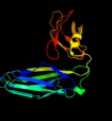


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qpxA_	 Alignment		100.0	35	PDB header: chaperone Chain: A; PDB Molecule: papd chaperone; PDBTitle: crystal structures of self-capping papd chaperone homodimers
2	c1qunA_	 Alignment		100.0	28	PDB header: chaperone/structural 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	24	PDB header: fibril protein Chain: B; PDB Molecule: putative fimbriae assembly chaperone; PDBTitle: salmonella enterica safi pilin in complex with the safb2 chaperone (type ii)
4	c1z9sA_	 Alignment		100.0	25	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	27	PDB header: chaperone Chain: A; PDB Molecule: sfac protein; PDBTitle: crystal structure of the periplasmic chaperone sfac
6	c3f6iB_	 Alignment		100.0	26	PDB header: chaperone Chain: B; PDB Molecule: chaperone protein faee; PDBTitle: structure of the semet labeled f4 fibril 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	d2j2za1	 Alignment		100.0	45	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: Pilus chaperone
9	d1p5va1	 Alignment		100.0	29	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: Pilus chaperone
10	d2co7b1	 Alignment		100.0	26	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: Pilus chaperone
11	d3bwuc1	 Alignment		100.0	32	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: Pilus chaperone

12	dl14ia1	Alignment		100.0	34	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: Pilus chaperone
13	d2j2za2	Alignment		99.8	26	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
14	d1p5va2	Alignment		99.7	22	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
15	d3bwuc2	Alignment		99.7	22	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
16	d2co7b2	Alignment		99.7	22	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
17	dl14ia2	Alignment		99.7	19	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
18	d1m1sa	Alignment		97.3	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like
19	dlrowa	Alignment		96.0	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like
20	c2qsvA	Alignment		95.7	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
21	d1grwa	Alignment	not modelled	95.4	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like
22	c1z9oB	Alignment	not modelled	94.6	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
23	d1mspa	Alignment	not modelled	93.8	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like
24	c3qisA	Alignment	not modelled	93.6	15	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	92.7	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
26	c3qbtH	Alignment	not modelled	90.8	14	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	dlwica	Alignment	not modelled	89.9	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like
						PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hydrocephalus-inducing protein

28	c2ys4A	Alignment	not modelled	87.5	16	homolog; PDBTitle: solution structure of the n-terminal papd-like domain of2 hydin protein from human
29	c3ac0B	Alignment	not modelled	80.2	14	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase i; PDBTitle: crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
30	d2vza2	Alignment	not modelled	79.7	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
31	c2qvka	Alignment	not modelled	73.2	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
32	d1hfua2	Alignment	not modelled	71.2	11	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
33	d1ejxb	Alignment	not modelled	66.3	14	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
34	d4ubpb	Alignment	not modelled	64.2	16	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
35	c2x41A	Alignment	not modelled	63.7	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
36	d1e42a1	Alignment	not modelled	60.9	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: Clathrin adaptor appendage domain Family: Alpha-adaptin ear subdomain-like
37	d1e9ya1	Alignment	not modelled	57.0	23	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
38	d2fwua1	Alignment	not modelled	56.3	8	Fold: Immunoglobulin-like beta-sandwich Superfamily: CalX-like Family: CalX-beta domain
39	c1e9za	Alignment	not modelled	47.5	23	PDB header: hydrolase Chain: A: PDB Molecule: urease subunit alpha; PDBTitle: crystal structure of helicobacter pylori urease
40	c3qgaD	Alignment	not modelled	45.5	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
41	d1aoza2	Alignment	not modelled	44.1	10	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
42	c3eujB	Alignment	not modelled	39.5	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
43	c1yyca	Alignment	not modelled	37.5	7	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	c3jt0B	Alignment	not modelled	37.3	15	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	d1gyca2	Alignment	not modelled	36.6	9	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
46	d1kyaa2	Alignment	not modelled	35.4	8	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
47	c3butA	Alignment	not modelled	34.5	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein af_0446; PDBTitle: crystal structure of protein af_0446 from archaeoglobus fulgidus
48	d1xo8a	Alignment	not modelled	32.6	7	Fold: Immunoglobulin-like beta-sandwich Superfamily: LEA14-like Family: LEA14-like
49	c3o0lB	Alignment	not modelled	31.6	13	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
50	d1v10a2	Alignment	not modelled	31.3	5	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
51	c1e42A	Alignment	not modelled	31.1	17	PDB header: endocytosis Chain: A: PDB Molecule: ap-2 complex subunit beta; PDBTitle: beta2-adaptin appendage domain, from clathrin adaptor ap2
52	d1ufga	Alignment	not modelled	29.4	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: Lamin A/C globular tail domain Family: Lamin A/C globular tail domain
53	d1k3ra1	Alignment	not modelled	28.6	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Hypothetical protein MTH1 (MT0001), insert domain
						PDB header: structural protein

