Phyre^2

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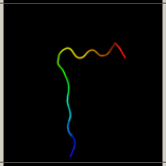
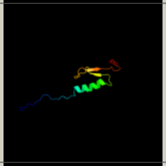
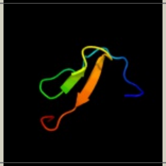
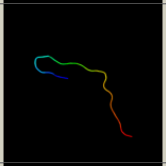
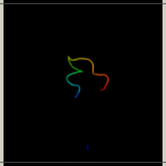
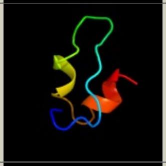
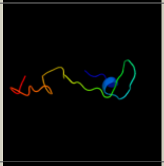
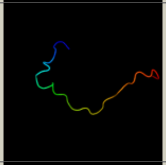
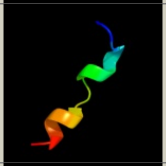
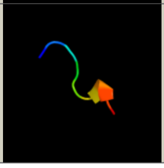
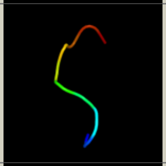
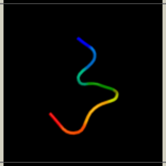
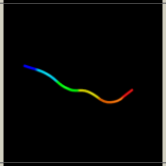
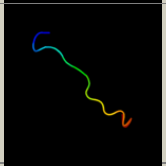
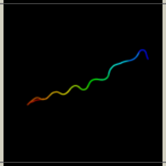
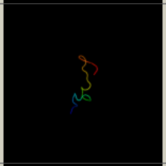
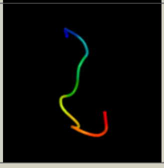
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bk7A_	Alignment		30.9	60	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**abc transporter atp-binding protein; **PDBTitle:** structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abysii
2	c2abyA_	Alignment		17.5	40	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ta0743; **PDBTitle:** solution structure of ta0743 from thermoplasma acidophilum
3	c2hlwA_	Alignment		17.1	16	**PDB header:**ligase, signaling protein **Chain:** A: **PDB Molecule:**ubiquitin-conjugating enzyme e2 variant 1; **PDBTitle:** solution structure of the human ubiquitin-conjugating2 enzyme variant uev1a
4	c1gthD_	Alignment		15.6	23	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
5	c2kvoA_	Alignment		15.4	32	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**photosystem ii reaction center psb28 protein; **PDBTitle:** solution nmr structure of photosystem ii reaction center psb28 protein2 from synechocystis sp.(strain pcc 6803), northeast structural3 genomics consortium target sgr171
6	c2gksB_	Alignment		13.9	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional sat/aps kinase; **PDBTitle:** crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
7	d3gata_	Alignment		12.7	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
8	c3u1xA_	Alignment		10.7	39	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycosyl hydrolase; **PDBTitle:** crystal structure of a putative glycosyl hydrolase (bdi_1869) from2 parabacteroides distasonis atcc 8503 at 1.70 a resolution
9	d2bs2b1	Alignment		9.8	24	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
10	c2kslA_	Alignment		9.8	38	**PDB header:**toxin **Chain:** A: **PDB Molecule:**u1-agatoxin-ta1a; **PDBTitle:** structure of the insecticidal toxin taitx-1
11	c1wsoA_	Alignment		9.4	78	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**orexin-a; **PDBTitle:** the solution structures of human orexin-a

12	c2kaeA_	Alignment		9.3	17	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**gata-type transcription factor; **PDBTitle:** data-driven model of med1:dna complex
13	c2gmhA_	Alignment		9.1	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**electron transfer flavoprotein-ubiquinone **PDBTitle:** structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
14	d1sj1a_	Alignment		9.0	30	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
15	c2nsvA_	Alignment		8.6	63	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**mating pheromone en-1; **PDBTitle:** nmr solution structure of the pheromone en-1
16	c3dnlG_	Alignment		8.5	67	**PDB header:**viral protein **Chain:** G: **PDB Molecule:**hiv-1 envelope glycoprotein gp120; **PDBTitle:** molecular structure for the hiv-1 gp120 trimer in the b12-2 bound state
17	d1nekb1	Alignment		8.4	38	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
18	c2rpvA_	Alignment		8.3	44	**PDB header:**immune system **Chain:** A: **PDB Molecule:**immunoglobulin g-binding protein g; **PDBTitle:** solution structure of gb1 with lbt probe
19	c3ivuB_	Alignment		8.1	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
20	d1fxra_	Alignment		8.0	30	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
21	d1lwha1	Alignment	not modelled	7.7	30	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
22	c2w3rG_	Alignment	not modelled	7.7	21	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**xanthine dehydrogenase; **PDBTitle:** crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine
23	d1xera_	Alignment	not modelled	7.6	44	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Archaeal ferredoxins
24	d1iw4a_	Alignment	not modelled	7.4	32	**Fold:**Kazal-type serine protease inhibitors **Superfamily:**Kazal-type serine protease inhibitors **Family:**Ovomucoid domain III-like
25	d7fd1a_	Alignment	not modelled	6.9	30	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
26	d2cm5a1	Alignment	not modelled	6.8	29	**Fold:**C2 domain-like **Superfamily:**C2 domain (Calcium/lipid-binding domain, CaLB) **Family:**Synaptotagmin-like (S variant)
27	d2vuti1	Alignment	not modelled	6.7	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
28	d2dlqa2	Alignment	not modelled	6.6	45	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
29	d5gata_	Alignment	not modelled	6.5	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain)

