Phyre2

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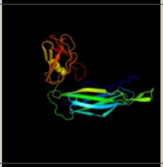
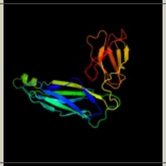
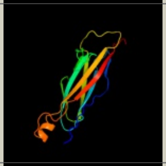
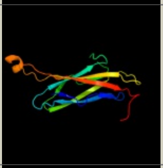
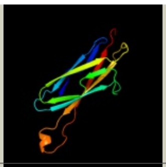
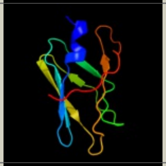
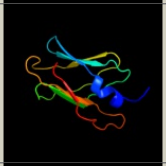
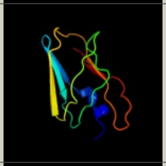
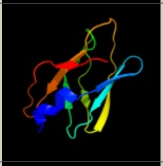
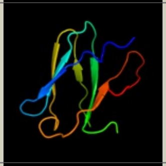
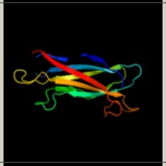
Description	P77249
Date	Thu Jan 5 12:26:49 GMT 2012
Unique Job ID	c98447ff7ee3d34f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qunA_	Alignment		100.0	48	**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	32	**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	29	**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	45	**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	27	**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	29	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone cupb2; **PDBTitle:** crystal structure of pseudomonas aeruginosa cupb2 chaperone
8	d3bwuc1	Alignment		100.0	58	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
9	d2co7b1	Alignment		100.0	32	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
10	d2j2za1	Alignment		100.0	34	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
11	d1p5va1	Alignment		100.0	38	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone

12	d1l4ia1	Alignment		100.0	54	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
13	d3bwuc2	Alignment		99.8	35	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
14	d1p5va2	Alignment		99.8	23	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
15	d2co7b2	Alignment		99.8	23	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
16	d1l4ia2	Alignment		99.7	33	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
17	d2j2za2	Alignment		99.6	23	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
18	d1m1sa_	Alignment		97.2	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
19	d1grwa_	Alignment		96.5	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
20	d1rowa_	Alignment		96.5	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
21	c2qsvA_	Alignment	not modelled	95.4	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
22	d1mspa_	Alignment	not modelled	95.2	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
23	c2e6jA_	Alignment	not modelled	94.3	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
24	c1z9oB_	Alignment	not modelled	93.2	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
25	c3o0lB_	Alignment	not modelled	92.9	7	**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
26	c3qisA_	Alignment	not modelled	91.8	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
27	c3qbtH_	Alignment	not modelled	90.5	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
						PDB header:structural genomics, unknown function **Chain:** A: **PDB Molecule:**hydrocephalus-inducing protein

