


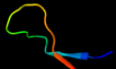

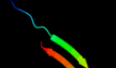

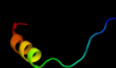





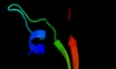





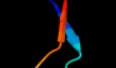





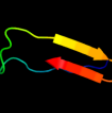
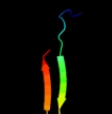

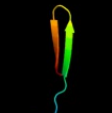
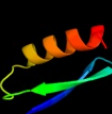



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rrlA_	 Alignment		99.9	59	PDB header: protein transport Chain: A: PDB Molecule: flagellar hook-length control protein; PDBTitle: solution structure of the c-terminal domain of the flik
2	d1k28a1	 Alignment		46.0	30	Fold: OB-fold Superfamily: gp5 N-terminal domain-like Family: gp4 N-terminal domain-like
3	d1byna_	 Alignment		35.7	36	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
4	d2pofa1	 Alignment		31.9	24	Fold: HIT-like Superfamily: HIT-like Family: CDH-like
5	c3ddcB_	 Alignment		30.8	17	PDB header: hydrolase/apoptosis Chain: B: PDB Molecule: ras association domain-containing family protein 5; PDBTitle: crystal structure of nore1a in complex with ras
6	c1uv7A_	 Alignment		27.0	24	PDB header: transport Chain: A: PDB Molecule: general secretion pathway protein m; PDBTitle: periplasmic domain of epsm from vibrio cholerae
7	d1uv7a_	 Alignment		27.0	24	Fold: RRF/tRNA synthetase additional domain-like Superfamily: General secretion pathway protein M, EpsM Family: General secretion pathway protein M, EpsM
8	d1bcoa1	 Alignment		26.9	29	Fold: mu transposase, C-terminal domain Superfamily: mu transposase, C-terminal domain Family: mu transposase, C-terminal domain
9	c2e62A_	 Alignment		26.7	31	PDB header: rna binding protein Chain: A: PDB Molecule: protein at5g25060; PDBTitle: solution structure of the cwf21 domain in protein aak25922
10	c1pdlC_	 Alignment		22.6	32	PDB header: hydrolase Chain: C: PDB Molecule: tail-associated lysozyme; PDBTitle: fitting of gp5 in the cryoem reconstruction of the t2 bacteriophage t4 baseplate
11	d2rnrbl	 Alignment		20.5	16	Fold: PH domain-like barrel Superfamily: PH domain-like Family: TFIIH domain

12	c2bolA	Alignment		19.2	16	PDB header: heat shock protein Chain: A: PDB Molecule: small heat shock protein; PDBTitle: crystal structure and assembly of tsp36, a metazoan small2 heat shock protein
13	d2gy9i1	Alignment		18.9	17	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
14	d2vqe1	Alignment		18.0	22	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
15	c3q9qB	Alignment		17.9	14	PDB header: chaperone Chain: B: PDB Molecule: heat shock protein beta-1; PDBTitle: hspb1 fragment second crystal form
16	c2enpA	Alignment		17.2	22	PDB header: transport protein Chain: A: PDB Molecule: b/k protein; PDBTitle: solution structure of the first c2 domain from human b/k2 protein
17	d2hiya1	Alignment		16.2	25	Fold: SP0830-like Superfamily: SP0830-like Family: SP0830-like
18	d2r83a1	Alignment		14.9	18	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
19	c2ns5A	Alignment		14.3	11	PDB header: signaling protein Chain: A: PDB Molecule: partitioning-defective 3 homolog; PDBTitle: the conserved n-terminal domain of par-3 adopts a novel pb1-2 like structure required for par-3 oligomerization and3 apical membrane localization
20	c3hugA	Alignment		14.0	33	PDB header: transcription/membrane protein Chain: A: PDB Molecule: rna polymerase sigma factor; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
21	c1qysA	Alignment	not modelled	13.6	14	PDB header: de novo protein Chain: A: PDB Molecule: top7; PDBTitle: crystal structure of top7: a computationally designed2 protein with a novel fold
22	c2d8kA	Alignment	not modelled	13.6	18	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: synaptotagmin vii; PDBTitle: solution structure of the first c2 domain of synaptotagmin2 vii
23	d1xuva	Alignment	not modelled	13.4	5	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
24	c2nnzA	Alignment	not modelled	12.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: solution structure of the hypothetical protein af2241 from2 archaeoglobus fulgidus
25	d2p5ka1	Alignment	not modelled	12.5	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
26	c2b3rA	Alignment	not modelled	12.5	19	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol-4-phosphate 3-kinase c2 domain- PDBTitle: crystal structure of the c2 domain of class ii phosphatidylinositi2e2 3-kinase c2
27	d1u0ua2	Alignment	not modelled	12.3	16	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
28	d1cfza	Alignment	not modelled	12.1	36	Fold: Phosphorylase/hydrolase-like Superfamily: HybD-like Family: Hydrogenase maturing endopeptidase HybD

