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Supporting Information

Intramolecular charge interactions as tool to control the coiled coil to amyloid transformation

Kevin Pagel,[a]+ Sara C. Wagner,[a]+ Raheleh Rezaei Araghi,[a] Hans v. Berlepsch,[b] Christoph Böttcher,[b] and Beate Koksch[a]*

[a] Institute for Chemistry and Biochemistry
Freie Universität Berlin
Takustrasse 3, 14195 Berlin (Germany)

[b] Research Centre for Electron Microscopy
Freie Universität Berlin
Fabeckstrasse 36a, 14195 Berlin (Germany)

A: Additional-TEM images.

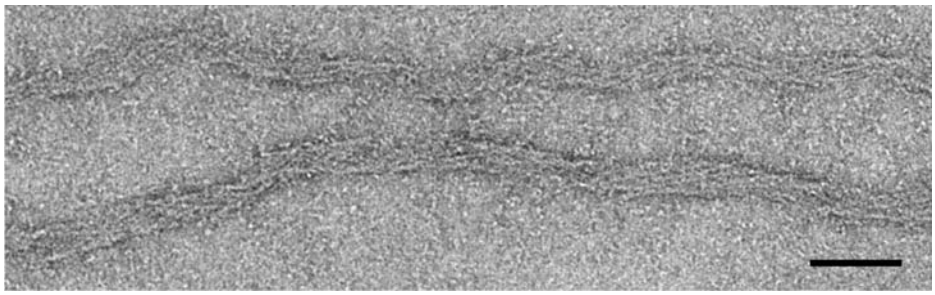

Figure SA1. TEM micrograph of PTA-stained amyloid fibrils formed by peptide A (600 μM) at pH 4.0 (10 mM acetate buffer). The protofilament substructure is visible. Scale bar: 50 nm.

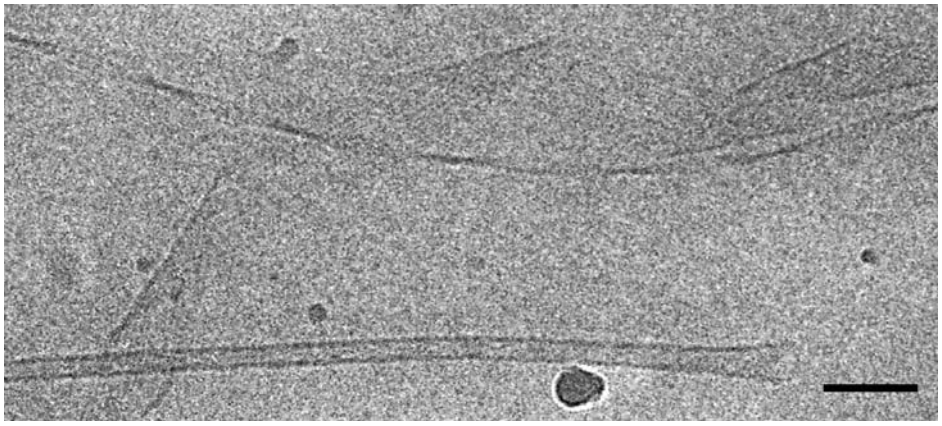

Figure SA2. Cryo-TEM micrograph of a 375 μM solution of peptide B at pH 7.4 (10 mM Tris/HCl buffer) showing different types of amyloid fibrils. Ribbons of variable width and a tubule are evident. Scale bar: 50 nm.

