Output Messages

Single TM helix:
Lowest energy helix-coil partition
Helix: 1 - 21, Stability: -24.4 (-17.6) kcal/mol
Helix 1: 1- 21 LLLLAILLTLLAVLFSLLILI
TM segments: 1(2- 20)
transfer energy = -25.2 kcal/mol; thickness/depth = 31.2+- 3.2 tilt = 29.+- 1.
Aa seq. for dimer: LLLLAILLTLLAVLFSLLILI
TM segment for dimer: 1 21

Model # 1 DGasc= -2.0 kcal/mol, DGstb= -18.6 kcal/mol, Easc= -21.9 kcal/mol, Rasym=0.0 A
Interhelix distance = 9.6 A, Angle = 10.
Key helix-helix interface residues ( ) :
LLLLAILL(T)LLAVLF(S)LLILI

Model # 2 DGasc= -2.0 kcal/mol, DGstb= -9.7 kcal/mol, Easc= -13.6 kcal/mol, Rasym=0.2 A
Interhelix distance = 8.4 A, Angle = 18.
Key helix-helix interface residues ( ) :
LLLL(A)ILLTLL(A)VLFSLLILI

Model # 3 DGasc= -2.8 kcal/mol, DGstb= -1.0 kcal/mol, Easc= -16.6 kcal/mol, Rasym=0.3 A
Interhelix distance = 8.0 A, Angle = -46.
Key interfacial residues ( ) :
LLLLAILLTLL(A)VLF(S)LLILI

Model # 4 DGasc= -1.4 kcal/mol, DGstb= -5.8 kcal/mol, Easc= -16.5 kcal/mol, Rasym=0.6 A
Interhelix distance = 8.1 A, Angle = -47.
Key interfacial residues ( ) :
LLLL(A)ILL(T)LLAVLFSLLILI

GLMOL Visualization

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Model 1

L L L L A I L L T L L A V L F S L L I L I

. . . . . T . . . . . S . . . . .

Model	ΔG_{asc}	ΔG_{stb}	E_{asc}	R_{asym}	Distance	Angle
	kcal/mol	kcal/mol	kcal/mol	Å	Å	Degrees
1	-2.0	-18.6	-21.9	0.0	9.6	10.0
2	-2.0	-9.7	-13.6	0.2	8.4	18.0
3	-2.8	-1.0	-16.6	0.3	8.0	-46.0
4	-1.4	-5.8	-16.5	0.6	8.1	-47.0

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pdb file

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