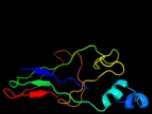
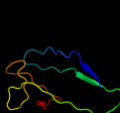
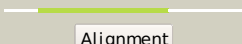
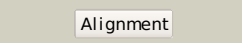
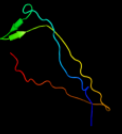
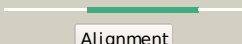
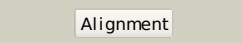
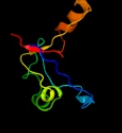
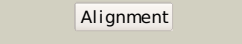
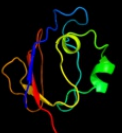
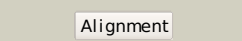
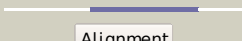
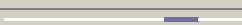


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2w07B_	 Alignment		94.8	19	PDB header: cell adhesion Chain: B: PDB Molecule: minor pilin subunit papf; PDBTitle: structural determinants of polymerization reactivity of the2 p pilus adaptor subunit papf
2	c3bfwA_	 Alignment		94.7	15	PDB header: structural protein/structural protein Chain: A: PDB Molecule: protein fimg; PDBTitle: crystal structure of truncated fimg (fimgt) in complex with the donor2 strand peptide of fimf (dsf)
3	c3jwnK_	 Alignment		94.1	17	PDB header: protein binding/cell adhesion Chain: K: PDB Molecule: protein fimf; PDBTitle: complex of fimc, fimf, fimg and fimh
4	c1klfP_	 Alignment		93.9	13	PDB header: chaperone/adhesin complex Chain: P: PDB Molecule: fimh protein; PDBTitle: fimh adhesin-fimc chaperone complex with d-mannose
5	c3jwnE_	 Alignment		93.8	16	PDB header: protein binding/cell adhesion Chain: E: PDB Molecule: protein fimf; PDBTitle: complex of fimc, fimf, fimg and fimh
6	d1ze3h1	 Alignment		93.3	12	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Pilus subunits
7	c3jwnL_	 Alignment		93.3	17	PDB header: protein binding/cell adhesion Chain: L: PDB Molecule: protein fimf; PDBTitle: complex of fimc, fimf, fimg and fimh
8	c3jwnF_	 Alignment		92.9	17	PDB header: protein binding/cell adhesion Chain: F: PDB Molecule: protein fimf; PDBTitle: complex of fimc, fimf, fimg and fimh
9	d1n12a_	 Alignment		87.9	14	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Pilus subunits
10	c2jtyA_	 Alignment		77.9	14	PDB header: structural protein Chain: A: PDB Molecule: type-1 fimbrial protein, a chain; PDBTitle: self-complemented variant of fima, the main subunit of type 1 pilus
11	d2uy6b1	 Alignment		70.7	13	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Pilus subunits

12	d2j2zb1	 Alignment		65.5	15	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Pilus subunits
13	d1pdkb_	 Alignment		60.7	9	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Pilus subunits
14	c2wmpB_	 Alignment		47.1	25	PDB header: chaperone Chain: B: PDB Molecule: pagp protein; PDBTitle: structure of the e. coli chaperone papd in complex with the pilin2 domain of the paggii adhesin
15	c2vsvB_	 Alignment		41.4	14	PDB header: protein-binding Chain: B: PDB Molecule: rhophilin-2; PDBTitle: crystal structure of the pdz domain of human rhophilin-2
16	c3qbtH_	 Alignment		34.1	11	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
17	d1r6ja_	 Alignment		29.6	28	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
18	c1r6jA_	 Alignment		29.6	28	PDB header: membrane protein Chain: A: PDB Molecule: syntenin 1; PDBTitle: ultrahigh resolution crystal structure of syntenin pdz2
19	c1nteA_	 Alignment		29.6	28	PDB header: signaling protein Chain: A: PDB Molecule: syntenin 1; PDBTitle: crystal structure analysis of the second pdz domain of2 syntenin
20	c3khfA_	 Alignment		21.2	16	PDB header: transferase Chain: A: PDB Molecule: microtubule-associated serine/threonine-protein PDBTitle: the crystal structure of the pdz domain of human microtubule2 associated serine/threonine kinase 3 (mast3)
21	c2kjmA_	 Alignment	not modelled	18.4	50	PDB header: rna binding protein Chain: A: PDB Molecule: histone rna hairpin-binding protein; PDBTitle: solution structure of slbp rna binding domain fragment
22	c3qglD_	 Alignment	not modelled	17.8	16	PDB header: protein binding Chain: D: PDB Molecule: sorting nexin-27; PDBTitle: crystal structure of pdz domain of sorting nexin 27 (snx27) in complex2 with the eseskv peptide corresponding to the c-terminal tail of girk3
23	d1eaqa_	 Alignment	not modelled	16.5	55	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: RUNT domain
24	d1ljma_	 Alignment	not modelled	16.0	55	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: RUNT domain
25	c1y7nA_	 Alignment	not modelled	15.9	22	PDB header: protein transport Chain: A: PDB Molecule: amyloid beta a4 precursor protein-binding family PDBTitle: solution structure of the second pdz domain of the human2 neuronal adaptor x11alpha
26	d1ry4a_	 Alignment	not modelled	11.8	20	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
27	c3l4fD_	 Alignment	not modelled	10.9	18	PDB header: signaling protein/protein binding Chain: D: PDB Molecule: sh3 and multiple ankyrin repeat domains protein PDBTitle: crystal structure of betapix coiled-coil domain and shank2 pdz complex
						Fold: GroES-like