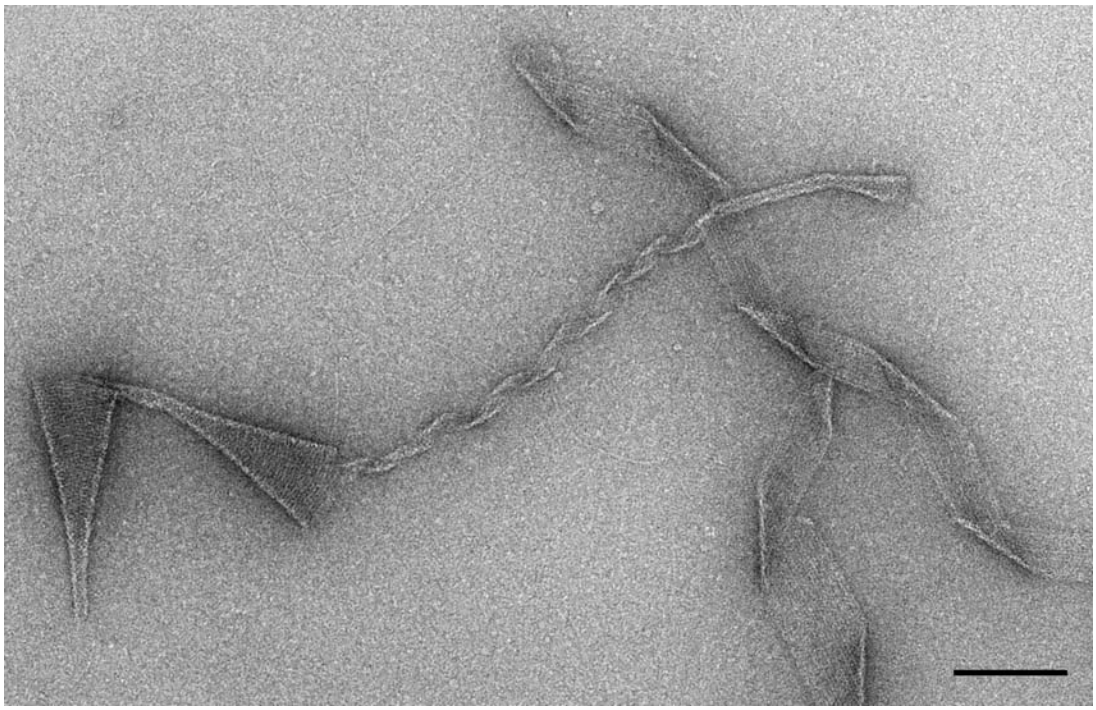

Figure SA3. TEM micrograph of UAc-stained amyloid fibrils formed by peptide B (160 μM) at pH 7.4 (10 mM Tris/HCl buffer). The protofilament substructure is visible. Scale bar: 100 nm.

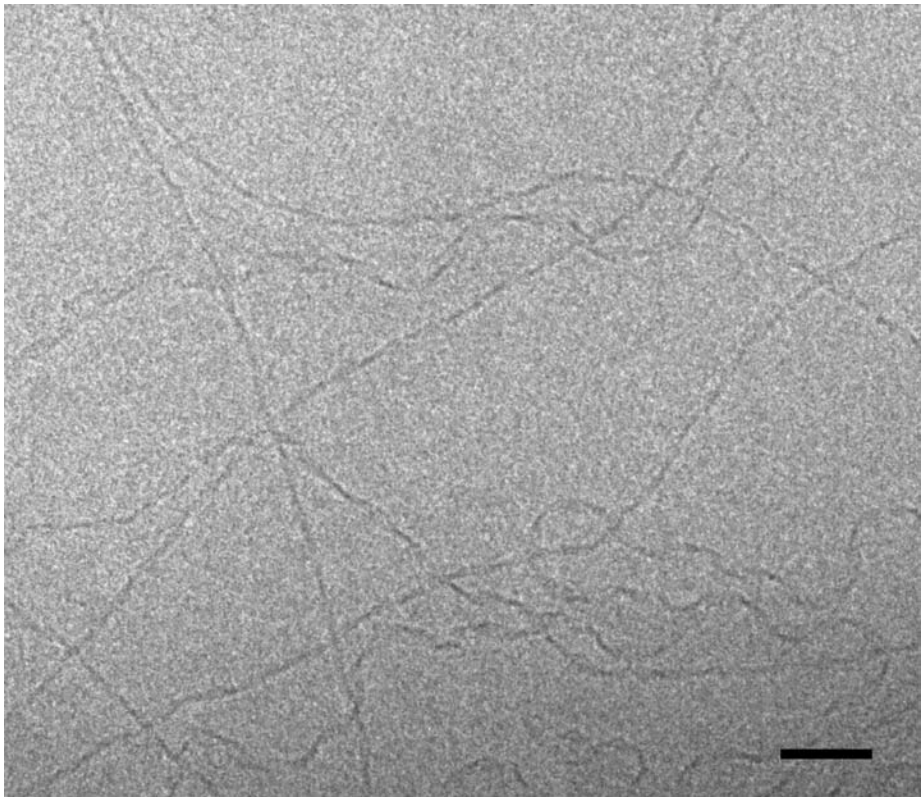

Figure SA4. Cryo-TEM micrograph of a 300 μM solution of peptide C at pH 4.0 (10 mM acetate buffer) showing stiff and curly amyloid fibrils, respectively. Scale bar: 50 nm.

