














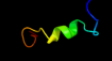

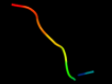


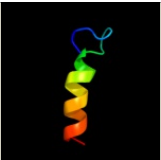


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rkoL_	 Alignment		91.3	13	PDB header: oxidoreductase Chain: L: PDB Molecule: nadh-quinone oxidoreductase subunit l; PDBTitle: crystal structure of the membrane domain of respiratory complex i from <i>E. coli</i> at 3.0 angstrom resolution
2	c1q2iA_	 Alignment		39.9	38	PDB header: antitumor protein Chain: A: PDB Molecule: pnc27; PDBTitle: nmr solution structure of a peptide from the mdm-2 binding2 domain of the p53 protein that is selectively cytotoxic to 3 cancer cells
3	c2jpmA_	 Alignment		22.9	11	PDB header: antimicrobial protein Chain: A: PDB Molecule: bacteriocin lactococcin-g subunit beta; PDBTitle: lactococcin g-b in tfe
4	d1lbqa_	 Alignment		17.9	18	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelatase
5	d1xn8a_	 Alignment		14.2	26	Fold: Hypothetical protein YqbG Superfamily: Hypothetical protein YqbG Family: Hypothetical protein YqbG
6	d1ufra_	 Alignment		9.8	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
7	c3rkoM_	 Alignment		9.2	16	PDB header: oxidoreductase Chain: M: PDB Molecule: nadh-quinone oxidoreductase subunit m; PDBTitle: crystal structure of the membrane domain of respiratory complex i from <i>E. coli</i> at 3.0 angstrom resolution
8	c2k8fB_	 Alignment		6.8	26	PDB header: transferase/transcription Chain: B: PDB Molecule: cellular tumor antigen p53; PDBTitle: structural basis for the regulation of p53 function by p300
9	c2vxSB_	 Alignment		6.7	27	PDB header: cytokine Chain: B: PDB Molecule: interleukin-17a; PDBTitle: structure of il-17a in complex with a potent, fully human2 neutralising antibody
10	c2rmrA_	 Alignment		5.7	34	PDB header: transcription Chain: A: PDB Molecule: paired amphipathic helix protein sin3a; PDBTitle: solution structure of msin3a pah1 domain

11 [d2hrca1](#)

Alignment



5.7

18

Fold:Chelatase-like
Superfamily:Chelatase
Family:Ferrochelatase