Phyre^2

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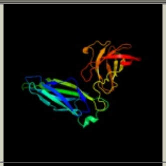
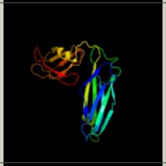
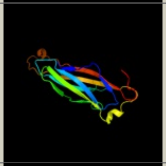
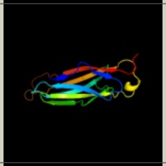
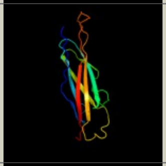
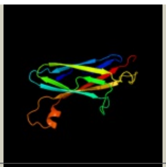
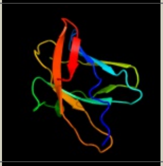
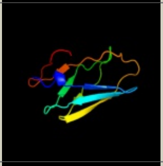
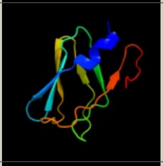
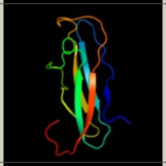
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qpxA_	Alignment		100.0	43	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**papd chaperone; **PDBTitle:** crystal structures of self-capping papd chaperone homodimers
2	c1qunA_	Alignment		100.0	34	**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	28	**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	c1z9sA_	Alignment		100.0	27	**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
5	c1l4iA_	Alignment		100.0	40	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**sfae protein; **PDBTitle:** crystal structure of the periplasmic chaperone sfae
6	c3f6iB_	Alignment		100.0	26	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone protein faee; **PDBTitle:** structure of the semet labeled f4 fibrial chaperone faee
7	c3q48B_	Alignment		100.0	34	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone cupb2; **PDBTitle:** crystal structure of pseudomonas aeruginosa cupb2 chaperone
8	d2j2za1	Alignment		100.0	50	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
9	d3bwuc1	Alignment		100.0	38	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
10	d2co7b1	Alignment		100.0	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
11	d1p5va1	Alignment		100.0	30	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone

12	d1l4ia1	Alignment		100.0	43	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
13	d2j2za2	Alignment		99.9	32	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
14	d3bwuc2	Alignment		99.8	32	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
15	d1p5va2	Alignment		99.7	21	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
16	d2co7b2	Alignment		99.7	23	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
17	d1l4ia2	Alignment		99.7	39	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
18	c2qsvA_	Alignment		97.8	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function from porphyromonas2 gingivalis w83
19	d1m1sa_	Alignment		97.4	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
20	d1rowa_	Alignment		96.4	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
21	c1z9oB_	Alignment	not modelled	96.2	17	**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
22	d1grwa_	Alignment	not modelled	96.2	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
23	d1mspa_	Alignment	not modelled	96.0	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
24	c2e6jA_	Alignment	not modelled	94.9	14	**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
25	c3qisA_	Alignment	not modelled	94.0	19	**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
26	c3qbtH_	Alignment	not modelled	92.5	19	**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
27	c2ys4A_	Alignment	not modelled	91.0	18	**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
						Fold: Immunoglobulin-like beta-sandwich

28	d1e42a1	Alignment	not modelled	86.5	17	**Superfamily:**Clathrin adaptor appendage domain **Family:**Alpha-adaptin ear subdomain-like
29	d1wica_	Alignment	not modelled	85.4	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
30	c3ac0B_	Alignment	not modelled	85.2	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase i; **PDBTitle:** crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
31	d2vzsa2	Alignment	not modelled	81.9	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
32	d1ejxb_	Alignment	not modelled	79.6	19	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
33	d4ubpb_	Alignment	not modelled	78.3	22	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
34	c2x41A_	Alignment	not modelled	75.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
35	d1e9ya1	Alignment	not modelled	73.1	21	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
36	c3qgaD_	Alignment	not modelled	69.8	18	**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
37	c1yycA_	Alignment	not modelled	68.0	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
38	c1e9zA_	Alignment	not modelled	66.6	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**urease subunit alpha; **PDBTitle:** crystal structure of helicobacter pylori urease
39	c3o0lB_	Alignment	not modelled	63.2	17	**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
40	d1ufga_	Alignment	not modelled	61.0	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
41	c1e42A_	Alignment	not modelled	60.7	17	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**ap-2 complex subunit beta; **PDBTitle:** beta2-adaptin appendage domain, from clathrin adaptor ap2
42	c2lllA_	Alignment	not modelled	52.5	12	**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
43	c2qvkA_	Alignment	not modelled	50.9	5	**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
44	c3ginB_	Alignment	not modelled	50.5	9	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**sodium/calcium exchanger 1; **PDBTitle:** crystal structure of e454k-cbd1
45	d1v8ha1	Alignment	not modelled	49.0	8	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**SoxZ-like
46	d1ifra_	Alignment	not modelled	48.9	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
47	c3jt0B_	Alignment	not modelled	44.1	14	**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	d2fwua1	Alignment	not modelled	41.2	7	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CalX-like **Family:**CalX-beta domain
49	d1kyaa2	Alignment	not modelled	40.5	10	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
50	d1hfua2	Alignment	not modelled	40.3	13	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
51	d1aoza2	Alignment	not modelled	35.3	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
52	c3eujB_	Alignment	not modelled	34.9	25	**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
53	d2dpka1	Alignment	not modelled	33.4	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CalX-like **Family:**CalX-beta domain

