Output Messages

Single TM helix:
Lowest energy helix-coil partition
Helix: 1 - 21, Stability: -25.6 (-18.4) kcal/mol
Helix 1: 1- 21 LLLLVALLLTLISLLFLLILI
TM segments: 1(2- 19)
transfer energy = -26.4 kcal/mol; thickness/depth = 31.6+- 4.2 tilt = 33.+- 3.
Aa seq. for dimer: LLLLVALLLTLISLLFLLILI
TM segment for dimer: 1 21

Model # 1 DGasc= -6.0 kcal/mol, DGstb= -6.5 kcal/mol, Easc= -22.2 kcal/mol, Rasym=0.0 A
Interhelix distance = 7.6 A, Angle = -59.
Key interfacial residues ( ) :
L(L)LLV(A)LLL(T)LISLLFLLILI

Model # 2 DGasc= -2.8 kcal/mol, DGstb= -20.2 kcal/mol, Easc= -25.8 kcal/mol, Rasym=0.1 A
Interhelix distance = 8.7 A, Angle = 22.
Key helix-helix interface residues ( ) :
LLLLV(A)LLLTLI(S)LLFLLILI

GLMOL Visualization

Model 1

L L L L V A L L L T L I S L L F L L I L I

. L . . . A . . . T . . . .

Model	ΔG_{asc}	ΔG_{stb}	E_{asc}	R_{asym}	Distance	Angle
	kcal/mol	kcal/mol	kcal/mol	Å	Å	Degrees
1	-6.0	-6.5	-22.2	0.0	7.6	-59.0
2	-2.8	-20.2	-25.8	0.1	8.7	22.0

Download Output File

pdb file

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