Phyre2

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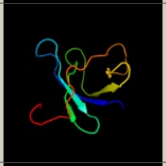
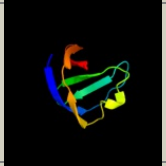
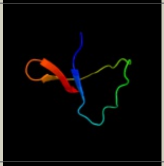
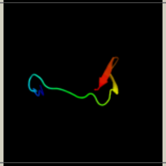
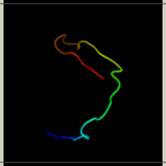
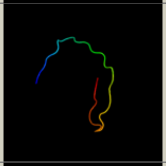
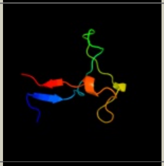
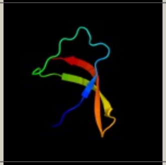
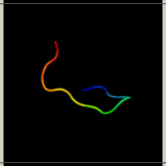
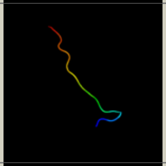
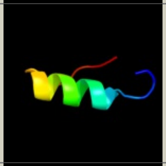
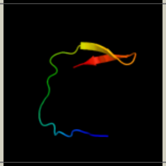
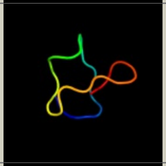
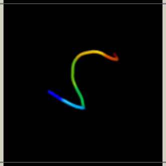
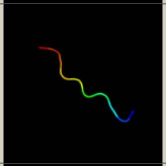
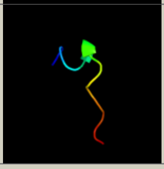
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jsoA_	Alignment		96.9	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**polymyxin resistance protein pmrd; **PDBTitle:** antimicrobial resistance protein
2	c2rqxA_	Alignment		96.7	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**polymyxin b resistance protein; **PDBTitle:** solution nmr structure of pmrd from klebsiella pneumoniae
3	c2k75A_	Alignment		59.1	7	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein ta0387; **PDBTitle:** solution nmr structure of the ob domain of ta0387 from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar80b.
4	c2kenA_	Alignment		35.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of the ob domain (residues 67-166)2 of mm0293 from methanosarcina mazei. northeast structural3 genomics consortium target mar214a.
5	d1giqa2	Alignment		27.9	17	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
6	d1r45a_	Alignment		25.3	21	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
7	c3bw8B_	Alignment		25.0	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mono-adp-ribosyltransferase c3; **PDBTitle:** crystal structure of the clostridium limosum c3 exoenzyme
8	c1xzzA_	Alignment		24.7	22	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**inositol 1,4,5-trisphosphate receptor type 1; **PDBTitle:** crystal structure of the ligand binding suppressor domain of type 12 inositol 1,4,5-trisphosphate receptor
9	c3dm3A_	Alignment		23.7	11	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication factor a; **PDBTitle:** crystal structure of a domain of a replication factor a2 protein, from methanocaldococcus jannaschii. northeast3 structural genomics target mjr118e
10	d1y0jb1	Alignment		20.5	38	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**C2HC finger
11	d1o7ia_	Alignment		18.8	10	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB

12	c2k9oA_	Alignment		18.2	36	**PDB header:**toxin **Chain:** A: **PDB Molecule:**vm24 scorpion toxin; **PDBTitle:** solution structure of vm24 synthetic scorpion toxin
13	d1wdia_	Alignment		18.1	38	**Fold:**QueA-like **Superfamily:**QueA-like **Family:**QueA-like
14	c2b68A_	Alignment		17.6	36	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**defensin; **PDBTitle:** solution structure of the recombinant crassostrea gigas2 defensin
15	d1giqa1	Alignment		17.2	17	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
16	c1hvwA_	Alignment		16.2	30	**PDB header:**toxin **Chain:** A: **PDB Molecule:**omega-atracotoxin-hv1a; **PDBTitle:** hairpinless mutant of omega-atracotoxin-hv1a
17	d1hvwa_	Alignment		16.2	30	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
18	c2k6uA_	Alignment		16.0	57	**PDB header:**hormone **Chain:** A: **PDB Molecule:**insulin-like 3 a chain; **PDBTitle:** the solution structure of a conformationally restricted2 fully active derivative of the human relaxin-like factor3 (rlf)
19	d2apja1	Alignment		15.9	40	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Putative acetylxylan esterase-like
20	c1i4oC_	Alignment		15.1	12	**PDB header:**apoptosis/hydrolase **Chain:** C: **PDB Molecule:**baculoviral iap repeat-containing protein 4; **PDBTitle:** crystal structure of the xiap/caspase-7 complex
21	d1vkya_	Alignment	not modelled	14.6	31	**Fold:**QueA-like **Superfamily:**QueA-like **Family:**QueA-like
22	d1bx7a_	Alignment	not modelled	14.0	42	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Huristasin-like
23	d1yq2a5	Alignment	not modelled	13.8	6	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
24	d1zmba1	Alignment	not modelled	13.5	30	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Putative acetylxylan esterase-like
25	c3u0jB_	Alignment	not modelled	13.3	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**type iii effector hopu1; **PDBTitle:** crystal structure of adp-ribosyltransferase hopu1 of pseudomonas2 syringae pv. tomato dc3000
26	d1fmta1	Alignment	not modelled	13.0	25	**Fold:**FMT C-terminal domain-like **Superfamily:**FMT C-terminal domain-like **Family:**Post formyltransferase domain
27	c1yy3A_	Alignment	not modelled	12.8	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**s-adenosylmethionine:trna ribosyltransferase- **PDBTitle:** structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea)
28	d1rm6c2	Alignment	not modelled	12.1	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
						Fold: Knottins (small inhibitors, toxins, lectins)

29	d1skza1	Alignment	not modelled	12.1	38	**Superfamily:**Leech antihemostatic proteins **Family:**Huristasin-like
30	d1iray2	Alignment	not modelled	11.4	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
31	d1l7la_	Alignment	not modelled	11.3	40	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**PA-IL, galactose-binding lectin 1
32	c2gwmA_	Alignment	not modelled	10.9	13	**PDB header:**transferase, toxin **Chain:** A: **PDB Molecule:**65 kda virulence protein; **PDBTitle:** crystal structure of the salmonella spvb atr domain
33	d1qs1a1	Alignment	not modelled	10.9	13	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
34	d1ejab_	Alignment	not modelled	10.4	31	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Huristasin-like
35	d1hmja_	Alignment	not modelled	10.2	8	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
36	c2yuzA_	Alignment	not modelled	10.0	11	**PDB header:**immune system **Chain:** A: **PDB Molecule:**myosin-binding protein c, slow-type; **PDBTitle:** solution structure of 4th immunoglobulin domain of slow2 type myosin-binding protein c
37	c2bovB_	Alignment	not modelled	9.9	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mono-adp-ribosyltransferase c3; **PDBTitle:** molecular recognition of an adp-ribosylating clostridium2 botulinum c3 exoenzyme by rala gtpase
38	d1dzfa2	Alignment	not modelled	9.8	15	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
39	d1eika_	Alignment	not modelled	9.3	15	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
40	d1wjja_	Alignment	not modelled	9.2	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
41	c3gabC_	Alignment	not modelled	8.7	50	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dna mismatch repair protein mutl; **PDBTitle:** c-terminal domain of bacillus subtilis mutl crystal form i
42	c1z0zC_	Alignment	not modelled	8.6	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**probable inorganic polyphosphate/atp-nad kinase; **PDBTitle:** crystal structure of a nad kinase from archaeoglobus2 fulgidus in complex with nad
43	d1z0sa1	Alignment	not modelled	8.6	14	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
44	c2h6oA_	Alignment	not modelled	8.6	26	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**major outer envelope glycoprotein gp350; **PDBTitle:** epstein barr virus major envelope glycoprotein
45	d1axha_	Alignment	not modelled	8.5	27	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
46	c3pt5A_	Alignment	not modelled	8.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nans (yjhs), a 9-o-acetyl n-acetylneuraminic acid esterase; **PDBTitle:** crystal structure of nans
47	d1ojqa_	Alignment	not modelled	8.3	27	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
48	c2cpcA_	Alignment	not modelled	8.2	6	**PDB header:**immune system **Chain:** A: **PDB Molecule:**kiaa0657 protein; **PDBTitle:** solution structure of rsgi ruh-030, an ig like domain from2 human cdna
49	c3bg4D_	Alignment	not modelled	8.1	38	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** D: **PDB Molecule:**guamerin; **PDBTitle:** the crystal structure of guamerin in complex with2 chymotrypsin and the development of an elastase-specific3 inhibitor
50	d1tdha3	Alignment	not modelled	7.9	43	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
51	c1wc6B_	Alignment	not modelled	7.9	28	**PDB header:**lyase **Chain:** B: **PDB Molecule:**adenylate cyclase; **PDBTitle:** soluble adenylyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate
52	d2c8aa1	Alignment	not modelled	7.8	24	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
53	c2kqdA_	Alignment	not modelled	7.8	50	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aprataxin and pnk-like factor; **PDBTitle:** first pbz domain of human aplf protein in complex with2 ribofuranosyladenosine
54	d2yt9a1	Alignment	not modelled	7.6	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
55	d1uzva_	Alignment	not modelled	7.6	15	**Fold:**Calcium-mediated lectin **Superfamily:**Calcium-mediated lectin **Family:**Calcium-mediated lectin

