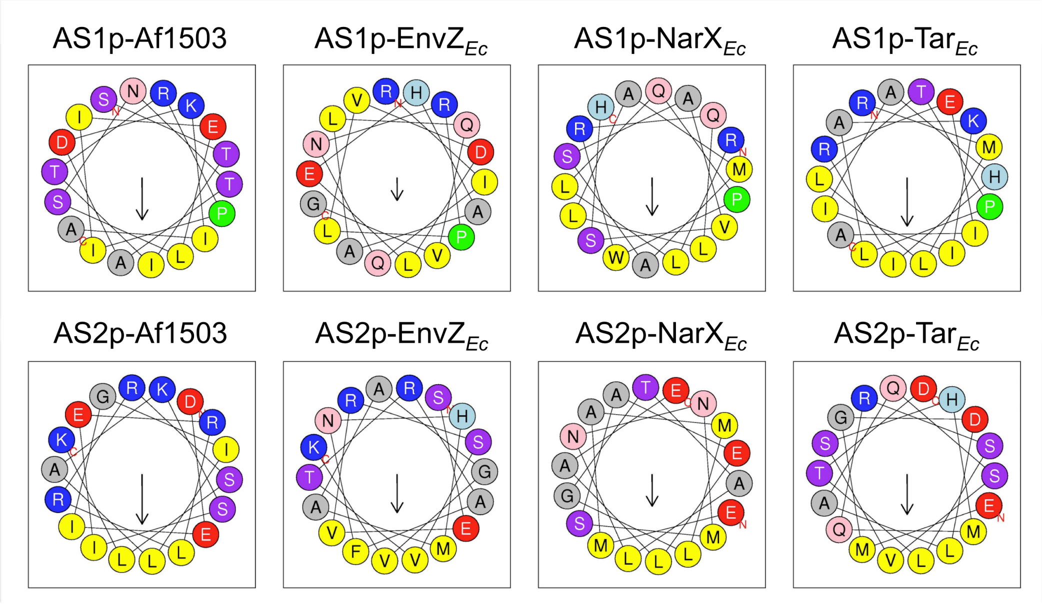
Supplemental information

Supplemental Figure 1. Helical-wheel projections of the AS1- and AS2-containing peptides used during this study. Various properties of the residue side chains are color-coded: hydrophobic (yellow), polar (purple), negatively charged (red), and positively charged (blue). Partially positive (slightly blue), partially negative (slightly red) and prolyl (green) residues are also indicated. An arrow representing the direction and magnitude of the hydrophobic moment is also displayed. A distinct hydrophobic surface is observed within AS1p-NarX$_{Ec}$ and AS1p-Tar$_{Ec}$ and, in both cases, two positively charged residues flank this hydrophobic surface.



Supplemental Table 1. Structural statistics for the ensemble of 25 structures of AS1p-Tar$_{Ec}$ in 10% negatively charged phospholipid bicelles.

Number of constraints		133 (59, 41, 33)
CYANA target function		0.84 ± 0.07 Å^2
Maximum distance violation		0.17 ± 0.02 Å
Backbone atom rmsd (Å)		
	All residues	1.04 ± 0.36
	Residue 9-19	0.63 ± 0.17
	Residue 12-18	0.32 ± 0.09
Ramachandran plot regions (%)		
	Most favored	83.8
	Allowed region	13.2
	Generously allowed	3
	Disallowed	0

References

[1] R. Gautier, D. Douguet, B. Antonny, G. Drin, HELIQUEST: a web server to screen sequences with specific alpha-helical properties, Bioinformatics 24 (2008) 2101-2102.