Phyre^2

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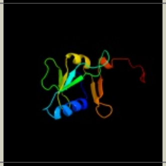
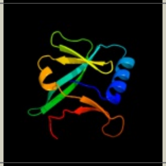
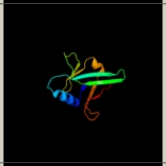
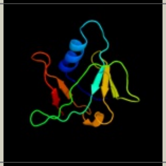
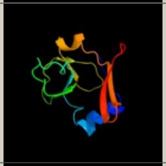
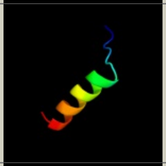
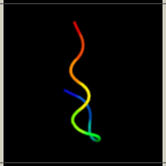
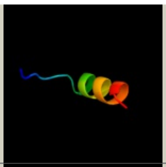
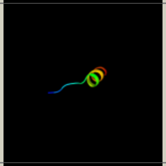
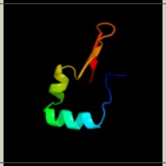
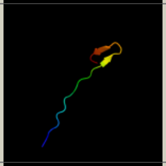
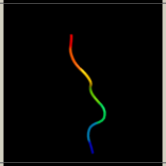
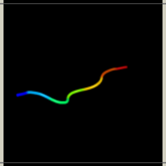
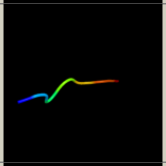
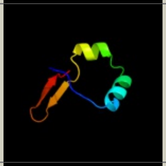
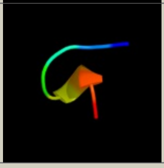
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2d2aA_	Alignment		100.0	47	**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	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein hi1723; **PDBTitle:** hi1723 solution structure
3	c1x0gA_	Alignment		100.0	31	**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	99	**Fold:**HesB-like domain **Superfamily:**HesB-like domain **Family:**HesB-like domain
5	c2k4zA_	Alignment		100.0	31	**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		100.0	33	**Fold:**HesB-like domain **Superfamily:**HesB-like domain **Family:**HesB-like domain
7	d2p2ea1	Alignment		98.9	19	**Fold:**HesB-like domain **Superfamily:**HesB-like domain **Family:**HesB-like domain
8	c2qgoA_	Alignment		98.7	15	**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	d2a6sa1	Alignment		19.1	10	**Fold:**RelE-like **Superfamily:**RelE-like **Family:**YoeB/Txe-like
10	d1sp2a_	Alignment		12.6	44	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
11	d1zfda_	Alignment		10.6	43	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2

12	c3kxeD_	Alignment		10.5	28	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**antitoxin protein pard-1; **PDBTitle:** a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
13	c3g5oC_	Alignment		10.0	13	**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
14	c2yujA_	Alignment		9.9	33	**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
15	c2kdxA_	Alignment		9.5	22	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
16	d1a1ia1	Alignment		9.4	29	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
17	d1aaya1	Alignment		9.0	29	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
18	d1ubdc3	Alignment		8.8	57	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
19	c1zc1A_	Alignment		8.7	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
20	c3c3jA_	Alignment		8.7	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
21	d1a1ha1	Alignment	not modelled	8.6	29	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
22	d1lk5a2	Alignment	not modelled	8.2	24	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
23	d1a1ga1	Alignment	not modelled	8.2	29	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
24	d1f2ig1	Alignment	not modelled	8.1	38	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
25	d1tf3a2	Alignment	not modelled	7.8	43	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
26	d1u86a1	Alignment	not modelled	7.8	29	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
27	d1wgea1	Alignment	not modelled	7.7	40	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
28	c3odpA_	Alignment	not modelled	7.5	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

29	c3a44D_	Alignment	not modelled	7.5	12	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
30	c2kvfA_	Alignment	not modelled	7.3	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
31	d1adta2	Alignment	not modelled	6.7	27	**Fold:**Zn-binding domains of ADDBP **Superfamily:**Zn-binding domains of ADDBP **Family:**Zn-binding domains of ADDBP
32	c2wh44_	Alignment	not modelled	6.6	80	**PDB header:**ribosome **Chain:** 4: **PDB Molecule:**50s ribosomal protein l31; **PDBTitle:** insights into translational termination from the structure2 of rf2 bound to the ribosome
33	c1gxsC_	Alignment	not modelled	6.6	14	**PDB header:**lyase **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
34	d1wmia1	Alignment	not modelled	6.4	0	**Fold:**RelE-like **Superfamily:**RelE-like **Family:**RelE-like
35	c2ab3A_	Alignment	not modelled	6.2	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
36	c3f1f4_	Alignment	not modelled	6.0	80	**PDB header:**ribosome **Chain:** 4: **PDB Molecule:**50s ribosomal protein l31; **PDBTitle:** crystal structure of a translation termination complex2 formed with release factor rf2. this file contains the 50s3 subunit of one 70s ribosome. the entire crystal structure4 contains two 70s ribosomes as described in remark 400.
37	d1m0sa2	Alignment	not modelled	6.0	22	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
38	d2h85a2	Alignment	not modelled	5.8	29	**Fold:**EndoU-like **Superfamily:**EndoU-like **Family:**Nsp15 C-terminal domain-like
39	d1ncsa_	Alignment	not modelled	5.7	43	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
40	d1u8sa1	Alignment	not modelled	5.6	32	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
41	d1qabe_	Alignment	not modelled	5.5	24	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
42	d1ywsa1	Alignment	not modelled	5.5	44	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
43	d2ayua1	Alignment	not modelled	5.4	27	**Fold:**NAP-like **Superfamily:**NAP-like **Family:**NAP-like
44	c2ayuA_	Alignment	not modelled	5.4	27	**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
45	c1bcrA_	Alignment	not modelled	5.3	20	**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
46	d2yt9a1	Alignment	not modelled	5.3	43	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
47	c3q3wB_	Alignment	not modelled	5.3	60	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** isopropylmalate isomerase small subunit from campylobacter jejuni.
48	c2hcuA_	Alignment	not modelled	5.3	60	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** crystal structure of smu.1381 (or leud) from streptococcus2 mutans
49	d1x6ea2	Alignment	not modelled	5.2	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
50	d2dlka2	Alignment	not modelled	5.2	57	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
51	d2glia3	Alignment	not modelled	5.1	29	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
52	c3kxeB_	Alignment	not modelled	5.1	24	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**toxin protein pare-1; **PDBTitle:** a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex