Output Messages

Single TM helix:
Lowest energy helix-coil partition
Helix: 1 - 21, Stability: -24.4 (-17.9) kcal/mol
Helix 1: 1- 21 LLLVALLIALLLTLLSLLILI
TM segments: 1(2- 20)
transfer energy = -25.5 kcal/mol; thickness/depth = 30.4+- 3.2 tilt = 35.+- 4.
Aa seq. for dimer: LLLVALLIALLLTLLSLLILI
TM segment for dimer: 1 21

Model # 1 DGasc= -2.4 kcal/mol, DGstb= -8.7 kcal/mol, Easc= -25.2 kcal/mol, Rasym=0.0 A
Interhelix distance = 8.4 A, Angle = 9.
Key helix-helix interface residues ( ) :
LLLVALLI(A)LLLTLL(S)LLILI

Model # 2 DGasc= -1.3 kcal/mol, DGstb= -2.0 kcal/mol, Easc= -19.0 kcal/mol, Rasym=1.5 A
Interhelix distance = 7.7 A, Angle = -46.
Key interfacial residues ( ) :
LLLV(A)LLI(A)LLLTLLSLLILI

GLMOL Visualization

Model 1

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

. . . . . A . . . . . S . . . . .

Model	ΔG_{asc}	ΔG_{stb}	E_{asc}	R_{asym}	Distance	Angle
	kcal/mol	kcal/mol	kcal/mol	Å	Å	Degrees
1	-2.4	-8.7	-25.2	0.0	8.4	9.0
2	-1.3	-2.0	-19.0	1.5	7.7	-46.0

Download Output File

pdb file

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