28	d1auua_	Alignment	not modelled	10.6	25	Superfamily: SacY-like RNA-binding domain Family: BglG-like antiterminator proteins
29	c1u39A_	Alignment	not modelled	10.2	16	PDB header: protein transport Chain: A: PDB Molecule: amyloid beta a4 precursor protein-binding, PDBTitle: auto-inhibition mechanism of x11s/mints family scaffold2 proteins revealed by the closed conformation of the tandem3 pdz domains
30	d1hcza1	Alignment	not modelled	10.1	20	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Cytochrome f, large domain Family: Cytochrome f, large domain
31	d2oz4a1	Alignment	not modelled	9.9	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C2 set domains
32	c2jtvA_	Alignment	not modelled	9.9	22	PDB header: structural genomics Chain: A: PDB Molecule: protein of unknown function; PDBTitle: solution structure of protein rpa3401, northeast structural genomics2 consortium target rpt7, ontario center for structural proteomics3 target rp3384
33	d1uf1a_	Alignment	not modelled	9.8	12	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
34	c7mdhA_	Alignment	not modelled	9.3	10	PDB header: chloroplastic malate dehydrogenase Chain: A: PDB Molecule: protein (malate dehydrogenase); PDBTitle: structural basis for light activation of a chloroplast enzyme. the2 structure of sorghum nadp-malate dehydrogenase in its oxidized form
35	c2eaqA_	Alignment	not modelled	9.3	13	PDB header: metal binding protein Chain: A: PDB Molecule: lim domain only protein 7; PDBTitle: crystal structure of pdz domain of kiaa0858 (lim), ms07932 from homo sapiens
36	d1b8pa2	Alignment	not modelled	9.0	10	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
37	c2zyzA_	Alignment	not modelled	8.9	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ttha1012; PDBTitle: crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
38	d1kwaa_	Alignment	not modelled	8.5	21	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
39	d1yq2a3	Alignment	not modelled	8.3	29	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: beta-Galactosidase/glucuronidase, N-terminal domain
40	d1y7na1	Alignment	not modelled	8.1	21	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
41	c2k8pA_	Alignment	not modelled	8.0	18	PDB header: signaling protein Chain: A: PDB Molecule: sclerostin; PDBTitle: characterisation of the structural features and2 interactions of sclerostin: molecular insight into a key3 regulator of wnt-mediated bone formation
42	d7mdha2	Alignment	not modelled	8.0	10	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
43	d1wioa2	Alignment	not modelled	7.4	43	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
44	c2z17A_	Alignment	not modelled	7.3	17	PDB header: protein binding Chain: A: PDB Molecule: pleckstrin homology sec7 and coiled-coil domains- PDBTitle: crystal sturcture of pdz domain from human pleckstrin2 homology, sec7
45	d1civa2	Alignment	not modelled	7.3	9	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
46	d1jz8a3	Alignment	not modelled	7.3	11	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: beta-Galactosidase/glucuronidase, N-terminal domain
47	c2d8iA_	Alignment	not modelled	7.2	16	PDB header: immune system, signaling protein Chain: A: PDB Molecule: t-cell lymphoma invasion and metastasis 1 PDBTitle: solution structure of the pdz domain of t-cell lymphoma2 invasion and metastasis 1 varian
48	c2w95B_	Alignment	not modelled	7.1	12	PDB header: cell adhesion Chain: B: PDB Molecule: discoidin-1 subunit a; PDBTitle: structure of the discoidin i from dictyostelium discoideum2 in complex with galnac at 1.75 angstrom resolution
49	c2fc6A_	Alignment	not modelled	6.9	27	PDB header: transcription Chain: A: PDB Molecule: target of egr1, member 1; PDBTitle: solution structure of the zf-cch domain of target of egr1,2 member 1 (nuclear)
50	c2jmrA_	Alignment	not modelled	6.8	13	PDB header: cell adhesion Chain: A: PDB Molecule: fimf; PDBTitle: nmr structure of the e. coli type 1 pilus subunit fimf
51	d2fc6a1	Alignment	not modelled	6.4	44	Fold: CCCH zinc finger Superfamily: CCCH zinc finger Family: CCCH zinc finger
52	c2kv8A_	Alignment	not modelled	6.3	19	PDB header: signaling protein Chain: A: PDB Molecule: regulator of g-protein signaling 12; PDBTitle: solution structure ofrgs12 pdz domain

53	d1gv0a2	Alignment	not modelled	6.2	8	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
54	c1wziA	Alignment	not modelled	6.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: structural basis for alteration of cofactor specificity of2 malate dehydrogenase from thermus flavus
55	d1be9a	Alignment	not modelled	6.0	13	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
56	d1y7ta2	Alignment	not modelled	5.9	14	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
57	d2zjrp1	Alignment	not modelled	5.7	15	Fold: Ribosomal protein L22 Superfamily: Ribosomal protein L22 Family: Ribosomal protein L22
58	c2xzzA	Alignment	not modelled	5.6	10	PDB header: transferase Chain: A: PDB Molecule: protein-glutamine gamma-glutamyltransferase k; PDBTitle: crystal structure of the human transglutaminase 1 beta-barrel domain
59	c2nncB	Alignment	not modelled	5.4	10	PDB header: ligand binding protein Chain: B: PDB Molecule: sulfur covalently-binding protein; PDBTitle: structure of the sulfur carrier protein soxy from chlorobium limicola2 f thiosulfatophilum
60	c1b8vA	Alignment	not modelled	5.3	12	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (malate dehydrogenase); PDBTitle: malate dehydrogenase from aquaspirillum arcticum
61	d1hyha2	Alignment	not modelled	5.1	15	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
62	c1xt5A	Alignment	not modelled	5.1	4	PDB header: immune system Chain: A: PDB Molecule: variable region-containing chitin-binding PDBTitle: crystal structure of vcbp3, domain 1, from branchiostoma2 floridae