B: x-ray studies.

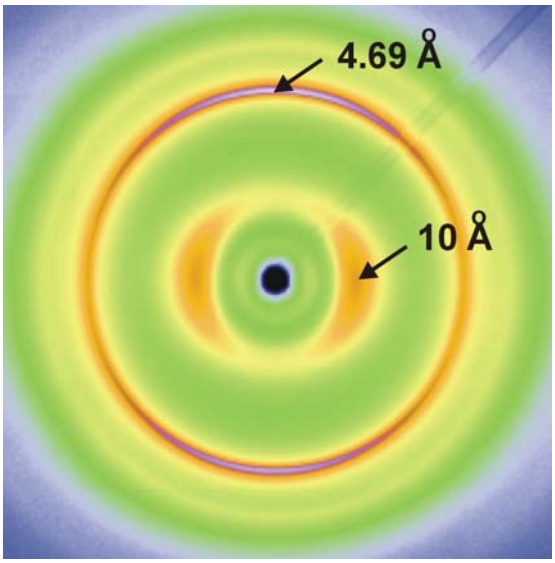

Figure SB1. 2D WAXS pattern from partially aligned dried fibril sample of peptide A. The fibril axis is vertical.

C: Kinetic studies.

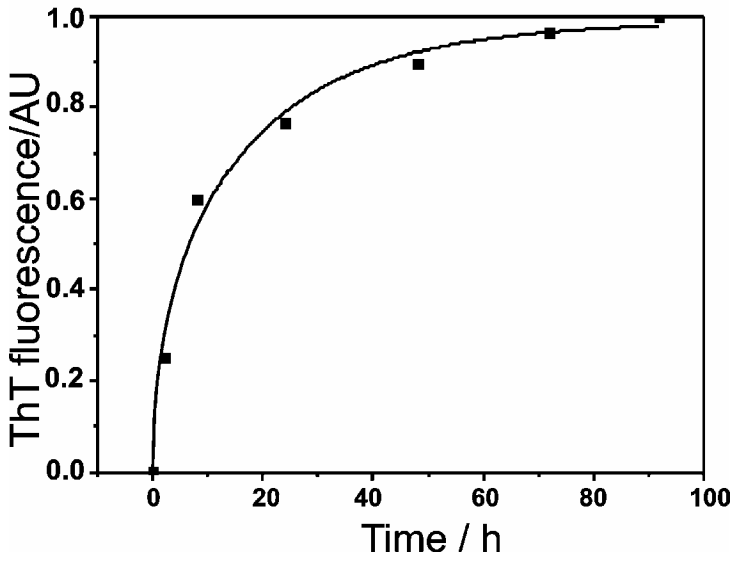

Figure SC1. ThT staining assay of peptide C (200 μM) at pH 7.4 and 4°C. The fluorescence intensity is given after normalization so that the final fluorescence intensity at the endpoint of the kinetic trace was 100%. The resulting plot of fluorescence intensity was fit to a single-exponential function *FL=a-bexp(-rt)* using the Origin Software (version 7.0, Microcal, USA).

D: Thermal denaturation experiments.

