Phyre²

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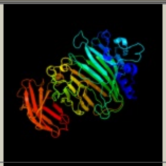
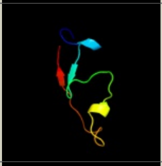
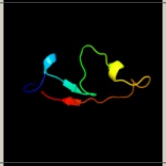
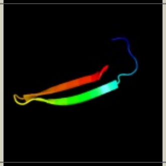
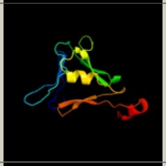
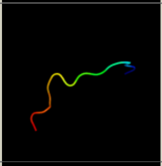
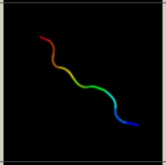
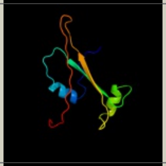
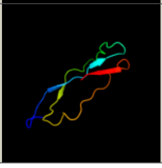
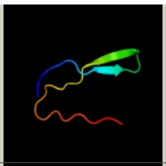
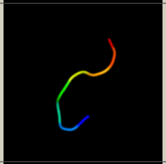
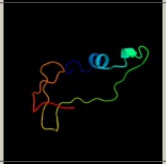
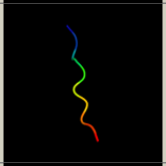
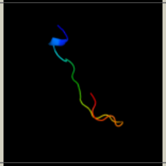
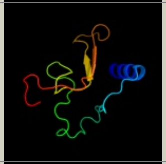
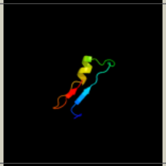
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1txkA_	Alignment		100.0	98	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glucans biosynthesis protein g; **PDBTitle:** crystal structure of escherichia coli opgg
2	d1txka2	Alignment		100.0	98	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**MdoG-like
3	d1txka1	Alignment		100.0	97	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
4	c1se9A_	Alignment		25.0	23	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**ubiquitin family; **PDBTitle:** structure of at3g01050, a ubiquitin-fold protein from2 arabidopsis thaliana
5	d1se9a_	Alignment		25.0	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
6	d2jnaa1	Alignment		23.4	26	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
7	c3r0eC_	Alignment		22.1	21	**PDB header:**sugar binding protein **Chain:** C: **PDB Molecule:**lectin; **PDBTitle:** structure of remusatia vivipara lectin
8	d2noca1	Alignment		21.8	14	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
9	d1nkra1	Alignment		21.3	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
10	c2r5oA_	Alignment		21.1	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative atp binding component of abc- **PDBTitle:** crystal structure of the c-terminal domain of wzt
11	c3o0lB_	Alignment		17.9	7	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a pfam duf1425 family member (shew_1734) from2 shewanella sp. pv-4 at 1.81 a resolution

12	c3on7C_	Alignment		17.0	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, iron/ascorbate family; **PDBTitle:** crystal structure of a putative oxygenase (so_2589) from shewanella2 oneidensis at 2.20 a resolution
13	c2l6mA_	Alignment		16.5	63	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein dicer; **PDBTitle:** structure of c-terminal dsrbd of the fission yeast dicer (dcr1)
14	d1oq1a_	Alignment		16.3	15	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Hypothetical protein YesU
15	c2qsdB_	Alignment		16.2	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** crystal structure of a protein il1583 from idiomarina loihiensis
16	d2dl2a1	Alignment		14.9	30	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
17	c2r3aA_	Alignment		14.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase suv39h2; **PDBTitle:** methyltransferase domain of human suppressor of variegation2 3-9 homolog 2
18	c3mpbA_	Alignment		14.6	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar isomerase; **PDBTitle:** z5688 from e. coli o157:h7 bound to fructose
19	c3rhfB_	Alignment		13.6	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative polyphosphate kinase 2 family protein; **PDBTitle:** crystal structure of polyphosphate kinase 2 from arthrobacter2 aurescens tc1
20	c2i1jA_	Alignment		12.7	35	**PDB header:**cell adhesion, membrane protein **Chain:** A: **PDB Molecule:**moesin; **PDBTitle:** moesin from spodoptera frugiperda at 2.1 angstroms resolution
21	d1ee8a2	Alignment	not modelled	12.1	28	**Fold:**N-terminal domain of MutM-like DNA repair proteins **Superfamily:**N-terminal domain of MutM-like DNA repair proteins **Family:**N-terminal domain of MutM-like DNA repair proteins
22	d3ehwa1	Alignment	not modelled	11.7	21	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
23	c3ooxA_	Alignment	not modelled	11.7	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative 2og-fe(ii) oxygenase family protein; **PDBTitle:** crystal structure of a putative 2og-fe(ii) oxygenase family protein2 (cc_0200) from caulobacter crescentus at 1.44 a resolution
24	d2ozga1	Alignment	not modelled	11.1	20	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**EF1021 C-terminal domain-like
25	d2k8ea1	Alignment	not modelled	10.7	19	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
26	c3exmA_	Alignment	not modelled	10.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatase sc4828; **PDBTitle:** crystal structure of the phosphatase sc4828 with the non-hydrolyzable2 nucleotide gpcp
27	c3f4fB_	Alignment	not modelled	10.3	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**deoxyuridine 5'-triphosphate nucleotidohydrolase; **PDBTitle:** crystal structure of dut1p, a dutpase from saccharomyces cerevisiae
28	d2k49a2	Alignment	not modelled	10.3	22	**Fold:**YegP-like **Superfamily:**YegP-like

