




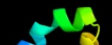







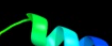



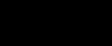



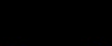

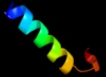









#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3i3fB_	 Alignment		40.8	15	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: hypothetical protein from giardia lamblia gl50803_14299
2	c3idwA_	 Alignment		40.7	25	PDB header: endocytosis Chain: A: PDB Molecule: actin cytoskeleton-regulatory complex protein sla1; PDBTitle: crystal structure of sla1 homology domain 2
3	c2rhfA_	 Alignment		38.1	20	PDB header: hydrolase Chain: A: PDB Molecule: dna helicase recq; PDBTitle: d. radiodurans recq hrhc domain 3
4	c1oxjA_	 Alignment		26.6	11	PDB header: rna binding protein Chain: A: PDB Molecule: rna-binding protein smaug; PDBTitle: crystal structure of the smaug rna binding domain
5	d2ewca1	 Alignment		22.8	24	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
6	d1oxja1	 Alignment		19.8	10	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
7	d2e1fa1	 Alignment		19.2	14	Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases
8	c3kjl_	 Alignment		18.3	35	PDB header: unknown function Chain: L: PDB Molecule: nmb1025 protein; PDBTitle: crystal structure of nmb1025, a member of yjgf protein family, from2 neisseria meningitidis (hexagonal crystal form)
9	c3k1rB_	 Alignment		18.2	25	PDB header: structural protein Chain: B: PDB Molecule: usher syndrome type-1g protein; PDBTitle: structure of harmonin npdz1 in complex with the sampm of2 sans
10	c2of5A_	 Alignment		17.9	19	PDB header: apoptosis Chain: A: PDB Molecule: death domain-containing protein cradd; PDBTitle: oligomeric death domain complex
11	c3lybC_	 Alignment		17.2	23	PDB header: hydrolase Chain: C: PDB Molecule: putative endoribonuclease; PDBTitle: structure of putative endoribonuclease(kp1_3112) from2 klebsiella pneumoniae

12	c2nv2U	Alignment		15.7	35	PDB header: lyase/transferase Chain: U: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
13	c2zbtB	Alignment		15.6	30	PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
14	c3oq9C	Alignment		13.9	22	PDB header: apoptosis Chain: C: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: structure of the fas/fadd death domain assembly
15	c1ow5A	Alignment		13.8	12	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase ste11; PDBTitle: nmr structure of the saccharomyces cerevisiae sam (sterile2 alpha motif) domain
16	d1ow5a	Alignment		13.8	12	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
17	d1onia	Alignment		13.3	27	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
18	d2cvla1	Alignment		13.2	27	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
19	d1d8ba	Alignment		13.2	24	Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases
20	c3bs7A	Alignment		12.9	32	PDB header: signaling protein Chain: A: PDB Molecule: protein aveugle; PDBTitle: crystal structure of the sterile alpha motif (sam) domain2 of hyphen/aveugle
21	c3bs5A	Alignment	not modelled	12.7	29	PDB header: signaling protein/membrane protein Chain: A: PDB Molecule: protein aveugle; PDBTitle: crystal structure of hcnk2-sam/dhyp-sam complex
22	c2eanA	Alignment	not modelled	11.3	24	PDB header: signaling protein Chain: A: PDB Molecule: connector enhancer of kinase suppressor of ras 2; PDBTitle: solution structure of the n-terminal sam-domain of human2 kiaa0902 protein (connector enhancer of kinase suppressor3 of ras 2)
23	d1hmja	Alignment	not modelled	11.2	33	Fold: RPB5-like RNA polymerase subunit Superfamily: RPB5-like RNA polymerase subunit Family: RPB5
24	d1qrva	Alignment	not modelled	11.1	16	Fold: HMG-box Superfamily: HMG-box Family: HMG-box
25	d3cx5g1	Alignment	not modelled	10.8	28	Fold: 14 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: 14 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: 14 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
26	c2eseA	Alignment	not modelled	10.1	29	PDB header: protein/rna complex Chain: A: PDB Molecule: vts1p; PDBTitle: structure of the sam domain of vts1p in complex with rna
27	c3bq7A	Alignment	not modelled	10.0	29	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase delta; PDBTitle: sam domain of diacylglycerol kinase delta1 (e35g)
28	c2fo9A	Alignment	not modelled	9.9	31	PDB header: rna binding protein Chain: A: PDB Molecule: protein vts1;

