



Supporting Information

Hydrophobic Tagging-Mediated Degradation of Transcription Coactivator SRC-1

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Scheme S1. Synthesis of YL2-HyT1 – 6.

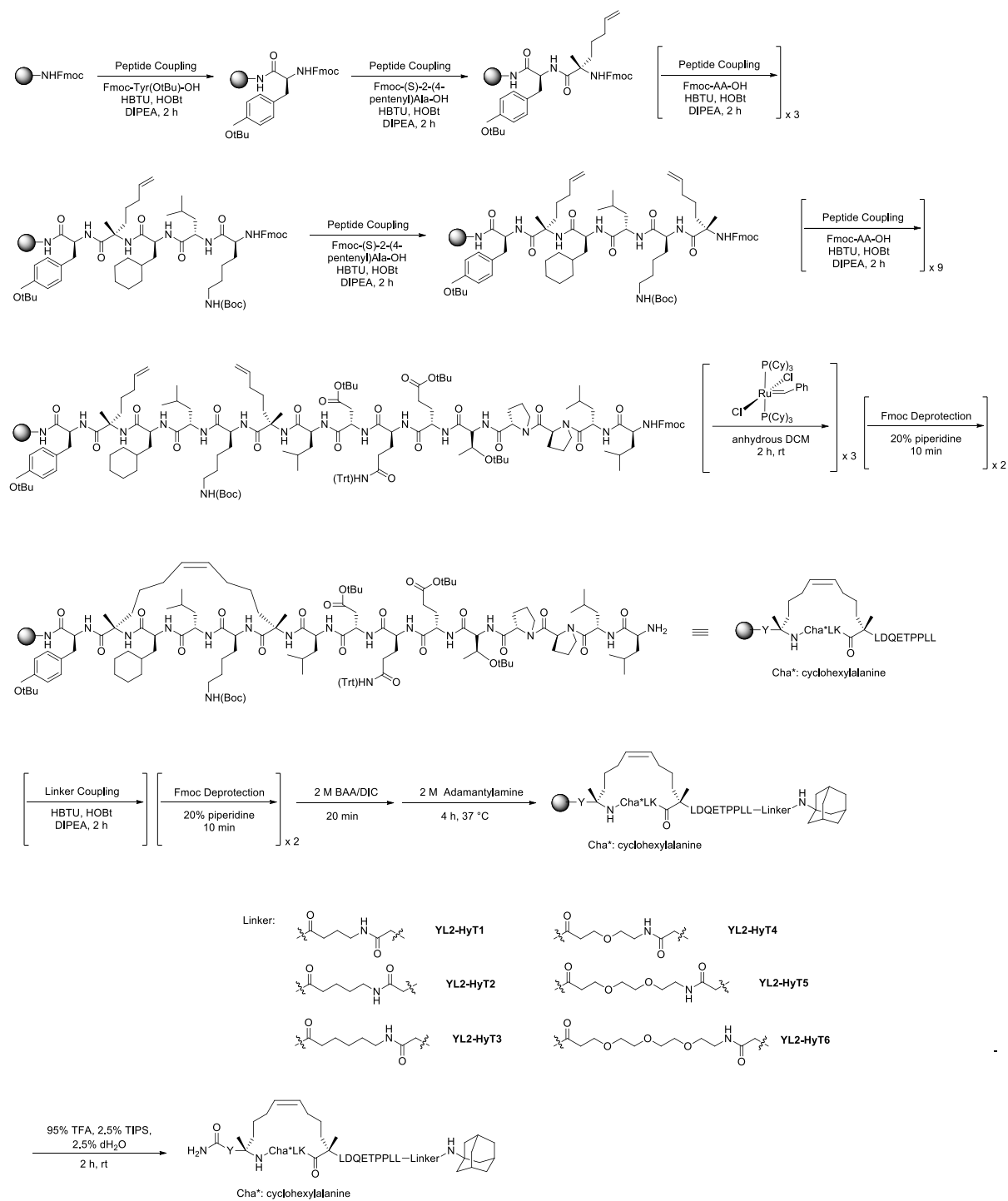
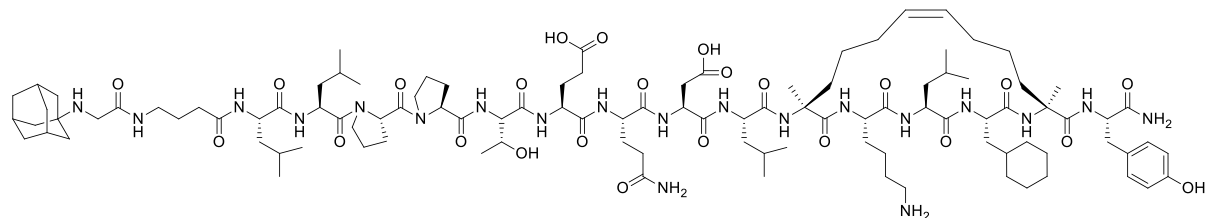
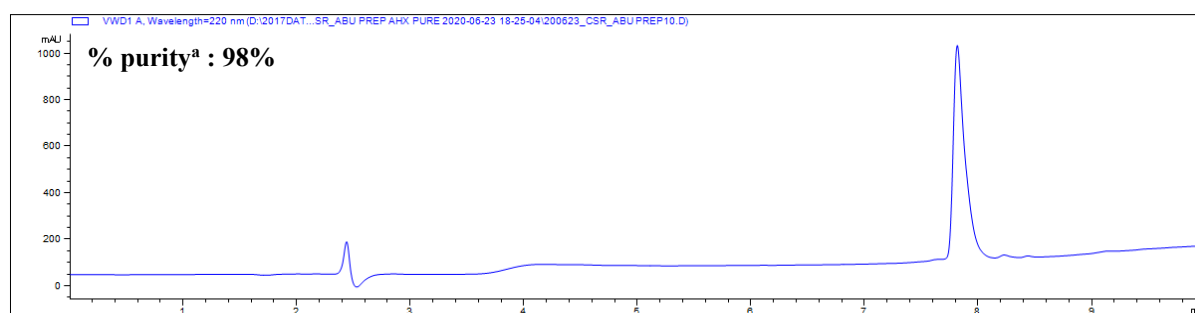
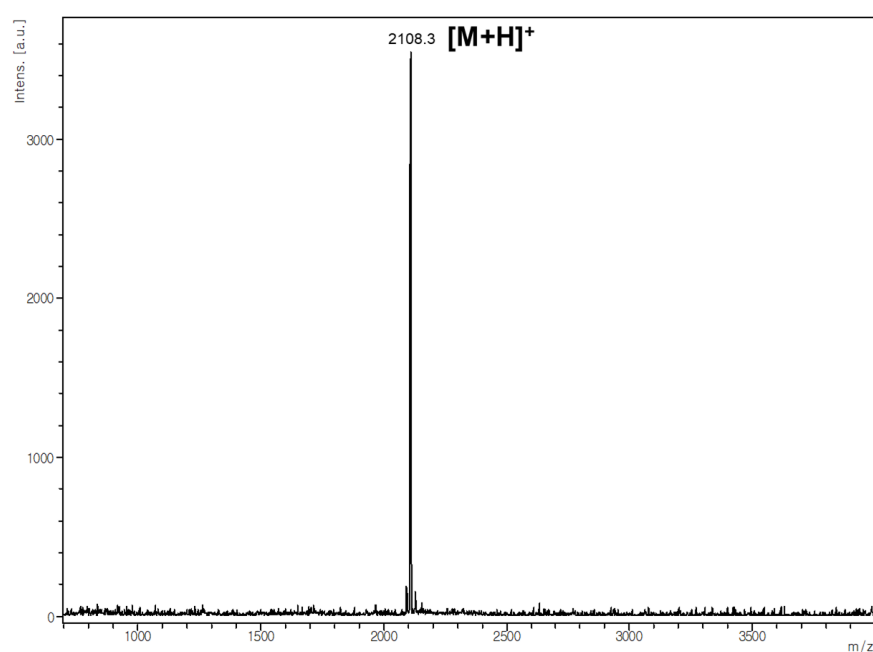


Figure S1. MALDI-TOF MS and LC data for purified YL2-HyT1 – 6.

