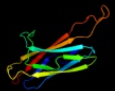
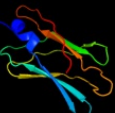
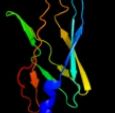
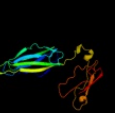
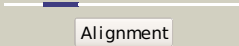
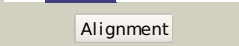
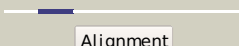
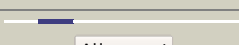
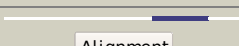
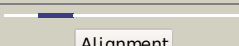
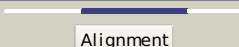
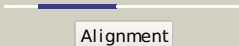
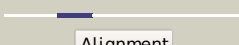
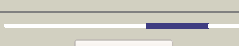
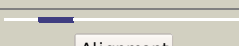
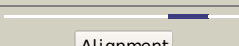


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2co7B_	 Alignment		100.0	32	PDB header: fibril protein Chain: B; PDB Molecule: putative fimbriae assembly chaperone; PDBTitle: salmonella enterica safi pilin in complex with the safb2 chaperone (type ii)
2	c1qunA_	 Alignment		100.0	35	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	c1z9sA_	 Alignment		100.0	31	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
4	c3q48B_	 Alignment		100.0	41	PDB header: chaperone Chain: B; PDB Molecule: chaperone cupb2; PDBTitle: crystal structure of pseudomonas aeruginosa cupb2 chaperone
5	c1l4iA_	 Alignment		100.0	34	PDB header: chaperone Chain: A; PDB Molecule: sfae protein; PDBTitle: crystal structure of the periplasmic chaperone sfae
6	c1qpxA_	 Alignment		100.0	35	PDB header: chaperone Chain: A; PDB Molecule: papd chaperone; PDBTitle: crystal structures of self-capping papd chaperone homodimers
7	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
8	d2co7b1	 Alignment		100.0	31	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: Pilus chaperone
9	d1p5va1	 Alignment		100.0	37	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: Pilus chaperone
10	d2j2za1	 Alignment		100.0	39	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: Pilus chaperone
11	d3bwuc1	 Alignment		100.0	39	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: Pilus chaperone

12	d1l4ia1	Alignment		100.0	41	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: Pilus chaperone
13	d1p5va2	Alignment		99.7	28	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
14	d3bwuc2	Alignment		99.7	23	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
15	d2co7b2	Alignment		99.6	34	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
16	d2j2za2	Alignment		99.6	26	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
17	d1l4ia2	Alignment		99.6	30	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
18	d1m1sa_	Alignment		97.9	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like
19	c2qsvA_	Alignment		97.7	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
20	d1rowa_	Alignment		97.6	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like
21	d1grwa_	Alignment	not modelled	97.2	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like
22	d1mspa_	Alignment	not modelled	96.9	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like
23	c1z9oB_	Alignment	not modelled	96.8	18	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	95.3	19	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	d1wica_	Alignment	not modelled	94.8	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like
26	c2ys4A_	Alignment	not modelled	94.7	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hydrocephalus-inducing protein homology; PDBTitle: solution structure of the n-terminal papd-like domain of2 hydin protein from human
27	c3qisA_	Alignment	not modelled	94.0	12	PDB header: hydrolase/protein binding Chain: A: PDB Molecule: inositol polyphosphate 5-phosphatase ocr1-1; PDBTitle: recognition of the f&h motif by the lowe syndrome protein ocr1
28	c3n0lB_	Alignment	not modelled	93.9	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein;

