Output Messages

Single TM helix:
Lowest energy helix-coil partition
Helix: 1 - 21, Stability: -17.4 (-10.9) kcal/mol
Helix 1: 1- 21 LLLTFLLGLLLGYLLSVLILI
TM segments: 1(2- 19)
transfer energy = -19.9 kcal/mol; thickness/depth = 30.8+- 3.8 tilt = 30.+- 16.
Aa seq. for dimer: LLLTFLLGLLLGYLLSVLILI
TM segment for dimer: 1 21

Model # 1 DGasc= -3.5 kcal/mol, DGstb= -12.8 kcal/mol, Easc= -25.5 kcal/mol, Rasym=0.1 A
Interhelix distance = 7.2 A, Angle = -28.
Key interfacial residues ( ) :
LLL(T)FLL(G)LLL(G)YLLSVLILI

Model # 2 DGasc= -2.4 kcal/mol, DGstb= -13.8 kcal/mol, Easc= -24.6 kcal/mol, Rasym=1.5 A
Interhelix distance = 6.4 A, Angle = 55.
Key helix-helix interface residues ( ) :
LLLT(F)LLGLLL(G)YLLSVLILI

Model # 3 DGasc= -2.2 kcal/mol, DGstb= -9.0 kcal/mol, Easc= -23.0 kcal/mol, Rasym=0.1 A
Interhelix distance = 9.7 A, Angle = 22.
Key helix-helix interface residues ( ) :
LLL(T)FL(L)GLL(L)GY(L)LSV(L)ILI

Model # 4 DGasc= -3.2 kcal/mol, DGstb= -0.5 kcal/mol, Easc= -20.4 kcal/mol, Rasym=0.8 A
Interhelix distance = 8.6 A, Angle = -46.
Key interfacial residues ( ) :
LLL(T)FLL(G)LLLGYLLSVLILI

GLMOL Visualization

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Model 1

L L L T F L L G L L L G Y L L S V L I L I

. . . T . . . G . . . G . . . .

Model	ΔG_{asc}	ΔG_{stb}	E_{asc}	R_{asym}	Distance	Angle
	kcal/mol	kcal/mol	kcal/mol	Å	Å	Degrees
1	-3.5	-12.8	-25.5	0.1	7.2	-28.0
2	-2.4	-13.8	-24.6	1.5	6.4	55.0
3	-2.2	-9.0	-23.0	0.1	9.7	22.0
4	-3.2	-0.5	-20.4	0.8	8.6	-46.0

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pdb file

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