YL2-HyT1



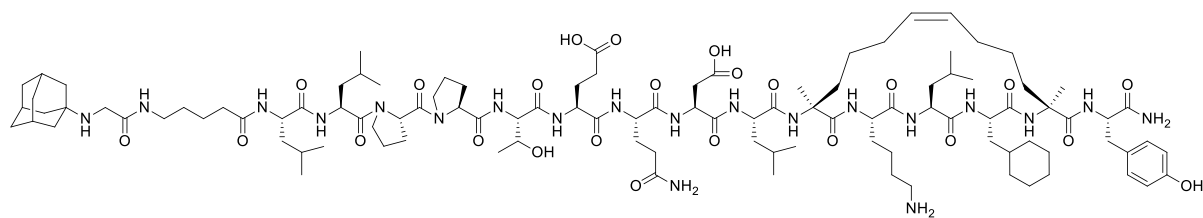
Calculated mass: 2107.27



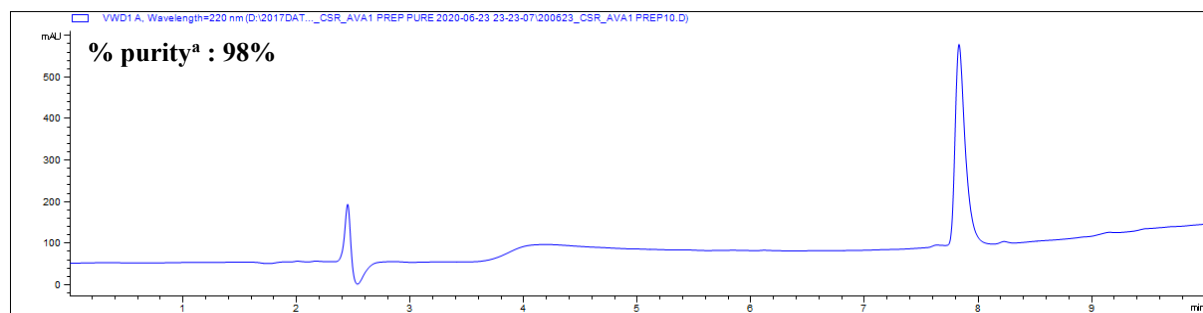
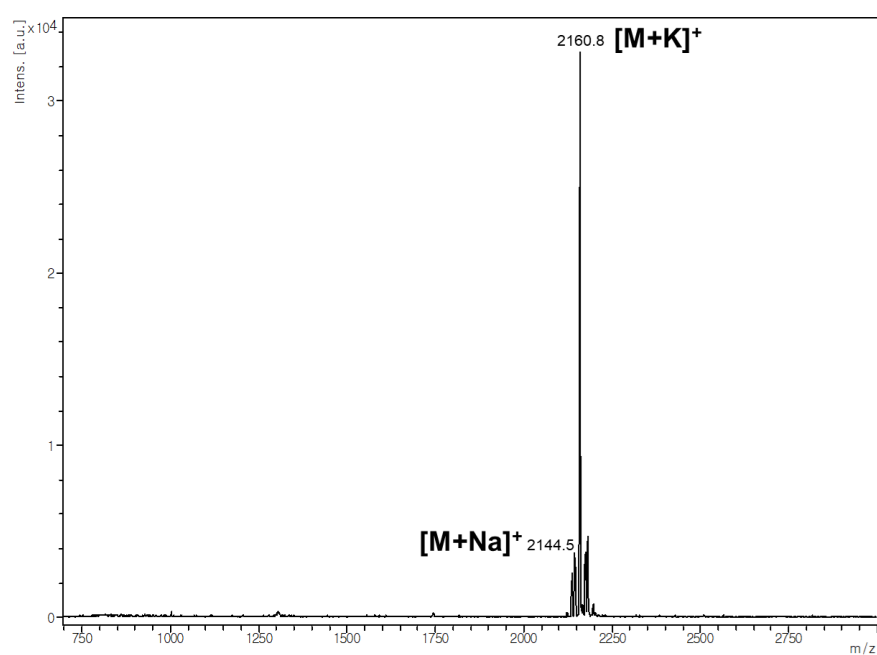
^a Determined by analytical reversed-phase HPLC of a product