54	c2IIIA_	Alignment	not modelled	27.7	13	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
55	d1v8ha1	Alignment	not modelled	24.4	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: SoxZ-like
56	d2q9oa2	Alignment	not modelled	23.8	10	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
57	d1lfra_	Alignment	not modelled	22.6	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: Lamin A/C globular tail domain Family: Lamin A/C globular tail domain
58	c1wkwB_	Alignment	not modelled	17.4	56	PDB header: translation/protein binding Chain: B: PDB Molecule: eukaryotic translation initiation factor 4e PDBTitle: crystal structure of the ternary complex of eif4e-m7pppa-2 4ebp1 peptide
59	d2v33a1	Alignment	not modelled	16.9	30	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain
60	c3rb7E_	Alignment	not modelled	15.8	7	PDB header: metal binding protein Chain: E: PDB Molecule: na/ca exchange protein; PDBTitle: crystal structure of cbd12 from calx1.2
61	c3h6aB_	Alignment	not modelled	15.4	7	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
62	d2dpka1	Alignment	not modelled	15.1	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: CalX-like Family: CalX-beta domain
63	c2frgP_	Alignment	not modelled	14.3	10	PDB header: immune system Chain: P: PDB Molecule: trem-like transcript-1; PDBTitle: structure of the immunoglobulin-like domain of human tlt-1
64	c3ginB_	Alignment	not modelled	13.9	15	PDB header: metal binding protein Chain: B: PDB Molecule: sodium/calcium exchanger 1; PDBTitle: crystal structure of e454k-cbd1
65	d1ivta_	Alignment	not modelled	13.0	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: Lamin A/C globular tail domain Family: Lamin A/C globular tail domain
66	d1jz8a2	Alignment	not modelled	11.7	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
67	d2f7fa1	Alignment	not modelled	11.2	38	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
68	c2qziA_	Alignment	not modelled	10.8	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	c2phgB_	Alignment	not modelled	10.5	50	PDB header: transcription Chain: B: PDB Molecule: alpha trans-inducing protein; PDBTitle: model for vp16 binding to tfiib
70	c2pheC_	Alignment	not modelled	10.1	50	PDB header: transcription Chain: C: PDB Molecule: alpha trans-inducing protein; PDBTitle: model for vp16 binding to pc4
71	d1eg3a3	Alignment	not modelled	8.7	50	Fold: WW domain-like Superfamily: WW domain Family: WW domain
72	c3hzpA_	Alignment	not modelled	8.0	43	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ntf2-like protein of unknown function; PDBTitle: crystal structure of ntf2-like protein of unknown function mn2a_05052 from prochlorococcus marinus (yp_291699.1) from prochlorococcus sp.3 nat2a at 1.40 a resolution
73	c3dqgC_	Alignment	not modelled	7.8	12	PDB header: chaperone Chain: C: PDB Molecule: heat shock 70 kda protein f; PDBTitle: peptide-binding domain of heat shock 70 kda protein f, mitochondrial2 precursor, from caenorhabditis elegans.
74	c3ohnA_	Alignment	not modelled	7.8	20	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane usher protein fimd; PDBTitle: crystal structure of the fimd translocation domain
75	c1skoA_	Alignment	not modelled	7.7	21	PDB header: signaling protein Chain: A: PDB Molecule: mitogen-activated protein kinase kinase 1 PDBTitle: mp1-p14 complex
76	c2oxgE_	Alignment	not modelled	7.6	16	PDB header: transport protein Chain: E: PDB Molecule: soxz protein; PDBTitle: the soxyz complex of paracoccus pantotrophus
77	d3cpta1	Alignment	not modelled	7.6	21	Fold: Profilin-like Superfamily: Roadblock/LC7 domain Family: Roadblock/LC7 domain
78	d1qgpa_	Alignment	not modelled	7.0	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
79	d1w8oa1	Alignment	not modelled	7.0	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
80	c2v0xB_	Alignment	not modelled	6.8	40	PDB header: cell cycle Chain: B: PDB Molecule: lamina-associated polypeptide 2 isoforms

