
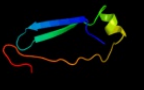









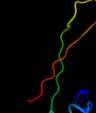





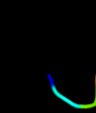






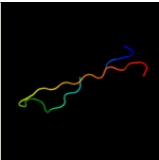
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1y6kr2	 Alignment		23.4	24	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
2	c3gqgD_	 Alignment		19.4	50	PDB header: splicing Chain: D: PDB Molecule: protein unc-119 homolog a; PDBTitle: crystal structure of the human retinal protein 4 (unc-1192 homolog a). northeast structural genomics consortium3 target hr3066a
3	d1sdwa2	 Alignment		18.3	17	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: PHM/PNGase F Family: Peptidylglycine alpha-hydroxylating monooxygenase, PHM
4	c2k8jX_	 Alignment		13.7	78	PDB header: viral protein Chain: X: PDB Molecule: p7tm2; PDBTitle: solution structure of hcv p7 tm2
5	c2k2waA_	 Alignment		12.4	27	PDB header: cell cycle Chain: A: PDB Molecule: recombination and dna repair protein; PDBTitle: second brct domain of nbs1
6	d1r4xa1	 Alignment		9.3	22	Fold: Immunoglobulin-like beta-sandwich Superfamily: Clathrin adaptor appendage domain Family: Coatomer appendage domain
7	c2lkaA_	 Alignment		9.2	100	PDB header: toxin Chain: A: PDB Molecule: toxin ts16; PDBTitle: new tricks of an old fold: structural versatility of scorpion toxins2 with common cysteine spacing
8	d2rnrb1	 Alignment		9.1	23	Fold: PH domain-like barrel Superfamily: PH domain-like Family: TFIIH domain
9	c2li3A_	 Alignment		8.3	100	PDB header: toxin Chain: A: PDB Molecule: potassium channel toxin kappa-ktx3.1; PDBTitle: structural and functional analysis of a novel potassium toxin2 argentinean scorpion tityus trivittatus reveals a new kappa sub-3 family
10	d1pzdal	 Alignment		7.6	22	Fold: Immunoglobulin-like beta-sandwich Superfamily: Clathrin adaptor appendage domain Family: Coatomer appendage domain
11	d1umga_	 Alignment		6.3	43	Fold: Sulfolobus fructose-1,6-bisphosphatase-like Superfamily: Sulfolobus fructose-1,6-bisphosphatase-like Family: Sulfolobus fructose-1,6-bisphosphatase-like

12	c1opmA	Alignment			6.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (peptidylglycine alpha-hydroxylating PDBTitle: oxidized (cu2+) peptidylglycine alpha-hydroxylating monooxygenase2 (phm) with bound substrate
13	c2dvkA	Alignment			5.7	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0130 protein ape0816; PDBTitle: crystal structure of hypothetical protein from aeropyrum pernix

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[c1pzdA](#)

Alignment



5.7

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PDB header:endocytosis/exocytosis
Chain: A: **PDB Molecule:**coatomer gamma subunit;
PDBTitle: structural identification of a conserved appendage domain2 in the carboxyl-terminus of the copi gamma-subunit.