Phyre^2

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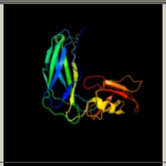
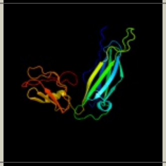
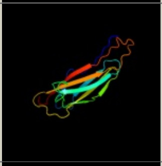
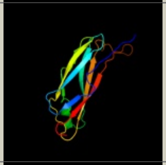
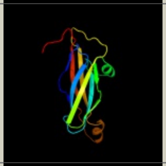
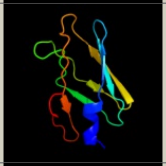
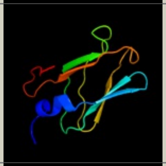
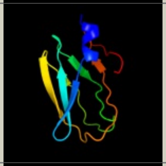
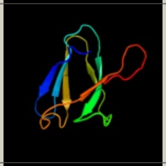
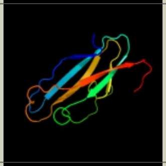
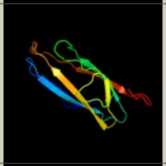
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1z9sA_	Alignment		100.0	29	**PDB header:**chaperone/immune system **Chain:** A: **PDB Molecule:**chaperone protein caf1m; **PDBTitle:** crystal structure of the native chaperone:subunit:subunit2 caf1m:caf1:caf1 complex
2	c1qunA_	Alignment		100.0	30	**PDB header:**chaperone/structural protein **Chain:** A: **PDB Molecule:**papd-like chaperone fimc; **PDBTitle:** x-ray structure of the fimc-fimh chaperone adhesin complex2 from uropathogenic e.coli
3	c2co7B_	Alignment		100.0	21	**PDB header:**fibril protein **Chain:** B: **PDB Molecule:**putative fimbriae assembly chaperone; **PDBTitle:** salmonella enterica safa pilin in complex with the safb2 chaperone (type ii)
4	c3q48B_	Alignment		100.0	33	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone cupb2; **PDBTitle:** crystal structure of pseudomonas aeruginosa cupb2 chaperone
5	c1qpxA_	Alignment		100.0	31	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**papd chaperone; **PDBTitle:** crystal structures of self-capping papd chaperone homodimers
6	c1l4iA_	Alignment		100.0	32	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**sfae protein; **PDBTitle:** crystal structure of the periplasmic chaperone sfae
7	c3f6iB_	Alignment		100.0	24	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone protein faee; **PDBTitle:** structure of the semet labeled f4 fibrial chaperone faee
8	d2co7b1	Alignment		100.0	26	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
9	d1p5va1	Alignment		100.0	35	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
10	d2j2za1	Alignment		100.0	36	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
11	d3bwuc1	Alignment		100.0	38	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone

12	d1l4ia1	Alignment		100.0	36	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
13	d3bwuc2	Alignment		99.7	22	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
14	d1p5va2	Alignment		99.7	18	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
15	d2co7b2	Alignment		99.6	15	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
16	d1l4ia2	Alignment		99.6	25	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
17	d2j2za2	Alignment		99.6	27	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
18	d1m1sa_	Alignment		97.8	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
19	d1rowa_	Alignment		97.3	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
20	d1grwa_	Alignment		97.2	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
21	c2qsvA_	Alignment	not modelled	96.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function from porphyromonas2 gingivalis w83
22	c1z9oB_	Alignment	not modelled	96.5	15	**PDB header:**protein binding/lipid binding protein **Chain:** B: **PDB Molecule:**vesicle-associated membrane protein-associated protein a; **PDBTitle:** 1.9 angstrom crystal structure of the rat vap-a msp homology domain in2 complex with the rat orp1 ffat motif
23	d1mspa_	Alignment	not modelled	95.8	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
24	c2ys4A_	Alignment	not modelled	95.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hydrocephalus-inducing protein homolog; **PDBTitle:** solution structure of the n-terminal papd-like domain of2 hydin protein from human
25	c2e6jA_	Alignment	not modelled	94.5	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hydin protein; **PDBTitle:** solution structure of the c-terminal papd-like domain from2 human hydin protein
26	d1wica_	Alignment	not modelled	93.6	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
27	c3qisA_	Alignment	not modelled	92.3	9	**PDB header:**hydrolase/protein binding **Chain:** A: **PDB Molecule:**inositol polyphosphate 5-phosphatase ocrl-1; **PDBTitle:** recognition of the f&h motif by the lowe syndrome protein ocrl
28	c3o0lB	Alignment	not modelled	91.2	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein;

