Phyre2

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Description	P31697
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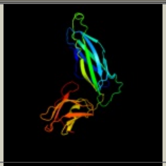
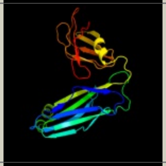
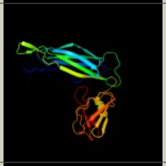
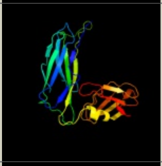
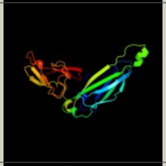
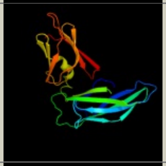
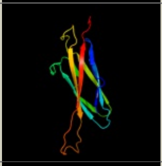
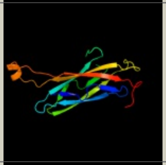
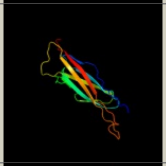
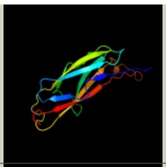
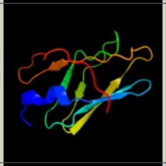
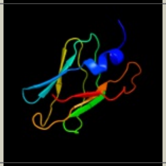
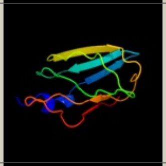
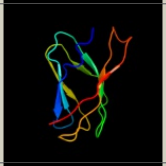
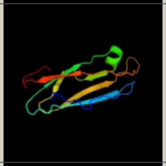
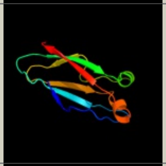
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qunA_	Alignment		100.0	99	**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	c1l4iA_	Alignment		100.0	71	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**sfae protein; **PDBTitle:** crystal structure of the periplasmic chaperone sfae
3	c2co7B_	Alignment		100.0	35	**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	36	**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	c1qpxA_	Alignment		100.0	33	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**papd chaperone; **PDBTitle:** crystal structures of self-capping papd chaperone homodimers
6	c3f6iB_	Alignment		100.0	33	**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	d3bwuc1	Alignment		100.0	100	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
9	d2j2za1	Alignment		100.0	36	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
10	d2co7b1	Alignment		100.0	39	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
11	d1l4ia1	Alignment		100.0	79	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone

12	d1p5va1	Alignment		100.0	42	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
13	d3bwuc2	Alignment		99.9	100	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
14	d1p5va2	Alignment		99.9	30	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
15	d1l4ia2	Alignment		99.8	63	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
16	d2co7b2	Alignment		99.8	29	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
17	d2j2za2	Alignment		99.7	28	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
18	d1m1sa_	Alignment		96.7	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
19	d1rowa_	Alignment		95.2	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
20	d1grwa_	Alignment		94.5	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
21	c2qsvA_	Alignment	not modelled	93.8	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
22	c1z9oB_	Alignment	not modelled	92.0	13	**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	92.0	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
24	c3qisA_	Alignment	not modelled	91.4	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
25	c2e6jA_	Alignment	not modelled	89.6	11	**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	c3qbtH_	Alignment	not modelled	88.9	10	**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	d2vzsa2	Alignment	not modelled	82.8	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
28	c3ac0B	Alignment	not modelled	79.3	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase i;

28	c3ac0B_	Alignment	not modelled	79.3	9	**PDBTitle:** crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
29	d1wica_	Alignment	not modelled	77.6	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
30	c3ginB_	Alignment	not modelled	76.9	8	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**sodium/calcium exchanger 1; **PDBTitle:** crystal structure of e454k-cbd1
31	c2ys4A_	Alignment	not modelled	69.3	10	**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
32	c2qvkA_	Alignment	not modelled	61.7	8	**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
33	d4ubpb_	Alignment	not modelled	61.6	14	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
34	d1ejxb_	Alignment	not modelled	60.9	10	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
35	d2dpka1	Alignment	not modelled	57.5	8	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CalX-like **Family:**CalX-beta domain
36	c2x41A_	Alignment	not modelled	56.5	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
37	d2fwua1	Alignment	not modelled	55.7	8	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CalX-like **Family:**CalX-beta domain
38	d1e9ya1	Alignment	not modelled	55.5	18	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
39	d1e42a1	Alignment	not modelled	55.4	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Clathrin adaptor appendage domain **Family:**Alpha-adaptin ear subdomain-like
40	c3h6aB_	Alignment	not modelled	52.6	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
41	c1e9zA_	Alignment	not modelled	42.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**urease subunit alpha; **PDBTitle:** crystal structure of helicobacter pylori urease
42	c3o0lB_	Alignment	not modelled	42.6	14	**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
43	c1yycA_	Alignment	not modelled	41.4	16	**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
44	c3eujB_	Alignment	not modelled	40.1	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
45	c3qgaD_	Alignment	not modelled	38.2	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
46	c3butA_	Alignment	not modelled	32.3	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
47	d1k3ra1	Alignment	not modelled	31.0	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Hypothetical protein MTH1 (MT0001), insert domain
48	c3jt0B_	Alignment	not modelled	29.7	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
49	d1xo8a_	Alignment	not modelled	29.3	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**LEA14-like **Family:**LEA14-like
50	c3rb7E_	Alignment	not modelled	26.1	9	**PDB header:**metal binding protein **Chain:** E: **PDB Molecule:**na/ca exchange protein; **PDBTitle:** crystal structure of cbd12 from calx1.2
51	c1e42A_	Alignment	not modelled	22.5	21	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**ap-2 complex subunit beta; **PDBTitle:** beta2-adaptin appendage domain, from clathrin adaptor ap2
52	d1jz8a2	Alignment	not modelled	21.1	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
53	d2f7fa1	Alignment	not modelled	20.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like