28	c3u0bB_	Alignment	not modelled	93.9	13	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	93.5	13	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
30	c1l9mB_	Alignment	not modelled	90.9	17	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	88.4	14	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	88.3	15	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
33	d4ubpb_	Alignment	not modelled	80.6	13	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
34	d1ejxb_	Alignment	not modelled	77.8	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
35	d2vzsa2	Alignment	not modelled	76.8	16	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
36	d1e9ya1	Alignment	not modelled	76.2	14	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
37	c2qvka_	Alignment	not modelled	75.9	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
38	d1w8oa1	Alignment	not modelled	75.8	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: Clathrin adaptor appendage domain Family: Alpha-adaptin ear subdomain-like
39	d1e42a1	Alignment	not modelled	71.6	25	Fold: Immunoglobulin-like beta-sandwich Superfamily: Lamin A/C globular tail domain Family: Lamin A/C globular tail domain
40	d1ufga_	Alignment	not modelled	68.9	26	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	c3qgaD_	Alignment	not modelled	68.2	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: fixg-related protein; PDBTitle: crystal structure of fixg-related protein from vibrio parahaemolyticus
42	c2r39A_	Alignment	not modelled	67.5	8	PDB header: hydrolase Chain: A: PDB Molecule: urease subunit alpha; PDBTitle: crystal structure of helicobacter pylori urease
43	c1e9za_	Alignment	not modelled	66.0	14	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
44	c2lIIA_	Alignment	not modelled	63.2	18	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	c3jt0B_	Alignment	not modelled	60.7	18	PDB header: hydrolase Chain: B: PDB Molecule: beta-mannosidase; PDBTitle: structure of a beta-mannosidase from bacteroides2 thetaiotaomicron
46	c2je8B_	Alignment	not modelled	59.9	13	PDB header: endocytosis Chain: A: PDB Molecule: ap-2 complex subunit beta; PDBTitle: beta2-adaptin appendage domain, from clathrin adaptor ap2
47	c1e42A_	Alignment	not modelled	53.7	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein apag; PDBTitle: solution structure of apag protein
48	c2f1eA_	Alignment	not modelled	49.1	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
49	c3eujB_	Alignment	not modelled	40.8	25	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
50	c3h6aB_	Alignment	not modelled	40.7	5	Fold: Immunoglobulin-like beta-sandwich Superfamily: Lamin A/C globular tail domain Family: Lamin A/C globular tail domain
51	d1lifr_	Alignment	not modelled	40.4	25	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-2; PDBTitle: structure of integrin alphaxbeta2 ectodomain
52	c3k6sB_	Alignment	not modelled	39.6	7	Fold: OB-fold

53	d1k3ra1	Alignment	not modelled	33.1	18	Superfamily: Nucleic acid-binding proteins Family: Hypothetical protein MTH1 (MT0001), insert domain
54	c2kl6A_	Alignment	not modelled	32.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the cardb domain of pf1109 from2 pyrococcus furiosus. northeast structural genomics3 consortium target pfr193a
55	d2fwua1	Alignment	not modelled	30.4	8	Fold: Immunoglobulin-like beta-sandwich Superfamily: CalX-like Family: CalX-beta domain
56	c3fcsA_	Alignment	not modelled	28.6	11	PDB header: cell adhesion/blood clotting Chain: A: PDB Molecule: integrin, alpha 2b; PDBTitle: structure of complete ectodomain of integrin aiibb3
57	dlivta_	Alignment	not modelled	28.4	28	Fold: Immunoglobulin-like beta-sandwich Superfamily: Lamin A/C globular tail domain Family: Lamin A/C globular tail domain
58	d1aoa2	Alignment	not modelled	21.7	15	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
59	c3ginB_	Alignment	not modelled	21.3	13	PDB header: metal binding protein Chain: B: PDB Molecule: sodium/calcium exchanger 1; PDBTitle: crystal structure of e454k-cbd1
60	d2je8a2	Alignment	not modelled	20.7	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
61	d2dpka1	Alignment	not modelled	19.9	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: CalX-like Family: CalX-beta domain
62	c2k6zA_	Alignment	not modelled	19.1	14	PDB header: metal transport Chain: A: PDB Molecule: putative uncharacterized protein ttha1943; PDBTitle: solution structures of copper loaded form pcua (trans2 conformation of the peptide bond involving the nitrogen of3 p14)
63	d1gpla1	Alignment	not modelled	15.3	20	Fold: Lipase/lipoxygenase domain (PLAT/LH2 domain) Superfamily: Lipase/lipoxygenase domain (PLAT/LH2 domain) Family: Colipase-binding domain
64	d1v10a2	Alignment	not modelled	14.4	8	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
65	d1tzaa_	Alignment	not modelled	12.7	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: ApaG-like Family: ApaG-like
66	d1xq4a_	Alignment	not modelled	12.6	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: ApaG-like Family: ApaG-like
67	c1l5gA_	Alignment	not modelled	12.6	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
68	d1etha1	Alignment	not modelled	12.5	21	Fold: Lipase/lipoxygenase domain (PLAT/LH2 domain) Superfamily: Lipase/lipoxygenase domain (PLAT/LH2 domain) Family: Colipase-binding domain
69	d1hfua2	Alignment	not modelled	12.3	5	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
70	c3isyA_	Alignment	not modelled	12.2	12	PDB header: protein binding Chain: A: PDB Molecule: intracellular proteinase inhibitor; PDBTitle: crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
71	d2q9oa2	Alignment	not modelled	11.7	13	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
72	d1hmja_	Alignment	not modelled	11.4	16	Fold: RPB5-like RNA polymerase subunit Superfamily: RPB5-like RNA polymerase subunit Family: RPB5
73	d2ccwa1	Alignment	not modelled	11.3	10	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
74	c1u8cB_	Alignment	not modelled	11.1	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
75	c1wkwb_	Alignment	not modelled	10.5	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
76	d1xvsa_	Alignment	not modelled	10.4	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: ApaG-like Family: ApaG-like
77	d1cc3a_	Alignment	not modelled	9.6	21	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
78	d1khua_	Alignment	not modelled	9.4	31	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: SMAD domain
79	c3rfrl_	Alignment	not modelled	9.3	16	PDB header: oxidoreductase Chain: I: PDB Molecule: pmob; PDBTitle: crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m

