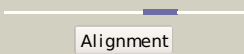
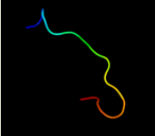
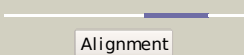

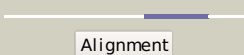
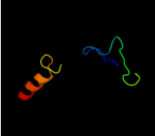

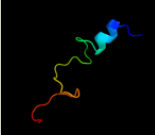
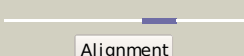
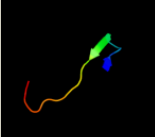
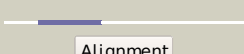
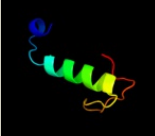
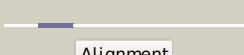

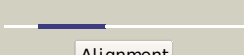




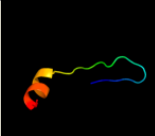

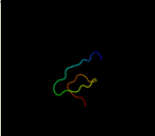








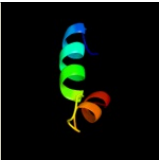
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2fd6u2</a>	 Alignment		16.1	25	<b>Fold:</b> Snake toxin-like <b>Superfamily:</b> Snake toxin-like <b>Family:</b> Extracellular domain of cell surface receptors
2	<a href="#">d1v0da_</a>	 Alignment		15.3	24	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> Caspase-activated DNase, CAD (DffB, DFF40)
3	<a href="#">c1v0dA_</a>	 Alignment		15.3	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna fragmentation factor 40 kda subunit; <b>PDBTitle:</b> crystal structure of caspase-activated dnase (cad)
4	<a href="#">c2vu9A_</a>	 Alignment		12.3	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> botulinum neurotoxin a heavy chain; <b>PDBTitle:</b> crystal structure of botulinum neurotoxin serotype a2 binding domain in complex with gt1b
5	<a href="#">c3ts3D_</a>	 Alignment		11.9	32	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> capsid polypeptide; <b>PDBTitle:</b> crystal structure of the projection domain of the turkey astrovirus2 capsid protein at 1.5 angstrom resolution
6	<a href="#">c2lfcA_</a>	 Alignment		11.3	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fumarate reductase, flavoprotein subunit; <b>PDBTitle:</b> solution nmr structure of fumarate reductase flavoprotein subunit from2 lactobacillus plantarum, northeast structural genomics consortium3 target lpr145j
7	<a href="#">c2w0cT_</a>	 Alignment		11.0	50	<b>PDB header:</b> virus <b>Chain:</b> T: <b>PDB Molecule:</b> protein p6; <b>PDBTitle:</b> x-ray structure of the entire lipid-containing2 bacteriophage pm2
8	<a href="#">d1p5dx1</a>	 Alignment		9.7	28	<b>Fold:</b> Phosphoglucomutase, first 3 domains <b>Superfamily:</b> Phosphoglucomutase, first 3 domains <b>Family:</b> Phosphoglucomutase, first 3 domains
9	<a href="#">d1hcia1</a>	 Alignment		8.8	25	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Spectrin repeat <b>Family:</b> Spectrin repeat
10	<a href="#">d1g03a_</a>	 Alignment		8.3	32	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
11	<a href="#">c2i9bF_</a>	 Alignment		8.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> urokinase plasminogen activator surface receptor; <b>PDBTitle:</b> crystal structure of atf-urokinase receptor complex

12	<a href="#">d1zy3a1</a>	Alignment		7.2	44	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Bcl-2 inhibitors of programmed cell death <b>Family:</b> Bcl-2 inhibitors of programmed cell death
13	<a href="#">d1o0la_</a>	Alignment		5.9	50	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Bcl-2 inhibitors of programmed cell death <b>Family:</b> Bcl-2 inhibitors of programmed cell death
14	<a href="#">d1pgl22</a>	Alignment		5.9	31	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses <b>Family:</b> Comoviridae-like VP
15	<a href="#">d1ny722</a>	Alignment		5.7	31	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses <b>Family:</b> Comoviridae-like VP
16	<a href="#">d1eijs_</a>	Alignment		5.7	19	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> Double-stranded DNA-binding domain <b>Family:</b> Double-stranded DNA-binding domain
17	<a href="#">c3jtpB_</a>	Alignment		5.4	10	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> adapter protein meca 1; <b>PDBTitle:</b> crystal structure of the c-terminal domain of meca

18 [d2crua1](#)

Alignment



5.2

12 **Fold:**RuvA C-terminal domain-like  
**Superfamily:**Double-stranded DNA-binding domain  
**Family:**Double-stranded DNA-binding domain