

Receptor-Templated Stapling of Intrinsically Disordered Peptide Ligands

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Supporting Information

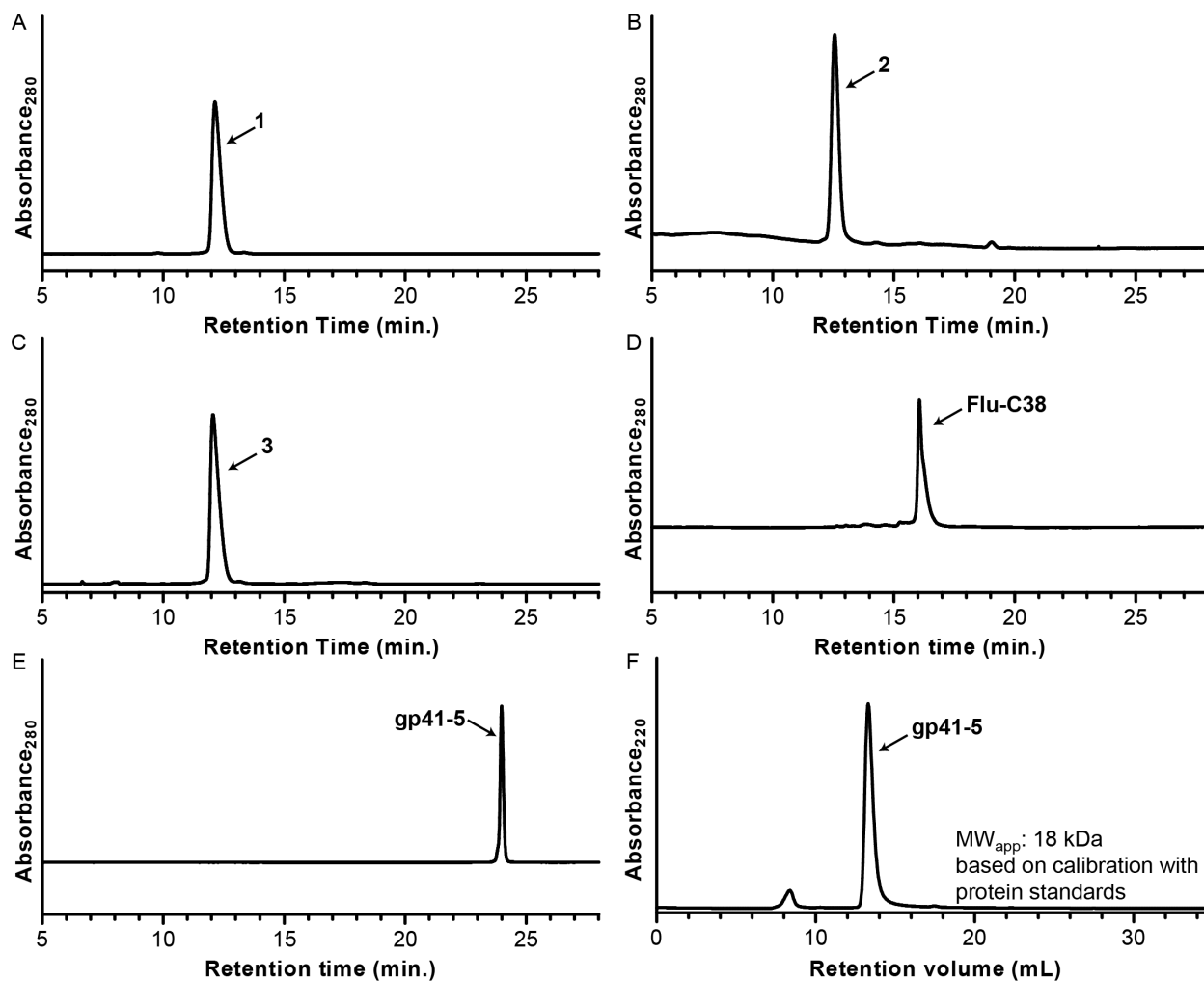


Figure S1. Chromatograms of purified peptides **1-3**, Flu-C38, and gp41-5. (A-E) HPLC chromatograms of peptides **1-3** (A-C, respectively), Flu-C38 (D) and gp41-5 (E). (F) Analytical GPC chromatogram of refolded gp41-5. Calculated molecular weight based on calibration with protein standards.