Figure S1. (Cont'd)

YL2-HyT2

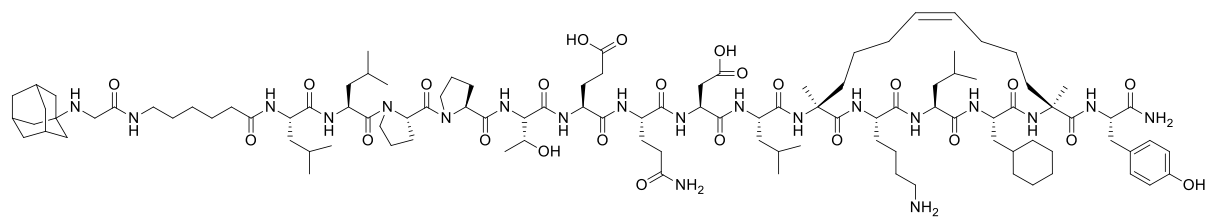


Calculated mass: 2121.29

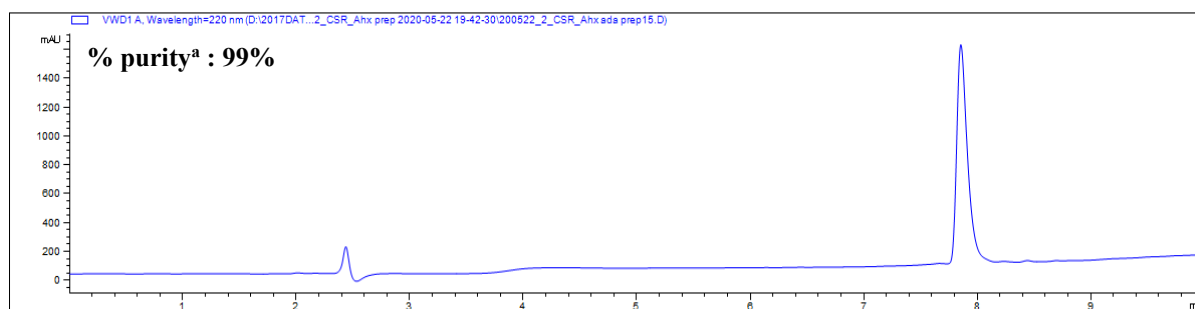


^a Determined by analytical reversed-phase HPLC of a product

YL2-HyT3



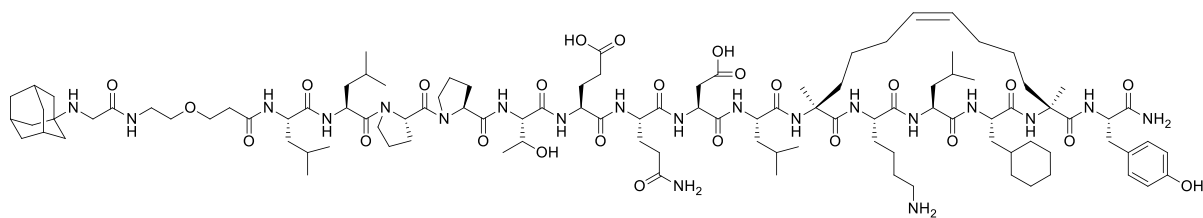
Mass spectrum showing relative intensity (a.u.) versus m/z . The base peak is at m/z 2136.5, labeled $[M+H]^+$. Other significant peaks are at m/z 2158.5, labeled $[M+Na]^+$, and m/z 2174.5, labeled $[M+K]^+$.



