Phyre2

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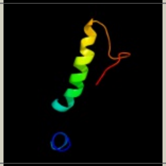
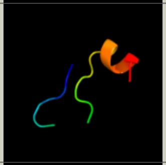
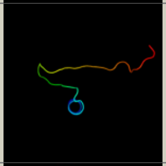
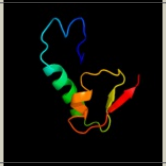
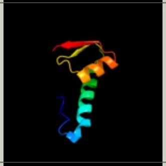
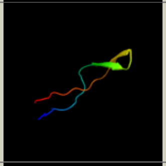
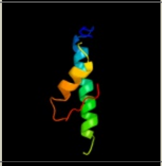
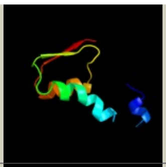
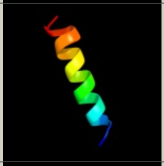
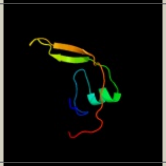
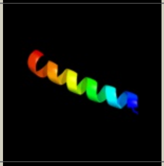
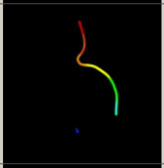
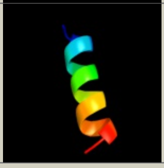
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gw6F_	Alignment		32.3	45	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**endo-n-acetylneuraminidase; **PDBTitle:** intramolecular chaperone
2	c3g79A_	Alignment		29.9	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ndp-n-acetyl-d-galactosaminuronic acid dehydrogenase; **PDBTitle:** crystal structure of ndp-n-acetyl-d-galactosaminuronic acid2 dehydrogenase from methanosarcina mazei go1
3	c1zy7A_	Alignment		25.2	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna-specific adenosine deaminase b1, isoform **PDBTitle:** crystal structure of the catalytic domain of an adenosine2 deaminase that acts on rna (hadar2) bound to inositol3 hexakisphosphate (ihp)
4	d2plga1	Alignment		24.2	31	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Tll0839-like
5	c3plnA_	Alignment		23.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** crystal structure of klebsiella pneumoniae udp-glucose 6-dehydrogenase2 complexed with udp-glucose
6	c1mv8A_	Alignment		20.9	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**gdp-mannose 6-dehydrogenase; **PDBTitle:** 1.55 a crystal structure of a ternary complex of gdp-mannose2 dehydrogenase from psuedomonas aeruginosa
7	d3er7a1	Alignment		20.1	41	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Exig0174-like
8	c1dliA_	Alignment		19.1	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-glucose dehydrogenase; **PDBTitle:** the first structure of udp-glucose dehydrogenase (udpgdh) reveals the2 catalytic residues necessary for the two-fold oxidation
9	c3prjB_	Alignment		17.8	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase.
10	c3ci9B_	Alignment		15.2	29	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat shock factor-binding protein 1; **PDBTitle:** crystal structure of the human hsbp1
11	c3ojlA_	Alignment		15.1	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cap5o; **PDBTitle:** native structure of the udp-n-acetyl-mannosamine dehydrogenase cap5o2 from staphylococcus aureus

12	c2y0dB_	Alignment		15.0	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**udp-glucose dehydrogenase; **PDBTitle:** bcec mutation y10k
13	c3m06F_	Alignment		14.0	43	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**tnf receptor-associated factor 2; **PDBTitle:** crystal structure of traf2
14	d1ttaa_	Alignment		13.0	18	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
15	c2keqA_	Alignment		13.0	23	**PDB header:**splicing **Chain:** A: **PDB Molecule:**dna polymerase iii alpha subunit, nucleic acid **PDBTitle:** solution structure of dnae intein from nostoc punctiforme
16	c1aq5C_	Alignment		12.5	45	**PDB header:**coiled-coil **Chain:** C: **PDB Molecule:**cartilage matrix protein; **PDBTitle:** high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures
17	c2lkaA_	Alignment		11.8	63	**PDB header:**toxin **Chain:** A: **PDB Molecule:**toxin ts16; **PDBTitle:** new tricks of an old fold: structural versatility of scorpion toxins2 with common cysteine spacing
18	c2oqqB_	Alignment		10.8	29	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor hy5; **PDBTitle:** crystal structure of hy5 leucine zipper homodimer from2 arabidopsis thaliana
19	d1rwha1	Alignment		10.4	32	**Fold:**alpha/alpha toroid **Superfamily:**Chondroitin AC/alginate lyase **Family:**Hyaluronate lyase-like catalytic, N-terminal domain
20	c3rylB_	Alignment		10.2	44	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**protein vpa1370; **PDBTitle:** dimerization domain of vibrio parahemolyticus vopl
21	d1f53a_	Alignment	not modelled	10.1	29	**Fold:**gamma-Crystallin-like **Superfamily:**gamma-Crystallin-like **Family:**Killer toxin-like protein SKLP
