
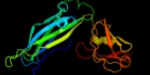

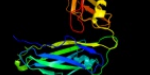
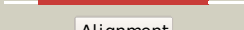

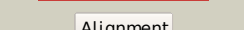
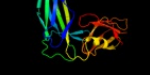
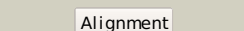
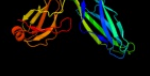




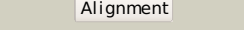

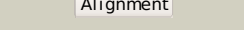

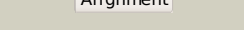

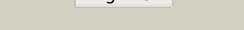

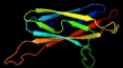




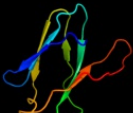

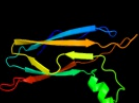

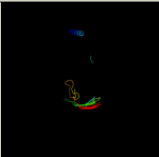


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2co7B_	 Alignment		100.0	32	PDB header: fibril protein Chain: B: PDB Molecule: putative fimbriae assembly chaperone; PDBTitle: salmonella enterica safi pilin in complex with the safb2 chaperone (type ii)
2	c1z9sA_	 Alignment		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	c1qunA_	 Alignment		100.0	32	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
4	c1l4iA_	 Alignment		100.0	32	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	c3q48B_	 Alignment		100.0	37	PDB header: chaperone Chain: B: PDB Molecule: chaperone cupb2; PDBTitle: crystal structure of pseudomonas aeruginosa cupb2 chaperone
7	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
8	d1p5va1	 Alignment		100.0	31	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: Pilus chaperone
9	d2co7b1	 Alignment		100.0	29	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: Pilus chaperone
10	d2j2za1	 Alignment		100.0	27	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	dl4ia1	Alignment		100.0	32	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: Pilus chaperone
13	d3bwuc2	Alignment		99.8	30	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
14	d1p5va2	Alignment		99.8	33	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
15	d2co7b2	Alignment		99.8	34	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
16	d1l4ia2	Alignment		99.7	31	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
17	d2j2za2	Alignment		99.6	28	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
18	d1m1sa	Alignment		97.8	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like
19	d1rowa	Alignment		97.5	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like
20	c2qsvA	Alignment		97.3	14	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	97.2	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like
22	d1mspa	Alignment	not modelled	96.9	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like
23	c1z9oB	Alignment	not modelled	96.4	21	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	96.0	14	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	c2ys4A	Alignment	not modelled	95.6	12	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
26	c3qisA	Alignment	not modelled	95.1	16	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	d1wica	Alignment	not modelled	94.3	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like
28	c3o1B	Alignment	not modelled	94.2	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein;

28	c3u0B_	Alignment	not modelled	94.2	10	PDBTitle: crystal structure of a pfam duf1425 family member (shew_1734) from2 shewanella sp. pv-4 at 1.81 a resolution PDB header: protein transport/hydrolase Chain: H: PDB Molecule: inositol polyphosphate 5-phosphatase ocr1-1; PDBTitle: crystal structure of ocr1 540-678 in complex with rab8a:gppnhp
29	c3qbth_	Alignment	not modelled	94.1	16	PDB header: oxidoreductase Chain: I: PDB Molecule: pmob; PDBTitle: crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
30	c3rfrl_	Alignment		89.6	20	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase i; PDBTitle: crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
31	c3ac0B_	Alignment	not modelled	87.5	18	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
32	c2x41A_	Alignment	not modelled	84.8	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
33	d2vza2_	Alignment	not modelled	81.6	26	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
34	d4ubpb_	Alignment	not modelled	74.6	15	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
35	d1ejxb_	Alignment	not modelled	70.1	11	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
36	d1e9ya1_	Alignment	not modelled	68.2	11	PDB header: endocytosis Chain: A: PDB Molecule: ap-2 complex subunit beta; PDBTitle: beta2-adaptin appendage domain, from clathrin adaptor ap2
37	c1e42A_	Alignment	not modelled	64.0	16	PDB header: hydrolase Chain: A: PDB Molecule: urease subunit alpha; PDBTitle: crystal structure of helicobacter pylori urease
38	c1e9zA_	Alignment	not modelled	62.6	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
39	c2IIIA_	Alignment	not modelled	61.5	19	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	c3qgaD_	Alignment	not modelled	61.2	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: Lamin A/C globular tail domain Family: Lamin A/C globular tail domain
41	d1ufga_	Alignment	not modelled	60.4	23	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
42	c3jt0B_	Alignment	not modelled	58.3	20	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
43	d1w8oa1_	Alignment	not modelled	54.9	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: Clathrin adaptor appendage domain Family: Alpha-adaptin ear subdomain-like
44	d1e42a1_	Alignment	not modelled	54.6	20	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 the domain
45	c3h6aB_	Alignment	not modelled	52.7	10	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-2; PDBTitle: structure of integrin alphaxbeta2 ectodomain
46	c3k6sB_	Alignment	not modelled	50.2	25	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
47	d1aoza2_	Alignment	not modelled	46.0	12	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
48	d1hfua2_	Alignment	not modelled	43.0	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
49	c1I9mB_	Alignment	not modelled	40.9	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein apag; PDBTitle: solution structure of apag protein
50	c2f1eA_	Alignment	not modelled	34.2	13	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
51	c2qvka_	Alignment	not modelled	33.3	11	PDB header: cell cycle Chain: B: PDB Molecule: chromosome partition protein mukf;
52	c2quvB_	Alignment	not modelled	33.1	23	

