Phyre^2

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Description	P75856
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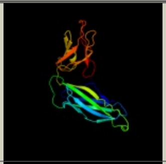
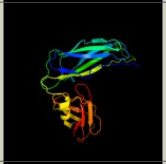
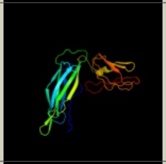
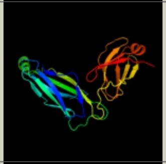
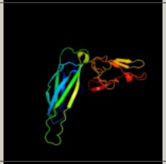
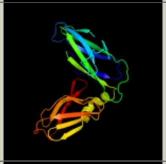
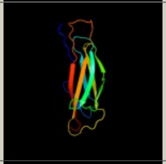
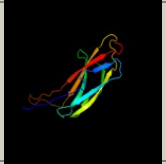
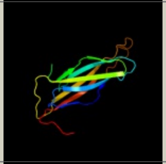
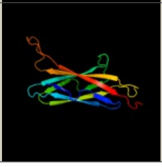
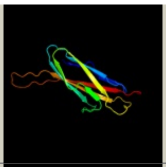
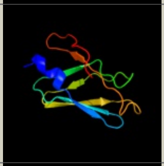
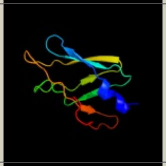
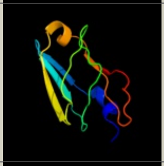
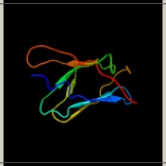
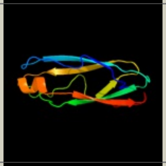
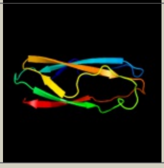
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qunA_	Alignment		100.0	46	**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	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
3	c2co7B_	Alignment		100.0	31	**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	46	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**sfae protein; **PDBTitle:** crystal structure of the periplasmic chaperone sfae
5	c1qpxA_	Alignment		100.0	29	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**papd chaperone; **PDBTitle:** crystal structures of self-capping papd chaperone homodimers
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	37	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone cupb2; **PDBTitle:** crystal structure of pseudomonas aeruginosa cupb2 chaperone
8	d2co7b1	Alignment		100.0	35	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
9	d1p5va1	Alignment		100.0	36	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
10	d2j2za1	Alignment		100.0	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
11	d3bwuc1	Alignment		100.0	48	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone

12	d1l4ia1	Alignment		100.0	46	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
13	d3bwuc2	Alignment		99.8	46	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
14	d1p5va2	Alignment		99.8	24	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
15	d1l4ia2	Alignment		99.8	49	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
16	d2co7b2	Alignment		99.8	24	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
17	d2j2za2	Alignment		99.7	23	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
18	d1m1sa_	Alignment		97.6	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
19	d1grwa_	Alignment		97.2	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
20	d1rowa_	Alignment		96.8	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
21	d1mspa_	Alignment	not modelled	96.5	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
22	c1z9oB_	Alignment	not modelled	95.9	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
23	c2qsvA_	Alignment	not modelled	94.6	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
24	c2e6jA_	Alignment	not modelled	94.1	16	**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	91.1	14	**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	d2vzsa2	Alignment	not modelled	91.0	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
27	c2ys4A_	Alignment	not modelled	90.3	20	**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	d1wica_	Alignment	not modelled	89.9	13	**Superfamily:**PapD-like **Family:**MSP-like
29	c3qbtH_	Alignment	not modelled	83.5	13	**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	d1ejxb_	Alignment	not modelled	79.2	14	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
31	d4ubpb_	Alignment	not modelled	78.3	22	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
32	c3ac0B_	Alignment	not modelled	77.3	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase i; **PDBTitle:** crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
33	c3h6aB_	Alignment	not modelled	76.4	10	**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
34	d2dpka1	Alignment	not modelled	76.4	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CalX-like **Family:**CalX-beta domain
35	d1e9ya1	Alignment	not modelled	73.3	26	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
36	c2x41A_	Alignment	not modelled	71.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
37	c3qgaD_	Alignment	not modelled	69.9	16	**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
38	c1e9zA_	Alignment	not modelled	66.2	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**urease subunit alpha; **PDBTitle:** crystal structure of helicobacter pylori urease
39	c3o0lB_	Alignment	not modelled	62.7	9	**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	c3ginB_	Alignment	not modelled	62.0	11	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**sodium/calcium exchanger 1; **PDBTitle:** crystal structure of e454k-cbd1
41	d1aoza2	Alignment	not modelled	57.9	13	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
42	d1e42a1	Alignment	not modelled	56.2	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Clathrin adaptor appendage domain **Family:**Alpha-adaptin ear subdomain-like
43	c3eujB_	Alignment	not modelled	52.1	18	**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	d1hfua2	Alignment	not modelled	50.5	13	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
45	c2qvkA_	Alignment	not modelled	48.8	17	**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
46	d1yq2a1	Alignment	not modelled	48.4	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
47	c3rb7E_	Alignment	not modelled	48.2	13	**PDB header:**metal binding protein **Chain:** E: **PDB Molecule:**na/ca exchange protein; **PDBTitle:** crystal structure of cbd12 from calx1.2
48	d1k3ra1	Alignment	not modelled	46.7	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Hypothetical protein MTH1 (MT0001), insert domain
49	c1e42A_	Alignment	not modelled	42.6	16	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**ap-2 complex subunit beta; **PDBTitle:** beta2-adaptin appendage domain, from clathrin adaptor ap2
50	c2je8B_	Alignment	not modelled	39.6	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-mannosidase; **PDBTitle:** structure of a beta-mannosidase from bacteroides2 thetaiotaomicron
51	c3jt0B_	Alignment	not modelled	38.1	10	**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
52	c3butA_	Alignment	not modelled	36.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein af_0446; **PDBTitle:** crystal structure of protein af_0446 from archaeoglobus fulgidus
53	c3e9uA_	Alignment	not modelled	36.3	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**na/ca exchange protein; **PDBTitle:** crystal structure of calx cbd2 domain

