

Supporting information for:

Glycine Substitution Reduces Antimicrobial Activity and Helical Stretch of diPGLa-H in Lipid Micelles

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Supporting Information includes:

Figure S1. NOESY spectra of Kiadin

Figure S2. NOESY spectra of DiPGLa-H

Figure S3. HSQC spectra of Kiadin and DiPGLa-H

Table S1 and S2. Chemical shifts (ppm), hydrogen bond strengths and temperature coefficients of Kiadin and diPGLa-H in SDS micelles

Table S3. Statistical information for the Kiadin and diPGLa-H NMR structures in SDS micelles

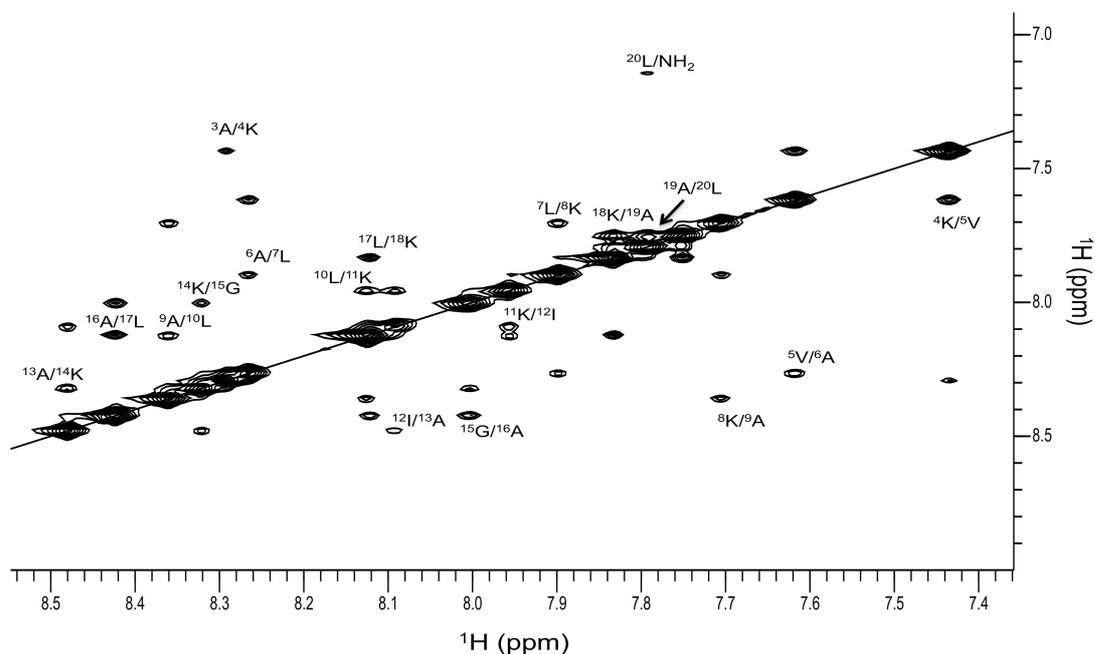


Figure S1 Expanded NH region of a NOESY spectrum ($\tau_{\text{mix}} = 150$ ms) for the 2 mM Kiadin in 150 mM SDS micelles (20 mM phosphate pH 7.4, 50 mM KCl, 0.05 mM DSS, 10%v D₂O) at 50°C. Annotations represent the sequential walk from *i* to *i*+1 residue.