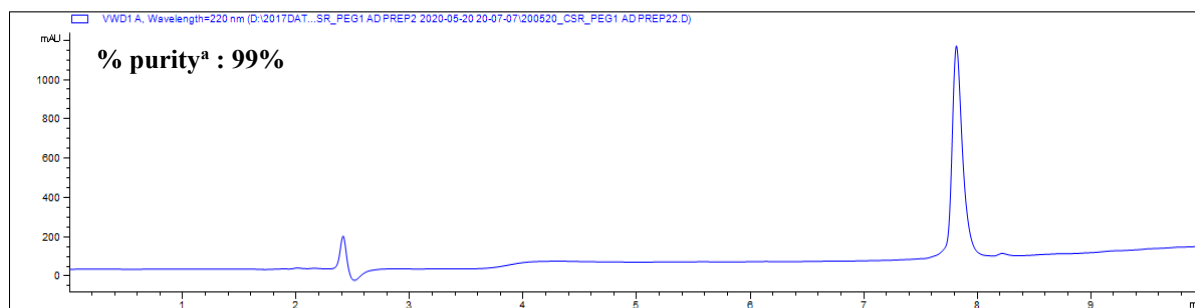
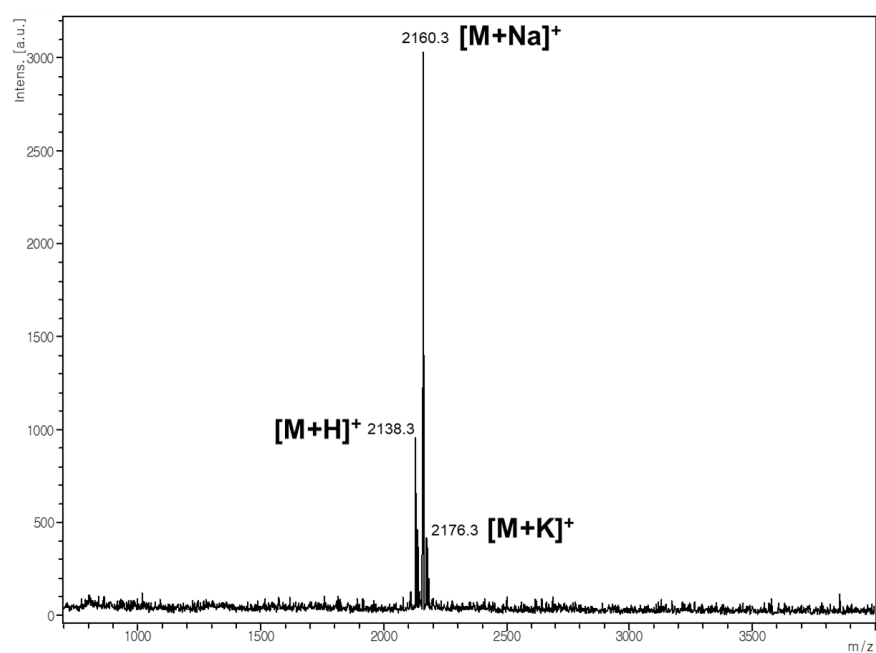
S5

Figure S1. (Cont'd)