28	[illegible]	Alignment	not modelled	91.2	15	**PDBTitle:** crystal structure of a pfam duf1425 family member (shew_1734) from2 shewanella sp. pv-4 at 1.81 a resolution
29	c3qbtH_	Alignment	not modelled	90.9	9	**PDB header:**protein transport/hydrolase **Chain:** H: **PDB Molecule:**inositol polyphosphate 5-phosphatase ocrl-1; **PDBTitle:** crystal structure of ocrl1 540-678 in complex with rab8a:gppnhp
30	d2vzsa2	Alignment	not modelled	90.8	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
31	c3ac0B_	Alignment	not modelled	88.8	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase i; **PDBTitle:** crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
32	c2x41A_	Alignment	not modelled	87.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
33	c2je8B_	Alignment	not modelled	83.2	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-mannosidase; **PDBTitle:** structure of a beta-mannosidase from bacteroides2 thetaiotaomicron
34	d4ubpb_	Alignment	not modelled	76.9	11	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
35	c3ginB_	Alignment	not modelled	75.6	9	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**sodium/calcium exchanger 1; **PDBTitle:** crystal structure of e454k-cbd1
36	d1ejxb_	Alignment	not modelled	72.8	8	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
37	d1e9ya1	Alignment	not modelled	71.0	11	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
38	c3qgaD_	Alignment	not modelled	65.2	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**fusion of urease beta and gamma subunits; **PDBTitle:** 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae
39	d2dpka1	Alignment	not modelled	62.8	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CalX-like **Family:**CalX-beta domain
40	c2qvkA_	Alignment	not modelled	58.6	11	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**sodium/calcium exchanger 1; **PDBTitle:** the second ca2+-binding domain of the na+-ca2+ exchanger is2 essential for regulation: crystal structures and3 mutational analysis
41	d1ufga_	Alignment	not modelled	56.4	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
42	d1e42a1	Alignment	not modelled	55.9	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Clathrin adaptor appendage domain **Family:**Alpha-adaptin ear subdomain-like
43	c1e9zA_	Alignment	not modelled	55.9	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**urease subunit alpha; **PDBTitle:** crystal structure of helicobacter pylori urease
44	d1k3ra1	Alignment	not modelled	49.1	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Hypothetical protein MTH1 (MT0001), insert domain
45	c2lllA_	Alignment	not modelled	49.0	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin-b2; **PDBTitle:** solution nmr structure of c-terminal globular domain of human lamin-2 b2, northeast structural genomics consortium target hr8546a
46	c2f1eA_	Alignment	not modelled	48.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein apag; **PDBTitle:** solution structure of apag protein
47	c3jt0B_	Alignment	not modelled	48.2	11	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**lamin-b1; **PDBTitle:** crystal structure of the c-terminal fragment (426-558)2 lamin-b1 from homo sapiens, northeast structural genomics3 consortium target hr5546a
48	c3eujB_	Alignment	not modelled	45.5	20	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**chromosome partition protein mukf; **PDBTitle:** crystal structure of muke-mukf(residues 292-443)-mukb(head2 domain)-atpgammas complex, symmetric dimer
49	c3rb7E_	Alignment	not modelled	45.2	10	**PDB header:**metal binding protein **Chain:** E: **PDB Molecule:**na/ca exchange protein; **PDBTitle:** crystal structure of cbd12 from calx1.2
50	c1e42A_	Alignment	not modelled	37.6	23	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**ap-2 complex subunit beta; **PDBTitle:** beta2-adaptin appendage domain, from clathrin adaptor ap2
51	d1aoza2	Alignment	not modelled	36.3	6	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
52	d1w8oa1	Alignment	not modelled	33.3	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
53	d1tzaa_	Alignment	not modelled	31.2	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ApaG-like **Family:**ApaG-like

