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A measure of helical propensity for amino acids in membrane environments

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The abstract and Table 1 were printed with a number of typographical errors which are corrected in the version below.

The frequent occurrence of β-sheet promoting residues such as Ile, Val, and Thr in the α-helical transmembrane segments of most integral membrane proteins suggests that the helical propensities of these residues are altered in the hydrophobic environment of the lipid bilayer. Systematic studies of model peptides by circular dichroism spectroscopy in various micellar/vesicular media allow the establishment of a ranking order of helical propensity for uncharged amino acids in the membrane environment. In contrast to their conformational preferences in water, the helical proclivity of amino acids in membranes is shown to be governed by their side chain hydrophobicity, and by the hydropathy of the local peptide segments in which the residues reside.

Table 1 Primary sequences and selected properties of host-guest peptides

Residue	Primary Sequences of AXA Peptides[1] (5 14)	$-\theta_{222}$[2] Aq.	SDS	LPG	DMPG	$P_\alpha(X)$[3]	Trp $\Delta\lambda_{max}$[4]
X	SKSK-**AXAAXAWAXA**-KSKSKS						
I	SKSK-**AIAAIAWAIA**-KSKSKS	4,800	25,700	23,900	23,000	1.08	13
L	SKSK-**ALAALAWALA**-KSKSKS	11,600	25,100	23,400	22,900	1.21	13
V	SKSK-**AVAAVAWAVA**-KSKSKS	1,700	25,000	23,100	22,400	1.06	13
M	SKSK-**AMAAMAWAMA**-KSKSKS	5,800	22,700	22,200	21,700	1.45	16
F	SKSK-**AFAAFAWAFA**-KSKSKS	1,000	21,500	21,000	19,400	1.13	13
A	SKSK-**AAAAAAWAAA**-KSKSKS	11,300	21,100	20,200	19,300	1.42	18
Q	SKSK-**AQAAQAWAQA**-KSKSKS	1,500	19,400	20,000	19,200	1.11	19
Y	SKSK-**AYAAYAWAYA**-KSKSKS	1,000	18,300	19,000	17,500	0.69	18
T	SKSK-**ATAATAWATA**-KSKSKS	2,300	16,600	18,700	16,600	0.83	18
S	SKSK-**ASAASAWASA**-KSKSKS	3,000	16,200	17,900	16,000	0.77	19
N	SKSK-**ANAANAWANA**-KSKSKS	1,900	13,800	16,000	13,300	0.67	19
G	SKSK-**AGAAGAWAGA**-KSKSKS	500	12,100	15,500	12,100	0.57	17
P	SKSK-**APAAPAWAPA**-KSKSKS	300	7,400	3,100	2,700	0.57	18

[1]See Methods section for preparation and characterization of peptides. Single letter codes of amino acids are used.
[2]Mean residue ellipticity (deg cm^2 $dmol^{-1}$) of the peptides at 222 nm (5 °C in aq. buffer, 25 °C in SDS, LPG, and DMPG). Values reported are based on triplicate measurements; estimated deviation, ± 1%. Peptide concentration was 30 mM for each peptide, determined by amino acid analysis[13]. Aq.: 10 mM sodium chloride, 10 mM phosphate, pH 7.0. SDS: 10 mM sodium dodecylsulfate micelles in Aq., pH 7.0. LPG: 5 mM egg lysophosphatidylglycerol micelles in 10 mM Tris-HCl, pH 7.0. DMPG: 3 mM unilamellar dimyristoylphosphatidylglycerol vesicles in 10 mM Tris-HCl, pH 7.0. See Methods for further details of sample preparation and CD measurements.
[3]P_α = Helical propensity parameter of amino acid (X) as given on the Chou-Fasman scale[5].
[4]λ_{max} = wavelength at which Trp fluorescence emission is maximal. For all peptides, λ_{max} (aq.) = 355 ± 1 nm. Blue shift for Trp emission, $D\lambda_{max}$ = Trp λ_{max} (aq.) - Trp λ_{max} (SDS). Excitation: 280 nm. Similar $D\lambda_{max}$ values were obtained for peptides in LPG micelles and DMPG vesicles (not shown).