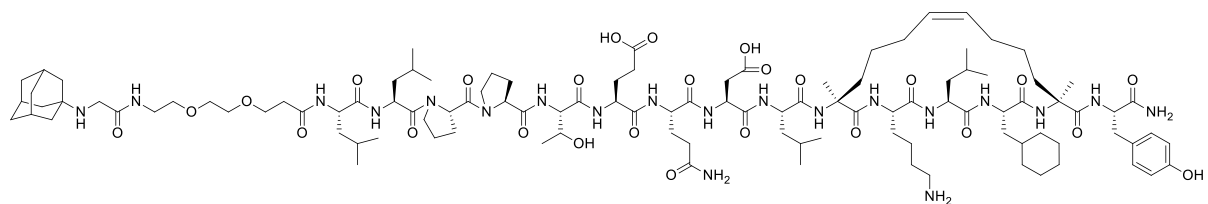
YL2-HyT4



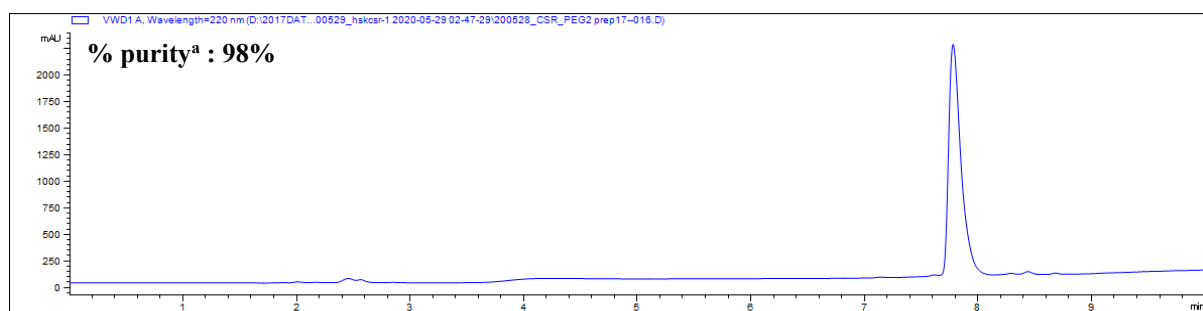
Calculated mass: 2137.28



^a Determined by analytical reversed-phase HPLC of a product

YL2-HyT5

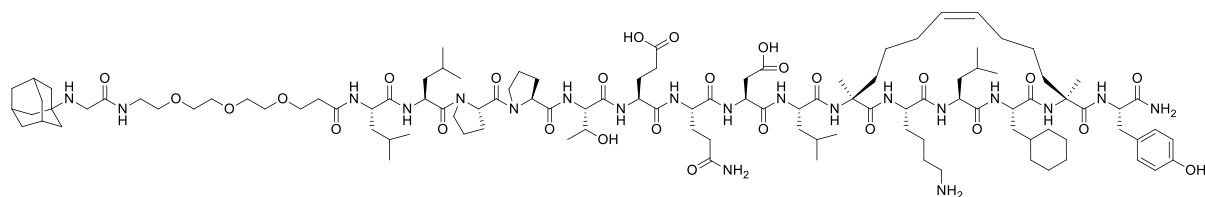
Mass spectrum of compound **1**. The x-axis represents the mass-to-charge ratio (m/z) from 0 to 4000, and the y-axis represents relative intensity from 0 to 2000+. The base peak is at m/z 2182.2, corresponding to the $[M+H]^+$ ion. A smaller peak is observed at m/z 2204.2, corresponding to the $[M+Na]^+$ ion.



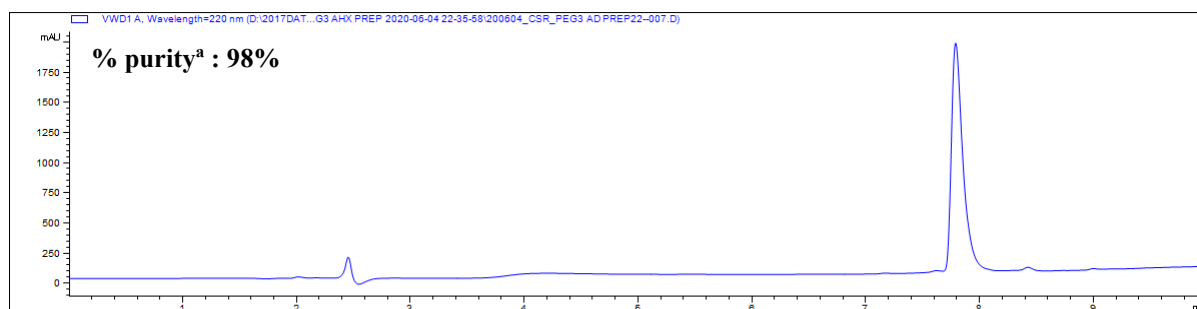
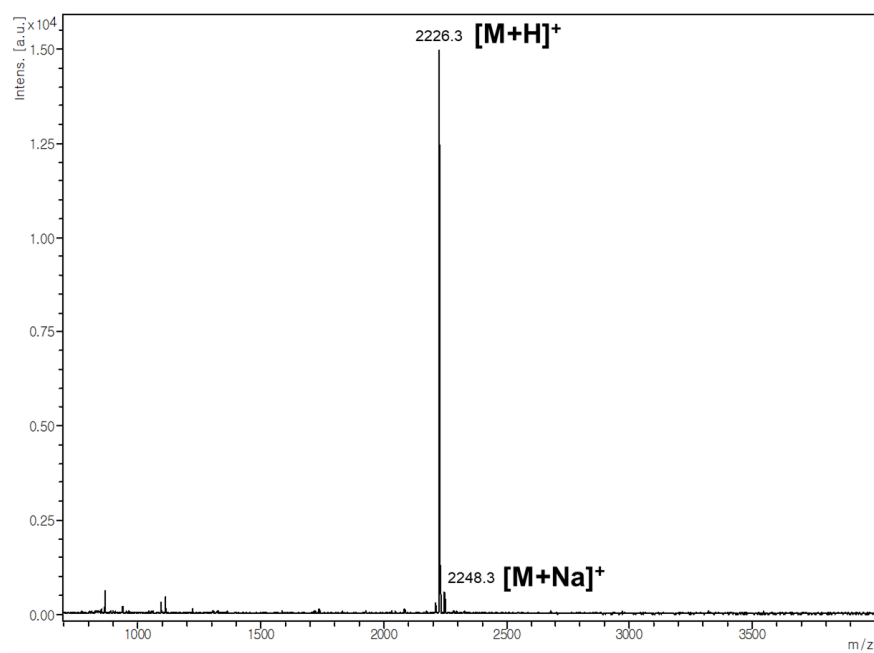
S7

