

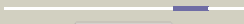


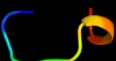



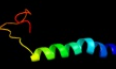









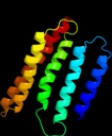

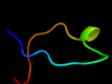
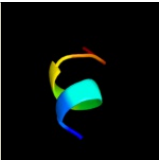


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3m7bA_</a>	 Alignment		100.0	40	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tellurite resistance protein teha homolog; <b>PDBTitle:</b> crystal structure of plant slac1 homolog teha
2	<a href="#">c2kncA_</a>	 Alignment		12.1	10	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
3	<a href="#">c3kysB_</a>	 Alignment		8.9	30	<b>PDB header:</b> transcription/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> 65 kda yes-associated protein; <b>PDBTitle:</b> crystal structure of human yap and tead complex
4	<a href="#">c1cn3F_</a>	 Alignment		8.3	33	<b>PDB header:</b> viral protein <b>Chain:</b> F: <b>PDB Molecule:</b> fragment of coat protein vp2; <b>PDBTitle:</b> interaction of polyomavirus internal protein vp2 with major2 capsid protein vp1 and implications for participation of3 vp2 in viral entry
5	<a href="#">c3dwwA_</a>	 Alignment		7.0	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> prostaglandin e synthase; <b>PDBTitle:</b> electron crystallographic structure of human microsomal2 prostaglandin e synthase 1
6	<a href="#">c3kcgA_</a>	 Alignment		6.3	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum
7	<a href="#">c1i25A_</a>	 Alignment		5.9	38	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> huwentoxin-ii; <b>PDBTitle:</b> three dimensional solution structure of huwentoxin-ii by 2d2 1h-nmr
8	<a href="#">d1i25a_</a>	 Alignment		5.9	38	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> omega toxin-like <b>Family:</b> Spider toxins
9	<a href="#">d1xioa_</a>	 Alignment		5.8	8	<b>Fold:</b> Family A G protein-coupled receptor-like <b>Superfamily:</b> Family A G protein-coupled receptor-like <b>Family:</b> Bacteriorhodopsin-like
10	<a href="#">c1xioA_</a>	 Alignment		5.8	8	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> anabaena sensory rhodopsin; <b>PDBTitle:</b> anabaena sensory rhodopsin
11	<a href="#">d4croa_</a>	 Alignment		5.5	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors

12 [c2rm9A](#)

Alignment



5.4

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**PDB header:**neuropeptide  
**Chain:** A: **PDB Molecule:**astressin2b;  
**PDBTitle:** astressin2b