Phyre2

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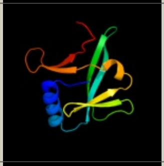
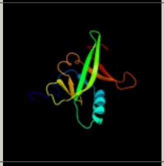
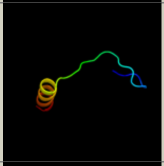
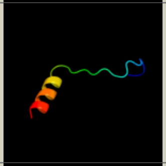
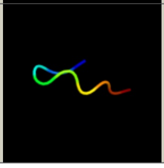
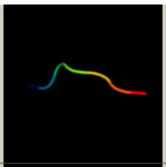
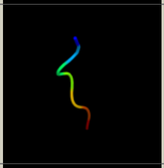
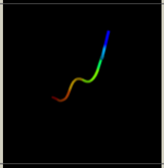
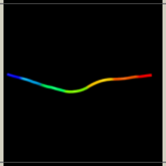
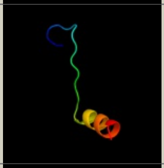
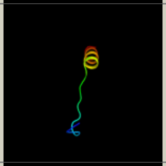
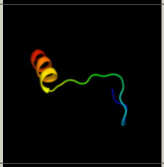
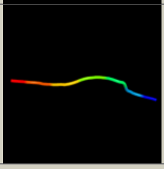
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2d2aA_	Alignment		100.0	100	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**sufa protein; **PDBTitle:** crystal structure of escherichia coli sufa involved in2 biosynthesis of iron-sulfur clusters
2	c2apnA_	Alignment		100.0	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein hi1723; **PDBTitle:** hi1723 solution structure
3	c1x0gA_	Alignment		100.0	35	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**isca; **PDBTitle:** crystal structure of isca with the [2fe-2s] cluster
4	d1s98a_	Alignment		100.0	44	**Fold:**HesB-like domain **Superfamily:**HesB-like domain **Family:**HesB-like domain
5	c2k4zA_	Alignment		100.0	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dsrr; **PDBTitle:** solution nmr structure of allochromatium vinosum dsrr:2 northeast structural genomics consortium target op5
6	d1nwba_	Alignment		99.9	26	**Fold:**HesB-like domain **Superfamily:**HesB-like domain **Family:**HesB-like domain
7	d2p2ea1	Alignment		98.7	14	**Fold:**HesB-like domain **Superfamily:**HesB-like domain **Family:**HesB-like domain
8	c2qgoA_	Alignment		98.4	9	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative fe-s biosynthesis protein; **PDBTitle:** crystal structure of a putative fe-s biosynthesis protein from2 lactobacillus acidophilus
9	c3pm7A_	Alignment		33.8	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of ef_3132 protein from enterococcus faecalis at the2 resolution 2a, northeast structural genomics consortium target efr184
10	d2frha1	Alignment		23.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
11	d1sp2a_	Alignment		21.1	44	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2

12	d1zfda_	Alignment		18.1	43	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
13	d1a1ia1	Alignment		16.5	29	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
14	d2glia3	Alignment		16.4	43	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
15	d1aaya1	Alignment		15.6	29	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
16	d1p4xa1	Alignment		15.6	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
17	d1ubdc3	Alignment		15.2	57	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
18	d1p4xa2	Alignment		15.2	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
19	c3obhA_	Alignment		14.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** x-ray crystal structure of protein sp_0782 (7-79) from streptococcus2 pneumoniae. northeast structural genomics consortium target spr104
20	d1a1ha1	Alignment		14.7	29	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
21	d1f2ig1	Alignment	not modelled	14.6	33	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
22	d1hsja1	Alignment	not modelled	14.2	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
23	d1a1ga1	Alignment	not modelled	14.2	29	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
24	c2kvfA_	Alignment	not modelled	14.1	38	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger and btb domain-containing protein 32; **PDBTitle:** structure of the three-cys2his2 domain of mouse testis zinc2 finger protein
25	c1p4xA_	Alignment	not modelled	13.8	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**staphylococcal accessory regulator a homologue; **PDBTitle:** crystal structure of sars protein from staphylococcus aureus
26	d1tf3a2	Alignment	not modelled	13.8	43	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
27	d1u86a1	Alignment	not modelled	11.7	44	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
28	d1vsra_	Alignment	not modelled	10.7	17	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Very short patch repair (VSR) endonuclease

