Phyre2

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Description	P42914
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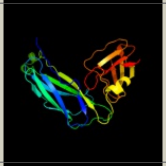
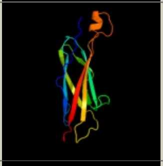
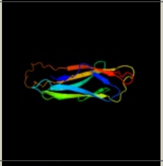
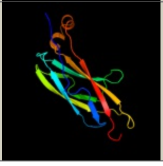
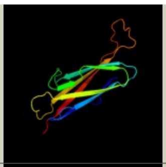
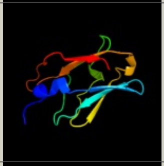
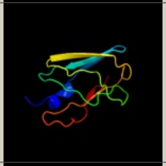
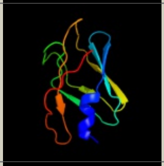
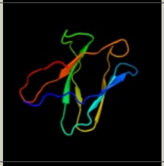
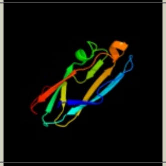
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qunA_	Alignment		100.0	40	**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
2	c1z9sA_	Alignment		100.0	30	**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
3	c2co7B_	Alignment		100.0	36	**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	c1l4iA_	Alignment		100.0	39	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**sfae protein; **PDBTitle:** crystal structure of the periplasmic chaperone sfae
5	c1qpxA_	Alignment		100.0	36	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**papd chaperone; **PDBTitle:** crystal structures of self-capping papd chaperone homodimers
6	c3f6iB_	Alignment		100.0	30	**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	36	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone cupb2; **PDBTitle:** crystal structure of pseudomonas aeruginosa cupb2 chaperone
8	d2co7b1	Alignment		100.0	39	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
9	d3bwuc1	Alignment		100.0	46	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
10	d2j2za1	Alignment		100.0	43	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
11	d1p5va1	Alignment		100.0	34	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone

12	d1l4ia1	Alignment		100.0	48	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
13	d3bwuc2	Alignment		99.9	30	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
14	d1p5va2	Alignment		99.8	28	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
15	d2co7b2	Alignment		99.8	30	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
16	d1l4ia2	Alignment		99.7	28	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
17	d2j2za2	Alignment		99.7	27	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
18	d1m1sa_	Alignment		97.2	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
19	d1grwa_	Alignment		96.9	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
20	d1rowa_	Alignment		96.6	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
21	d1mspa_	Alignment	not modelled	96.1	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
22	c2qsvA_	Alignment	not modelled	95.7	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function from porphyromonas2 gingivalis w83
23	c1z9oB_	Alignment	not modelled	94.6	14	**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
24	c2e6jA_	Alignment	not modelled	92.3	19	**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	d2vzsa2	Alignment	not modelled	92.0	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
26	c3o0lB_	Alignment	not modelled	91.6	12	**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
27	c2ys4A_	Alignment	not modelled	88.5	22	**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
28	c3qbtH_	Alignment	not modelled	87.8	12	**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
29	c3qisA_	Alignment	not modelled	87.6	12	**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
30	d1wica_	Alignment	not modelled	82.7	7	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
31	d1ejxb_	Alignment	not modelled	76.3	18	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
32	d4ubpb_	Alignment	not modelled	75.4	19	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
33	c3ac0B_	Alignment	not modelled	74.1	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase i; **PDBTitle:** crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
34	d2dpka1	Alignment	not modelled	71.8	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CalX-like **Family:**CalX-beta domain
35	d1e9ya1	Alignment	not modelled	69.3	23	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
36	c3ginB_	Alignment	not modelled	64.1	10	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**sodium/calcium exchanger 1; **PDBTitle:** crystal structure of e454k-cbd1
37	c1e9zA_	Alignment	not modelled	61.2	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**urease subunit alpha; **PDBTitle:** crystal structure of helicobacter pylori urease
38	d1k3ra1	Alignment	not modelled	55.7	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Hypothetical protein MTH1 (MT0001), insert domain
39	c3qgaD_	Alignment	not modelled	54.5	20	**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
40	c2x41A_	Alignment	not modelled	49.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
41	c2je8B_	Alignment	not modelled	49.1	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-mannosidase; **PDBTitle:** structure of a beta-mannosidase from bacteroides2 thetaiotaomicron
42	c3jt0B_	Alignment	not modelled	43.2	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
43	c3eujB_	Alignment	not modelled	41.5	33	**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
44	d1aoza2	Alignment	not modelled	41.3	15	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
45	c3rb7E_	Alignment	not modelled	41.3	16	**PDB header:**metal binding protein **Chain:** E: **PDB Molecule:**na/ca exchange protein; **PDBTitle:** crystal structure of cbd12 from calx1.2
46	c3h6aB_	Alignment	not modelled	37.8	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
47	d1hfua2	Alignment	not modelled	32.5	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
48	d1kyaa2	Alignment	not modelled	31.5	10	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
49	d1jz8a2	Alignment	not modelled	31.0	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
50	d1ufga_	Alignment	not modelled	27.8	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
51	c2vzvB_	Alignment	not modelled	24.8	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exo-beta-d-glucosaminidase; **PDBTitle:** substrate complex of amycolatopsis orientalis exo-2 chitosanase csxa e541a with chitosan
52	d1e42a1	Alignment	not modelled	24.5	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Clathrin adaptor appendage domain **Family:**Alpha-adaptin ear subdomain-like
53	d2q9oa2	Alignment	not modelled	20.8	24	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
54	c3k6sB_	Alignment	not modelled	20.6	22	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-2; **PDBTitle:** structure of integrin alphaxbeta2 ectodomain

