

Rickmore\_11 HHPred results. 34 of 115 AA align with gp6. Helix-coil-helix.

Template alignment | CDD

1. **PF05135.12 ; Phage\_connect\_1 ; Phage gp6-like head-tail connector protein**  
 Probability: 71.52 E-value: 15.0 Score: 23.87 Aligned Cols: 34 Identities: 15% Similarity: 0.095

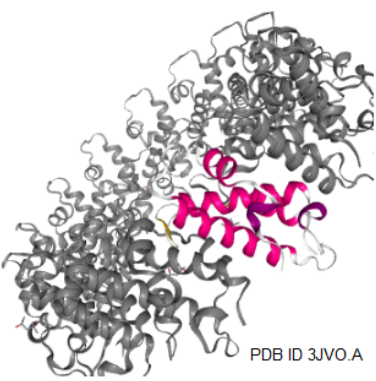
Q ss_pred		HHHHHHHhCCCCccccChhHHHHHHHHHHHHHHH	
Q Rickmore_Draft	6	LNSTKKILGIDADYDVFDMVIMHINSAFSTLHQ	39 (115)
Q Consensus	6	L~SiKk~LGI~e~y~FD~DlimhINS~f~L~Q	39 (115)
		+.. +.. +++..+...- .. ... +++...+..	
T Consensus	4	l~k~L~i~D~l~i~A~i~	37 (113)
T PF05135.12	4	LERCRILCGISKDNTKKLGLLSVLLLEKAREDEIA	37 (113)
T ss_pred		HHHHHHHhCCCCc hhhHHHHHHHHHHHHHHH	

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## Gp6 - Q9MBY2 (Q9MBY2\_BPHK7)

Protein Feature View of PDB entries mapped to a UniProtKB sequence

Number of PDB entries for Q9MBY2: 1



PDB ID 3JVO.A

Organism: Bacteriophage HK97 Length: 108 UniProt

Other Gene names: 6

This protein in other organisms (by gene name):  
 Q9MBY2 - Enterobacteria phage HK97 1

If I'm looking at this right, only the first three helices are matching with HHPred, and the rest is not.

