Output Messages

Single TM helix:
Lowest energy helix-coil partition
Helix: 1 - 21, Stability: -23.5 (-16.5) kcal/mol
Helix 1: 1- 21 LLLTLLLGVLLGLLLAFLILI
TM segments: 1(2- 20)
transfer energy = -22.7 kcal/mol; thickness/depth = 31.2+- 3.6 tilt = 1.+- 13.
Aa seq. for dimer: LLLTLLLGVLLGLLLAFLILI
TM segment for dimer: 1 21

Model # 1 DGasc= -7.5 kcal/mol, DGstb= -18.9 kcal/mol, Easc= -29.5 kcal/mol, Rasym=0.1 A
Interhelix distance = 5.7 A, Angle = -46.
Key interfacial residues ( ) :
LLLTLLL(G)VLL(G)LLLAFLILI

Model # 2 DGasc= -5.1 kcal/mol, DGstb= -3.0 kcal/mol, Easc= -25.5 kcal/mol, Rasym=0.1 A
Interhelix distance = 6.0 A, Angle = 57.
Key helix-helix interface residues ( ) :
LLLT(L)LLGVLL(G)LLLAFLILI

GLMOL Visualization

Model 1

L L L T L L L G V L L G L L L A F L I L I

. . . . . G . . . G . . . . . .

Model	ΔG_{asc}	ΔG_{stb}	E_{asc}	R_{asym}	Distance	Angle
	kcal/mol	kcal/mol	kcal/mol	Å	Å	Degrees
1	-7.5	-18.9	-29.5	0.1	5.7	-46.0
2	-5.1	-3.0	-25.5	0.1	6.0	57.0

Download Output File

pdb file

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