Output Messages

Single TM helix:
Lowest energy helix-coil partition
Helix: 1 - 21, Stability: -21.9 (-15.7) kcal/mol
Helix 1: 1- 21 LLLVFLLGTLLGLLLAILILI
TM segments: 1(2- 20)
transfer energy = -25.6 kcal/mol; thickness/depth = 30.4+- 4.6 tilt = 37.+- 15.
Aa seq. for dimer: LLLVFLLGTLLGLLLAILILI
TM segment for dimer: 1 21

Model # 1 DGasc= -10.5 kcal/mol, DGstb= -12.5 kcal/mol, Easc= -26.7 kcal/mol, Rasym=0.5 A
Interhelix distance = 6.5 A, Angle = -44.
Key interfacial residues ( ) :
LLLVFLL(G)TLL(G)LLLAILILI

Model # 2 DGasc= -7.2 kcal/mol, DGstb= -3.0 kcal/mol, Easc= -18.2 kcal/mol, Rasym=0.1 A
Interhelix distance = 8.4 A, Angle = 37.
Key helix-helix interface residues ( ) :
LLLV(F)LLGTLL(G)LLLAILILI

Model # 3 DGasc= -5.1 kcal/mol, DGstb= -8.5 kcal/mol, Easc= -23.3 kcal/mol, Rasym=0.3 A
Interhelix distance = 7.3 A, Angle = -8.
Key interfacial residues ( ) :
LLLVFLL(G)TLL(G)LLL(A)ILILI

GLMOL Visualization

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Model 1

L L L V F L L G T L L G L L L A I 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	-10.5	-12.5	-26.7	0.5	6.5	-44.0
2	-7.2	-3.0	-18.2	0.1	8.4	37.0
3	-5.1	-8.5	-23.3	0.3	7.3	-8.0

Download Output File

pdb file

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