22	c3c8xA_	Alignment	not modelled	10.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** crystal structure of the ligand binding domain of human ephrin a22 (epha2) receptor protein kinase
23	c1cosA_	Alignment	not modelled	10.0	50	**PDB header:**alpha-helical bundle **Chain:** A: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
24	c1cosC_	Alignment	not modelled	10.0	50	**PDB header:**alpha-helical bundle **Chain:** C: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
25	c1cosB_	Alignment	not modelled	10.0	50	**PDB header:**alpha-helical bundle **Chain:** B: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
26	c3gg2B_	Alignment	not modelled	9.9	45	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sugar dehydrogenase, udp-glucose/gdp-mannose **PDBTitle:** crystal structure of udp-glucose 6-dehydrogenase from2 porphyromonas gingivalis bound to product udp-glucuronate
27	c3f59A_	Alignment	not modelled	9.7	45	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**ankyrin-1; **PDBTitle:** crystal structure of zu5-ank, the spectrin binding region of human2 erythroid ankyrin
28	c2h1xB_	Alignment	not modelled	9.6	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**5-hydroxyisourate hydrolase (formerly known as **PDBTitle:** crystal structure of 5-hydroxyisourate hydrolase

						(formerly2 known as trp, transthyretin related protein)
29	d2it9a1	Alignment	not modelled	9.2	42	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**PMN2A0962/syc2379c-like
30	d2bvca1	Alignment	not modelled	8.9	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Glutamine synthetase, N-terminal domain **Family:**Glutamine synthetase, N-terminal domain
31	c1coiA_	Alignment	not modelled	8.8	50	**PDB header:**alpha-helical bundle **Chain:** A: **PDB Molecule:**coil-vald; **PDBTitle:** designed trimeric coiled coil-vald
32	d1mv8a1	Alignment	not modelled	8.6	55	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**UDP-glucose/GDP-mannose dehydrogenase dimerisation domain
33	d1f52a1	Alignment	not modelled	8.3	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Glutamine synthetase, N-terminal domain **Family:**Glutamine synthetase, N-terminal domain
34	d1dlja1	Alignment	not modelled	8.2	43	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**UDP-glucose/GDP-mannose dehydrogenase dimerisation domain
35	c2jgoC_	Alignment	not modelled	7.8	50	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l9c; **PDBTitle:** stucture of the arsenated de novo designed peptide coil ser2 l9c
36	c3ljmA_	Alignment	not modelled	7.8	50	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l9c; **PDBTitle:** structure of de novo designed apo peptide coil ser l9c
37	c2jgoA_	Alignment	not modelled	7.8	50	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l9c; **PDBTitle:** stucture of the arsenated de novo designed peptide coil ser2 l9c
38	c3ljmB_	Alignment	not modelled	7.8	50	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l9c; **PDBTitle:** structure of de novo designed apo peptide coil ser l9c
39	c3ljmC_	Alignment	not modelled	7.8	50	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l9c; **PDBTitle:** structure of de novo designed apo peptide coil ser l9c
40	c2jgoB_	Alignment	not modelled	7.8	50	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l9c; **PDBTitle:** stucture of the arsenated de novo designed peptide coil ser2 l9c
41	d1vq3a_	Alignment	not modelled	7.5	17	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
42	c3hroA_	Alignment	not modelled	7.5	35	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**transient receptor potential (trp) channel **PDBTitle:** crystal structure of a c-terminal coiled coil domain of2 transient receptor potential (trp) channel subfamily p3 member 2 (trpp2, polycystic kidney disease 2)
43	c2pnvA_	Alignment	not modelled	7.5	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**small conductance calcium-activated potassium **PDBTitle:** crystal structure of the leucine zipper domain of small-2 conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus
44	c3rj1S_	Alignment	not modelled	7.4	31	**PDB header:**transcription **Chain:** S: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 18; **PDBTitle:** architecture of the mediator head module