						Family: Erythroid transcription factor GATA-1
30	c1dwlA_	Alignment	not modelled	6.5	40	**PDB header:**electron transfer **Chain:** A: **PDB Molecule:**ferredoxin i; **PDBTitle:** the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
31	c1s6wA_	Alignment	not modelled	6.4	83	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**hepcidin; **PDBTitle:** solution structure of hybrid white striped bass hepcidin
32	c2xglB_	Alignment	not modelled	6.4	31	**PDB header:**antibiotic **Chain:** B: **PDB Molecule:**colicin-m immunity protein; **PDBTitle:** the x-ray structure of the escherichia coli colicin m immunity2 protein demonstrates the presence of a disulphide bridge, which is3 functionally essential
33	d1y0ja1	Alignment	not modelled	6.0	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
34	d1zata1	Alignment	not modelled	5.9	17	**Fold:**L,D-transpeptidase catalytic domain-like **Superfamily:**L,D-transpeptidase catalytic domain-like **Family:**L,D-transpeptidase catalytic domain-like
35	c1t4vL_	Alignment	not modelled	5.8	40	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** L: **PDB Molecule:**prothrombin; **PDBTitle:** crystal structure analysis of a novel oxyguanidine bound to thrombin
36	c3c27A_	Alignment	not modelled	5.8	40	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**thrombin light chain; **PDBTitle:** cyanofluorophenylacetamides as orally efficacious thrombin inhibitors
37	c2r2mA_	Alignment	not modelled	5.8	40	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**thrombin light chain; **PDBTitle:** 2-(2-chloro-6-fluorophenyl)acetamides as potent thrombin inhibitors
38	c1t4uL_	Alignment	not modelled	5.8	40	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** L: **PDB Molecule:**prothrombin; **PDBTitle:** crystal structure analysis of a novel oxyguanidine bound to thrombin
39	d2fug91	Alignment	not modelled	5.8	57	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
40	c2fugG_	Alignment	not modelled	5.8	57	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**nadh-quinone oxidoreductase chain 9; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
41	d1bc6a_	Alignment	not modelled	5.8	40	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
42	c1m8pB_	Alignment	not modelled	5.7	38	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfate adenylyltransferase; **PDBTitle:** crystal structure of p. chrysogenum atp sulfurylase in the t-state
43	c2c3yA_	Alignment	not modelled	5.6	63	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase; **PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
44	d1xeba_	Alignment	not modelled	5.6	21	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
45	d2c42a5	Alignment	not modelled	5.5	50	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
46	d2it9a1	Alignment	not modelled	5.5	29	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**PMN2A0962/syc2379c-like
47	d1h98a_	Alignment	not modelled	5.5	44	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
48	d1gnfa_	Alignment	not modelled	5.4	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
49	c1p8vB_	Alignment	not modelled	5.4	40	**PDB header:**membrane protein/hydrolase **Chain:** B: **PDB Molecule:**prothrombin; **PDBTitle:** crystal structure of the complex of platelet receptor gpib-alpha and2 alpha-thrombin at 2.6a
50	d1gtea5	Alignment	not modelled	5.4	50	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
51	d1iqza_	Alignment	not modelled	5.2	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
52	c1g8gB_	Alignment	not modelled	5.2	38	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfate adenylyltransferase; **PDBTitle:** atp sulfurylase from s. cerevisiae: the binary product complex with2 aps
53	d2nvna1	Alignment	not modelled	5.1	29	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**PMN2A0962/syc2379c-like
54	d1pcfa_	Alignment	not modelled	5.1	18	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**Transcriptional coactivator PC4 C-terminal domain
55	c3immC_	Alignment	not modelled	5.1	31	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative secreted glycosylhydrolase; **PDBTitle:** crystal structure of putative glycosyl hydrolase (yp_001301887.1) from2 parabacteroides distasonis atcc 8503 at 2.00 a resolution

56	d1hfel2	Alignment	not modelled	5.1	50	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
57	c2kvfA_	Alignment	not modelled	5.1	50	**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