54	c1yycA_	Alignment	not modelled	34.8	20	**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
55	d2fwua1	Alignment	not modelled	34.1	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CalX-like **Family:**CalX-beta domain
56	c3e9tD_	Alignment	not modelled	32.6	10	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**na/ca exchange protein; **PDBTitle:** crystal structure of apo-form calx cbd1 domain
57	d1kyaa2	Alignment	not modelled	29.5	10	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
58	d2huha1	Alignment	not modelled	29.5	22	**Fold:**C2 domain-like **Superfamily:**Smr-associated domain-like **Family:**Smr-associated domain
59	d1jz8a2	Alignment	not modelled	28.5	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
60	d1gyca2	Alignment	not modelled	25.3	9	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
61	c1l5gA_	Alignment	not modelled	24.9	10	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha v; **PDBTitle:** crystal structure of the extracellular segment of integrin avb3 in2 complex with an arg-gly-asp ligand
62	d1xo8a_	Alignment	not modelled	22.4	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**LEA14-like **Family:**LEA14-like
63	d1r7aa1	Alignment	not modelled	21.6	23	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
64	d1ufga_	Alignment	not modelled	20.6	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
65	d1w8oa1	Alignment	not modelled	17.8	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
66	c2lllA_	Alignment	not modelled	15.5	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
67	d1ifra_	Alignment	not modelled	14.8	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
68	c2qziA_	Alignment	not modelled	14.1	17	**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.
69	c2vzvB_	Alignment	not modelled	14.0	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
70	c1wkwB_	Alignment	not modelled	13.9	38	**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
71	d1hmja_	Alignment	not modelled	11.3	3	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
72	c2f1eA_	Alignment	not modelled	11.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein apag; **PDBTitle:** solution structure of apag protein
73	c3i3fB_	Alignment	not modelled	11.1	16	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** hypothetical protein from giardia lamblia gl50803_14299
74	c3of6D_	Alignment	not modelled	8.8	12	**PDB header:**immune system **Chain:** D: **PDB Molecule:**pre t-cell antigen receptor alpha; **PDBTitle:** human pre-t cell receptor crystal structure
75	c2zooA_	Alignment	not modelled	8.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nitrite reductase; **PDBTitle:** crystal structure of nitrite reductase from pseudoalteromonas2 haloplanktis tac125
76	d1ivta_	Alignment	not modelled	8.2	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
77	c1zpuE_	Alignment	not modelled	7.9	17	**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
78	c2phgB_	Alignment	not modelled	7.8	50	**PDB header:**transcription **Chain:** B: **PDB Molecule:**alpha trans-inducing protein; **PDBTitle:** model for vp16 binding to tfiib
79	c2pheC_	Alignment	not modelled	7.7	50	**PDB header:**transcription **Chain:** C: **PDB Molecule:**alpha trans-inducing protein; **PDBTitle:** model for vp16 binding to pc4
80	d1ty0a1	Alignment	not modelled	7.7	50	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins

						Family: Superantigen toxins, N-terminal domain
81	c2ph7B_	Alignment	not modelled	7.4	40	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein af_2093; **PDBTitle:** crystal structure of af2093 from archaeoglobus fulgidus
82	d1tzaa_	Alignment	not modelled	6.9	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ApaG-like **Family:**ApaG-like
83	d1eu3a1	Alignment	not modelled	6.4	24	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
84	c1hymB_	Alignment	not modelled	5.5	27	**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)
85	c2b9kA_	Alignment	not modelled	5.5	13	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**antimicrobial peptide lci; **PDBTitle:** solution structure of lci, an amp from bacillus subtilis
86	c2l02B_	Alignment	not modelled	5.4	8	**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
87	c1pzdA_	Alignment	not modelled	5.4	10	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**coatomer gamma subunit; **PDBTitle:** structural identification of a conserved appendage domain2 in the carboxyl-terminus of the copi gamma-subunit.
88	c1egpB_	Alignment	not modelled	5.3	22	**PDB header:**proteinase inhibitor **Chain:** B: **PDB Molecule:**eglin-c; **PDBTitle:** proteinase inhibitor eglin c with hydrolysed reactive center
89	d1v7wa1	Alignment	not modelled	5.2	10	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glycosyltransferase family 36 C-terminal domain
90	d1pkoa_	Alignment	not modelled	5.1	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)