Figure S1. (Cont'd)

YL2-HyT6



Calculated mass: 2225.33



^a Determined by analytical reversed-phase HPLC of a product

Figure S2. Western blot analysis of SRC-1 levels in MDA-MB-231 cells after treatment of YL2-HyT1 – 6 for 12 h. The SRC-1 levels (%) were normalized to GAPDH and DMSO controls.

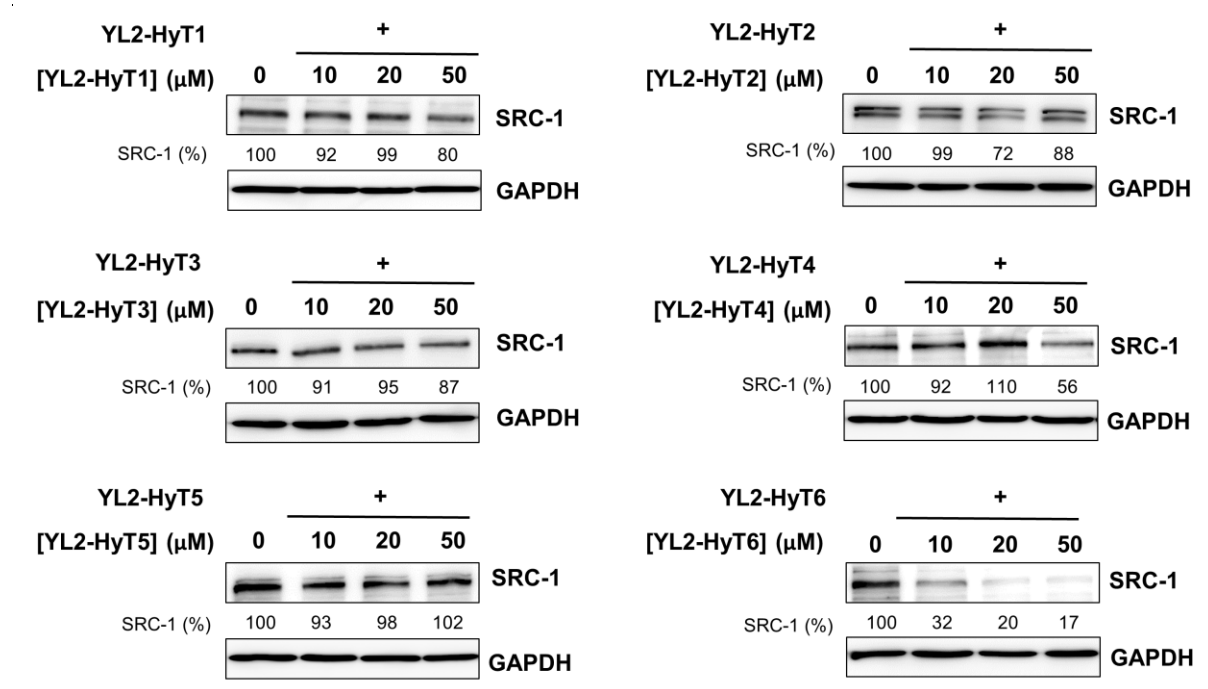


Figure S3. Western blot analysis of SRC-1 levels in MDA-MB-231 cells after treatment of YL2-HyT1 – 6 for 24 h. The SRC-1 levels (%) were normalized to GAPDH and DMSO controls.