52	c3eupB	Alignment	not modelled	33.1	93	PDBTitle: crystal structure of muke-mukf(residues 292-443)-mukb(head2 domain)-atpgammas complex, symmetric dimer PDB header: structural genomics, unknown function Chain: A: PDB Molecule: fixg-related protein; PDBTitle: crystal structure of fixg-related protein from vibrio parahaemolyticus
53	c2r39A	Alignment	not modelled	33.0	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
54	c1u8cB	Alignment	not modelled	32.2	21	Fold: Immunoglobulin-like beta-sandwich Superfamily: Lamin A/C globular tail domain Family: Lamin A/C globular tail domain
55	d1lfra	Alignment	not modelled	32.0	21	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multi domain cupredoxins
56	d1gyca2	Alignment	not modelled	28.3	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Hypothetical protein MTH1 (MT0001), insert domain
57	d1k3ra1	Alignment	not modelled	27.3	24	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multi domain cupredoxins
58	d1v10a2	Alignment	not modelled	26.9	13	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
59	c1l5gA	Alignment	not modelled	25.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: methane monooxygenase subunit b2; PDBTitle: crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
60	c3rgbA	Alignment	not modelled	24.7	20	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multi domain cupredoxins
61	d1kyaa2	Alignment	not modelled	24.0	13	PDB header: oxidoreductase, membrane protein Chain: I: PDB Molecule: particulate methane monooxygenase, b subunit; PDBTitle: crystal structure of particulate methane monooxygenase
62	c1yewl	Alignment	not modelled	24.0	21	PDB header: cell adhesion/blood clotting Chain: A: PDB Molecule: integrin, alpha 2b; PDBTitle: structure of complete ectodomain of integrin aiiibb3
63	c3fcsA	Alignment	not modelled	22.5	15	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multi domain cupredoxins
64	d2q9oa2	Alignment	not modelled	20.9	19	PDB header: metal binding protein Chain: B: PDB Molecule: sodium/calcium exchanger 1; PDBTitle: crystal structure of e454k-cbd1
65	c3ginB	Alignment	not modelled	19.9	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: CalX-like Family: CalX-beta domain
66	d2fwua1	Alignment	not modelled	19.6	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains
67	d1ex0a2	Alignment	not modelled	18.1	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: CalX-like Family: CalX-beta domain
68	d2dpka1	Alignment	not modelled	17.2	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains
69	d1vjja2	Alignment	not modelled	16.7	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: Heat shock protein 70kD (HSP70), peptide-binding domain Family: Heat shock protein 70kD (HSP70), peptide-binding domain
70	d1g0da2	Alignment	not modelled	16.0	2	PDB header: oxidase Chain: A: PDB Molecule: laccase; PDBTitle: structure of rigidoporus lignosus laccase from hemihedrally2 twinned crystals
71	d1u00a2	Alignment	not modelled	16.0	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: ApaG-like Family: ApaG-like
72	c1v10A	Alignment	not modelled	15.6	11	PDB header: membrane protein Chain: D: PDB Molecule: na/ca exchange protein; PDBTitle: crystal structure of apo-form calx cbd1 domain
73	d1tzaa	Alignment	not modelled	15.0	13	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Carbohydrate-binding domain Family: Cellulose-binding domain family II
74	c3e9tD	Alignment	not modelled	14.7	8	Fold: Immunoglobulin-like beta-sandwich Superfamily: Lamin A/C globular tail domain Family: Lamin A/C globular tail domain
75	d1lexha	Alignment	not modelled	14.6	12	PDB header: cell adhesion/blood clotting Chain: B: PDB Molecule: integrin beta-3; PDBTitle: structure of headpiece of integrin aiiibb3 in open conformation
76	d1ivta	Alignment	not modelled	13.7	22	PDB header: lipoprotein Chain: A: PDB Molecule: uncharacterized lipoprotein yjha; PDBTitle: crystal structure of the yjha protein from bacillus2 subtilis, northeast structural genomics consortium target3 sr562
77	c3fcuB	Alignment	not modelled	13.7	21	PDB header: hydrolase (serine proteinase) Chain: B: PDB Molecule: hydrolyzed cucurbita maxima trypsin
78	c3cfuA	Alignment	not modelled	12.2	16	