29	d1l7da2	Alignment	not modelled	10.0	20	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**L-alanine dehydrogenase-like
30	d1ncsa_	Alignment	not modelled	10.0	43	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
31	d2dlka2	Alignment	not modelled	9.7	57	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
32	c1bcrA_	Alignment	not modelled	9.7	15	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**serine carboxypeptidase ii; **PDBTitle:** complex of the wheat serine carboxypeptidase, cpdw-ii, with the2 microbial peptide aldehyde inhibitor, antipain, and arginine at room3 temperature
33	d2yt9a1	Alignment	not modelled	9.6	43	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
34	d2h85a2	Alignment	not modelled	9.5	29	**Fold:**EndoU-like **Superfamily:**EndoU-like **Family:**Nsp15 C-terminal domain-like
35	c3me5A_	Alignment	not modelled	9.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cytosine-specific methyltransferase; **PDBTitle:** crystal structure of putative dna cytosine methylase from shigella2 flexneri 2a str. 301
36	c2kdxA_	Alignment	not modelled	9.3	26	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
37	c2ab3A_	Alignment	not modelled	9.3	67	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**znf29; **PDBTitle:** solution structures and characterization of hiv rre iib rna2 targeting zinc finger proteins
38	d1x6ea2	Alignment	not modelled	9.0	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
39	c2yujA_	Alignment	not modelled	9.0	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation 1-like; **PDBTitle:** solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1
40	d1rp0a1	Alignment	not modelled	8.8	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Thi4-like
41	c1zc1A_	Alignment	not modelled	8.5	23	**PDB header:**protein turnover **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation protein 1; **PDBTitle:** ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites
42	c3a44D_	Alignment	not modelled	8.3	17	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
43	c1va1A_	Alignment	not modelled	8.2	57	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor sp1; **PDBTitle:** solution structure of transcription factor sp1 dna binding2 domain (zinc finger 1)
44	d1jj7a_	Alignment	not modelled	8.0	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
45	c3c3jA_	Alignment	not modelled	7.9	38	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of tagatose-6-phosphate ketose/aldose isomerase from2 escherichia coli
46	c1znmA_	Alignment	not modelled	7.8	38	**PDB header:**zinc finger **Chain:** A: **PDB Molecule:**yy1; **PDBTitle:** a zinc finger with an artificial beta-turn, original2 sequence taken from the third zinc finger domain of the3 human transcriptional repressor protein yy1 (ying and yang4 1, a delta transcription factor), nmr, 34 structures
47	d1wgea1	Alignment	not modelled	7.7	40	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
48	c3odpA_	Alignment	not modelled	7.1	38	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of a putative tagatose-6-phosphate ketose/aldose2 isomerase (nt01cx_0292) from clostridium novyi nt at 2.35 a3 resolution
49	c2qrlA_	Alignment	not modelled	7.1	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase, nad+, l-lysine- **PDBTitle:** crystal structure of oxalylglycine-bound saccharopine2 dehydrogenase (l-lys forming) from saccharomyces cerevisiae
50	d1wmia1	Alignment	not modelled	7.1	7	**Fold:**RelE-like **Superfamily:**RelE-like **Family:**RelE-like
51	c2nq2C_	Alignment	not modelled	7.0	16	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**hypothetical abc transporter atp-binding protein **PDBTitle:** an inward-facing conformation of a putative metal-chelate2 type abc transporter.
52	c3g5oC_	Alignment	not modelled	6.9	20	**PDB header:**toxin/antitoxin **Chain:** C: **PDB Molecule:**uncharacterized protein rv2866; **PDBTitle:** the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
						PDB header:lyase

53	c1gxsC_	Alignment	not modelled	6.7	18	**Chain:** C: **PDB Molecule:**p-(s)-hydroxymandelonitrile lyase chain a; **PDBTitle:** crystal structure of hydroxynitrile lyase from sorghum2 bicolor in complex with inhibitor benzoic acid: a novel3 cyanogenic enzyme
54	d2cota1	Alignment	not modelled	6.6	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
55	c3nbbC_	Alignment	not modelled	6.5	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**peroxisomal primary amine oxidase; **PDBTitle:** crystal structure of mutant y305f expressed in e. coli in the copper2 amine oxidase from hansenula polymorpha
56	c2entA_	Alignment	not modelled	6.0	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**krueppel-like factor 15; **PDBTitle:** solution structure of the second c2h2-type zinc finger2 domain from human krueppel-like factor 15
57	c1ekmC_	Alignment	not modelled	5.8	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**copper amine oxidase; **PDBTitle:** crystal structure at 2.5 a resolution of zinc-substituted2 copper amine oxidase of hansenula polymorpha expressed in3 escherichia coli
58	d2bs2b2	Alignment	not modelled	5.8	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
59	d2fbia1	Alignment	not modelled	5.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
60	d1ywsa1	Alignment	not modelled	5.7	40	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
61	d1qabe_	Alignment	not modelled	5.6	24	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
62	d1kt7a_	Alignment	not modelled	5.5	16	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
63	d1jgsa_	Alignment	not modelled	5.5	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
64	d2cota2	Alignment	not modelled	5.4	67	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
65	c2ayuA_	Alignment	not modelled	5.4	10	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**nucleosome assembly protein; **PDBTitle:** the structure of nucleosome assembly protein suggests a mechanism for2 histone binding and shuttling
66	d2ayua1	Alignment	not modelled	5.4	10	**Fold:**NAP-like **Superfamily:**NAP-like **Family:**NAP-like
67	c3g3zA_	Alignment	not modelled	5.3	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
68	d1a1ia3	Alignment	not modelled	5.3	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
69	c3h5jA_	Alignment	not modelled	5.2	60	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** leud_1-168 small subunit of isopropylmalate isomerase (rv2987c) from2 mycobacterium tuberculosis
70	c3o2eA_	Alignment	not modelled	5.1	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**bola-like protein; **PDBTitle:** crystal structure of a bol-like protein from babesia bovis
71	d1u85a1	Alignment	not modelled	5.1	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2