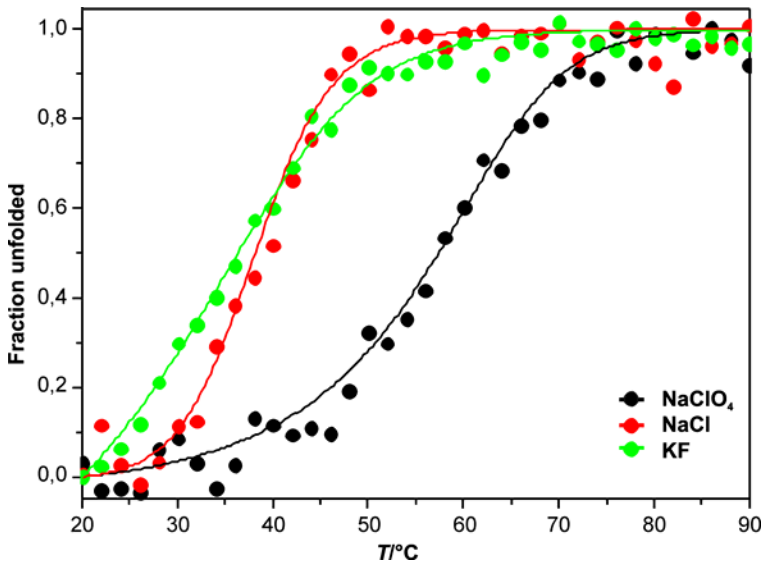

Figure SD1. CD denaturation profiles of peptide C at 50 µM and pH 7.4 (10 mM Tris/HCl buffer) in the presence of 3 M salt. 3 M guanidine hydrochloride were added as denaturation reagent.

E: Additional CD spectra.

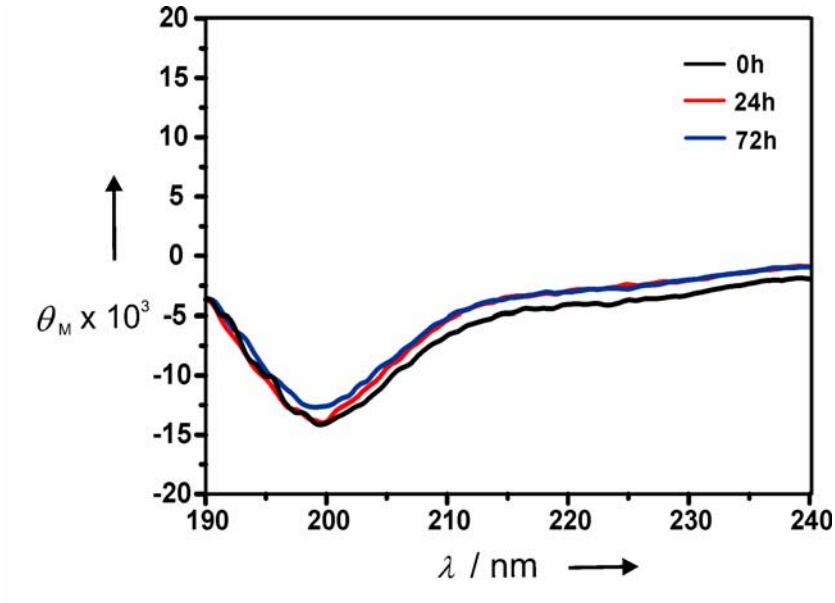

Figure SE1. CD spectra of 250 µM peptide A at pH 4.0 (10 mM acetate buffer).

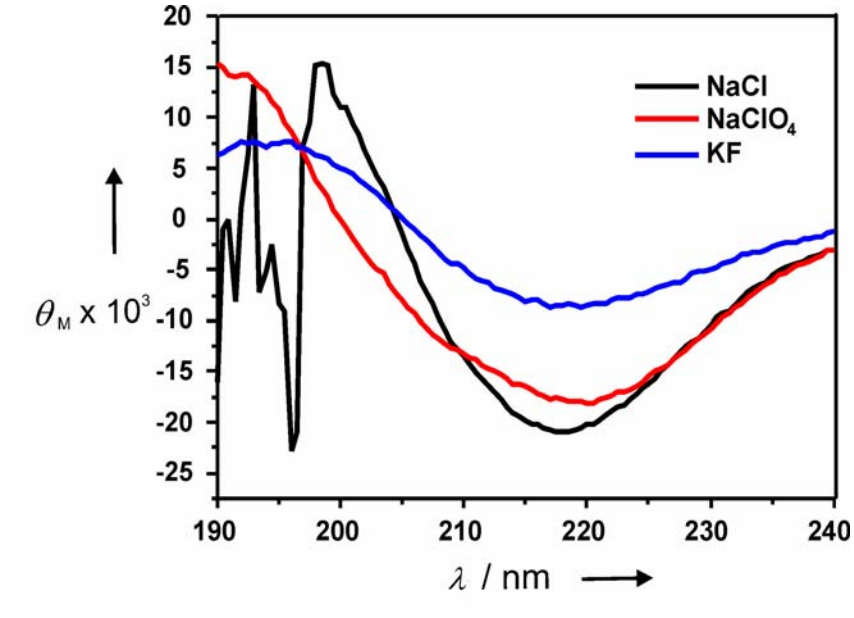

Figure SE2. CD spectra of 69 μM peptide C at pH 7.4 (10 mM Tris/HCl buffer) in the presence of 1 M salt. Spectra were taken immediately after dissolution of the peptide.