28	c2ys4A_	Alignment	not modelled	88.0	12	homolog; **PDBTitle:** solution structure of the n-terminal papd-like domain of2 hydin protein from human
29	d2vzsa2	Alignment	not modelled	82.1	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
30	d1wica_	Alignment	not modelled	78.1	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
31	c3ginB_	Alignment	not modelled	71.9	11	**PDB header:**metal binding protein **Chain: B: PDB Molecule:**sodium/calcium exchanger 1; **PDBTitle:** crystal structure of e454k-cbd1
32	d1ufga_	Alignment	not modelled	71.8	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
33	d2dpka1	Alignment	not modelled	69.4	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CalX-like **Family:**CalX-beta domain
34	d4ubpb_	Alignment	not modelled	68.0	22	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
35	d1ejxb_	Alignment	not modelled	65.7	14	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
36	d1kyaa2	Alignment	not modelled	63.5	6	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
37	d1aoza2	Alignment	not modelled	63.0	26	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
38	d1e9ya1	Alignment	not modelled	62.1	21	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
39	d1hfua2	Alignment	not modelled	60.3	10	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
40	c2lllA_	Alignment	not modelled	55.9	18	**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
41	c3h6aB_	Alignment	not modelled	54.1	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
42	d1ifra_	Alignment	not modelled	53.9	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
43	d2q9oa2	Alignment	not modelled	53.3	23	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
44	c3jt0B_	Alignment	not modelled	52.8	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
45	c1e9zA_	Alignment	not modelled	50.6	21	**PDB header:**hydrolase **Chain: A: PDB Molecule:**urease subunit alpha; **PDBTitle:** crystal structure of helicobacter pylori urease
46	d1k3ra1	Alignment	not modelled	50.4	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Hypothetical protein MTH1 (MT0001), insert domain
47	c2je8B_	Alignment	not modelled	50.2	7	**PDB header:**hydrolase **Chain: B: PDB Molecule:**beta-mannosidase; **PDBTitle:** structure of a beta-mannosidase from bacteroides2 thetaiotaomicron
48	d1v10a2	Alignment	not modelled	48.6	10	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
49	c2qvkA_	Alignment	not modelled	47.4	10	**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
50	c3qgaD_	Alignment	not modelled	46.2	17	**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
51	c3eujB_	Alignment	not modelled	44.9	15	**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
52	d1e42a1	Alignment	not modelled	44.7	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Clathrin adaptor appendage domain **Family:**Alpha-adaptin ear subdomain-like
53	c3e9uA_	Alignment	not modelled	40.5	12	**PDB header:**membrane protein **Chain: A: PDB Molecule:**na/ca exchange protein; **PDBTitle:** crystal structure of calx cbd2 domain
						PDB header:metal binding protein

54	c3rb7E_	Alignment	not modelled	37.4	12	**Chain:** E: **PDB Molecule:**na/ca exchange protein; **PDBTitle:** crystal structure of cbd12 from calx1.2
55	c3ac0B_	Alignment	not modelled	33.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase i; **PDBTitle:** crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
56	c1yycA_	Alignment	not modelled	31.9	13	**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	d1gyca2	Alignment	not modelled	30.3	3	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
58	d1ivta_	Alignment	not modelled	27.5	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
59	d1xo8a_	Alignment	not modelled	23.7	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**LEA14-like **Family:**LEA14-like
60	c2vzvB_	Alignment	not modelled	22.5	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exo-beta-d-glucosaminidase; **PDBTitle:** substrate complex of amycolatopsis orientalis exo-2 chitosanase csxa e541a with chitosan
61	c3butA_	Alignment	not modelled	21.3	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein af_0446; **PDBTitle:** crystal structure of protein af_0446 from archaeoglobus fulgidus
62	c1a65A_	Alignment	not modelled	21.1	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**laccase; **PDBTitle:** type-2 cu-depleted laccase from coprinus cinereus
63	d1hmja_	Alignment	not modelled	20.9	26	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
64	c2x41A_	Alignment	not modelled	20.7	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
65	c2l02B_	Alignment	not modelled	19.4	16	**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
66	d1w8oa1	Alignment	not modelled	16.3	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
67	d1r7aa1	Alignment	not modelled	15.9	13	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
68	c3ppsD_	Alignment	not modelled	15.7	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**laccase; **PDBTitle:** crystal structure of an ascomycete fungal laccase from thielavia2 arenaria
69	c1asqB_	Alignment	not modelled	15.4	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ascorbate oxidase; **PDBTitle:** x-ray structures and mechanistic implications of three functional2 derivatives of ascorbate oxidase from zucchini: reduced-, peroxide-,3 and azide-forms
70	c2q9oA_	Alignment	not modelled	15.4	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**laccase-1; **PDBTitle:** near-atomic resolution structure of a melanocarpus albomyces laccase
71	d2fwua1	Alignment	not modelled	14.6	8	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CalX-like **Family:**CalX-beta domain
72	c1v10A_	Alignment	not modelled	14.6	9	**PDB header:**oxidase **Chain:** A: **PDB Molecule:**laccase; **PDBTitle:** structure of rigidoporus lignosus laccase from hemihedrally2 twinned crystals
73	c1wkwB_	Alignment	not modelled	14.0	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
74	c1gycA_	Alignment	not modelled	12.1	3	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**laccase 2; **PDBTitle:** crystal structure determination at room temperature of a2 laccase from trametes versicolor in its oxidised form3 containing a full complement of copper ions
75	c3of6D_	Alignment	not modelled	12.0	12	**PDB header:**immune system **Chain:** D: **PDB Molecule:**pre t-cell antigen receptor alpha; **PDBTitle:** human pre-t cell receptor crystal structure
76	d1yq2a1	Alignment	not modelled	11.6	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
77	c3e9tD_	Alignment	not modelled	11.5	11	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**na/ca exchange protein; **PDBTitle:** crystal structure of apo-form calx cbd1 domain
78	c2f7fA_	Alignment	not modelled	11.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase, putative; **PDBTitle:** crystal structure of enterococcus faecalis putative nicotinate2 phosphoribosyltransferase, new york structural genomics consortium
79	c1e42A_	Alignment	not modelled	11.0	16	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**ap-2 complex subunit beta;

