Output Messages

Single TM helix:
Lowest energy helix-coil partition
Helix: 1 - 21, Stability: -22.6 (-16.5) kcal/mol
Helix 1: 1- 21 LLLYALLLALLVSLLTILILI
TM segments: 1(2- 19)
transfer energy = -21.9 kcal/mol; thickness/depth = 32.0+- 5.0 tilt = 31.+- 22.
Aa seq. for dimer: LLLYALLLALLVSLLTILILI
TM segment for dimer: 1 21

Model # 1 DGasc= -4.6 kcal/mol, DGstb= -1.5 kcal/mol, Easc= -19.1 kcal/mol, Rasym=0.1 A
Interhelix distance = 7.2 A, Angle = -54.
Key interfacial residues ( ) :
LLLYALL(L)ALL(V)SLLTILILI

Model # 2 DGasc= -3.7 kcal/mol, DGstb= -5.0 kcal/mol, Easc= -21.0 kcal/mol, Rasym=0.5 A
Interhelix distance = 7.4 A, Angle = -43.
Key interfacial residues ( ) :
LLLY(A)LLL(A)LLVSLLTILILI

Model # 3 DGasc= -1.0 kcal/mol, DGstb= -6.8 kcal/mol, Easc= -22.5 kcal/mol, Rasym=0.2 A
Interhelix distance = 9.0 A, Angle = 11.
Key helix-helix interface residues ( ) :
L(L)LYALLL(A)LLVSLLTILILI

GLMOL Visualization

GLMOL Visualization

Model 1

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

. . . . . L . . . V . . . . . .

Model	ΔG_{asc}	ΔG_{stb}	E_{asc}	R_{asym}	Distance	Angle
	kcal/mol	kcal/mol	kcal/mol	Å	Å	Degrees
1	-4.6	-1.5	-19.1	0.1	7.2	-54.0
2	-3.7	-5.0	-21.0	0.5	7.4	-43.0
3	-1.0	-6.8	-22.5	0.2	9.0	11.0

Download Output File

pdb file

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