Supporting Information

Hydrophobic blocks facilitate lipid compatibility and translocon recognition of transmembrane protein sequences

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Table S1: Ser-Leu peptide % gel-shift, tryptophan fluorescence and helicity in SDS micelles

*Calculated % peptide gel-shift from SDS-PAGE migration rates. SL_{amp}, SL_{scr1}, SL_{scr2} all travelled significantly faster than the Leu-block peptides ($p < 0.01$). Within the Leu-block series, S3L9 is the slowest traveling ($p < 0.01$). S5L9 travels significantly faster than S3L9, S2L9 and S1L9 ($p < 0.05$) but not S0L9, S9L9. Error values are reported as standard deviation.

†Tryptophan blue shifts were obtained from subtracting the maximum emission peak in SDS from the emission of free Trp in aqueous solution (350 nm). For the majority of peptides, significant differences are found in their blue shifts ($p < 0.05$) with the exception of SL_{amp} and S0L9, SL_{scr2}; S0L9 and S9L9; SL_{scr2}, S9L9 and S5L9; S1L9 and S2L9; S2L9 and SL_{scr1}. Error values are reported as standard deviation.

‡Helicity in SDS micelles measured by MRE at 222 nm. Significant variations in helicity are observed among the Ser-Leu peptides. LSL and SL_{scr1}, SL_{scr2} are significantly less helical than the Leu-block peptides (with the exception S1L9) and SL_{amp} ($p < 0.05$). SL_{amp} is significantly more helical than all peptides except for S9L9, S5L9 and S3L9 ($p < 0.05$). Among the Leu-block peptides, S1L9 is significant less helical than S9L9, S5L9, and S3L9 ($p< 0.05$). Significant differences also exist between S0L9 and S3L9; S2L9 and S3L9 ($p < 0.05$). Error values are reported as standard deviation.

Peptide	% Gel-shift* (SDS-PAGE)	Trp Blue shift† (nm)	MRE x 10^3 (deg cm^2 $dmol^{-1}$)‡ at 222 nm
		Non-Leu-block	
SL_n	N/A	N/A	N/A
LSL	N/A	N/A	-5.1 ± 0.8
SL_{scr1}	27.3 ± 3.0	28 ± 0.0	-6.2 ± 1.2
SL_{scr2}	30.0 ± 3.5	24 ± 1.0	-5.4 ± 1.4
SL_{amp}	42.2 ± 2.5	24 ± 1.9	-12.6 ± 1.2
		Leu-block	
S9L9	86.0 ± 3.3	22 ± 0.0	-11.3 ± 1.5
S5L9	74.2 ± 7.2	20 ± 0.0	-11.1 ± 0.0
S3L9	111.7 ± 6.9	15 ± 1.1	-12.4 ± 0.6
S2L9	99.6 ± 5.6	29 ± 1.0	-9.4 ± 0.6
S1L9	91.3 ± 5.5	29 ± 1.1	-7.8 ± 1.4
S0L9	88.3 ± 5.6	24 ± 0.0	-8.8 ± 1.2

Table S2: Ser-Leu peptide helicity and blue shift in POPC liposomes

[*]Helicity in POPC liposomes measured by MRE at 222 nm. S9L9 is significantly less helical than the other Ser-Leu peptides ($p < 0.01$). Values represent the average of at least 3 independent experiments. Error values are recorded as standard deviation.

[†]Tryptophan blue shifts were obtained from subtracting the maximum emission peak in POPC liposomes from the emission of free Trp in aqueous solution (350 nm). SL_{amp} has a significantly smaller blue shift than the Leu-block peptides with the exception of S9L9 ($p < 0.001$). Significant variations in blue shift were found between Leu-block peptides. S9L9 has the smallest blue shift of the Leu-block peptides ($p < 0.05$). S5L9 has a significantly larger blue shift than S1L9 and S2L9 ($p < 0.05$) and S3L9 has a significantly larger blue shift than S1L9 ($p < 0.01$). Values represent the average of at least 3 independent experiments. Error values are reported as standard deviation.

Peptide	MRE x 10^3 (deg cm^2 $dmol^{-1}$)[*] at 222 nm	Blue Shift[†] (nm)
	Non-Leu-block	
SL_{amp}	**-10.2 ± 1.1**	**18 ± 0.0**
	Leu-block	
S9L9	**-7.4 ± 0.4**	**27 ± 0.6**
S5L9	**-10.6 ± 0.6**	**29 ± 0.6**
S3L9	**-11.6 ± 0.5**	**28 ± 0.0**
S2L9	**-10.2 ± 0.7**	**26 ± 0.6**
S1L9	**-11.8 ± 0.5**	**25 ± 1.0**
S0L9	**-11.8 ± 0.6**	**22 ± 0.0**

Figure S1. Ser-Leu peptide helicities in HPLC solvents. CD spectra of Ser-Leu peptides in HPLC solvents (60% solvent A, 40% solvent B). *A)* Non-Leu-block peptides. *B)* Leu-block peptides. Ser-Leu peptides exhibit similar helicity with the exception of LSL and SL_{scr1} which are notably less helical. Spectra shown are an average of at least 2 independent experiments.