						Family: YegP-like
29	d1p1la_	Alignment	not modelled	9.9	30	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
30	c2l3bA_	Alignment	not modelled	9.8	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein found in conjugate transposon; **PDBTitle:** solution nmr structure of the bt_0084 lipoprotein from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr376
31	d1qcsa1	Alignment	not modelled	9.8	57	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
32	c2p8zS_	Alignment	not modelled	9.8	67	**PDB header:**translation **Chain:** S: **PDB Molecule:**elongation factor tu-b; **PDBTitle:** fitted structure of adpr-eef2 in the 80s:adpr-2 eef2:gdpnp:sordarin cryo-em reconstruction
33	d1ix2a_	Alignment	not modelled	9.6	43	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Copper resistance protein C (CopC, PcoC)
34	d1h95a_	Alignment	not modelled	9.5	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
35	d1e09a_	Alignment	not modelled	9.5	13	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
36	d1ef1a2	Alignment	not modelled	9.4	35	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Third domain of FERM
37	d1ml9a_	Alignment	not modelled	9.2	17	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Histone lysine methyltransferases
38	c3camB_	Alignment	not modelled	9.0	33	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**cold-shock domain family protein; **PDBTitle:** crystal structure of the cold shock domain protein from neisseria2 meningitidis
39	d1xbwa_	Alignment	not modelled	8.9	32	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PG130-like
40	c3ehwA_	Alignment	not modelled	8.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dutp pyrophosphatase; **PDBTitle:** human dutpase in complex with alpha,beta-imido-dutp and mg2+:2 visualization of the full-length c-termini in all monomers and3 suggestion for an additional metal ion binding site
41	d1kr4a_	Alignment	not modelled	8.7	10	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
42	d1kfia4	Alignment	not modelled	8.7	10	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
43	d3bida1	Alignment	not modelled	8.6	14	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
44	d1dq3a3	Alignment	not modelled	8.5	27	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
45	d1svba1	Alignment	not modelled	8.4	26	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
46	d1ukua_	Alignment	not modelled	8.4	0	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
47	d1erna1	Alignment	not modelled	8.4	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
48	d1ja1a3	Alignment	not modelled	8.4	33	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
49	d1pjca1	Alignment	not modelled	8.3	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
50	d1b2pa_	Alignment	not modelled	8.3	21	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
51	c3d3zA_	Alignment	not modelled	8.3	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**actibind; **PDBTitle:** crystal structure of actibind a t2 rnase
52	d1euwa_	Alignment	not modelled	8.1	20	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
53	d1a8pa2	Alignment	not modelled	8.1	44	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
54	d1fdra2	Alignment	not modelled	8.0	22	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases

55	c2rocB_	Alignment	not modelled	7.9	44	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-binding component 3; **PDBTitle:** solution structure of mcl-1 complexed with puma
56	c2wclA_	Alignment	not modelled	7.6	29	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**general odorant-binding protein 1; **PDBTitle:** structure of bmori gobp2 (general odorant binding protein 2)2 with (8e,10z)-hexadecadien-1-ol
57	d3pmga4	Alignment	not modelled	7.6	13	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
58	d1y0ka1	Alignment	not modelled	7.5	24	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**PA4535-like
59	d1h4ra2	Alignment	not modelled	7.5	35	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Third domain of FERM
60	c3a0jB_	Alignment	not modelled	7.5	33	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cold shock protein; **PDBTitle:** crystal structure of cold shock protein 1 from thermus2 thermophilus hb8
61	d2jn4a1	Alignment	not modelled	7.3	13	**Fold:**NifT/FixU barrel-like **Superfamily:**NifT/FixU-like **Family:**NifT/FixU
62	c2jn4A_	Alignment	not modelled	7.3	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein fixu, nift; **PDBTitle:** solution nmr structure of protein rp4601 from2 rhodopseudomonas palustris. northeast structural genomics3 consortium target rpt2; ontario center for structural4 proteomics target rp4601.
63	d1cgta2	Alignment	not modelled	7.3	25	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**Starch-binding domain
64	d1f20a2	Alignment	not modelled	7.3	44	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
65	d1nkra2	Alignment	not modelled	7.2	38	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
66	c2l7qA_	Alignment	not modelled	7.2	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein found in conjugate transposon; **PDBTitle:** solution nmr structure of conjugate transposon protein bvu_1572(27-2 141) from bacteroides vulgatus, northeast structural genomics3 consortium target bvr155
67	d1ddga2	Alignment	not modelled	7.0	38	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
68	c1meqA_	Alignment	not modelled	7.0	67	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**exterior membrane glycoprotein (gp120); **PDBTitle:** hiv gp120 c5
69	c3oruA_	Alignment	not modelled	7.0	11	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**duf1989 family protein; **PDBTitle:** crystal structure of a duf1989 family protein (tm1040_0329) from2 silicibacter sp. tm1040 at 1.11 a resolution
70	d3bmva2	Alignment	not modelled	7.0	18	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**Starch-binding domain
71	d1isna2	Alignment	not modelled	6.9	35	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Third domain of FERM
72	d2bk0a1	Alignment	not modelled	6.8	23	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
73	c1ibtC_	Alignment	not modelled	6.8	31	**PDB header:**lyase **Chain:** C: **PDB Molecule:**histidine decarboxylase beta chain; **PDBTitle:** structure of the d53,54n mutant of histidine decarboxylase at-170 c
74	c2kl5A_	Alignment	not modelled	6.8	45	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yutd; **PDBTitle:** solution nmr structure of protein yutd from b.subtilis, northeast2 structural genomics consortium target sr232
75	c2l1nA_	Alignment	not modelled	6.8	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of the protein yp_399305.1
76	c1wrgA_	Alignment	not modelled	6.8	100	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**light-harvesting protein b-880, beta chain; **PDBTitle:** light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum
77	c2kvhA_	Alignment	not modelled	6.7	75	**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
78	c1ckwA_	Alignment	not modelled	6.7	12	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**protein (cystic fibrosis transmembrane **PDBTitle:** cystic fibrosis transmembrane conductance regulator:2 solution structures of peptides based on the phe508 region,3 the most common site of disease-causing delta-f508 mutation
79	d2hv2a1	Alignment	not modelled	6.7	16	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**EF1021 C-terminal domain-like

80	d1x9na2	Alignment	not modelled	6.7	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
81	c2ns2A_	Alignment	not modelled	6.6	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**spindlin-1; **PDBTitle:** crystal structure of spindlin1
82	d1m4ka2	Alignment	not modelled	6.6	38	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
83	d2zpya2	Alignment	not modelled	6.6	35	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Third domain of FERM
84	c2eiuE_	Alignment	not modelled	6.5	38	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**hypothetical protein aq_1627; **PDBTitle:** crystal structure of a putative protein (aq1627) from aquifex aeolicus
85	c3n6yA_	Alignment	not modelled	6.5	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**immunoglobulin-like protein; **PDBTitle:** crystal structure of an immunoglobulin-like protein (pa1606) from2 pseudomonas aeruginosa at 1.50 a resolution
86	d1hska2	Alignment	not modelled	6.4	23	**Fold:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Superfamily:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
87	d1j19a2	Alignment	not modelled	6.4	35	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Third domain of FERM
88	d1vhfa_	Alignment	not modelled	6.4	10	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
89	d1txca1	Alignment	not modelled	6.4	20	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
90	d2oq1a2	Alignment	not modelled	6.3	15	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
91	c1ckxA_	Alignment	not modelled	6.3	18	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cystic fibrosis transmembrane conductance **PDBTitle:** cystic fibrosis transmembrane conductance regulator:2 solution structures of peptides based on the phe508 region,3 the most common site of disease-causing delta-f508 mutation
92	c2ys2A_	Alignment	not modelled	6.2	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cytoplasmic tyrosine-protein kinase bmx; **PDBTitle:** solution structure of the btk motif of human cytoplasmic2 tyrosine-protein kinase bmx
93	c2wsfG_	Alignment	not modelled	6.2	29	**PDB header:**photosynthesis **Chain:** G: **PDB Molecule:**photosystem i reaction center subunit v, **PDBTitle:** improved model of plant photosystem i
94	d1g6pa_	Alignment	not modelled	6.2	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
95	d1dmla1	Alignment	not modelled	6.1	29	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
96	d1rnja_	Alignment	not modelled	6.1	21	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
97	d1njha_	Alignment	not modelled	6.1	10	**Fold:**Hypothetical protein YojF **Superfamily:**Hypothetical protein YojF **Family:**Hypothetical protein YojF
98	d1gawa2	Alignment	not modelled	6.0	44	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
99	d1gg3a2	Alignment	not modelled	6.0	25	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Third domain of FERM