Phyre2

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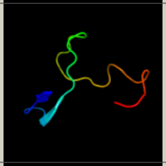
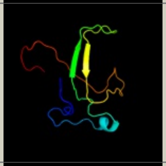
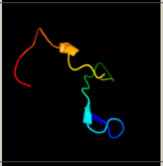
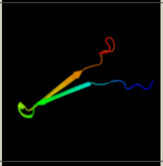
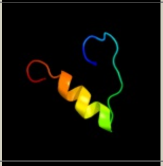
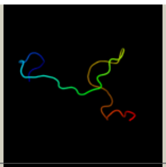
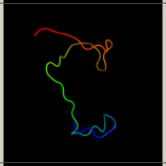
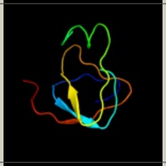
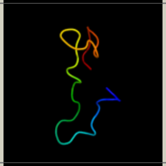
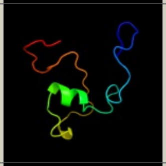
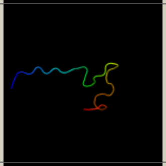
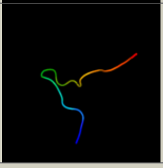
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2oy7A_	Alignment		95.2	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer surface protein a; **PDBTitle:** the crystal structure of ospa mutant
2	d1x3za1	Alignment		52.2	19	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
3	d1ulva3	Alignment		45.0	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CBD9-like **Family:**Glucodextranase, domain C
4	c1n7dA_	Alignment		44.1	11	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**low-density lipoprotein receptor; **PDBTitle:** extracellular domain of the ldl receptor
5	c3eswA_	Alignment		31.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine **PDBTitle:** complex of yeast pngase with glcnac2-iac.
6	c3mswA_	Alignment		30.2	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein with unknown function (bf3112) from2 bacteroides fragilis nctc 9343 at 1.90 a resolution
7	d1oeya_	Alignment		29.6	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
8	d2f4ma1	Alignment		29.4	18	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
9	c2ivzD_	Alignment		26.0	11	**PDB header:**protein transport/hydrolase **Chain:** D: **PDB Molecule:**protein tolb; **PDBTitle:** structure of tolb in complex with a peptide of the colicin2 e9 t-domain
10	c3rwxA_	Alignment		24.5	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hypothetical bacterial outer membrane protein; **PDBTitle:** crystal structure of a hypothetical bacterial outer membrane protein2 (bf2706) from bacteroides fragilis nctc 9343 at 2.40 a resolution
11	c2w8bB_	Alignment		23.3	12	**PDB header:**protein transport/membrane protein **Chain:** B: **PDB Molecule:**protein tolb; **PDBTitle:** crystal structure of processed tolb in complex with pal

12	c1mjeA_	Alignment		23.3	28	**PDB header:**gene regulation/antitumor protein/dna **Chain:** A: **PDB Molecule:**breast cancer 2; **PDBTitle:** structure of a brca2-dss1-ssdna complex
13	c1miuA_	Alignment		23.0	27	**PDB header:**gene regulation/antitumor protein **Chain:** A: **PDB Molecule:**breast cancer type 2 susceptibility protein; **PDBTitle:** structure of a brca2-dss1 complex
14	d1khda2	Alignment		22.8	35	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
15	c2kijA_	Alignment		22.7	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the actuator domain of the copper-2 transporting atpase atp7a
16	c2fz0A_	Alignment		22.2	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**v-snare component of the vacuolar snare complex **PDBTitle:** identification of yeast r-snare nyv1p as a novel longin2 domain protein
17	c1j5qB_	Alignment		21.5	26	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**major capsid protein; **PDBTitle:** the structure and evolution of the major capsid protein of a large,2 lipid-containing, dna virus.
18	d1qs0b1	Alignment		18.8	32	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
19	d1o5ua_	Alignment		18.5	8	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Hypothetical protein TM1112
20	d1bcga_	Alignment		16.2	35	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Long-chain scorpion toxins
21	c2hc8A_	Alignment	not modelled	15.5	30	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
22	c1iyjB_	Alignment	not modelled	15.2	27	**PDB header:**gene regulation/antitumor protein **Chain:** B: **PDB Molecule:**breast cancer susceptibility; **PDBTitle:** structure of a brca2-dss1 complex
23	c3e5zA_	Alignment	not modelled	14.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative gluconolactonase; **PDBTitle:** x-ray structure of the putative gluconolactonase in protein family2 pf08450. northeast structural genomics consortium target drr130.
