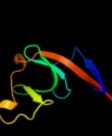
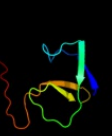
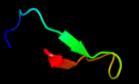
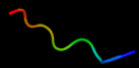
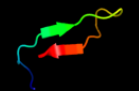
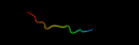


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jhfa2	 Alignment		100.0	33	Fold: LexA/Signal peptidase Superfamily: LexA/Signal peptidase Family: LexA-related
2	d1umua_	 Alignment		100.0	98	Fold: LexA/Signal peptidase Superfamily: LexA/Signal peptidase Family: LexA-related
3	c3k2zA_	 Alignment		99.9	33	PDB header: hydrolase Chain: A: PDB Molecule: lexa repressor; PDBTitle: crystal structure of a lexa protein from thermotoga maritima
4	c1jhhB_	 Alignment		99.9	32	PDB header: hydrolase Chain: B: PDB Molecule: lexa repressor; PDBTitle: lexa s119a mutant
5	c2hnfA_	 Alignment		99.9	29	PDB header: viral protein Chain: A: PDB Molecule: repressor protein ci101-229dm-k192a; PDBTitle: structure of a hyper-cleavable monomeric fragment of phage2 lambda repressor containing the cleavage site region
6	d1f39a_	 Alignment		99.8	34	Fold: LexA/Signal peptidase Superfamily: LexA/Signal peptidase Family: LexA-related
7	c3bdnB_	 Alignment		99.7	32	PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor
8	c2fjrB_	 Alignment		99.6	10	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
9	c2fkdkK_	 Alignment		98.7	18	PDB header: transcription regulator Chain: K: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of the c-terminal domain of bacteriophage2 186 repressor
10	d1b12a_	 Alignment		97.5	21	Fold: LexA/Signal peptidase Superfamily: LexA/Signal peptidase Family: Type 1 signal peptidase
11	d1nnxa_	 Alignment		15.0	18	Fold: OB-fold Superfamily: Hypothetical protein YgiW Family: Hypothetical protein YgiW

12	d1hr0w_	Alignment		14.9	32	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
13	d1jt8a_	Alignment		14.6	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
14	d1d7qa_	Alignment		14.0	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
15	c2uwqA_	Alignment		10.5	38	PDB header: apoptosis Chain: A: PDB Molecule: apoptosis-stimulating of p53 protein 2; PDBTitle: solution structure of aspp2 n-terminus
16	d2p84a1	Alignment		10.1	22	Fold: YopX-like Superfamily: YopX-like Family: YopX-like
17	d1ah9a_	Alignment		9.8	32	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
18	c2oqkA_	Alignment		9.1	27	PDB header: translation Chain: A: PDB Molecule: putative translation initiation factor eif-1a; PDBTitle: crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
19	c2zpmA_	Alignment		7.5	11	PDB header: hydrolase Chain: A: PDB Molecule: regulator of sigma e protease; PDBTitle: crystal structure analysis of pdz domain b
20	d1zvpa1	Alignment		5.8	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: VC0802-like
21	d2vgna1	Alignment	not modelled	5.3	14	Fold: Sm-like fold Superfamily: Dom34/Pelota N-terminal domain-like Family: Dom34/Pelota N-terminal domain-like