Phyre^2

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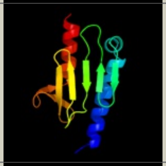
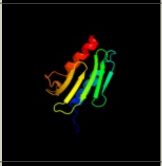
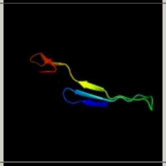
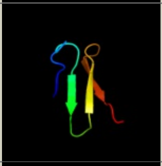
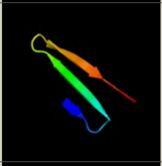
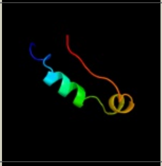
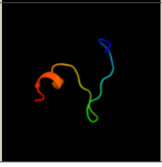
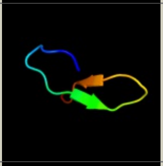
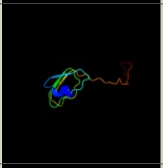
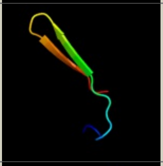
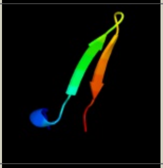
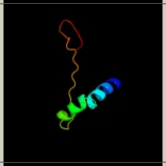
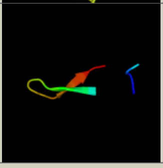
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ew4a_	Alignment		100.0	100	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
2	d1ekga_	Alignment		100.0	25	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
3	d2ga5a1	Alignment		100.0	27	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
4	d2fqla1	Alignment		100.0	28	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
5	d1xkpb1	Alignment		61.4	11	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
6	c1q40C_	Alignment		32.2	43	**PDB header:**translation **Chain:** C: **PDB Molecule:**mrna transport regulator mtr2; **PDBTitle:** crystal structure of the c. albicans mtr2-mex67 m domain complex
7	d1mbya_	Alignment		29.1	13	**Fold:**Polo-box domain **Superfamily:**Polo-box domain **Family:**Swapped Polo-box domain
8	d2ebsa1	Alignment		23.9	24	**Fold:**7-bladed beta-propeller **Superfamily:**Oligoxyloglucan reducing end-specific cellobiohydrolase **Family:**Oligoxyloglucan reducing end-specific cellobiohydrolase
9	d2ogqa2	Alignment		22.1	26	**Fold:**Polo-box domain **Superfamily:**Polo-box domain **Family:**Polo-box duplicated region
10	d3e11a1	Alignment		21.0	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
11	d1q42a_	Alignment		20.4	43	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**NTF2-like

12	c1umwB_	Alignment		19.5	22	**PDB header:**kinase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase plk; **PDBTitle:** structure of a human plk1 polo-box domain/phosphopeptide2 complex
13	c2bsgA_	Alignment		18.8	20	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**fibritin; **PDBTitle:** the modeled structure of fibritin (gpwac) of bacteriophage2 t4 based on cryo-em reconstruction of the extended tail of3 bacteriophage t4
14	c2v5iA_	Alignment		18.1	24	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**salmonella typhimurium db7155 bacteriophage det7 **PDBTitle:** structure of the receptor-binding protein of bacteriophage2 det7: a podoviral tailspike in a myovirus
15	d2azeb1	Alignment		14.4	23	**Fold:**E2F-DP heterodimerization region **Superfamily:**E2F-DP heterodimerization region **Family:**E2F dimerization segment
16	c3aabA_	Alignment		12.9	32	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**putative uncharacterized protein st1653; **PDBTitle:** small heat shock protein hsp14.0 with the mutations of i120f and i122f2 in the form i crystal
17	d2h50a1	Alignment		12.7	26	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**HSP20
18	c2v1lA_	Alignment		12.4	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** structure of the conserved hypothetical protein vc1805 from2 pathogenicity island vpi-2 of vibrio cholerae o1 biovar3 eltor str. n16961 shares structural homology with the4 human p32 protein
19	d1gmea_	Alignment		11.6	26	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**HSP20
20	c3nrlB_	Alignment		11.6	50	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rumgna_01417; **PDBTitle:** crystal structure of protein rumgna_01417 from ruminococcus gnavus,2 northeast structural genomics consortium target ugr76
21	c2qlvB_	Alignment	not modelled	11.3	16	**PDB header:**transferase/protein binding **Chain:** B: **PDB Molecule:**protein sip2; **PDBTitle:** crystal structure of the heterotrimer core of the s.2 cerevisiae ampk homolog snf1
22	c3nmeA_	Alignment	not modelled	11.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sex4 glucan phosphatase; **PDBTitle:** structure of a plant phosphatase
23	c3btpA_	Alignment	not modelled	11.1	33	**PDB header:**dna binding protein, chaperone **Chain:** A: **PDB Molecule:**single-strand dna-binding protein; **PDBTitle:** crystal structure of agrobacterium tumefaciens vire2 in complex with2 its chaperone vire1: a novel fold and implications for dna binding
24	d2qlvb1	Alignment	not modelled	11.0	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**AMPK-beta glycogen binding domain-like
25	c3igmA_	Alignment	not modelled	11.0	10	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**pf14_0633 protein; **PDBTitle:** a 2.2a crystal structure of the ap2 domain of pf14_0633 from p.2 falciparum, bound as a domain-swapped dimer to its cognate dna
26	d1gmeb_	Alignment	not modelled	10.6	26	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**HSP20
27	d2f15a1	Alignment	not modelled	10.2	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**AMPK-beta glycogen binding domain-like
28	d2je8a2	Alignment	not modelled	9.5	6	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain

29	d1yuaa2	Alignment	not modelled	8.9	18	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Prokaryotic DNA topoisomerase I, a C-terminal fragment
30	d1z0mb1	Alignment	not modelled	8.7	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**AMPK-beta glycogen binding domain-like
31	c2euzA_	Alignment	not modelled	8.6	33	**PDB header:**cell cycle/dna **Chain:** A: **PDB Molecule:**ndt80 protein; **PDBTitle:** structure of a ndt80-dna complex (mse mutant mc5t)
32	d1mnna_	Alignment	not modelled	8.6	33	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**DNA-binding domain from NDT80
33	c3glaA_	Alignment	not modelled	8.3	26	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**low molecular weight heat shock protein; **PDBTitle:** crystal structure of the hspa from xanthomonas axonopodis
34	c1yuaA_	Alignment	not modelled	7.8	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**topoisomerase i; **PDBTitle:** c-terminal domain of escherichia coli topoisomerase i
35	d1z0na1	Alignment	not modelled	7.6	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**AMPK-beta glycogen binding domain-like
36	c2yz0A_	Alignment	not modelled	7.5	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase gcn2; **PDBTitle:** solution structure of rwd/gi domain of saccharomyces2 cerevisiae gcn2
37	c2vecA_	Alignment	not modelled	7.4	19	**PDB header:**cytosolic protein **Chain:** A: **PDB Molecule:**pirin-like protein yhak; **PDBTitle:** the crystal structure of the protein yhak from escherichia2 coli
38	d1veha_	Alignment	not modelled	6.8	18	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
39	d1xhja_	Alignment	not modelled	6.7	8	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
40	c2pmzQ_	Alignment	not modelled	6.1	28	**PDB header:**translation, transferase **Chain:** Q: **PDB Molecule:**dna-directed rna polymerase subunit a; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
41	d2p3ya1	Alignment	not modelled	6.1	19	**Fold:**VPA0735-like **Superfamily:**VPA0735-like **Family:**VPA0735-like
42	c2p3yA_	Alignment	not modelled	6.1	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein vpa0735; **PDBTitle:** crystal structure of vpa0735 from vibrio parahaemolyticus. northeast2 structural genomics target vpr109
43	c3q9qB_	Alignment	not modelled	6.0	16	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**heat shock protein beta-1; **PDBTitle:** hspb1 fragment second crystal form
44	d1shsa_	Alignment	not modelled	6.0	16	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**HSP20
45	c1shsD_	Alignment	not modelled	6.0	16	**PDB header:**heat shock protein **Chain:** D: **PDB Molecule:**small heat shock protein; **PDBTitle:** small heat shock protein from methanococcus jannaschii
46	c3n23E_	Alignment	not modelled	5.6	17	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the high affinity complex between ouabain and the2 e2p form of the sodium-potassium pump
47	c2wj5A_	Alignment	not modelled	5.5	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein beta-6; **PDBTitle:** rat alpha crystallin domain
48	c2k38A_	Alignment	not modelled	5.5	40	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**cupiennin-1a; **PDBTitle:** cupiennin 1a, nmr, minimized average structure
49	d1j1la_	Alignment	not modelled	5.4	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Pirin-like
50	c3k6qB_	Alignment	not modelled	5.4	7	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**putative ligand binding protein; **PDBTitle:** crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
51	d1ro0a_	Alignment	not modelled	5.3	36	**Fold:**Prim-pol domain **Superfamily:**Prim-pol domain **Family:**Bifunctional DNA primase/polymerase N-terminal domain
52	c2x6vB_	Alignment	not modelled	5.2	7	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**t-box transcription factor tbx5; **PDBTitle:** crystal structure of human tbx5 in the dna-bound and dna-2 free form
53	d1p5ta_	Alignment	not modelled	5.1	21	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Phosphotyrosine-binding domain (PTB)