54	d1ifra_	Alignment	not modelled	30.7	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
55	d1hfua2	Alignment	not modelled	30.4	6	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
56	c2r39A_	Alignment	not modelled	30.3	3	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**fixg-related protein; **PDBTitle:** crystal structure of fixg-related protein from vibrio parahaemolyticus
57	d2fwua1	Alignment	not modelled	26.2	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CalX-like **Family:**CalX-beta domain
58	c1yycA_	Alignment	not modelled	25.7	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative late embryogenesis abundant protein; **PDBTitle:** solution structure of a putative late embryogenesis2 abundant (lea) protein at2g46140.1
59	c3isyA_	Alignment	not modelled	24.0	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intracellular proteinase inhibitor; **PDBTitle:** crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
60	d1kyaa2	Alignment	not modelled	23.7	4	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
61	c3cfuA_	Alignment	not modelled	23.2	11	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**uncharacterized lipoprotein yjha; **PDBTitle:** crystal structure of the yjha protein from bacillus2 subtilis. northeast structural genomics consortium target3 sr562
62	d1xo8a_	Alignment	not modelled	22.4	7	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**LEA14-like **Family:**LEA14-like
63	d1v8ha1	Alignment	not modelled	22.2	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**SoxZ-like
64	d1v10a2	Alignment	not modelled	21.0	10	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
65	c3butA_	Alignment	not modelled	20.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein af_0446; **PDBTitle:** crystal structure of protein af_0446 from archaeoglobus fulgidus
66	c2vzvB_	Alignment	not modelled	17.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exo-beta-d-glucosaminidase; **PDBTitle:** substrate complex of amycolatopsis orientalis exo-2 chitosanase csxa e541a with chitosan
67	d1ivta_	Alignment	not modelled	17.1	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
68	d1gyca2	Alignment	not modelled	16.1	8	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
69	d1xq4a_	Alignment	not modelled	16.0	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ApaG-like **Family:**ApaG-like
70	d1jz8a2	Alignment	not modelled	15.7	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
71	d1v7wa1	Alignment	not modelled	15.1	12	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glycosyltransferase family 36 C-terminal domain
72	d1ahsa_	Alignment	not modelled	14.8	25	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Top domain of virus capsid protein
73	c2l02B_	Alignment	not modelled	14.6	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein bt2368 from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr375
74	c1l9mB_	Alignment	not modelled	14.4	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein-glutamine glutamyltransferase e3; **PDBTitle:** three-dimensional structure of the human transglutaminase 32 enzyme: binding of calcium ions change structure for3 activation
75	c1wkwB_	Alignment	not modelled	13.7	67	**PDB header:**translation/protein binding **Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 4e **PDBTitle:** crystal structure of the ternary complex of eif4e-m7gpppa-2 4ebp1 peptide
76	d1ex0a2	Alignment	not modelled	12.8	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Transglutaminase, two C-terminal domains **Family:**Transglutaminase, two C-terminal domains
77	c2l0dA_	Alignment	not modelled	12.4	21	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**cell surface protein; **PDBTitle:** solution nmr structure of putative cell surface protein ma_4588 (272-2 376 domain) from methanosarcina acetivorans, northeast structural3 genomics consortium target mvr254a
78	d2pwwa1	Alignment	not modelled	11.9	17	**Fold:**TBP-like **Superfamily:**YugN-like **Family:**YugN-like
79	c3h6aB_	Alignment	not modelled	11.8	6	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-4; **PDBTitle:** structure of the calx-beta domain of integrin beta42

						crystallized in the presence of calcium
80	d1cuoa_	Alignment	not modelled	11.5	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
81	c3k6sB_	Alignment	not modelled	11.1	11	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-2; **PDBTitle:** structure of integrin alphaxbeta2 ectodomain
82	d1xvsa_	Alignment	not modelled	10.5	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ApaG-like **Family:**ApaG-like
83	d1hmja_	Alignment	not modelled	9.8	23	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
84	d2ccwa1	Alignment	not modelled	9.7	14	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
85	c3qe5A_	Alignment	not modelled	9.3	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**major cell-surface adhesin pac; **PDBTitle:** complete structure of streptococcus mutans antigen i/ii carboxy-2 terminus
86	c2h47C_	Alignment	not modelled	9.3	17	**PDB header:**oxidoreductase/electron transport **Chain:** C: **PDB Molecule:**azurin; **PDBTitle:** crystal structure of an electron transfer complex between2 aromatic amine dephydrogenase and azurin from alcaligenes3 faecalis (form 1)
87	d1vjja2	Alignment	not modelled	9.2	5	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Transglutaminase, two C-terminal domains **Family:**Transglutaminase, two C-terminal domains
88	c2f7fA_	Alignment	not modelled	9.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase, putative; **PDBTitle:** crystal structure of enterococcus faecalis putative nicotinate2 phosphoribosyltransferase, new york structural genomics consortium
89	d1cc3a_	Alignment	not modelled	9.1	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
90	c2kl6A_	Alignment	not modelled	8.9	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of the cardb domain of pf1109 from2 pyrococcus furiosus. northeast structural genomics3 consortium target pfr193a
91	c1v7wA_	Alignment	not modelled	8.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**chitobiose phosphorylase; **PDBTitle:** crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac
92	d1g0da2	Alignment	not modelled	8.7	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Transglutaminase, two C-terminal domains **Family:**Transglutaminase, two C-terminal domains
93	c2qziA_	Alignment	not modelled	8.5	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of a conserved protein of unknown function from2 streptococcus thermophilus lmg 18311.
94	d2q9oa2	Alignment	not modelled	8.5	9	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
95	c2ii8F_	Alignment	not modelled	8.0	16	**PDB header:**signaling protein **Chain:** F: **PDB Molecule:**anabaena sensory rhodopsin transducer protein; **PDBTitle:** anabaena sensory rhodopsin transducer
96	c3rfrI_	Alignment	not modelled	7.9	18	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**pmob; **PDBTitle:** crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
97	d1dd1a_	Alignment	not modelled	7.9	15	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**SMAD domain
98	c3tqzA_	Alignment	not modelled	7.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deoxyuridine 5'-triphosphate nucleotidohydrolase; **PDBTitle:** structure of a deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)2 from coxiella burnetii
99	d1jzga_	Alignment	not modelled	7.8	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like