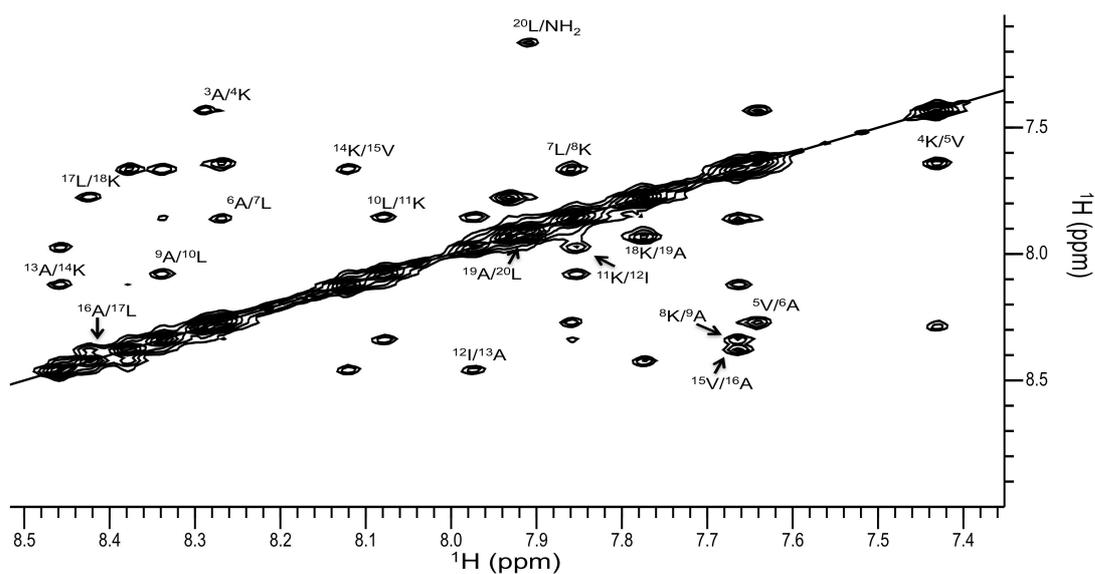


Figure S2 Expanded NH region of a NOESY spectrum ($\tau_{\text{mix}} = 150$ ms) for the 2 mM diPGLa-H in 150 mM SDS micelles (20 mM phosphate pH 7.4, 50 mM KCl, 0.05 mM DSS, 10%v D₂O) at 50°C. Annotations represent the sequential walk from residue *i* to *i*+1 residue.

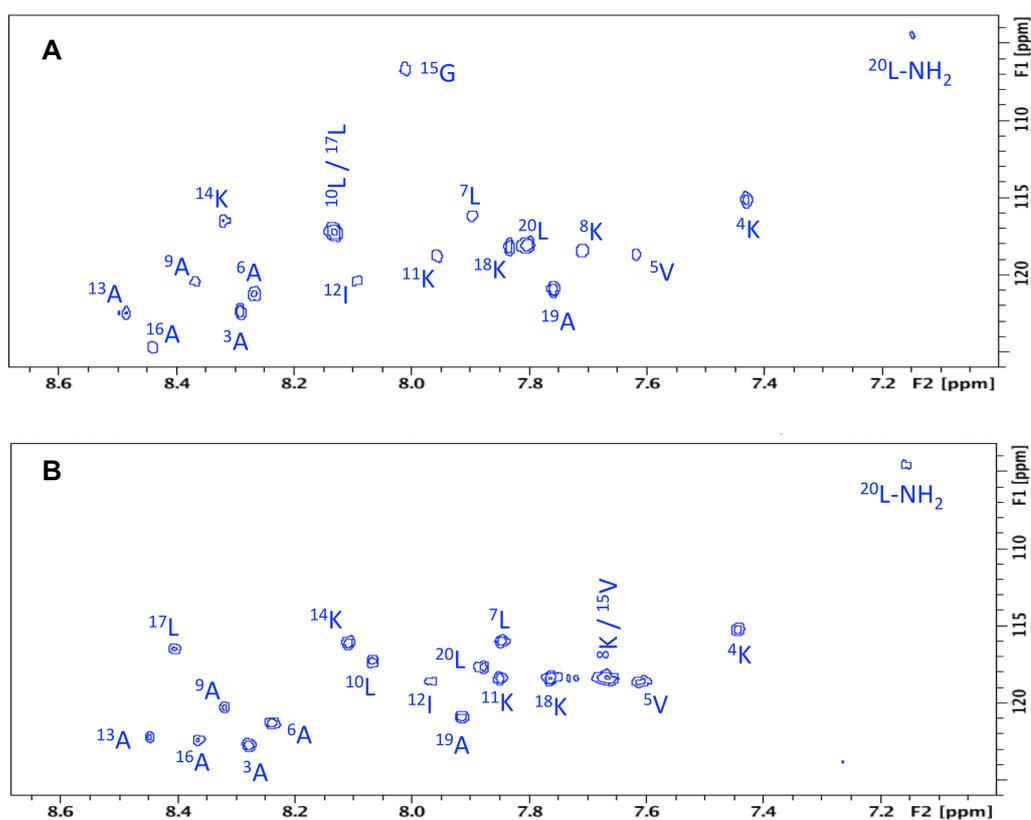


Figure S3 ¹⁵N ¹H HSQC spectra of: (A) Kiadin, and (B) DiPGLa-H in 150 mM SDS micelles (20 mM phosphate pH 7.4, 50 mM KCl, 0.05 mM DSS, 10%v D₂O) at 50°C. Annotations represent the sequential walk from residue *i* to *i*+1 residue.

