Output Messages

Single TM helix:
Lowest energy helix-coil partition
Helix: 1 - 21, Stability: -20.2 (-13.9) kcal/mol
Helix 1: 1- 21 LLLAFLLGLLLGTLLTVLILI
TM segments: 1(2- 19)
transfer energy = -22.9 kcal/mol; thickness/depth = 31.2+- 3.6 tilt = 37.+- 5.
Aa seq. for dimer: LLLAFLLGLLLGTLLTVLILI
TM segment for dimer: 1 21

Model # 1 DGasc= -16.6 kcal/mol, DGstb= -16.9 kcal/mol, Easc= -32.0 kcal/mol, Rasym=0.0 A
Interhelix distance = 6.0 A, Angle = -46.
Key interfacial residues ( ) :
LLLAFLL(G)LLL(G)TLLTVLILI

Model # 2 DGasc= -5.0 kcal/mol, DGstb= -17.6 kcal/mol, Easc= -25.3 kcal/mol, Rasym=0.2 A
Interhelix distance = 7.1 A, Angle = -29.
Key interfacial residues ( ) :
LLL(A)FLL(G)LLLGTLLTVLILI

Model # 3 DGasc= -5.3 kcal/mol, DGstb= -0.1 kcal/mol, Easc= -23.1 kcal/mol, Rasym=1.1 A
Interhelix distance = 8.3 A, Angle = -35.
Key interfacial residues ( ) :
LLLAFLLGLLL(G)TLL(T)VLILI

Model # 4 DGasc= -2.6 kcal/mol, DGstb= -11.5 kcal/mol, Easc= -21.6 kcal/mol, Rasym=0.5 A
Interhelix distance = 8.6 A, Angle = 40.
Key helix-helix interface residues ( ) :
LLLAF(L)LGLLLG(T)LLTVLILI

GLMOL Visualization

GLMOL Visualization

Model 1

L L L A F L L G L L L G T L L T V 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	-16.6	-16.9	-32.0	0.0	6.0	-46.0
2	-5.0	-17.6	-25.3	0.2	7.1	-29.0
3	-5.3	-0.1	-23.1	1.1	8.3	-35.0
4	-2.6	-11.5	-21.6	0.5	8.6	40.0

Download Output File

pdb file

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