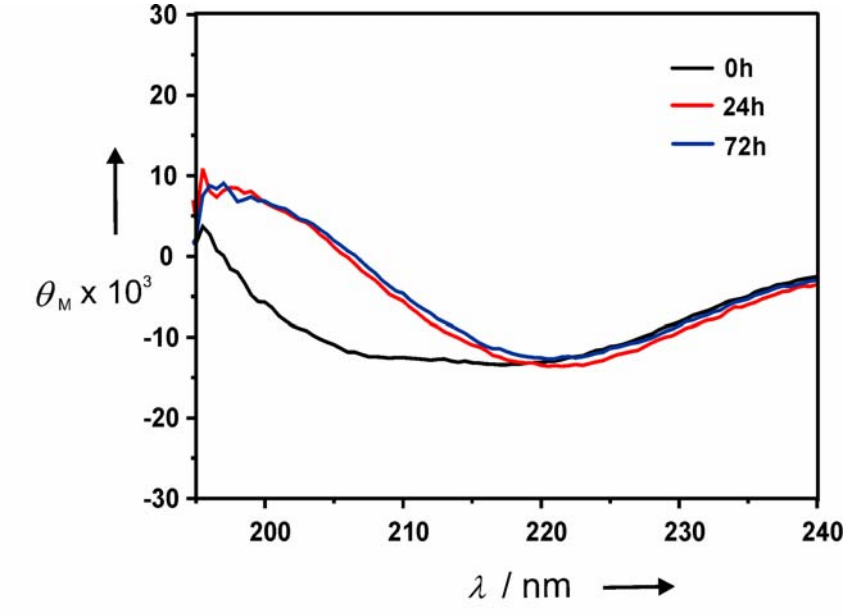

Figure SE3. CD spectra of 95 μM peptide C at pH 7.4 (10 mM Tris/HCl buffer) in the presence of 3 M $NaClO_4$.

