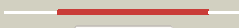




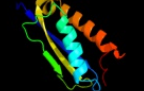

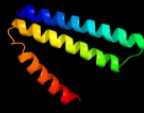

















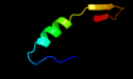
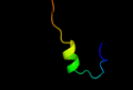

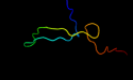


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vv5D_	 Alignment		100.0	18	PDB header: membrane protein Chain: D: PDB Molecule: small-conductance mechanosensitive channel; PDBTitle: the open structure of mscs
2	d2vv5a1	 Alignment		99.8	23	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Mechanosensitive channel protein MscS (YggB), middle domain
3	d2vv5a2	 Alignment		99.2	19	Fold: Ferredoxin-like Superfamily: Mechanosensitive channel protein MscS (YggB), C-terminal domain Family: Mechanosensitive channel protein MscS (YggB), C-terminal domain
4	d2vv5a3	 Alignment		98.7	14	Fold: Mechanosensitive channel protein MscS (YggB), transmembrane region Superfamily: Mechanosensitive channel protein MscS (YggB), transmembrane region Family: Mechanosensitive channel protein MscS (YggB), transmembrane region
5	d1nz9a_	 Alignment		80.7	22	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
6	d1nppa2	 Alignment		78.9	17	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
7	d2hqha1	 Alignment		78.6	30	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
8	c2kvqG	 Alignment		76.8	13	PDB header: transcription Chain: G: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of nuse:nusg-ctd complex
9	c2jvva_	 Alignment		76.8	13	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of e. coli nusg carboxyterminal domain
10	c2e6zA	 Alignment		74.6	13	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt5; PDBTitle: solution structure of the second kow motif of human2 transcription elongation factor spt5
11	c2zkrt_	 Alignment		70.4	13	PDB header: ribosomal protein/rna Chain: T: PDB Molecule: rna expansion segment es39 part iii; PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map

12	c2l82A_	Alignment		69.5	16	PDB header: de novo protein Chain: A: PDB Molecule: designed protein or32; PDBTitle: solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or32
13	d1t9ha1	Alignment		63.1	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
14	c3p8bB_	Alignment		61.1	30	PDB header: transferase/transcription Chain: B: PDB Molecule: transcription antitermination protein nusg; PDBTitle: x-ray crystal structure of pyrococcus furiosus transcription2 elongation factor spt4/5
15	d1u0la1	Alignment		60.0	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
16	c2rcnA_	Alignment		59.5	19	PDB header: hydrolase Chain: A: PDB Molecule: probable gtpase engc; PDBTitle: crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium.
17	d2gvha1	Alignment		56.7	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
18	c2gvhC_	Alignment		54.3	18	PDB header: hydrolase Chain: C: PDB Molecule: agr_1_2016p; PDBTitle: crystal structure of acyl-coa hydrolase (15159470) from agrobacterium2 tumefaciens at 2.65 a resolution
19	d2eyqa1	Alignment		53.7	16	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
20	c2yv5A_	Alignment		52.5	17	PDB header: hydrolase Chain: A: PDB Molecule: yjeq protein; PDBTitle: crystal structure of yjeq from aquifex aeolicus
21	d1whka_	Alignment	not modelled	52.5	16	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
22	d1whma_	Alignment	not modelled	51.6	16	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
23	d1y7ua1	Alignment	not modelled	50.9	25	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
24	c1t9ha_	Alignment	not modelled	50.7	22	PDB header: hydrolase Chain: A: PDB Molecule: probable gtpase engc; PDBTitle: the crystal structure of yloq, a circularly permuted gtpase.
25	c3b7kA_	Alignment	not modelled	50.3	25	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 12; PDBTitle: human acyl-coenzyme a thioesterase 12
26	d2gvha2	Alignment	not modelled	45.3	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
27	c1m1gB_	Alignment	not modelled	44.2	18	PDB header: transcription Chain: B: PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of aquifex aeolicus n-utilization2 substance g (nusg), space group p2(1)
28	d2coya1	Alignment	not modelled	43.8	28	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
						PDB header: ribosome Chain: S: PDB Molecule: rpl26;