54	c3rfrl_	Alignment	not modelled	19.4	19	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**pmob; **PDBTitle:** crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
55	c2f7fA_	Alignment	not modelled	18.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase, putative; **PDBTitle:** crystal structure of enterococcus faecalis putative nicotinate2 phosphoribosyltransferase, new york structural genomics consortium
56	d1r7aa1	Alignment	not modelled	18.3	20	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
57	d1kyaa2	Alignment	not modelled	17.4	9	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
58	d1w8oa1	Alignment	not modelled	16.9	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
59	d1ufga_	Alignment	not modelled	16.6	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
60	c3e9uA_	Alignment	not modelled	16.1	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**na/ca exchange protein; **PDBTitle:** crystal structure of calx cbd2 domain
61	c1pzdA_	Alignment	not modelled	15.7	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.
62	d1aoza2	Alignment	not modelled	13.6	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
63	c2vzvB_	Alignment	not modelled	13.6	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exo-beta-d-glucosaminidase; **PDBTitle:** substrate complex of amycolatopsis orientalis exo-2 chitosanase csxa e541a with chitosan
64	c3k6sB_	Alignment	not modelled	13.1	11	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-2; **PDBTitle:** structure of integrin alphaxbeta2 ectodomain
65	d1hfua2	Alignment	not modelled	12.4	14	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
66	d1pkoa_	Alignment	not modelled	11.3	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
67	d1v7wa1	Alignment	not modelled	11.1	12	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glycosyltransferase family 36 C-terminal domain
68	c1l9mB_	Alignment	not modelled	10.4	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
69	c1r4xA_	Alignment	not modelled	9.9	12	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**coatomer gamma subunit; **PDBTitle:** crystal structure analys of the gamma-copi appendage domain
70	d1ifra_	Alignment	not modelled	9.5	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
71	c3e9tD_	Alignment	not modelled	9.3	10	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**na/ca exchange protein; **PDBTitle:** crystal structure of apo-form calx cbd1 domain
72	c1wkwB_	Alignment	not modelled	9.2	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
73	c2lllA_	Alignment	not modelled	9.2	11	**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
74	c2zooA_	Alignment	not modelled	8.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nitrite reductase; **PDBTitle:** crystal structure of nitrite reductase from pseudoalteromonas2 haloplanktis tac125
75	d1ivta_	Alignment	not modelled	8.0	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
76	c2l02B_	Alignment	not modelled	8.0	12	**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
77	d1gyca2	Alignment	not modelled	7.7	9	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
78	d1hmja_	Alignment	not modelled	6.8	13	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
						PDB header:unknown function

79	c3pdgA_	Alignment	not modelled	6.8	21	**Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
80	c2pheC_	Alignment	not modelled	6.6	50	**PDB header:**transcription **Chain:** C: **PDB Molecule:**alpha trans-inducing protein; **PDBTitle:** model for vp16 binding to pc4
81	c1u8cB_	Alignment	not modelled	6.5	11	**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
82	c2qziA_	Alignment	not modelled	6.5	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.
83	c2phgB_	Alignment	not modelled	6.4	50	**PDB header:**transcription **Chain:** B: **PDB Molecule:**alpha trans-inducing protein; **PDBTitle:** model for vp16 binding to tfiib
84	d2plta_	Alignment	not modelled	6.4	11	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
85	d1eu3a1	Alignment	not modelled	5.7	20	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
86	c3nuhB_	Alignment	not modelled	5.7	40	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** a domain insertion in e. coli gyrb adopts a novel fold that plays a2 critical role in gyrase function
87	c2z4dA_	Alignment	not modelled	5.6	21	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**26s proteasome regulatory subunit rpn13; **PDBTitle:** nmr structures of yeast proteasome component rpn13
88	d1v8ha1	Alignment	not modelled	5.5	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**SoxZ-like