79	c1e42A_	Alignment	not modelled	11.0	10	**PDBTitle:** beta2-adaptin appendage domain, from clathrin adaptor ap2
80	d1eu3a1	Alignment	not modelled	10.6	24	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
81	c3pe9D_	Alignment	not modelled	10.3	16	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
82	c2vqiA_	Alignment	not modelled	9.9	19	**PDB header:**transport **Chain:** A: **PDB Molecule:**outer membrane usher protein papc; **PDBTitle:** structure of the p pilus usher (papc) translocation pore
83	d1jz8a2	Alignment	not modelled	9.5	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
84	c3k6sB_	Alignment	not modelled	9.4	11	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-2; **PDBTitle:** structure of integrin alphaxbeta2 ectodomain
85	c2pheC_	Alignment	not modelled	9.2	33	**PDB header:**transcription **Chain:** C: **PDB Molecule:**alpha trans-inducing protein; **PDBTitle:** model for vp16 binding to pc4
86	c2phgB_	Alignment	not modelled	9.1	33	**PDB header:**transcription **Chain:** B: **PDB Molecule:**alpha trans-inducing protein; **PDBTitle:** model for vp16 binding to tfiib
87	c2aenH_	Alignment	not modelled	7.9	10	**PDB header:**viral protein **Chain:** H: **PDB Molecule:**outer capsid protein vp4, vp8* core; **PDBTitle:** crystal structure of the rotavirus strain ds-1 vp8* core
88	c2r2yA_	Alignment	not modelled	7.6	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein adrm1; **PDBTitle:** crystal structure of the proteasomal rpn13 pru-domain
89	c2z59A_	Alignment	not modelled	7.6	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein adrm1; **PDBTitle:** complex structures of mouse rpn13 (22-130aa) and ubiquitin
90	c2dv6F_	Alignment	not modelled	7.2	10	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nitrite reductase; **PDBTitle:** crystal structure of nitrite reductase from hyphomicrobium2 denitrificans
91	c2z4dA_	Alignment	not modelled	6.7	17	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**26s proteasome regulatory subunit rpn13; **PDBTitle:** nmr structures of yeast proteasome component rpn13
92	c3g7mA_	Alignment	not modelled	6.2	18	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**xylanase inhibitor tl-xi; **PDBTitle:** structure of the thaumatin-like xylanase inhibitor tlxi
93	c2kr0A_	Alignment	not modelled	6.1	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**proteasomal ubiquitin receptor adrm1; **PDBTitle:** a proteasome protein
94	d1t4za_	Alignment	not modelled	6.0	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**KaiB-like
95	c1u8cB_	Alignment	not modelled	6.0	13	**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
96	d1lm8v_	Alignment	not modelled	5.9	21	**Fold:**Prealbumin-like **Superfamily:**VHL **Family:**VHL
97	d1kqra_	Alignment	not modelled	5.9	9	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**vp4 sialic acid binding domain
98	c1kriA_	Alignment	not modelled	5.9	9	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vp4; **PDBTitle:** nmr solution structures of the rhesus rotavirus vp4 sialic2 acid binding domain without ligand
99	d2plta_	Alignment	not modelled	5.7	14	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like