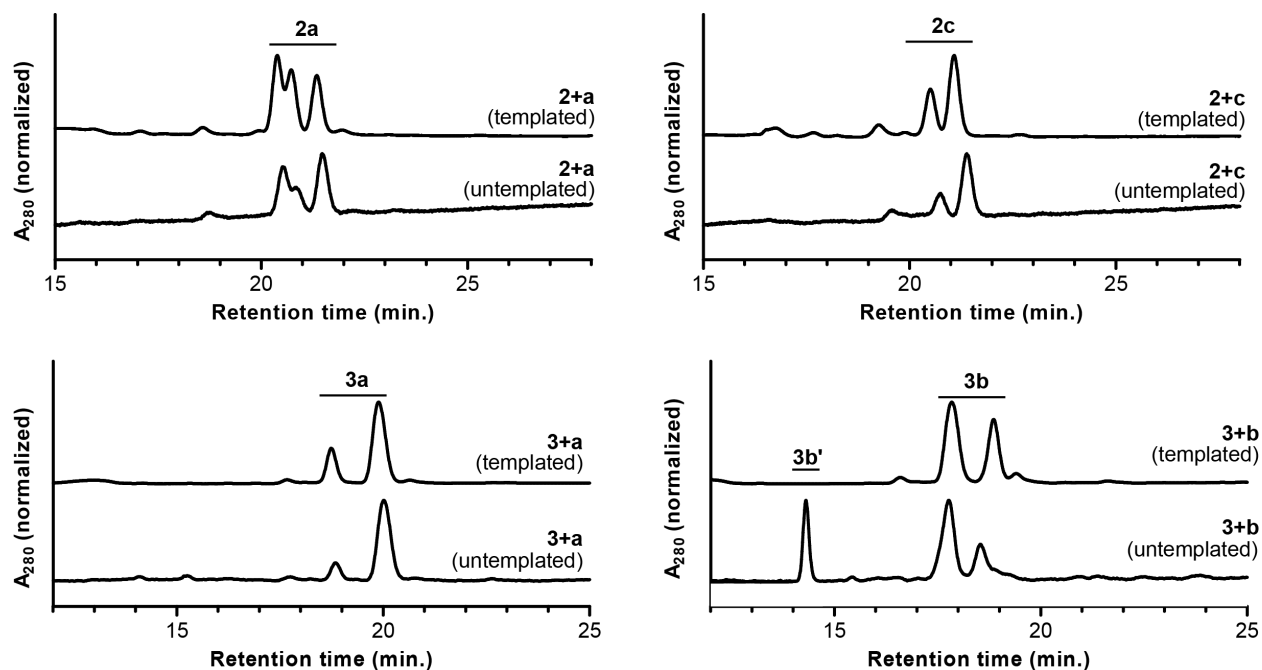


Figure S2. HPLC chromatograms of peptide stapling reactions carried out in the presence (“templated”) or absence (“untemplated”) of the gp41-5 protein receptor. Each reaction consists of 10 μ M peptide, 40 μ M linker, and 10 μ M gp41-5 (if present) in pH 7 phosphate buffer.

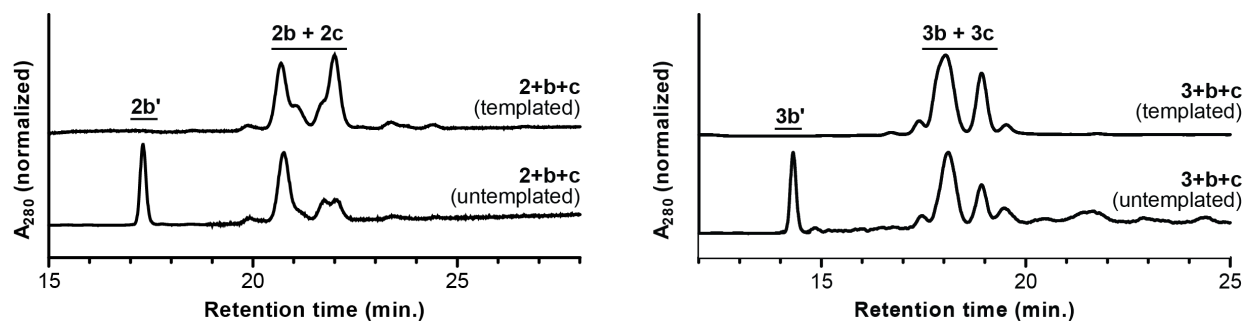


Figure S3. HPLC chromatograms of peptide stapling reactions carried out in the presence (“templated”) or absence (“untemplated”) of the gp41-5 protein receptor. Each reaction consists of 10 μ M peptide, 40 μ M each linker (**b** and **c**), and 10 μ M gp41-5 (if present) in pH 7 phosphate buffer.