54	c2oxgE_	Alignment	not modelled	33.4	11	**PDB header:**transport protein **Chain:** E: **PDB Molecule:**soxz protein; **PDBTitle:** the soxyz complex of paracoccus pantotrophus
55	c3butA_	Alignment	not modelled	29.4	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein af_0446; **PDBTitle:** crystal structure of protein af_0446 from archaeoglobus fulgidus
56	d1jz8a2	Alignment	not modelled	28.3	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
57	c3h6aB_	Alignment	not modelled	27.0	8	**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
58	d2q9oa2	Alignment	not modelled	25.3	23	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
59	d1xo8a_	Alignment	not modelled	23.3	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**LEA14-like **Family:**LEA14-like
60	d1w8oa1	Alignment	not modelled	22.5	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
61	d1ivta_	Alignment	not modelled	21.6	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
62	d1k3ra1	Alignment	not modelled	20.0	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Hypothetical protein MTH1 (MT0001), insert domain
63	d1v10a2	Alignment	not modelled	20.0	11	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
64	c3hs8A_	Alignment	not modelled	19.0	13	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**adaptor protein complex ap-2, alpha 2 subunit; **PDBTitle:** intersectin 1-peptide-ap2 alpha ear complex
65	c2kutA_	Alignment	not modelled	16.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of gmr58a from geobacter metallireducens.2 northeast structural genomics consortium target gmr58a
66	c2frgP_	Alignment	not modelled	16.3	14	**PDB header:**immune system **Chain:** P: **PDB Molecule:**trem-like transcript-1; **PDBTitle:** structure of the immunoglobulin-like domain of human tlt-1
67	c1wkwB_	Alignment	not modelled	15.7	44	**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
68	c3isyA_	Alignment	not modelled	14.1	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
69	c2vzvB_	Alignment	not modelled	13.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exo-beta-d-glucosaminidase; **PDBTitle:** substrate complex of amycolatopsis orientalis exo-2 chitosanase csxa e541a with chitosan
70	d1hmja_	Alignment	not modelled	13.7	23	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
71	c2l0dA_	Alignment	not modelled	12.9	15	**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
72	c3rfrI_	Alignment	not modelled	12.8	11	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**pmob; **PDBTitle:** crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
73	c3ts3D_	Alignment	not modelled	11.6	27	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**capsid polyprotein; **PDBTitle:** crystal structure of the projection domain of the turkey astrovirus2 capsid protein at 1.5 angstrom resolution
74	d1gyca2	Alignment	not modelled	10.9	8	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
75	c1ky6A_	Alignment	not modelled	10.7	13	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**alpha-adaptin c; **PDBTitle:** ap-2 clathrin adaptor alpha-appendage in complex with epsin2 dpw peptide
76	c1zeqX_	Alignment	not modelled	9.9	7	**PDB header:**metal binding protein **Chain:** X: **PDB Molecule:**cation efflux system protein cusf; **PDBTitle:** 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
77	d2huha1	Alignment	not modelled	9.9	27	**Fold:**C2 domain-like **Superfamily:**Smr-associated domain-like **Family:**Smr-associated domain
78	d2v33a1	Alignment	not modelled	9.8	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
79	c2qziA_	Alignment	not modelled	9.4	29	**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.
						PDB header:transferase

80	c1l9mB_	Alignment	not modelled	8.8	17	**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
81	c2phgB_	Alignment	not modelled	8.7	50	**PDB header:**transcription **Chain:** B: **PDB Molecule:**alpha trans-inducing protein; **PDBTitle:** model for vp16 binding to tfiib
82	c2pheC_	Alignment	not modelled	8.5	50	**PDB header:**transcription **Chain:** C: **PDB Molecule:**alpha trans-inducing protein; **PDBTitle:** model for vp16 binding to pc4
83	c3i74B_	Alignment	not modelled	7.9	18	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**subtilisin-like protease; **PDBTitle:** crystal structure of the plant subtilisin-like protease sbt3 in2 complex with a chloromethylketone inhibitor
84	c2je8B_	Alignment	not modelled	7.2	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-mannosidase; **PDBTitle:** structure of a beta-mannosidase from bacteroides2 thetaiotaomicron
85	c3rb7E_	Alignment	not modelled	7.2	8	**PDB header:**metal binding protein **Chain:** E: **PDB Molecule:**na/ca exchange protein; **PDBTitle:** crystal structure of cbd12 from calx1.2
86	c2kl6A_	Alignment	not modelled	7.2	10	**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
87	d2f7fa1	Alignment	not modelled	6.8	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
88	c1z8yF_	Alignment	not modelled	6.1	11	**PDB header:**virus **Chain:** F: **PDB Molecule:**spike glycoprotein e1; **PDBTitle:** mapping the e2 glycoprotein of alphaviruses
89	c3k6sB_	Alignment	not modelled	6.0	21	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-2; **PDBTitle:** structure of integrin alphaxbeta2 ectodomain
90	d1eg3a3	Alignment	not modelled	5.7	38	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
91	d1cuoa_	Alignment	not modelled	5.5	11	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like