56	d1xiwb_	Alignment	not modelled	7.6	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
57	d1pcfa_	Alignment	not modelled	7.6	31	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**Transcriptional coactivator PC4 C-terminal domain
58	c2eo1A_	Alignment	not modelled	7.4	11	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**cdna flj14124 fis, clone mamma1002498; **PDBTitle:** solution structure of the ig domain of human obscn protein
59	d1m0da_	Alignment	not modelled	7.3	31	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Endonuclease I (Holliday junction resolvase)
60	c2pmzV_	Alignment	not modelled	7.2	23	**PDB header:**translation, transferase **Chain:** V: **PDB Molecule:**dna-directed rna polymerase subunit h; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
61	c3ncvB_	Alignment	not modelled	7.0	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dna mismatch repair protein mutl; **PDBTitle:** ngol
62	c2zfnA_	Alignment	not modelled	7.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**regulator of ty1 transposition protein 109; **PDBTitle:** self-acetylation mediated histone h3 lysine 56 acetylation by rtt109
63	d1qs1a2	Alignment	not modelled	6.9	13	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
64	c2jtdA_	Alignment	not modelled	6.9	3	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**myomesin-1; **PDBTitle:** skelemin immunoglobulin c2 like domain 4
65	c3mr7B_	Alignment	not modelled	6.7	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenylate/guanylate cyclase/hydrolase, alpha/beta fold **PDBTitle:** crystal structure of adenylate/guanylate cyclase/hydrolase from2 silicibacter pomeroyi
66	d1usra_	Alignment	not modelled	6.6	11	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
67	c3ehkC_	Alignment	not modelled	6.5	12	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**prunin; **PDBTitle:** crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
68	c1rwuA_	Alignment	not modelled	6.5	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0250 protein ybed; **PDBTitle:** solution structure of conserved protein ybed from e. coli
69	d1rwua_	Alignment	not modelled	6.5	13	**Fold:**Ferredoxin-like **Superfamily:**YbeD/HP0495-like **Family:**YbeD-like
70	d1rgoa2	Alignment	not modelled	6.5	57	**Fold:**CCCH zinc finger **Superfamily:**CCCH zinc finger **Family:**CCCH zinc finger
71	d1wwbx_	Alignment	not modelled	6.3	7	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
72	d1wd2a_	Alignment	not modelled	6.2	30	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
73	d2nqra2	Alignment	not modelled	6.0	13	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
74	d1jz8a5	Alignment	not modelled	5.8	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
75	d2isya2	Alignment	not modelled	5.7	33	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
76	c2k50A_	Alignment	not modelled	5.7	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**replication factor a related protein; **PDBTitle:** solution nmr structure of the replication factor a related2 protein from methanobacterium thermoautotrophicum.3 northeast structural genomics target tr91a.
77	d6paxa1	Alignment	not modelled	5.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
78	c2zkqi_	Alignment	not modelled	5.5	11	**PDB header:**ribosomal protein/rna **Chain:** I: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
79	d2cu3a1	Alignment	not modelled	5.4	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
80	c2j58G_	Alignment	not modelled	5.2	25	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**outer membrane lipoprotein wza; **PDBTitle:** the structure of wza
81	d1s04a_	Alignment	not modelled	5.2	16	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain

82	c1ti2F_	 Alignment	not modelled	5.2	67	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**pyrogallol hydroxytransferase small subunit; **PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
83	d1g3wa2	 Alignment	not modelled	5.1	29	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain