Phyre2

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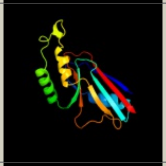
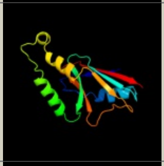
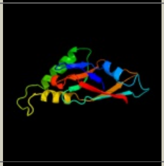
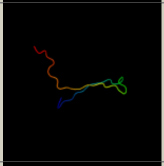
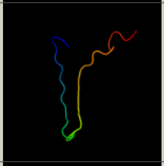
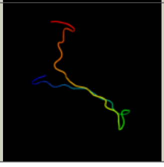
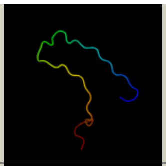
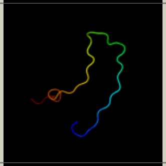
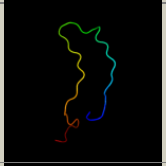
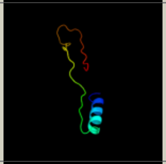
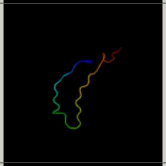
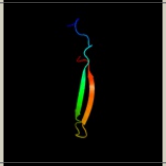
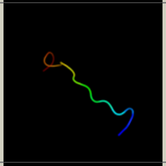
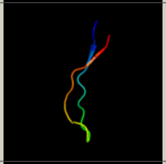
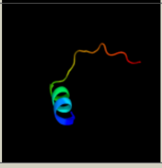
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2p6cB_	Alignment		100.0	26	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**aq_2013 protein; **PDBTitle:** crystal structure of hypothetical protein aq_2013 from aquifex2 aeolicus vf5.
2	d1vmja_	Alignment		100.0	27	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
3	d1vpha_	Alignment		100.0	23	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
4	c1ve0A_	Alignment		100.0	27	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein (st2072); **PDBTitle:** crystal structure of uncharacterized protein st2072 from sulfolobus2 tokodaii
5	c2p6hB_	Alignment		100.0	26	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of hypothetical protein ape1520 from aeropyrum2 pernix k1
6	d1vmfa_	Alignment		100.0	28	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
7	d1vmha_	Alignment		100.0	29	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
8	c2cu5C_	Alignment		100.0	27	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**conserved hypothetical protein tt1486; **PDBTitle:** crystal structure of the conserved hypothetical protein tt1486 from2 thermus thermophilus hb8
9	d1ojja_	Alignment		44.4	17	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolase family 7 catalytic core
10	c2rfyB_	Alignment		40.6	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cellulose 1,4-beta-cellobiosidase; **PDBTitle:** crystal structure of cellobiohydrolase from melanocarpus2 albomyces complexed with cellobiose
11	d1gpia_	Alignment		40.6	17	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolase family 7 catalytic core

12	d1q9ha_	Alignment		36.7	14	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolase family 7 catalytic core
13	d3ovwa_	Alignment		35.3	23	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolase family 7 catalytic core
14	d2v3ia1	Alignment		35.3	17	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolase family 7 catalytic core
15	d1f06a2	Alignment		30.3	15	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
16	d1egla_	Alignment		28.9	17	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolase family 7 catalytic core
17	c2kmcA_	Alignment		24.1	14	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**fermitin family homolog 1; **PDBTitle:** solution structure of the n-terminal domain of kindlin-1
18	d2qmwa2	Alignment		18.6	0	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
19	c3hi2D_	Alignment		14.3	11	**PDB header:**dna binding protein/toxin **Chain:** D: **PDB Molecule:**motility quorum-sensing regulator mqsr; **PDBTitle:** structure of the n-terminal domain of the e. coli antitoxin mqsa2 (ygit/b3021) in complex with the e. coli toxin mqsr (ygiu/b3022)
20	c2l57A_	Alignment		13.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
21	d2j0pa1	Alignment	not modelled	11.9	10	**Fold:**Heme iron utilization protein-like **Superfamily:**Heme iron utilization protein-like **Family:**HemS/ChuS-like
22	c2qmwA_	Alignment	not modelled	11.2	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of the prephenate dehydratase (pdt) from2 staphylococcus aureus subsp. aureus mu50
23	d2drpa2	Alignment	not modelled	10.7	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
24	d1phza1	Alignment	not modelled	10.5	0	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
25	d2hq2a1	Alignment	not modelled	10.2	10	**Fold:**Heme iron utilization protein-like **Superfamily:**Heme iron utilization protein-like **Family:**HemS/ChuS-like
26	c3luyA_	Alignment	not modelled	10.1	6	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable chorismate mutase; **PDBTitle:** putative chorismate mutase from bifidobacterium adolescentis
27	d1rkea1	Alignment	not modelled	10.0	24	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
28	d1j5ya2	Alignment	not modelled	9.7	10	**Fold:**HPr-like **Superfamily:**Putative transcriptional regulator TM1602, C-terminal domain **Family:**Putative transcriptional regulator TM1602, C-terminal domain

29	c3m45D_	Alignment	not modelled	9.6	13	**PDB header:**cell adhesion **Chain:** D: **PDB Molecule:**cell adhesion molecule 2; **PDBTitle:** crystal structure of ig1 domain of mouse syncam 2
30	c3mwbA_	Alignment	not modelled	8.9	6	**PDB header:**lyase **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a
31	d1i8fa_	Alignment	not modelled	7.8	6	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
32	d1cl1a_	Alignment	not modelled	7.6	33	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
33	d1n8ia_	Alignment	not modelled	7.3	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Malate synthase G **Family:**Malate synthase G
34	c3gqqD_	Alignment	not modelled	6.8	17	**PDB header:**splicing **Chain:** D: **PDB Molecule:**protein unc-119 homolog a; **PDBTitle:** crystal structure of the human retinal protein 4 (unc-1192 homolog a). northeast structural genomics consortium3 target hr3066a
35	d1t01a1	Alignment	not modelled	6.7	21	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
36	d1rutx4	Alignment	not modelled	5.9	30	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
37	c3i38L_	Alignment	not modelled	5.2	24	**PDB header:**chaperone **Chain:** L: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578