28	c2ie9A	Alignment	not modelled	9.5	31	PDBTitle: solution structure of the vts1 sam domain in the presence2 of rna PDB header: transcription Chain: B: PDB Molecule: bcl2-antagonist of cell death; PDBTitle: the crystal structure of bcl-xl in complex with full-length2 bad
29	c2bzwB	Alignment	not modelled	9.6	50	PDB header: hydrolase Chain: B: PDB Molecule: l-psp putative endoribonuclease; PDBTitle: crystal structure of l-psp putative endoribonuclease from uncultured2 organism
30	c3r0pB	Alignment	not modelled	9.6	15	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
31	d1ucva	Alignment	not modelled	9.0	12	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
32	d1kw4a	Alignment	not modelled	9.0	13	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
33	d1ddfa	Alignment	not modelled	8.2	22	Fold: DEATH domain Superfamily: DEATH domain Family: DEATH domain, DD
34	c2kg5A	Alignment	not modelled	8.2	24	PDB header: signaling protein Chain: A: PDB Molecule: arf-gap, rho-gap domain, ank repeat and ph PDBTitle: nmr solution structure of arap3-sam
35	c3quwA	Alignment	not modelled	8.1	12	PDB header: protein binding Chain: A: PDB Molecule: protein mmf1; PDBTitle: crystal structure of yeast mmf1
36	c2eaoA	Alignment	not modelled	8.0	35	PDB header: signaling protein, transferase Chain: A: PDB Molecule: ephrin type-b receptor 1; PDBTitle: solution structure of the c-terminal sam-domain of mouse2 ephrin type-b receptor 1 precursor (ec 2.7.1.112)
37	c3lmeE	Alignment	not modelled	7.9	19	PDB header: translation Chain: E: PDB Molecule: possible translation initiation inhibitor; PDBTitle: structure of probable translation initiation inhibitor from2 (rpa2473) from rhodopseudomonas palustris
38	d1hsma	Alignment	not modelled	7.7	21	Fold: HMG-box Superfamily: HMG-box Family: HMG-box
39	c3i7tA	Alignment	not modelled	7.7	31	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of rv2704, a member of highly conserved2 yjgf/yer057c/uk114 family, from mycobacterium tuberculosis
40	d2d59a1	Alignment	not modelled	7.4	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
41	c2hueB	Alignment	not modelled	7.2	56	PDB header: dna binding protein Chain: B: PDB Molecule: histone h3; PDBTitle: structure of the h3-h4 chaperone asf1 bound to histones h3 and h4
42	c3nquA	Alignment	not modelled	7.0	44	PDB header: dna binding protein Chain: A: PDB Molecule: histone h3-like centromeric protein a; PDBTitle: crystal structure of partially trypsinized (cenp-a/h4)2 heterotetramer
43	c2qkqA	Alignment	not modelled	6.9	35	PDB header: transferase Chain: A: PDB Molecule: ephrin type-b receptor 4; PDBTitle: structure of the sam domain of human ephrin type-b receptor2 4
44	d1eika	Alignment	not modelled	6.9	40	Fold: RPB5-like RNA polymerase subunit Superfamily: RPB5-like RNA polymerase subunit Family: RPB5
45	d1ui0a	Alignment	not modelled	6.8	32	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Mug-like
46	d1v38a	Alignment	not modelled	6.7	12	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
47	d1ulqa1	Alignment	not modelled	6.7	27	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
48	c1g5jB	Alignment	not modelled	6.7	50	PDB header: apoptosis Chain: B: PDB Molecule: bad protein; PDBTitle: complex of bcl-xl with peptide from bad
49	d1o4va	Alignment	not modelled	6.7	29	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
50	d1sgga	Alignment	not modelled	6.6	27	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
51	c2yfwC	Alignment	not modelled	6.5	44	PDB header: cell cycle Chain: C: PDB Molecule: histone h3-like centromeric protein cse4; PDBTitle: heterotetramer structure of kluyveromyces lactis cse4,h4
52	d2a1ja1	Alignment	not modelled	6.4	33	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
53	d1w7pd1	Alignment	not modelled	6.4	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
54	c3k12F	Alignment	not modelled	6.3	38	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: uncharacterized protein a6v7t0; PDBTitle: crystal structure of an uncharacterized protein a6v7t0 from2 pseudomonas aeruginosa

81	d1mz4a_	Alignment	not modelled	5.1	17	Superfamily: Cytochrome c Family: monodomain cytochrome c
82	d1b0xa_	Alignment	not modelled	5.1	29	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
83	c1b0xA_	Alignment	not modelled	5.1	29	PDB header: transferase Chain: A: PDB Molecule: protein (epha4 receptor tyrosine kinase); PDBTitle: the crystal structure of an eph receptor sam domain reveals2 a mechanism for modular dimerization.
84	d1gt0d_	Alignment	not modelled	5.1	26	Fold: HMG-box Superfamily: HMG-box Family: HMG-box
85	d1j7ha_	Alignment	not modelled	5.1	26	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
86	d1icha_	Alignment	not modelled	5.0	21	Fold: DEATH domain Superfamily: DEATH domain Family: DEATH domain, DD