29	d1zx8a1	Alignment	not modelled	12.0	17	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: TM1367-like
30	d1uowa_	Alignment	not modelled	12.0	18	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
31	d2cfxa1	Alignment	not modelled	11.7	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
32	d3b7sa2	Alignment	not modelled	11.5	6	Fold: Leukotriene A4 hydrolase N-terminal domain Superfamily: Leukotriene A4 hydrolase N-terminal domain Family: Leukotriene A4 hydrolase N-terminal domain
33	d1dsya_	Alignment	not modelled	11.4	16	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
34	d1go3e2	Alignment	not modelled	11.3	18	Fold: Dodecin subunit-like Superfamily: N-terminal, heterodimerisation domain of RBP7 (RpoE) Family: N-terminal, heterodimerisation domain of RBP7 (RpoE)
35	d1u0ma2	Alignment	not modelled	11.2	20	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
36	d2cg4a1	Alignment	not modelled	11.1	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
37	d1b4aa1	Alignment	not modelled	11.0	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
38	d2j0wa3	Alignment	not modelled	11.0	9	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
39	d2j07a2	Alignment	not modelled	10.7	27	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
40	d1cc1l_	Alignment	not modelled	10.7	26	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nickel-iron hydrogenase, large subunit
41	d1f9na1	Alignment	not modelled	10.7	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
42	c2jvfA_	Alignment	not modelled	10.5	29	PDB header: de novo protein Chain: A: PDB Molecule: de novo protein m7; PDBTitle: solution structure of m7, a computationally-designed2 artificial protein
43	c2nscA_	Alignment	not modelled	10.5	17	PDB header: chaperone Chain: A: PDB Molecule: trigger factor; PDBTitle: structures of and interactions between domains of trigger factor from2 themotoga maritima
44	d2c35b2	Alignment	not modelled	10.3	45	Fold: Dodecin subunit-like Superfamily: N-terminal, heterodimerisation domain of RBP7 (RpoE) Family: N-terminal, heterodimerisation domain of RBP7 (RpoE)
45	d1wuill	Alignment	not modelled	10.3	19	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nickel-iron hydrogenase, large subunit
46	d1rh8a_	Alignment	not modelled	10.3	23	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
47	d1dqva2	Alignment	not modelled	10.3	26	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
48	d1rsya_	Alignment	not modelled	10.2	35	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
49	c2jqzA_	Alignment	not modelled	10.2	31	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase smurf2; PDBTitle: solution structure of the c2 domain of human smurf2
50	d1ilga1	Alignment	not modelled	10.1	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
51	c1b4aA_	Alignment	not modelled	10.0	32	PDB header: repressor Chain: A: PDB Molecule: arginine repressor; PDBTitle: structure of the arginine repressor from bacillus stearothermophilus
52	d2vv5a2	Alignment	not modelled	9.9	11	Fold: Ferredoxin-like Superfamily: Mechanosensitive channel protein MscS (YggB), C-terminal domain Family: Mechanosensitive channel protein MscS (YggB), C-terminal domain
53	d1txka1	Alignment	not modelled	9.8	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
54	d1imua_	Alignment	not modelled	9.7	10	Fold: Ribosome binding protein Y (YfiA homologue) Superfamily: Ribosome binding protein Y (YfiA homologue) Family: Ribosome binding protein Y (YfiA homologue)
55	c3ereD_	Alignment	not modelled	9.6	37	PDB header: dna binding protein/dna Chain: D: PDB Molecule: arginine repressor; PDBTitle: crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator

56	c2dmgA	Alignment	not modelled	9.5	18	PDB header: lipid binding protein Chain: A: PDB Molecule: kiaa1228 protein; PDBTitle: solution structure of the third c2 domain of kiaa12282 protein
57	c3bbnl	Alignment	not modelled	9.5	17	PDB header: ribosome Chain: I: PDB Molecule: ribosomal protein s9; PDBTitle: homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
58	d1y14b2	Alignment	not modelled	9.4	36	Fold: Dodecin subunit-like Superfamily: N-terminal, heterodimerisation domain of RBP7 (RpoE) Family: N-terminal, heterodimerisation domain of RBP7 (RpoE)
59	c2q3xA	Alignment	not modelled	9.3	20	PDB header: transport protein Chain: A: PDB Molecule: regulating synaptic membrane exocytosis protein 1; PDBTitle: the rim1alpha c2b domain
60	d2cu6a1	Alignment	not modelled	8.9	16	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
61	c2chdA	Alignment	not modelled	8.9	35	PDB header: protein transport Chain: A: PDB Molecule: rabphilin-3a; PDBTitle: crystal structure of the c2a domain of rabphilin-3a
62	d1pa4a	Alignment	not modelled	8.9	15	Fold: Alpha-lytic protease prodomain-like Superfamily: Ribosome-binding factor A, RbfA Family: Ribosome-binding factor A, RbfA
63	c3k12F	Alignment	not modelled	8.9	19	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: uncharacterized protein a6v7t0; PDBTitle: crystal structure of an uncharacterized protein a6v7t0 from2 pseudomonas aeruginosa
64	d2cyya1	Alignment	not modelled	8.8	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
65	d2oo3a1	Alignment	not modelled	8.7	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: LPG1296-like
66	d1a25a	Alignment	not modelled	8.5	14	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
67	c2kyzA	Alignment	not modelled	8.4	17	PDB header: metal binding protein Chain: A: PDB Molecule: heavy metal binding protein; PDBTitle: nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
68	c3tqmD	Alignment	not modelled	8.3	13	PDB header: protein binding Chain: D: PDB Molecule: ribosome-associated factor y; PDBTitle: structure of an ribosomal subunit interface protein from coxiella2 burnetii
69	d1oiza1	Alignment	not modelled	8.1	25	Fold: RuvA C-terminal domain-like Superfamily: CRAL/TRIO N-terminal domain Family: CRAL/TRIO N-terminal domain
70	c3gtzA	Alignment	not modelled	8.1	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative translation initiation inhibitor; PDBTitle: crystal structure of a putative translation initiation inhibitor from2 salmonella typhimurium
71	d1dqva1	Alignment	not modelled	8.1	14	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
72	d1k0ra4	Alignment	not modelled	8.0	25	Fold: Transcription factor NusA, N-terminal domain Superfamily: Transcription factor NusA, N-terminal domain Family: Transcription factor NusA, N-terminal domain
73	c2dvzA	Alignment	not modelled	7.9	7	PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of a periplasmic transporter
74	d1u0bb1	Alignment	not modelled	7.8	38	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
75	d2qgsa2	Alignment	not modelled	7.8	27	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
76	d1bi5a2	Alignment	not modelled	7.6	13	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
77	d1f46a	Alignment	not modelled	7.5	26	Fold: TBP-like Superfamily: Cell-division protein ZipA, C-terminal domain Family: Cell-division protein ZipA, C-terminal domain
78	c2ds4A	Alignment	not modelled	7.5	7	PDB header: protein binding Chain: A: PDB Molecule: tripartite motif protein 45; PDBTitle: solution structure of the filamin domain from human2 tripartite motif protein 45
79	c3d01G	Alignment	not modelled	7.4	7	PDB header: structural genomics, unknown function Chain: G: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the protein atu1372 with unknown function from2 agrobacterium tumefaciens
80	d1fe0a	Alignment	not modelled	7.4	18	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
81	d1e3db	Alignment	not modelled	7.4	18	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nickel-iron hydrogenase, large subunit
						Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase

82	d1bkna2	Alignment	not modelled	7.3	6	II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
83	d1lb2b	Alignment	not modelled	7.3	32	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
84	d1aoya	Alignment	not modelled	7.2	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
85	d1ugka	Alignment	not modelled	7.2	19	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
86	c2v51E	Alignment	not modelled	7.2	29	PDB header: structural protein/contractile protein Chain: E: PDB Molecule: mk1/myocardin-like protein 1; PDBTitle: structure of mal-rpel1 complexed to actin
87	c2kzfA	Alignment	not modelled	7.2	20	PDB header: ribosomal protein Chain: A: PDB Molecule: ribosome-binding factor a; PDBTitle: solution nmr structure of the thermotoga maritima protein tm0855 a2 putative ribosome binding factor a
88	d2qqra2	Alignment	not modelled	7.2	27	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
89	c1u0bB	Alignment	not modelled	7.1	31	PDB header: ligase/rna Chain: B: PDB Molecule: cysteiny1 trna; PDBTitle: crystal structure of cysteiny1-trna synthetase binary2 complex with trnacs
90	d1g0da2	Alignment	not modelled	7.0	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains
91	d1dnpa2	Alignment	not modelled	7.0	41	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
92	c2klrA	Alignment	not modelled	6.9	12	PDB header: chaperone Chain: A: PDB Molecule: alpha-crystallin b chain; PDBTitle: solid-state nmr structure of the alpha-crystallin domain in alphab-2 crystallin oligomers
93	c3lybC	Alignment	not modelled	6.9	21	PDB header: hydrolase Chain: C: PDB Molecule: putative endoribonuclease; PDBTitle: structure of putative endoribonuclease(kp1_3112) from2 klebsiella pneumoniae
94	c2v51F	Alignment	not modelled	6.9	44	PDB header: structural protein/contractile protein Chain: F: PDB Molecule: mk1/myocardin-like protein 1; PDBTitle: structure of mal-rpel1 complexed to actin
95	c2e85B	Alignment	not modelled	6.9	21	PDB header: hydrolase Chain: B: PDB Molecule: hydrogenase 3 maturation protease; PDBTitle: crystal structure of the hydrogenase 3 maturation protease
96	d1wlha1	Alignment	not modelled	6.8	20	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
97	c2gjhA	Alignment	not modelled	6.8	21	PDB header: de novo protein Chain: A: PDB Molecule: designed protein; PDBTitle: nmr structure of cfr (c-terminal fragment of2 computationally designed novel-topology protein top7)
98	c2r83B	Alignment	not modelled	6.7	36	PDB header: endocytosis, exocytosis Chain: B: PDB Molecule: synaptotagmin-1; PDBTitle: crystal structure analysis of human synaptotagmin 1 c2a-c2b
99	d2ns9a1	Alignment	not modelled	6.7	9	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like