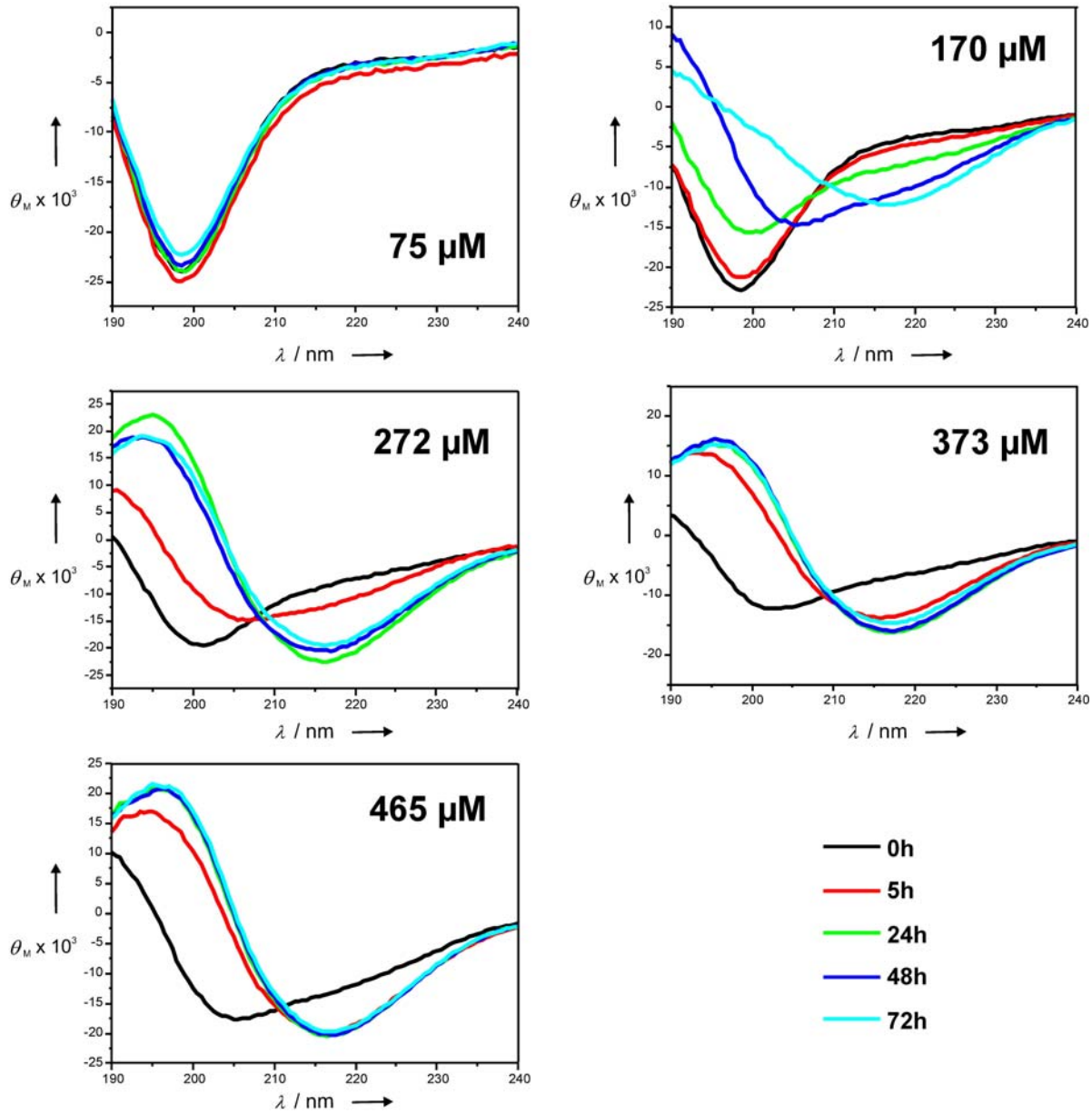

Figure SE4. CD spectra of peptide B at pH 7.4 (10 mM Tris/HCl buffer) and different concentrations.

F: HPLC Data

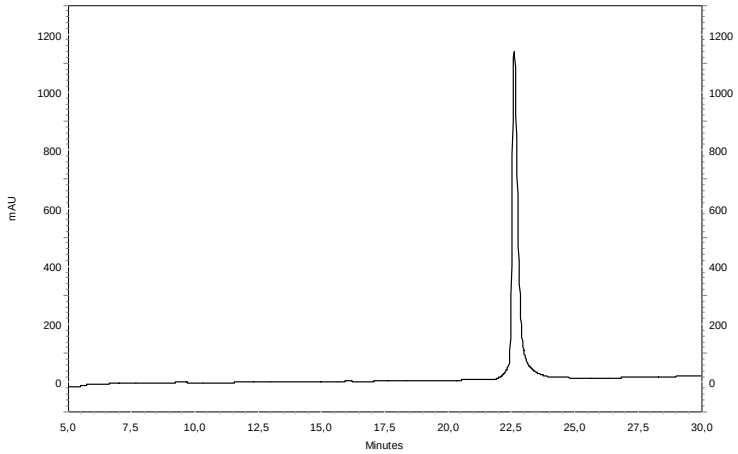

Figure SF1: HPLC Chromatogram of 150 µM peptide A (t_r = 22.6 minutes).

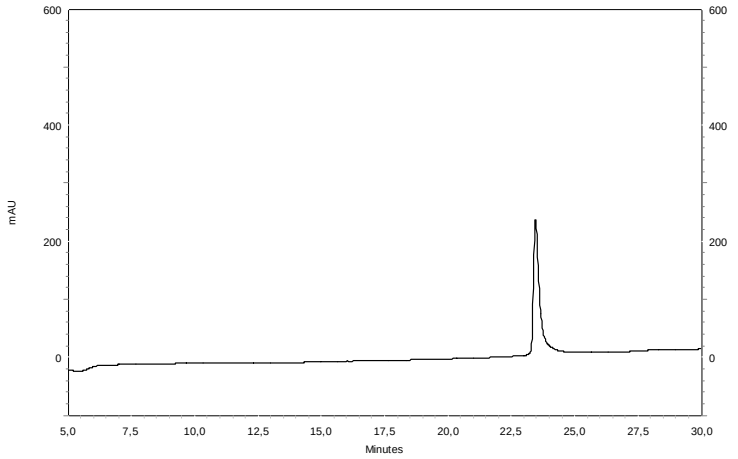

Figure SF2: HPLC Chromatogramm of 150 µM peptide B (t_r = 23.2 minutes).