Table S1: Chemical shifts, hydrogen bond strengths and temperature coefficients of Kiadin in SDS micelles

	H _N (ppm)	H _α (ppm)	H _β (ppm)	H _γ (ppm)	H _δ / H _ε (ppm)	Hydrogen bond strength	Δδ/ΔT (ppb/K)
1 Lys	-	4.10	2.15	1.94	1.59	W	
2 Ile	-	3.95	2.01	-	-	W	
3 Ala	8.30	3.98	1.48			W	-5.6
4 Lys	7.44	4.01	1.95	-	-	W	0
5 Val	7.62	3.70	2.2	0.97		W	-1.8
6 Ala	8.27	3.95	1.42			W	-5.3
7 Leu	7.90	4.05	1.81	-	-	W	-4.1
8 Lys	7.71	4.01	2.04	-	-	W	-2.4
9 Ala	8.36	3.98	1.46			W-M	-4.4
10 Leu	8.13	3.99	1.94	-	-	S	-5.5
11 Lys	7.96	3.93	2.02	-	-	W	-5.1
12 Ile	8.10	3.82	2.01	-	-	S	-5.6
13 Ala	8.48	3.98	1.47			S	-5.6
14 Lys	8.32	3.92	2.00	-	-	W	-3.9
15 Gly	8.01	3.88				W	-2.4
16 Ala	8.43	4.14	1.48			S	-6.2
17 Leu	8.13	4.05	1.87	-	-	S	-5.5
18 Lys	7.84	4.07	1.94	-	-	W	-4.9
19 Ala	7.76	4.22	1.50			W	-2.6
20 Leu	7.80	4.20	1.83	1.63	-	W	-5.0

Table S2: Chemical shifts (ppm), hydrogen bond strengths and temperature coefficients of diPGLa-H in SDS micelles

	H _N (ppm)	H _α (ppm)	H _β (ppm)	H _γ (ppm)	Hydrogen bond strength	Δδ/ΔT (ppb/K)
1 Lys	-	4.09	2.13	-		
2 Ile	-	3.94	2.04	-		
3 Ala	8.28	4.00	1.48		W	-5.9
4 Lys	7.43	4.03	1.94	-	W	0
5 Val	7.63	3.69	2.20	1.08, 0.96	W	-2.6
6 Ala	8.26	3.94	1.43		W	-5.9
7 Leu	7.85	4.05	1.81	-	W	-4.6
8 Lys	7.66	4.02	2.06	-	W	-1.9
9 Ala	8.33	3.97	1.45		M	-4.8
10 Leu	8.07	3.98	1.93	-	S	-4.9
11 Lys	7.85	3.94	2.04	-	W	-4.6
12 Ile	7.97	3.73	2.01	1.48, 0.89	S	-5.5
13 Ala	8.45	3.92	1.47		S	-6.2
14 Lys	8.11	3.89	2.05	-	W	-5.3
15 Val	7.66	3.71	2.27	1.15, 1.00	W	-1.9
16 Ala	8.37	3.99	1.44		M-S	-4.3
17 Leu	8.42	4.00	1.85	-	S	-7.5
18 Lys	7.77	4.07	1.96	-	W	-3.7
19 Ala	7.93	4.22	1.50		W	-2.2
20 Leu	7.90	4.22	1.82	-	W	-5.5

Table S3: Statistical information for the Kiadin and diPGLa-H NMR structures in SDS micelles			
		Kiadin	diPGLa-H
Distance restraints	Total	154	156
	Intra residue	59	62
	Inter	95	94
	Sequential	63	61
	Short range (seq)	95	94
	Short range (non-seq)	32	33
Atomic RMSD (Å) from average structure			
	Backbone (1-20)	0.52	0.47
	Backbone (3-18)	0.39	0.32
Violations from experimental restraints			
	NOE violations (> 0.3 Å)	1	0
	Average violation (Å)	0.57	-
Molprobit statistics			
	Clashes (> 0.4 Å / 1000 atoms)	8.13±4.3	12.90±2.99
	Poor rotamers	0.60±0.49	0.30±0.46
	Ramachandran outliers (%)	0	0
	Ramachandran favoured (%)	99.44±1.67	99.44± 1.67
	MolProbit score	1.80±0.48	1.84± 0.31
	MolProbit score percentile	79.5±19.23	81.1±15.01