Output Messages

Single TM helix:
Lowest energy helix-coil partition
Helix: 1 - 21, Stability: -19.5 (-13.4) kcal/mol
Helix 1: 1- 21 LLLTFLLGVLLGLLLGALILI
TM segments: 1(2- 20)
transfer energy = -20.6 kcal/mol; thickness/depth = 31.2+- 4.4 tilt = 1.+- 16.
Aa seq. for dimer: LLLTFLLGVLLGLLLGALILI
TM segment for dimer: 1 21

Model # 1 DGasc= -6.7 kcal/mol, DGstb= -13.1 kcal/mol, Easc= -25.5 kcal/mol, Rasym=0.1 A
Interhelix distance = 6.4 A, Angle = -45.
Key interfacial residues ( ) :
LLLTFLL(G)VLL(G)LLLGALILI

Model # 2 DGasc= -6.7 kcal/mol, DGstb= -1.7 kcal/mol, Easc= -24.7 kcal/mol, Rasym=0.2 A
Interhelix distance = 6.0 A, Angle = -47.
Key interfacial residues ( ) :
LLLTFLLGVLL(G)LLL(G)ALILI

Model # 3 DGasc= -2.8 kcal/mol, DGstb= -6.9 kcal/mol, Easc= -27.2 kcal/mol, Rasym=0.1 A
Interhelix distance = 5.9 A, Angle = 57.
Key helix-helix interface residues ( ) :
LLLT(F)LLGVLL(G)LLLGALILI

GLMOL Visualization

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Model 1

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

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Model	ΔG_{asc}	ΔG_{stb}	E_{asc}	R_{asym}	Distance	Angle
	kcal/mol	kcal/mol	kcal/mol	Å	Å	Degrees
1	-6.7	-13.1	-25.5	0.1	6.4	-45.0
2	-6.7	-1.7	-24.7	0.2	6.0	-47.0
3	-2.8	-6.9	-27.2	0.1	5.9	57.0

Download Output File

pdb file

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