Output Messages

Single TM helix:
Lowest energy helix-coil partition
Helix: 1 - 21, Stability: -22.3 (-15.5) kcal/mol
Helix 1: 1- 21 LLLSYLLTLLLAFLLSILILI
TM segments: 1(2- 20)
transfer energy = -19.9 kcal/mol; thickness/depth = 30.8+- 3.2 tilt = 25.+- 18.
Aa seq. for dimer: LLLSYLLTLLLAFLLSILILI
TM segment for dimer: 1 21

Model # 1 DGasc= -7.7 kcal/mol, DGstb= -4.3 kcal/mol, Easc= -24.3 kcal/mol, Rasym=0.0 A
Interhelix distance = 7.4 A, Angle = -31.
Key interfacial residues ( ) :
LLL(S)YLL(T)LLLAFLLSILILI

Model # 2 DGasc= -4.4 kcal/mol, DGstb= -13.7 kcal/mol, Easc= -26.5 kcal/mol, Rasym=0.1 A
Interhelix distance = 9.1 A, Angle = 19.
Key helix-helix interface residues ( ) :
LLLS(Y)LLTLLL(A)FLLSILILI

Model # 3 DGasc= -3.9 kcal/mol, DGstb= -7.4 kcal/mol, Easc= -24.5 kcal/mol, Rasym=1.0 A
Interhelix distance = 7.9 A, Angle = -43.
Key interfacial residues ( ) :
LLLSYLL(T)LLL(A)FLLSILILI

Model # 4 DGasc= -3.3 kcal/mol, DGstb= -2.3 kcal/mol, Easc= -21.7 kcal/mol, Rasym=0.3 A
Interhelix distance = 9.6 A, Angle = -8.
Key interfacial residues ( ) :
LLLSYLL(T)LL(L)(A)FL(L)(S)ILILI

GLMOL Visualization

GLMOL Visualization

Model 1

L L L S Y L L T L L L A F L L S I L I L I

. . . S . . . T . . . .

Model	ΔG_{asc}	ΔG_{stb}	E_{asc}	R_{asym}	Distance	Angle
	kcal/mol	kcal/mol	kcal/mol	Å	Å	Degrees
1	-7.7	-4.3	-24.3	0.0	7.4	-31.0
2	-4.4	-13.7	-26.5	0.1	9.1	19.0
3	-3.9	-7.4	-24.5	1.0	7.9	-43.0
4	-3.3	-2.3	-21.7	0.3	9.6	-8.0

Download Output File

pdb file

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