55	d1hmja_	Alignment	not modelled	19.0	13	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
56	c1yycA_	Alignment	not modelled	18.9	12	**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
57	c2qvkA_	Alignment	not modelled	18.7	9	**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
58	c3butA_	Alignment	not modelled	16.9	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein af_0446; **PDBTitle:** crystal structure of protein af_0446 from archaeoglobus fulgidus
59	d1xo8a_	Alignment	not modelled	16.9	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**LEA14-like **Family:**LEA14-like
60	d1r7aa1	Alignment	not modelled	15.8	24	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
61	c3e9uA_	Alignment	not modelled	15.7	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**na/ca exchange protein; **PDBTitle:** crystal structure of calx cbd2 domain
62	c2lllA_	Alignment	not modelled	15.0	14	**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
63	d1ifra_	Alignment	not modelled	14.7	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
64	d1w8oa1	Alignment	not modelled	13.5	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
65	c2f1eA_	Alignment	not modelled	13.5	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein apag; **PDBTitle:** solution structure of apag protein
66	d1yq2a1	Alignment	not modelled	13.2	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
67	d1gyca2	Alignment	not modelled	13.0	10	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
68	c2l02B_	Alignment	not modelled	12.8	19	**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
69	d2fwua1	Alignment	not modelled	11.9	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CalX-like **Family:**CalX-beta domain
70	c1v7wA_	Alignment	not modelled	11.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**chitobiose phosphorylase; **PDBTitle:** crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac
71	d1ivta_	Alignment	not modelled	10.4	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
72	d1pkoa_	Alignment	not modelled	9.2	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
73	d2huha1	Alignment	not modelled	8.9	16	**Fold:**C2 domain-like **Superfamily:**Smr-associated domain-like **Family:**Smr-associated domain
74	c2q9oA_	Alignment	not modelled	8.1	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**laccase-1; **PDBTitle:** near-atomic resolution structure of a melanocarpus albomyces laccase
75	c3of6D_	Alignment	not modelled	8.0	21	**PDB header:**immune system **Chain:** D: **PDB Molecule:**pre t-cell antigen receptor alpha; **PDBTitle:** human pre-t cell receptor crystal structure
76	c2pheC_	Alignment	not modelled	7.9	67	**PDB header:**transcription **Chain:** C: **PDB Molecule:**alpha trans-inducing protein; **PDBTitle:** model for vp16 binding to pc4
77	c2phgB_	Alignment	not modelled	7.8	67	**PDB header:**transcription **Chain:** B: **PDB Molecule:**alpha trans-inducing protein; **PDBTitle:** model for vp16 binding to tfiib
78	c2qziA_	Alignment	not modelled	7.4	25	**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.
79	c3ppsD_	Alignment	not modelled	7.4	27	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**laccase; **PDBTitle:** crystal structure of an ascomycete fungal laccase from thielavia2 arenaria
80	c1wkwB_	Alignment	not modelled	7.3	63	**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
81	c1a65A_	Alignment	not modelled	7.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**laccase; **PDBTitle:** type-2 cu-depleted laccase from coprinus cinereus
82	c1hymB_	Alignment	not modelled	7.0	31	**PDB header:**hydrolase (serine proteinase) **Chain:** B: **PDB Molecule:**hydrolyzed cucurbita maxima trypsin inhibitor v; **PDBTitle:** hydrolyzed trypsin inhibitor (cmti-v, minimized average nmr2 structure)
83	c1u8cB_	Alignment	not modelled	7.0	22	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** a novel adaptation of the integrin psi domain revealed from its2 crystal structure
84	c1zpuE_	Alignment	not modelled	6.8	12	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**iron transport multicopper oxidase fet3; **PDBTitle:** crystal structure of fet3p, a multicopper oxidase that functions in2 iron import
85	c1z65A_	Alignment	not modelled	6.8	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**prion-like protein doppel; **PDBTitle:** mouse doppel 1-30 peptide
86	d1cuoa_	Alignment	not modelled	5.6	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
87	c3i3fB_	Alignment	not modelled	5.5	9	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** hypothetical protein from giardia lamblia gl50803_14299