24	d1pk6c_	Alignment	not modelled	14.0	27	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
25	d1ei5a1	Alignment	not modelled	13.9	32	**Fold:**Streptavidin-like **Superfamily:**D-aminopeptidase, middle and C-terminal domains **Family:**D-aminopeptidase, middle and C-terminal domains
26	c1dskA_	Alignment	not modelled	13.6	100	**PDB header:**viral peptide **Chain:** A: **PDB Molecule:**vpr protein; **PDBTitle:** nmr solution structure of vpr59_86, 20 structures
27	c2kz5A_	Alignment	not modelled	13.5	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor nf-e2 45 kda subunit; **PDBTitle:** solution nmr structure of transcription factor nf-e2 subunit's dna2 binding domain from homo sapiens, northeast structural genomics3 consortium target hr4653b
28	d1miua3	Alignment	not modelled	13.4	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB

29	c2x12A_	Alignment	not modelled	13.2	23	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**fimbriae-associated protein fap1; **PDBTitle:** ph-induced modulation of streptococcus parasanguinis2 adhesion by fap1 fimbriae
30	d1bcoa1	Alignment	not modelled	13.2	17	**Fold:**mu transposase, C-terminal domain **Superfamily:**mu transposase, C-terminal domain **Family:**mu transposase, C-terminal domain
31	d1vk8a_	Alignment	not modelled	13.1	14	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
32	c2ka3C_	Alignment	not modelled	13.0	36	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**emilin-1; **PDBTitle:** structure of emilin-1 c1q-like domain
33	d1pzqa_	Alignment	not modelled	12.6	32	**Fold:**Dimerisation interlock **Superfamily:**Docking domain A of the erythromycin polyketide synthase (DEBS) **Family:**Docking domain A of the erythromycin polyketide synthase (DEBS)
34	d1pk6b_	Alignment	not modelled	12.5	27	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
35	d1iyjb3	Alignment	not modelled	12.4	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
36	c2cseU_	Alignment	not modelled	12.2	19	**PDB header:**virus **Chain:** U: **PDB Molecule:**guanylyltransferase; **PDBTitle:** features of reovirus outer-capsid protein mu1 revealed by2 electron and image reconstruction of the virion at 7.0-a3 resolution
37	d2joya1	Alignment	not modelled	11.9	7	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L14e
38	d1brwa3	Alignment	not modelled	11.6	26	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
39	d1lxna_	Alignment	not modelled	11.5	15	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
40	c3bmxB_	Alignment	not modelled	11.5	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized lipoprotein ybbd; **PDBTitle:** beta-n-hexosaminidase (ybbd) from bacillus subtilis
41	d1c3ha_	Alignment	not modelled	11.3	31	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
42	c3dczA_	Alignment	not modelled	11.2	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative rnfg subunit of electron transport complex; **PDBTitle:** crystal structure of a putative rnfg subunit of electron transport2 complex (tm0246) from thermotoga maritima at 1.65 a resolution
43	d1m3ya2	Alignment	not modelled	11.0	33	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group II dsDNA viruses VP **Family:**Major capsid protein vp54
44	d1uerc2	Alignment	not modelled	10.9	20	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
45	c1zrxA_	Alignment	not modelled	10.9	23	**PDB header:**antimicrobial protein, antibiotic **Chain:** A: **PDB Molecule:**stomoxyn; **PDBTitle:** solution structure of stomoxyn in h20/tfe 50%
46	c3fnkA_	Alignment	not modelled	10.9	23	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**cellulosomal scaffoldin adaptor protein b; **PDBTitle:** crystal structure of the second type ii cohesin module from2 the cellulosomal adaptor scaa scaffoldin of acetivibrio3 cellulolyticus
47	d2tpta3	Alignment	not modelled	10.7	26	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
48	c3izcN_	Alignment	not modelled	10.6	21	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein rpl14 (l14e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