						PDBTitle: the dimerization domain of lap2alpha
81	d1u00a2	Alignment	not modelled	6.8	25	Fold: Heat shock protein 70kD (HSP70), peptide-binding domain Superfamily: Heat shock protein 70kD (HSP70), peptide-binding domain Family: Heat shock protein 70kD (HSP70), peptide-binding domain
82	c2ai4A_	Alignment	not modelled	6.7	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein so1698; PDBTitle: structure of protein of unknown function so1698 from shewanella2 oneidensis
83	d1r7aa1	Alignment	not modelled	6.2	20	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
84	d2huha1	Alignment	not modelled	6.2	16	Fold: C2 domain-like Superfamily: Smr-associated domain-like Family: Smr-associated domain
85	c1z8yF_	Alignment	not modelled	6.2	25	PDB header: virus Chain: F: PDB Molecule: spike glycoprotein e1; PDBTitle: mapping the e2 glycoprotein of alphaviruses
86	d1t4za_	Alignment	not modelled	5.9	22	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: KaiB-like
87	c3e9tD_	Alignment	not modelled	5.7	10	PDB header: membrane protein Chain: D: PDB Molecule: na/ca exchange protein; PDBTitle: crystal structure of apo-form calx cbd1 domain
88	c1zpuE_	Alignment	not modelled	5.6	8	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
89	c3nuhB_	Alignment	not modelled	5.6	20	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
90	c3of6D_	Alignment	not modelled	5.6	21	PDB header: immune system Chain: D: PDB Molecule: pre t-cell antigen receptor alpha; PDBTitle: human pre-t cell receptor crystal structure
91	c1i9mB_	Alignment	not modelled	5.5	14	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
92	d1nyna_	Alignment	not modelled	5.5	23	Fold: FYSH domain Superfamily: FYSH domain Family: Hypothetical protein Yhr087W
93	c2vzvB_	Alignment	not modelled	5.3	13	PDB header: hydrolase Chain: B: PDB Molecule: exo-beta-d-glucosaminidase; PDBTitle: substrate complex of amycolatopsis orientalis exo-2 chitosanase csxa e541a with chitosan
94	d1hmja_	Alignment	not modelled	5.2	16	Fold: RPB5-like RNA polymerase subunit Superfamily: RPB5-like RNA polymerase subunit Family: RPB5
95	d1cuoa_	Alignment	not modelled	5.1	7	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
96	d1pkoa_	Alignment	not modelled	5.1	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
97	c3ppsD_	Alignment	not modelled	5.1	11	PDB header: oxidoreductase Chain: D: PDB Molecule: laccase; PDBTitle: crystal structure of an ascomycete fungal laccase from thielavia2 arenaria
98	c3e9uA_	Alignment	not modelled	5.1	8	PDB header: membrane protein Chain: A: PDB Molecule: na/ca exchange protein; PDBTitle: crystal structure of calx cbd2 domain
99	c2y38A_	Alignment	not modelled	5.0	10	PDB header: structural protein Chain: A: PDB Molecule: laminin subunit alpha-5; PDBTitle: laminin alpha5 chain n-terminal fragment