45	d2nvna1	Alignment	not modelled	7.2	50	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**PMN2A0962/syc2379c-like
46	d1hn0a2	Alignment	not modelled	7.1	38	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Chondroitin ABC lyase I, N-terminal domain
47	d1tfpa_	Alignment	not modelled	7.0	25	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
48	c3ssbJ_	Alignment	not modelled	6.9	57	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** J: **PDB Molecule:**inducible metalloproteinase inhibitor protein; **PDBTitle:** structure of insect metalloproteinase inhibitor in complex with2 thermolysin
49	c1q2kA_	Alignment	not modelled	6.7	46	**PDB header:**toxin **Chain:** A: **PDB Molecule:**neurotoxin bmk37; **PDBTitle:** solution structure of bmbktx1 a new potassium channel2 blocker from the chinese scorpion buthus martensi karsch
50	d1k8ib2	Alignment	not modelled	6.5	37	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
51	c3e8yX_	Alignment	not modelled	6.5	46	**PDB header:**toxin **Chain:** X: **PDB Molecule:**potassium channel toxin alpha-ktx 19.1; **PDBTitle:** xray structure of scorpion toxin bmbktx1
52	c2fwvA_	Alignment	not modelled	6.2	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein mtubf_01000852; **PDBTitle:** crystal structure of rv0813
53	c2jmzA_	Alignment	not modelled	6.1	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein mj0781; **PDBTitle:** solution structure of a klba intein precursor from2 methanococcus jannaschii

54	d1eaic_	Alignment	not modelled	6.0	50	**Fold:**Serine protease inhibitors **Superfamily:**Serine protease inhibitors **Family:**ATI-like
55	d1mylb_	Alignment	not modelled	5.9	50	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
56	c1i4oC_	Alignment	not modelled	5.9	67	**PDB header:**apoptosis/hydrolase **Chain:** C: **PDB Molecule:**baculoviral iap repeat-containing protein 4; **PDBTitle:** crystal structure of the xiap/caspase-7 complex
57	d1f86a_	Alignment	not modelled	5.9	18	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
58	d1un7a1	Alignment	not modelled	5.9	40	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA
59	d1t11a2	Alignment	not modelled	5.9	17	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
60	c3u5ga_	Alignment	not modelled	5.9	43	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein s0-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
61	d1oo2a_	Alignment	not modelled	5.9	21	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
62	c1i7wB_	Alignment	not modelled	5.8	40	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**epithelial-cadherin; **PDBTitle:** beta-catenin/phosphorylated e-cadherin complex
63	c2xzn5_	Alignment	not modelled	5.8	43	**PDB header:**ribosome **Chain:** 5: **PDB Molecule:**ribosomal protein s26e containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
64	c2zw2B_	Alignment	not modelled	5.6	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
65	c2dadA_	Alignment	not modelled	5.6	20	**PDB header:**oncoprotein **Chain:** A: **PDB Molecule:**absent in melanoma 1 protein; **PDBTitle:** solution structure of the fifth crystall domain of the non-2 lens protein, absent in melanoma 1
66	c3batB_	Alignment	not modelled	5.6	33	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**myosin heavy chain, striated muscle/general **PDBTitle:** crystal structure of the n-terminal region of the scallop2 myosin rod, monoclinic (p21) form
67	d2uubc1	Alignment	not modelled	5.4	36	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
68	d1kgia_	Alignment	not modelled	5.3	18	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
69	d1okia1	Alignment	not modelled	5.3	44	**Fold:**gamma-Crystallin-like **Superfamily:**gamma-Crystallin-like **Family:**Crystallins/Ca-binding development proteins
70	d1ataa_	Alignment	not modelled	5.2	42	**Fold:**Serine protease inhibitors **Superfamily:**Serine protease inhibitors **Family:**ATI-like
71	d1rhoa_	Alignment	not modelled	5.2	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
72	d1u58a2	Alignment	not modelled	5.1	38	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
73	d1t6ca2	Alignment	not modelled	5.1	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase