

Start: 57,852 (Glimmer)

MRQRLKIAAAEDGLTYAQLLVSLLDLRDDRHRHQRAAQASPLHRPRAETA

Start: 57,555

MLPIKCPDVRQRLKIAAAEDGLTYAQLLVSLLDLRDDRHRHQRAAQASPLHRPRAETA

Start: 57,492

MVNPKRPHRAFQQTPAKPATILMLPIKCPDVRQRLKIAAAEDGLTYAQLLVSLLDLRDDRHRHQRAAQASPLHRPRAETA

57,492. Structure starts upstream of the predicted beta sheet

57,555. Structure starts in the beta sheet

57,852. Structure starts within the alpha helix

Template alignment | Template 3D Structure | PDBe

20.6SBW_A CdbA; nucleoid ribbon-helix-helix, DNA BINDING PROTEIN; 2.24A {Myxococcus xanthus DK 1622}

Probability: 97.86% E-value: 0.00018, Score: 45.31, Aligned cols: 44, Identities: 7%, Similarity: 0.15, Template Neff: 6.5

Q ss_pred		QeEEEEECCHHHHHHHHHHHcCCCHHHHHHHHHhhHHHH	
Q Uvasi_70_57492	19	ATILLPIKCPPDVRQRLKIAAAEDGLTYAQLLVSLLDLRDDRHR	62 (81)
Q Consensus	19	~v~TIkVp~LR~RIK~Aa~Gtm~eLI~n~L~n~n~n~r	62 (81)
		.+.+.+ + +++..+ ..++.+ .++ +.	
T Consensus	5	~n~Vsv~lp~l~n~l~n~lA~n~n~rS~s~lI~n~AL~nyL~n~n	48 (67)
T 6SBW_A	5	DKRKQSLYFPEEMLKEIQEEATRQDRSLSWVQQAWKIARERIK	48 (67)
T ss_dssp		CCCCCCCCCHHHHHHHHHHHHTTCCCHHHHHHHHHHHHHHH	
T ss_pred		CcceeEeECCHHHHHHHHHHHcCCCHHHHHHHHHHHHHHH	

If translation starts at 57,492, a 7aa beta strand is predicted, and full ribbon-helix-helix motif is present.