49	c2jpnA_	Alignment	not modelled	10.5	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase uvsw; **PDBTitle:** solution structure of t4 bacteriophage helicase uvsw.1
50	c3h1sB_	Alignment	not modelled	10.2	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**superoxide dismutase; **PDBTitle:** crystal structure of superoxide dismutase from francisella tularensis2 subsp. tularensis schu s4
51	c3iz5N_	Alignment	not modelled	10.2	13	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein l14 (l14e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
52	c1m4xC_	Alignment	not modelled	10.0	33	**PDB header:**virus **Chain:** C: **PDB Molecule:**pbcv-1 virus capsid; **PDBTitle:** pbcv-1 virus capsid, quasi-atomic model
53	c1trlB_	Alignment	not modelled	10.0	19	**PDB header:**hydrolase (metalloprotease) **Chain:** B: **PDB Molecule:**thermolysin fragment 255 - 316; **PDBTitle:** nmr solution structure of the c-terminal fragment 255-3162 of thermolysin: a dimer formed by subunits having the3 native

						structure
54	d2pyta1	Alignment	not modelled	10.0	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**EutQ-like
55	c2oajA_	Alignment	not modelled	10.0	12	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**protein sni1; **PDBTitle:** crystal structure of sro7 from s. cerevisiae
56	c2jttD_	Alignment	not modelled	9.9	36	**PDB header:**calcium binding protein/antitumor protei **Chain:** D: **PDB Molecule:**calcyclin-binding protein; **PDBTitle:** solution structure of calcium loaded s100a6 bound to c-2 terminal siah-1 interacting protein
57	d1lxja_	Alignment	not modelled	9.5	12	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
58	c3lk6A_	Alignment	not modelled	9.3	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipoprotein ybbd; **PDBTitle:** beta-n-hexosaminidase n318d mutant (ybbd_n318d) from bacillus subtilis
59	c3jroA_	Alignment	not modelled	9.1	13	**PDB header:**transport protein, structural protein **Chain:** A: **PDB Molecule:**fusion protein of protein transport protein sec13 **PDBTitle:** nup84-nup145c-sec13 edge element of the npc lattice
60	c2gacA_	Alignment	not modelled	9.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosylasparaginase; **PDBTitle:** t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum
61	d1sknp_	Alignment	not modelled	9.0	11	**Fold:**A DNA-binding domain in eukaryotic transcription factors **Superfamily:**A DNA-binding domain in eukaryotic transcription factors **Family:**A DNA-binding domain in eukaryotic transcription factors
62	d1ejxc1	Alignment	not modelled	9.0	26	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**alpha-Subunit of urease
63	d1dfma_	Alignment	not modelled	8.9	47	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease BglII
64	c2jtmA_	Alignment	not modelled	8.9	29	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of sso6901 from sulfolobus solfataricus2 p2
65	d1jnpa_	Alignment	not modelled	8.7	24	**Fold:**Oncogene products **Superfamily:**Oncogene products **Family:**Oncogene products
66	d1a1xa_	Alignment	not modelled	8.7	19	**Fold:**Oncogene products **Superfamily:**Oncogene products **Family:**Oncogene products
67	c3nv4A_	Alignment	not modelled	8.7	28	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**galectin 9 short isoform variant; **PDBTitle:** crystal structure of human galectin-9 c-terminal crd in complex with2 sialyllactose
68	c2ksnA_	Alignment	not modelled	8.6	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin domain-containing protein 2; **PDBTitle:** solution structure of the n-terminal domain of dc-ubp/ubtd2
69	d1pk6a_	Alignment	not modelled	8.6	22	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
70	c1bdeA_	Alignment	not modelled	8.4	27	**PDB header:**aids **Chain:** A: **PDB Molecule:**vpr protein; **PDBTitle:** helical structure of polypeptides from the c-terminal half2 of hiv-1 vpr, nmr, 20 structures
71	c3nqhA_	Alignment	not modelled	8.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyl hydrolase; **PDBTitle:** crystal structure of a glycosyl hydrolase (bt_2959) from bacteroides2 thetaiotaomicron vpi-5482 at 2.11 a resolution
72	d2f1fa1	Alignment	not modelled	8.3	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
73	d1f00i2	Alignment	not modelled	8.3	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
74	d1xata_	Alignment	not modelled	8.3	21	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
75	c2vtwF_	Alignment	not modelled	8.2	32	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**fiber protein 2; **PDBTitle:** structure of the c-terminal head domain of the fowl2 adenovirus type 1 short fibre
76	c1gv3B_	Alignment	not modelled	8.2	11	**PDB header:**manganese superoxide dismutase **Chain:** B: **PDB Molecule:**manganese superoxide dismutase; **PDBTitle:** the 2.0 angstrom resolution structure of the catalytic2 portion of a cyanobacterial membrane-bound manganese3 superoxide dismutase
77	c1dfwA_	Alignment	not modelled	8.2	57	**PDB header:**immune system **Chain:** A: **PDB Molecule:**lung surfactant protein b; **PDBTitle:** conformational mapping of the n-terminal segment of2 surfactant protein b in lipid using 13c-enhanced fourier3 transform infrared spectroscopy (ftir)
78	d1x6va1	Alignment	not modelled	8.2	19	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
79	d2pc6a2	Alignment	not modelled	8.1	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like

80	c2wlgA_	Alignment	not modelled	7.9	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polysialic acid o-acetyltransferase; **PDBTitle:** crystallographic analysis of the polysialic acid o-2 acetyltransferase oatwy
81	d1e9yb1	Alignment	not modelled	7.9	26	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**alpha-Subunit of urease
82	d1o91a_	Alignment	not modelled	7.9	31	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
83	c1o91B_	Alignment	not modelled	7.9	31	**PDB header:**collagen **Chain:** B: **PDB Molecule:**collagen alpha 1(viii) chain; **PDBTitle:** crystal structure of a collagen viii nc1 domain trimer
84	c2iu9C_	Alignment	not modelled	7.8	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine **PDBTitle:** chlamydia trachomatis lpxd with 100mm udpglcnac (complex ii)
85	d2q09a1	Alignment	not modelled	7.8	80	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
86	d2jdqd1	Alignment	not modelled	7.7	20	**Fold:**PB2 C-terminal domain-like **Superfamily:**PB2 C-terminal domain-like **Family:**PB2 C-terminal domain-like
87	d2i5ua1	Alignment	not modelled	7.7	17	**Fold:**DnaD domain-like **Superfamily:**DnaD domain-like **Family:**DnaD domain
88	d1w9pa2	Alignment	not modelled	7.6	18	**Fold:**FKBP-like **Superfamily:**Chitinase insertion domain **Family:**Chitinase insertion domain
89	d1jsga_	Alignment	not modelled	7.5	24	**Fold:**Oncogene products **Superfamily:**Oncogene products **Family:**Oncogene products
90	d2hqya2	Alignment	not modelled	7.5	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**FemXAB nonribosomal peptidyltransferases
91	d1azpa_	Alignment	not modelled	7.5	17	**Fold:**SH3-like barrel **Superfamily:**Chromo domain-like **Family:**"Histone-like" proteins from archaea
92	c2a03A_	Alignment	not modelled	7.5	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fe-superoxide dismutase homolog; **PDBTitle:** superoxide dismutase protein from plasmodium berghei
93	c3cl5A_	Alignment	not modelled	7.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hemagglutinin-esterase; **PDBTitle:** structure of coronavirus hemagglutinin-esterase in complex with 4,9-o-2 diacetyl sialic acid
94	d1r7aa1	Alignment	not modelled	7.4	36	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
95	d1thqa_	Alignment	not modelled	7.4	50	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane enzyme PagP
96	d1zaka2	Alignment	not modelled	7.4	33	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
97	c2kjmA_	Alignment	not modelled	7.4	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**histone rna hairpin-binding protein; **PDBTitle:** solution structure of slbp rna binding domain fragment
98	c1t3dB_	Alignment	not modelled	7.3	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** crystal structure of serine acetyltransferase from e.coli at 2.2a
99	d1s6la1	Alignment	not modelled	7.3	44	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MerB N-terminal domain-like