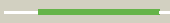












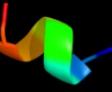
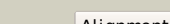


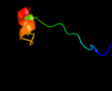









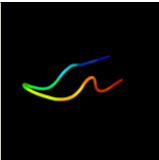


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1e9ra_	 Alignment		50.1	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
2	d2pvaa_	 Alignment		12.9	36	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Penicillin V acylase
3	c2hezB_	 Alignment		11.5	21	PDB header: hydrolase Chain: B: PDB Molecule: bile salt hydrolase; PDBTitle: bifidobacterium longum bile salt hydrolase
4	c1shzF_	 Alignment		10.4	13	PDB header: signaling protein Chain: F: PDB Molecule: rho guanine nucleotide exchange factor 1; PDBTitle: crystal structure of the p115rhogef rgrgs domain in a2 complex with galpha(13):galpha(i1) chimera
5	c2bjgB_	 Alignment		10.3	29	PDB header: hydrolase Chain: B: PDB Molecule: choloylglycine hydrolase; PDBTitle: crystal structure of conjugated bile acid hydrolase from2 clostridium perfringens in complex with reaction products3 taurine and deoxycholate
6	d1iapa_	 Alignment		10.3	13	Fold: Regulator of G-protein signaling, RGS Superfamily: Regulator of G-protein signaling, RGS Family: Regulator of G-protein signaling, RGS
7	d1htjF_	 Alignment		9.2	25	Fold: Regulator of G-protein signaling, RGS Superfamily: Regulator of G-protein signaling, RGS Family: Regulator of G-protein signaling, RGS
8	c1htjF_	 Alignment		9.2	25	PDB header: signaling protein Chain: F: PDB Molecule: kiaa0380; PDBTitle: structure of the rgs-like domain from pdz-rhogef
9	d2jxta1	 Alignment		9.0	12	Fold: RplX-like Superfamily: RplX-like Family: RplX-like
10	c1tu3J_	 Alignment		8.7	33	PDB header: protein transport Chain: J: PDB Molecule: rab gtpase binding effector protein 1; PDBTitle: crystal structure of rab5 complex with rabaptin5 c-terminal2 domain
11	c3aqbC_	 Alignment		8.4	50	PDB header: transferase Chain: C: PDB Molecule: component a of hexaprenyl diphosphate synthase; PDBTitle: m. luteus b-p 26 heterodimeric hexaprenyl diphosphate synthase in2 complex with magnesium

12	d2f4ia1	Alignment		7.4	15	Fold: OB-fold Superfamily: TM0957-like Family: TM0957-like
13	c3ipjB_	Alignment		6.6	40	PDB header: transferase Chain: B: PDB Molecule: pts system, iiabc component; PDBTitle: the crystal structure of one domain of the pts system, iiabc component2 from clostridium difficile
14	c2oqcB_	Alignment		6.0	42	PDB header: hydrolase Chain: B: PDB Molecule: penicillin v acylase; PDBTitle: crystal structure of penicillin v acylase from bacillus subtilis
15	c1ibaA_	Alignment		5.9	40	PDB header: phosphotransferase Chain: A: PDB Molecule: glucose permease; PDBTitle: glucose permease (domain iib), nmr, 11 structures
16	c3hbcA_	Alignment		5.6	42	PDB header: hydrolase Chain: A: PDB Molecule: choloylglycine hydrolase; PDBTitle: crystal structure of choloylglycine hydrolase from bacteroides2 thetaiotaomicron vpi

17 [d3bp8c1](#)

Alignment



5.2

40

Fold:Homing endonuclease-like
Superfamily:Glucose permease domain IIB
Family:Glucose permease domain IIB