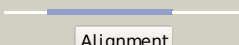






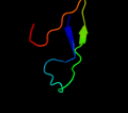
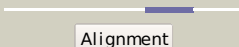



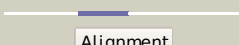

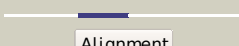

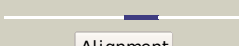






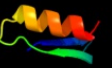

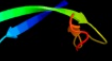
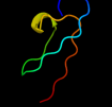

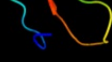

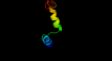


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2pc9B_</a>	 Alignment		20.4	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoenolpyruvate carboxykinase [atp]; <b>PDBTitle:</b> crystal structure of atp-dependent phosphoenolpyruvate carboxykinase2 from thermus thermophilus hb8
2	<a href="#">c2h12C_</a>	 Alignment		19.8	12	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> citrate synthase; <b>PDBTitle:</b> structure of acetobacter aceti citrate synthase complexed2 with oxaloacetate and carboxymethyl dethia coenzyme a (cmx)
3	<a href="#">d1bqga2</a>	 Alignment		17.2	23	<b>Fold:</b> Enolase N-terminal domain-like <b>Superfamily:</b> Enolase N-terminal domain-like <b>Family:</b> Enolase N-terminal domain-like
4	<a href="#">d2a9da1</a>	 Alignment		16.2	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Molybdenum-containing oxidoreductases-like dimerisation domain
5	<a href="#">c3f4yF_</a>	 Alignment		11.9	31	<b>PDB header:</b> viral protein <b>Chain:</b> F: <b>PDB Molecule:</b> mutant peptide derived from hiv gp41 chr domain; <b>PDBTitle:</b> hiv gp41 six-helix bundle containing a mutant chr alpha-2 peptide sequence
6	<a href="#">d1ogpa1</a>	 Alignment		10.9	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Molybdenum-containing oxidoreductases-like dimerisation domain
7	<a href="#">c2eqjA_</a>	 Alignment		10.1	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> metal-response element-binding transcription <b>PDBTitle:</b> solution structure of the tudor domain of metal-response2 element-binding transcription factor 2
8	<a href="#">c2e5pA_</a>	 Alignment		9.5	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> phd finger protein 1; <b>PDBTitle:</b> solution structure of the tudor domain of phd finger2 protein 1 (phf1 protein)
9	<a href="#">d1z1ba1</a>	 Alignment		9.4	32	<b>Fold:</b> DNA-binding domain <b>Superfamily:</b> DNA-binding domain <b>Family:</b> lambda integrase N-terminal domain
10	<a href="#">c1kjkA_</a>	 Alignment		9.4	32	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> solution structure of the lambda integrase amino-terminal2 domain
11	<a href="#">c3c4tA_</a>	 Alignment		9.1	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoribonuclease dicer; <b>PDBTitle:</b> structure of rnaseiiiib and dsrna binding domains of mouse dicer

12	<a href="#">c1o0wB_</a>	Alignment		8.7	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ribonuclease iii; <b>PDBTitle:</b> crystal structure of ribonuclease iii (tm1102) from2 thermotoga maritima at 2.0 a resolution
13	<a href="#">d1x47a1</a>	Alignment		8.2	26	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
14	<a href="#">c2enpA_</a>	Alignment		8.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> b/k protein; <b>PDBTitle:</b> solution structure of the first c2 domain from human b/k2 protein
15	<a href="#">c2e5qA_</a>	Alignment		8.0	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> phd finger protein 19; <b>PDBTitle:</b> solution structure of the tudor domain of phd finger2 protein 19, isoform b [homo sapiens]
16	<a href="#">d2fd6u2</a>	Alignment		7.4	6	<b>Fold:</b> Snake toxin-like <b>Superfamily:</b> Snake toxin-like <b>Family:</b> Extracellular domain of cell surface receptors
17	<a href="#">d1stua_</a>	Alignment		7.3	19	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
18	<a href="#">d2bv3a4</a>	Alignment		6.9	26	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/efEF-2 domains III and V
19	<a href="#">c3ts3D_</a>	Alignment		6.9	26	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> capsid polyprotein; <b>PDBTitle:</b> crystal structure of the projection domain of the turkey astrovirus2 capsid protein at 1.5 angstrom resolution
20	<a href="#">d1ef1c_</a>	Alignment		6.2	14	<b>Fold:</b> Non-globular all-alpha subunits of globular proteins <b>Superfamily:</b> Moesin tail domain <b>Family:</b> Moesin tail domain
21	<a href="#">d2gl5a2</a>	Alignment	not modelled	6.1	15	<b>Fold:</b> Enolase N-terminal domain-like <b>Superfamily:</b> Enolase N-terminal domain-like <b>Family:</b> Enolase N-terminal domain-like
22	<a href="#">d2bo3a1</a>	Alignment	not modelled	5.9	16	<b>Fold:</b> HP0242-like <b>Superfamily:</b> HP0242-like <b>Family:</b> HP0242-like
23	<a href="#">d1m06f_</a>	Alignment	not modelled	5.8	75	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> ssDNA viruses <b>Family:</b> Microviridae-like VP
24	<a href="#">d1x48a1</a>	Alignment	not modelled	5.7	23	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
25	<a href="#">d1hi9a_</a>	Alignment	not modelled	5.5	10	<b>Fold:</b> Dipeptide transport protein <b>Superfamily:</b> Dipeptide transport protein <b>Family:</b> Dipeptide transport protein
26	<a href="#">d1t0aa_</a>	Alignment	not modelled	5.5	16	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> lpsF-like <b>Family:</b> lpsF-like
27	<a href="#">c1h2IG_</a>	Alignment	not modelled	5.4	35	<b>PDB header:</b> dna-binding protein <b>Chain:</b> G: <b>PDB Molecule:</b> dna repair protein rad52 homolog; <b>PDBTitle:</b> human rad52 protein, n-terminal domain
28	<a href="#">d1w55a2</a>	Alignment	not modelled	5.2	16	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> lpsF-like <b>Family:</b> lpsF-like
29	<a href="#">d1pyma3</a>	Alignment	not modelled	5.2	22	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Hypothetical protein Ta0289 C-terminal domain

				Family:Hypothetical protein Ta0289 C-terminal domain	
30	<a href="#">c3kysB_</a>	Alignment	not modelled	5.1	29
				PDB header:transcription/protein binding Chain: B: PDB Molecule:65 kda yes-associated protein; PDBTitle: crystal structure of human yap and tead complex	