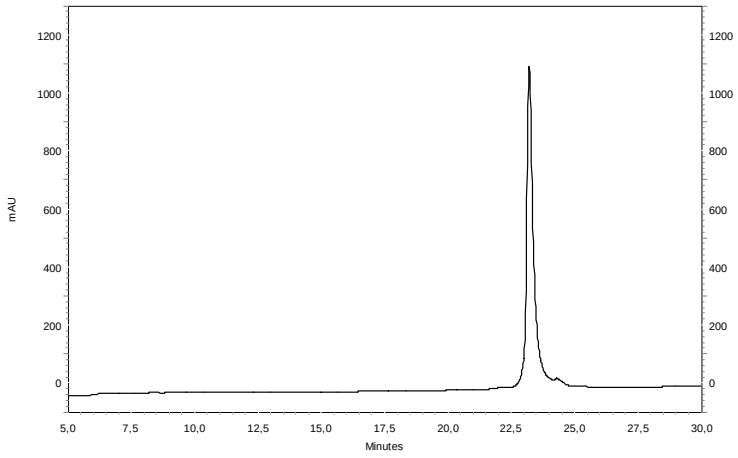

Figure SF3: HPLC Chromatogramm of 150 µM peptide B (t_r = 23.4 minutes).

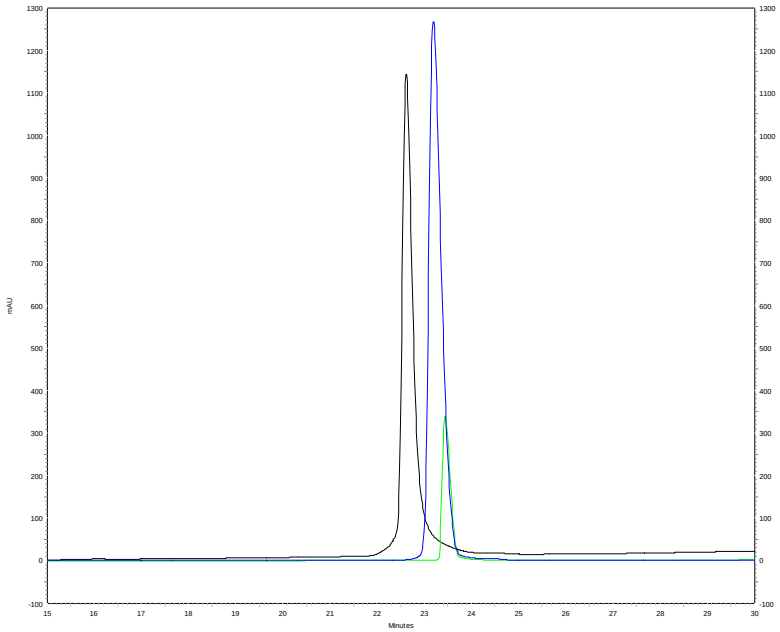

Figure SF4: Magnified HPLC Chromatograms of peptides A (black), B (green), and C (blue) at peptide concentration of 150 µM. The purity of all three peptides was >95%.

Preparative and analytical HPLC was performed at a flow rate of 1 mL min^{-1} using the following gradient and columns.

Gradient: Solvent A H_2O, 0.1% (v/v) Trifluoroacetic acid

Solvent B Acetonitrile, 0.1% (v/v) Trifluoroacetic acid

0 min	95% A
30 min	30% A
32 min	0% A
35 min	0% A
37 min	95% A
40 min	95% A

Columns: Analytical HPLC: Phenomenex® Luna C8 10µm, 250 x 4.6 mm, (Phenomenex Inc., Torrance, CA, USA)

Preparative HPLC:Phenomenex® Luna C8 10µm, 250mm x 21.2mm, (Phenomenex Inc., Torrance, CA, USA)

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