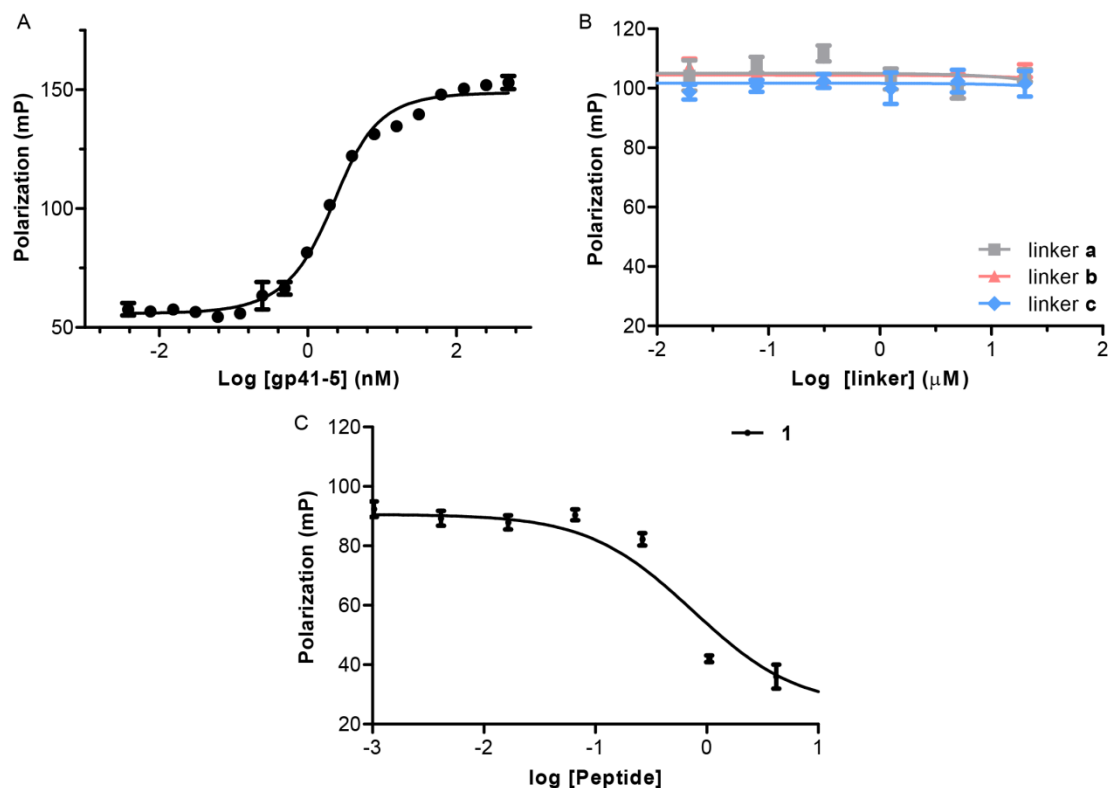


Figure S4. Fluorescence polarization curves. (A) Direct binding fluorescence polarization assay showing titration of gp41-5 into 2 nM Flu-C38. (B) Fluorescence polarization (FP) inhibition of the interaction between Flu-C38 and gp41-5 by linkers **a-c**. No disruption of the binding interaction is observed. (C) Fluorescence polarization (FP) inhibition curve for peptide **1** competitively displacing Flu-C38 from the gp41-5 receptor.

Table S1. MALDI-TOF Data for peptides **1-3**, their cyclic products, protein gp41-5, and Flu-C38.

Peptide	$[M+H]^+$ (m/z)	
	Calculated	Observed
1	2812.5	2812.3
2	2816.5	2816.5
2a	2914.5	2914.6
2b	2914.5	2914.7
2b'	2932.5	2932.7*
2c	2920.4	2920.2
3	2816.5	2816.3
3a	2914.5	2914.8
3b	2914.5	2914.2
3b'	2932.5	2932.8*
3c	2920.4	2920.5
gp41-5	22228.7 [†]	22232.1 [†]
Flu-C38	5089.3	5089.5

*Second species observed at 2949.5.

[†]Calculated and observed average $[M+H]^+$ masses