Output Messages

Single TM helix:
Lowest energy helix-coil partition
Helix: 1 - 21, Stability: -22.1 (-15.1) kcal/mol
Helix 1: 1- 21 LLLSYLLVALLTLLLSFLILI
TM segments: 1(2- 19)
transfer energy = -20.5 kcal/mol; thickness/depth = 31.2+- 2.8 tilt = 29.+- 23.
Aa seq. for dimer: LLLSYLLVALLTLLLSFLILI
TM segment for dimer: 1 21

Model # 1 DGasc= -8.6 kcal/mol, DGstb= -7.1 kcal/mol, Easc= -27.9 kcal/mol, Rasym=0.3 A
Interhelix distance = 9.7 A, Angle = 25.
Key helix-helix interface residues ( ) :
LLLS(Y)LL(V)ALL(T)LL(L)SFL(I)LI

Model # 2 DGasc= -8.8 kcal/mol, DGstb= -2.1 kcal/mol, Easc= -25.0 kcal/mol, Rasym=0.5 A
Interhelix distance = 8.3 A, Angle = -41.
Key interfacial residues ( ) :
LLLSYLL(V)ALL(T)LLLSFLILI

Model # 3 DGasc= -6.6 kcal/mol, DGstb= -1.2 kcal/mol, Easc= -21.6 kcal/mol, Rasym=0.8 A
Interhelix distance = 8.0 A, Angle = -27.
Key interfacial residues ( ) :
LLL(S)YLL(V)ALLTLLLSFLILI

Model # 4 DGasc= -5.3 kcal/mol, DGstb= -2.9 kcal/mol, Easc= -24.6 kcal/mol, Rasym=0.0 A
Interhelix distance = 8.0 A, Angle = 54.
Key helix-helix interface residues ( ) :
LLLS(Y)LLVALL(T)LLLSFLILI

Model # 5 DGasc= -2.6 kcal/mol, DGstb= -6.6 kcal/mol, Easc= -20.1 kcal/mol, Rasym=0.6 A
Interhelix distance =10.0 A, Angle = -7.
Key interfacial residues ( ) :
LLL(S)YLL(V)AL(L)(T)LL(L)SFLILI

GLMOL Visualization

GLMOL Visualization

Model 1

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

. . . . Y . . V . . . T . . L . . . I . .

Model	ΔG_{asc}	ΔG_{stb}	E_{asc}	R_{asym}	Distance	Angle
	kcal/mol	kcal/mol	kcal/mol	Å	Å	Degrees
1	-8.6	-7.1	-27.9	0.3	9.7	25.0
2	-8.8	-2.1	-25.0	0.5	8.3	-41.0
3	-6.6	-1.2	-21.6	0.8	8.0	-27.0
4	-5.3	-2.9	-24.6	0.0	8.0	54.0
5	-2.6	-6.6	-20.1	0.6	10.0	-7.0

Download Output File

pdb file

Print this page