80	c3fcuB	 Alignment	not modelled	9.1	10	PDB header: cell adhesion/blood clotting Chain: B: PDB Molecule: integrin beta-3; PDBTitle: structure of headpiece of integrin aiibb3 in open conformation
81	d1kha	 Alignment	not modelled	8.8	31	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: SMAD domain
82	c1kha	 Alignment	not modelled	8.8	31	PDB header: transcription Chain: A: PDB Molecule: smad2; PDBTitle: crystal structure of a phosphorylated smad2
83	c3cfuA	 Alignment	not modelled	8.6	15	PDB header: lipoprotein Chain: A: PDB Molecule: uncharacterized lipoprotein yjha; PDBTitle: crystal structure of the yjha protein from bacillus subtilis. northeast structural genomics consortium target3 sr562
84	c2h47C	 Alignment	not modelled	8.3	14	PDB header: oxidoreductase/electron transport Chain: C: PDB Molecule: azurin; PDBTitle: crystal structure of an electron transfer complex between2 aromatic amine dehydrogenase and azurin from alcaligenes3 faecalis (form 1)
85	d1rkra	 Alignment	not modelled	8.3	14	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
86	d1ex0a3	 Alignment	not modelled	8.2	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains
87	d1dd1a	 Alignment	not modelled	8.1	23	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: SMAD domain
88	d1gyca2	 Alignment	not modelled	8.0	11	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
89	c3rb7E	 Alignment	not modelled	8.0	13	PDB header: metal binding protein Chain: E: PDB Molecule: na/ca exchange protein; PDBTitle: crystal structure of cbd12 from calx1.2
90	c1hymB	 Alignment	not modelled	7.9	29	PDB header: hydrolase (serine proteinase) Chain: B: PDB Molecule: hydrolyzed cucurbita maxima trypsin inhibitor v; PDBTitle: hydrolyzed trypsin inhibitor (cmli-v, minimized average nmr2 structure)
91	c3hs0B	 Alignment	not modelled	7.3	14	PDB header: immune system Chain: B: PDB Molecule: cobra venom factor; PDBTitle: cobra venom factor (cvf) in complex with human factor b
92	d1x9la	 Alignment	not modelled	7.3	10	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: DR1885-like metal-binding protein Family: DR1885-like metal-binding protein
93	d1exha	 Alignment	not modelled	7.3	18	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Carbohydrate-binding domain Family: Cellulose-binding domain family II
94	d1ygsa	 Alignment	not modelled	7.2	23	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: SMAD domain
95	d1jzga	 Alignment	not modelled	7.2	21	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
96	d1cuoa	 Alignment	not modelled	7.0	21	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
97	d1xo8a	 Alignment	not modelled	7.0	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: LEA14-like Family: LEA14-like
98	d1g0da2	 Alignment	not modelled	6.9	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains
99	c2pheC	 Alignment	not modelled	6.8	50	PDB header: transcription Chain: C: PDB Molecule: alpha trans-inducing protein; PDBTitle: model for vp16 binding to pc4