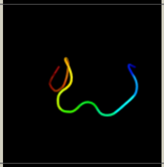
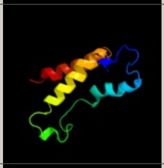
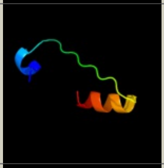
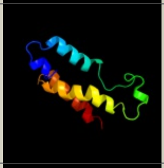
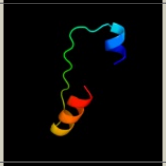
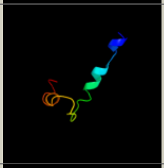
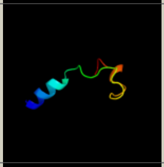
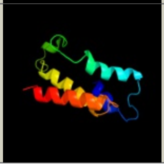
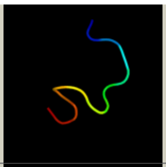
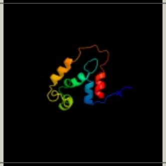
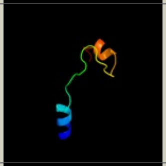
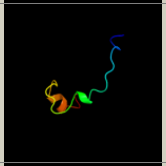
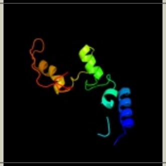
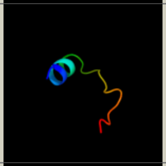
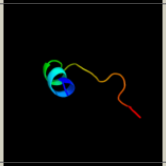
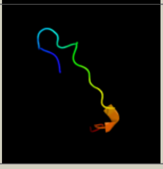
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1n7oa1	 Alignment		69.9	11	**Fold:**alpha/alpha toroid **Superfamily:**Chondroitin AC/alginate lyase **Family:**Hyaluronate lyase-like catalytic, N-terminal domain
2	d2d0ta1	 Alignment		49.8	12	**Fold:**Indolic compounds 2,3-dioxygenase-like **Superfamily:**Indolic compounds 2,3-dioxygenase-like **Family:**Indoleamine 2,3-dioxygenase-like
3	d1kyfa1	 Alignment		33.3	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Clathrin adaptor appendage domain **Family:**Alpha-adaptin ear subdomain-like
4	d1rwha1	 Alignment		32.2	10	**Fold:**alpha/alpha toroid **Superfamily:**Chondroitin AC/alginate lyase **Family:**Hyaluronate lyase-like catalytic, N-terminal domain
5	c1qysA_	 Alignment		26.2	19	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7; **PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold
6	d1f1sa1	 Alignment		23.7	5	**Fold:**alpha/alpha toroid **Superfamily:**Chondroitin AC/alginate lyase **Family:**Hyaluronate lyase-like catalytic, N-terminal domain
7	c2jvfA_	 Alignment		19.1	26	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
8	d1e85a_	 Alignment		19.0	3	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
9	d1mqva_	 Alignment		18.5	20	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
10	d2nr7a1	 Alignment		18.3	20	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**NMB1012-like
11	d1x1ia1	 Alignment		17.5	6	**Fold:**alpha/alpha toroid **Superfamily:**Chondroitin AC/alginate lyase **Family:**Hyaluronate lyase-like catalytic, N-terminal domain

12	c1ky6A_	Alignment		15.1	29	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**alpha-adaptin c; **PDBTitle:** ap-2 clathrin adaptor alpha-appendage in complex with epsin2 dpw peptide
13	c3zriA_	Alignment		13.2	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**clpb protein; **PDBTitle:** n-domain of clpv from vibrio cholerae
14	d2j8wa1	Alignment		12.5	17	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
15	d1gqaa_	Alignment		12.4	23	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
16	c2c2xB_	Alignment		11.5	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase- **PDBTitle:** three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
17	c2ckcA_	Alignment		10.7	14	**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
18	d2ckca1	Alignment		10.7	14	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
19	c1q2iA_	Alignment		10.1	20	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**pnc27; **PDBTitle:** nmr solution structure of a peptide from the mdm-2 binding2 domain of the p53 protein that is selectively cytotoxic to3 cancer cells
20	d1t57a_	Alignment		9.0	29	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
21	d1s0pa_	Alignment	not modelled	8.9	18	**Fold:**N-terminal domain of adenylylcyclase associated protein, CAP **Superfamily:**N-terminal domain of adenylylcyclase associated protein, CAP **Family:**N-terminal domain of adenylylcyclase associated protein, CAP
22	d1b6aa1	Alignment	not modelled	8.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Methionine aminopeptidase, insert domain
23	d1s05a_	Alignment	not modelled	7.9	4	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
24	d3e2ba1	Alignment	not modelled	7.2	14	**Fold:**DLC **Superfamily:**DLC **Family:**DLC
25	d2ikba1	Alignment	not modelled	6.9	10	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**NMB1012-like
26	d1hdma2	Alignment	not modelled	6.9	22	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
27	c3ajfA_	Alignment	not modelled	6.4	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** structural insigths into dsrna binding and rna silencing suppression2 by ns3 protein of rice hoja blanca tenuivirus
28	d1pwka_	Alignment	not modelled	6.3	11	**Fold:**DLC **Superfamily:**DLC **Family:**DLC

29	d1k8ia2	Alignment	not modelled	6.2	22	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
30	c2o35A_	Alignment	not modelled	6.2	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein duf1244; **PDBTitle:** protein of unknown function (duf1244) from sinorhizobium meliloti
31	d2o35a1	Alignment	not modelled	6.2	38	**Fold:**SMc04008-like **Superfamily:**SMc04008-like **Family:**SMc04008-like
32	d1u69a_	Alignment	not modelled	6.1	44	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**3-demethylubiquinone-9 3-methyltransferase
33	d1vkma_	Alignment	not modelled	6.1	25	**Fold:**Indigoidine synthase A-like **Superfamily:**Indigoidine synthase A-like **Family:**Indigoidine synthase A-like
34	d2f53d2	Alignment	not modelled	6.0	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
35	d1cmia_	Alignment	not modelled	5.8	11	**Fold:**DLC **Superfamily:**DLC **Family:**DLC
36	d1vp8a_	Alignment	not modelled	5.8	21	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
37	d2bnqd2	Alignment	not modelled	5.8	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
38	d1cpqa_	Alignment	not modelled	5.7	13	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
39	c3fybA_	Alignment	not modelled	5.5	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein of unknown function (duf1244); **PDBTitle:** crystal structure of a protein of unknown function (duf1244) from2 alcanivorax borkumensis
40	d2foka4	Alignment	not modelled	5.3	17	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease FokI, C-terminal (catalytic) domain
41	c2vuxB_	Alignment	not modelled	5.2	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ribonucleoside-diphosphate reductase subunit m2 b; **PDBTitle:** human ribonucleotide reductase, subunit m2 b