Output Messages

Single TM helix:
Lowest energy helix-coil partition
Helix: 1 - 21, Stability: -25.5 (-17.3) kcal/mol
Helix 1: 1- 21 LLLLLWLLTVLIALLSFLILI
TM segments: 1(2- 19)
transfer energy = -25.0 kcal/mol; thickness/depth = 32.0+- 3.0 tilt = 33.+- 24.
Aa seq. for dimer: LLLLLWLLTVLIALLSFLILI
TM segment for dimer: 1 21

Model # 1 DGasc= -4.7 kcal/mol, DGstb= -8.1 kcal/mol, Easc= -28.7 kcal/mol, Rasym=1.4 A
Interhelix distance = 7.7 A, Angle = -51.
Key interfacial residues ( ) :
LLLLLWLL(T)VLI(A)LLSFLILI

Model # 2 DGasc= -1.7 kcal/mol, DGstb= -13.8 kcal/mol, Easc= -21.3 kcal/mol, Rasym=1.1 A
Interhelix distance = 9.2 A, Angle = 14.
Key helix-helix interface residues ( ) :
LLLLLWLL(T)VLIALL(S)FLILI

GLMOL Visualization

Model 1

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

. . . . . T . . . A . . . . . .

Model	ΔG_{asc}	ΔG_{stb}	E_{asc}	R_{asym}	Distance	Angle
	kcal/mol	kcal/mol	kcal/mol	Å	Å	Degrees
1	-4.7	-8.1	-28.7	1.4	7.7	-51.0
2	-1.7	-13.8	-21.3	1.1	9.2	14.0

Download Output File

pdb file

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