79	c1hymB_	Alignment	not modelled	11.7	29	inhibitor v; PDBTitle: hydrolyzed trypsin inhibitor (cmli-v, minimized average nmr2 structure)
80	c2h47C_	Alignment	not modelled	11.1	10	PDB header: oxidoreductase/electron transport Chain: C: PDB Molecule: azurin; PDBTitle: crystal structure of an electron transfer complex between 2 aromatic amine dehydrogenase and azurin from <i>Alcaligenes faecalis</i> (form 1)
81	d1cc3a_	Alignment	not modelled	11.1	3	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
82	d2ccwa1	Alignment	not modelled	10.9	3	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
83	c2qv2A_	Alignment	not modelled	10.7	23	PDB header: hydrolase Chain: A: PDB Molecule: inositol polyphosphate 5-phosphatase ocr1-1; PDBTitle: a role of the Lowe syndrome protein ocr1 in early steps of 2 the endocytic pathway
84	d1cuoa_	Alignment	not modelled	10.6	7	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
85	d1jzga_	Alignment	not modelled	9.5	3	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
86	d1hmja_	Alignment	not modelled	9.3	13	Fold: RPB5-like RNA polymerase subunit Superfamily: RPB5-like RNA polymerase subunit Family: RPB5
87	d1dkza2	Alignment	not modelled	8.9	6	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
88	c1yycA_	Alignment	not modelled	8.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative late embryogenesis abundant protein; PDBTitle: solution structure of a putative late embryogenesis 2 abundant (lea) protein at2g46140.1
89	c2pheC_	Alignment	not modelled	8.9	67	PDB header: transcription Chain: C: PDB Molecule: alpha trans-inducing protein; PDBTitle: model for vp16 binding to pc4
90	c2je8B_	Alignment	not modelled	8.8	12	PDB header: hydrolase Chain: B: PDB Molecule: beta-mannosidase; PDBTitle: structure of a beta-mannosidase from <i>Bacteroides thetaiotaomicron</i>
91	d1rkra_	Alignment	not modelled	8.7	7	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
92	c1pzdA_	Alignment	not modelled	8.7	22	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: coatamer gamma subunit; PDBTitle: structural identification of a conserved appendage domain 2 in the carboxyl-terminus of the copI gamma-subunit.
93	c2phgB_	Alignment	not modelled	8.5	67	PDB header: transcription Chain: B: PDB Molecule: alpha trans-inducing protein; PDBTitle: model for vp16 binding to tfiib
94	d1v54g_	Alignment	not modelled	8.0	17	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIa Family: Mitochondrial cytochrome c oxidase subunit VIa
95	d1nwpa_	Alignment	not modelled	7.7	7	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
96	c3tqzA_	Alignment	not modelled	7.4	20	PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: structure of a deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)2 from <i>Coxiella burnetii</i>
97	d1xo8a_	Alignment	not modelled	7.3	22	Fold: Immunoglobulin-like beta-sandwich Superfamily: LEA14-like Family: LEA14-like
98	d1j6qa_	Alignment	not modelled	7.3	17	Fold: OB-fold Superfamily: Heme chaperone CcmE Family: Heme chaperone CcmE
99	c1j6qa_	Alignment	not modelled	7.3	17	PDB header: chaperone Chain: A: PDB Molecule: cytochrome c maturation protein e; PDBTitle: solution structure and characterization of the heme 2 chaperone ccme