29	c4a1cS_	Alignment	not modelled	43.0	18	PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
30	d1ylia1	Alignment	not modelled	42.3	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
31	d1vpma_	Alignment	not modelled	41.1	32	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
32	d2cqaa1	Alignment	not modelled	38.8	28	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TIP49 domain
33	c4a2iV_	Alignment	not modelled	38.8	21	PDB header: ribosome/hydrolase Chain: V: PDB Molecule: putative ribosome biogenesis gtpase rsga; PDBTitle: cryo-electron microscopy structure of the 30s subunit in complex with2 the yjeq biogenesis factor
34	d1vqot1	Alignment	not modelled	38.5	32	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal proteins L24p and L21e
35	c1u0lB_	Alignment	not modelled	37.0	22	PDB header: hydrolase Chain: B: PDB Molecule: probable gtpase engc; PDBTitle: crystal structure of yjeq from thermotoga maritima
36	c2v1oF_	Alignment	not modelled	35.1	11	PDB header: hydrolase Chain: F: PDB Molecule: cytosolic acyl coenzyme a thioester hydrolase; PDBTitle: crystal structure of n-terminal domain of acyl-coa2 thioesterase 7
37	d2cp6a1	Alignment	not modelled	35.0	29	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
38	d2do3a1	Alignment	not modelled	33.9	22	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: SPT5 KOW domain-like
39	d1ppje2	Alignment	not modelled	33.7	8	Fold: Single transmembrane helix Superfamily: ISP transmembrane anchor Family: ISP transmembrane anchor
40	c3iz5Y_	Alignment	not modelled	31.8	18	PDB header: ribosome Chain: Y: PDB Molecule: 60s ribosomal protein l26 (l24p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
41	d1yvca1	Alignment	not modelled	31.4	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TRAM domain
42	d1yeza1	Alignment	not modelled	30.7	11	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TRAM domain
43	c2qq2C_	Alignment	not modelled	30.0	11	PDB header: hydrolase Chain: C: PDB Molecule: cytosolic acyl coenzyme a thioester hydrolase; PDBTitle: crystal structure of c-terminal domain of human acyl-coa thioesterase2 7
44	d2coza1	Alignment	not modelled	29.7	17	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
45	c2xhcA_	Alignment	not modelled	29.3	22	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
46	d1bcce2	Alignment	not modelled	28.6	8	Fold: Single transmembrane helix Superfamily: ISP transmembrane anchor Family: ISP transmembrane anchor
47	c2z0wA_	Alignment	not modelled	27.7	24	PDB header: protein binding Chain: A: PDB Molecule: cap-gly domain-containing linker protein 4; PDBTitle: crystal structure of the 2nd cap-gly domain in human restin-2 like protein 2 reveals a swapped-dimer
48	c3d6lA_	Alignment	not modelled	27.1	23	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of cj0915, a hexameric hotdog fold2 thioesterase of campylobacter jejuni
49	d2e3ha1	Alignment	not modelled	26.9	33	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
50	d2cp5a1	Alignment	not modelled	26.9	14	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
51	d2cp3a1	Alignment	not modelled	26.7	33	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
52	c2eisA_	Alignment	not modelled	26.5	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein tthb207; PDBTitle: x-ray structure of acyl-coa hydrolase-like protein, tt1379, from2 thermus thermophilus hb8
53	d2e3ia1	Alignment	not modelled	26.4	14	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
54	d1whja_	Alignment	not modelled	25.8	32	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain

55	c2e4hA_	Alignment	not modelled	24.7	30	PDB header: structural protein Chain: A: PDB Molecule: restin; PDBTitle: solution structure of cytoskeletal protein in complex with2 tubulin tail
56	d1ayia_	Alignment	not modelled	24.6	24	Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins
57	d2cowa1	Alignment	not modelled	24.2	22	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
58	d2cp2a1	Alignment	not modelled	23.8	19	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
59	d2vlqa1	Alignment	not modelled	23.4	24	Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins
60	c3owvA_	Alignment	not modelled	23.3	15	PDB header: hydrolase Chain: A: PDB Molecule: dna-entry nuclease; PDBTitle: structural insights into catalytic and substrate binding mechanisms of2 the strategic endo nuclease from streptococcus pneumoniae
61	c2no8A_	Alignment	not modelled	22.2	30	PDB header: immune system Chain: A: PDB Molecule: colicin-e2 immunity protein; PDBTitle: nmr structure analysis of the colicin immunity protein im2
62	d2cp0a1	Alignment	not modelled	22.2	22	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
63	c3mayE_	Alignment	not modelled	20.1	27	PDB header: heme-binding protein Chain: E: PDB Molecule: possible exported protein; PDBTitle: crystal structure of a secreted mycobacterium tuberculosis heme-2 binding protein
64	d1gxha_	Alignment	not modelled	19.9	30	Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins
65	c3lwgb_	Alignment	not modelled	19.4	4	PDB header: unknown function Chain: B: PDB Molecule: hp0420 homologue; PDBTitle: crystal structure of hp0420-homologue c46a from helicobacter2 felis
66	d1njib1	Alignment	not modelled	18.8	33	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Eukaryotic ODC-like
67	d1whha_	Alignment	not modelled	17.4	21	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
68	d2btva_	Alignment	not modelled	17.2	26	Fold: Reovirus inner layer core protein p3 Superfamily: Reovirus inner layer core protein p3 Family: Orbivirus core
69	c2zqeA_	Alignment	not modelled	16.4	35	PDB header: dna binding protein Chain: A: PDB Molecule: imuts2 protein; PDBTitle: crystal structure of the smr domain of thermus thermophilus imuts2
70	d2cbpa_	Alignment	not modelled	16.2	25	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
71	d1i9ga_	Alignment	not modelled	15.8	8	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: tRNA(1-methyladenosine) methyltransferase-like
72	d2toda1	Alignment	not modelled	15.6	33	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Eukaryotic ODC-like
73	d2je6i1	Alignment	not modelled	15.1	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
74	c2btvB_	Alignment	not modelled	14.7	26	PDB header: virus Chain: B: PDB Molecule: protein (vp3 core protein); PDBTitle: atomic model for bluetongue virus (btv) core
75	d1y4oa1	Alignment	not modelled	14.3	19	Fold: Profilin-like Superfamily: Roadblock/LC7 domain Family: Roadblock/LC7 domain
76	d2ot2a1	Alignment	not modelled	13.7	20	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
77	d1sroa_	Alignment	not modelled	13.7	12	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
78	c1s1iU_	Alignment	not modelled	13.4	18	PDB header: ribosome Chain: U: PDB Molecule: 60s ribosomal protein l26-a; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
79	d1bbua1	Alignment	not modelled	13.3	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
80	d1ws8a_	Alignment	not modelled	12.6	21	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
						Fold: OB-fold

81	d1e1oa1	Alignment	not modelled	12.3	19	Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
82	d1e32a3	Alignment	not modelled	12.2	21	Fold: Cdc48 domain 2-like Superfamily: Cdc48 domain 2-like Family: Cdc48 domain 2-like
83	d2g50a1	Alignment	not modelled	12.1	14	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
84	d3d3ra1	Alignment	not modelled	12.1	25	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
85	d1r4va	Alignment	not modelled	11.8	23	Fold: Histone-fold Superfamily: Histone-fold Family: Bacterial histone-fold protein
86	d1g7sa1	Alignment	not modelled	11.7	26	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
87	c2qlwA	Alignment	not modelled	11.6	21	PDB header: isomerase Chain: A: PDB Molecule: rhau; PDBTitle: crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
88	c2qlxA	Alignment	not modelled	11.6	21	PDB header: isomerase Chain: A: PDB Molecule: l-rhamnose mutarotase; PDBTitle: crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose
89	d1wwia1	Alignment	not modelled	11.5	14	Fold: Histone-fold Superfamily: Histone-fold Family: Bacterial histone-fold protein
90	d1ubea2	Alignment	not modelled	11.5	7	Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain
91	c2gutA	Alignment	not modelled	11.5	23	PDB header: transcription Chain: A: PDB Molecule: arc/mediator, positive cofactor 2 glutamine/q- PDBTitle: solution structure of the trans-activation domain of the2 human co-activator arc105
92	d1mo6a2	Alignment	not modelled	11.5	7	Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain
93	c3d3rA	Alignment	not modelled	11.4	25	PDB header: chaperone Chain: A: PDB Molecule: hydrogenase assembly chaperone hupc/hupf; PDBTitle: crystal structure of the hydrogenase assembly chaperone hupc/hupf2 family protein from shewanella oneidensis mr-1
94	d1d7ka1	Alignment	not modelled	11.2	33	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Eukaryotic ODC-like
95	c3g7gG	Alignment	not modelled	11.1	18	PDB header: structural genomics, unknown function Chain: G: PDB Molecule: upf0311 protein ca_c3321; PDBTitle: crystal structure of the protein with unknown function from2 clostridium acetobutylicum atcc 824
96	d1g7sa2	Alignment	not modelled	11.1	19	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
97	d1e0ta1	Alignment	not modelled	11.1	21	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
98	d1jera	Alignment	not modelled	11.0	29	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
99	c1jerA	Alignment	not modelled	11.0	29	PDB header: electron transport Chain: A: PDB Molecule: cucumber stellacyanin; PDBTitle: cucumber stellacyanin, cu2+, ph 7.0