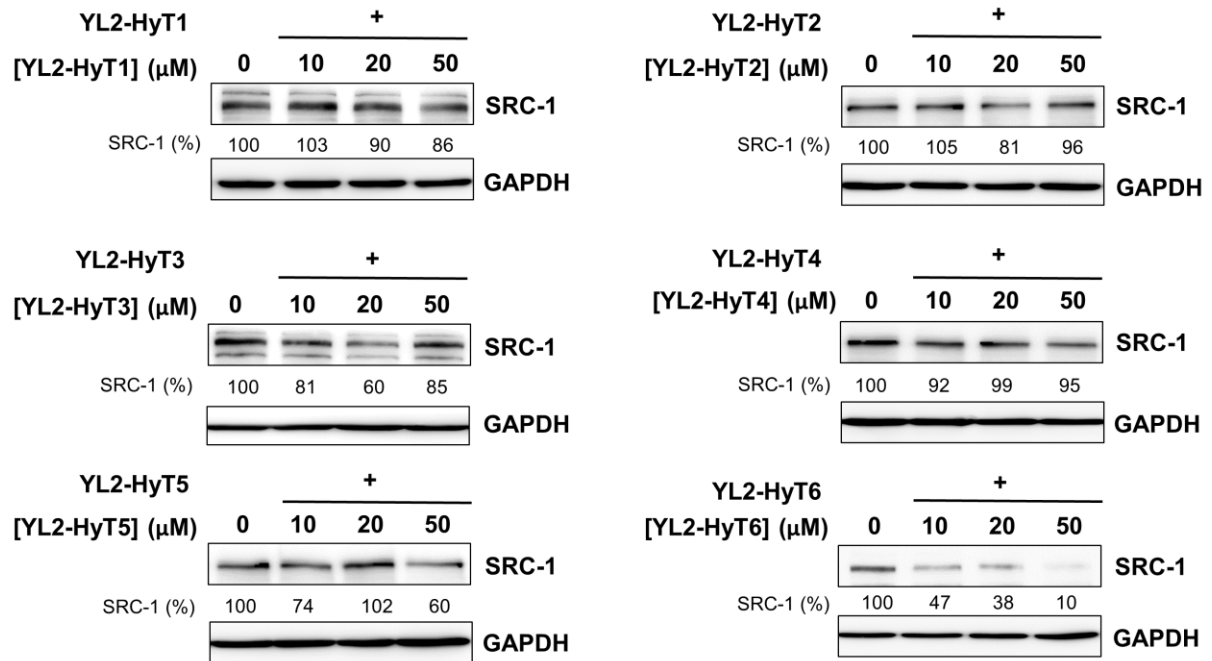
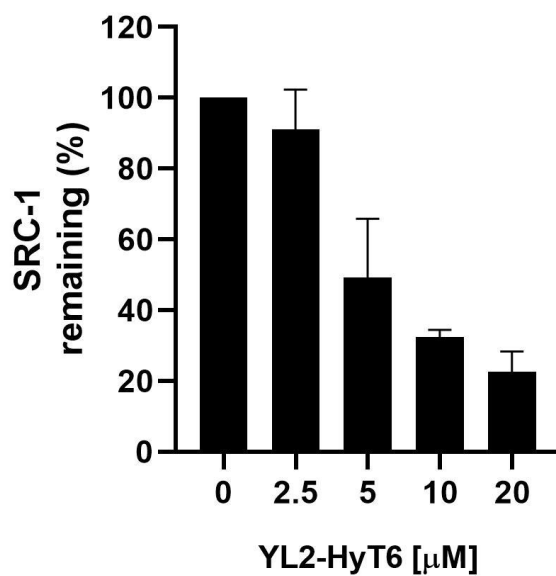
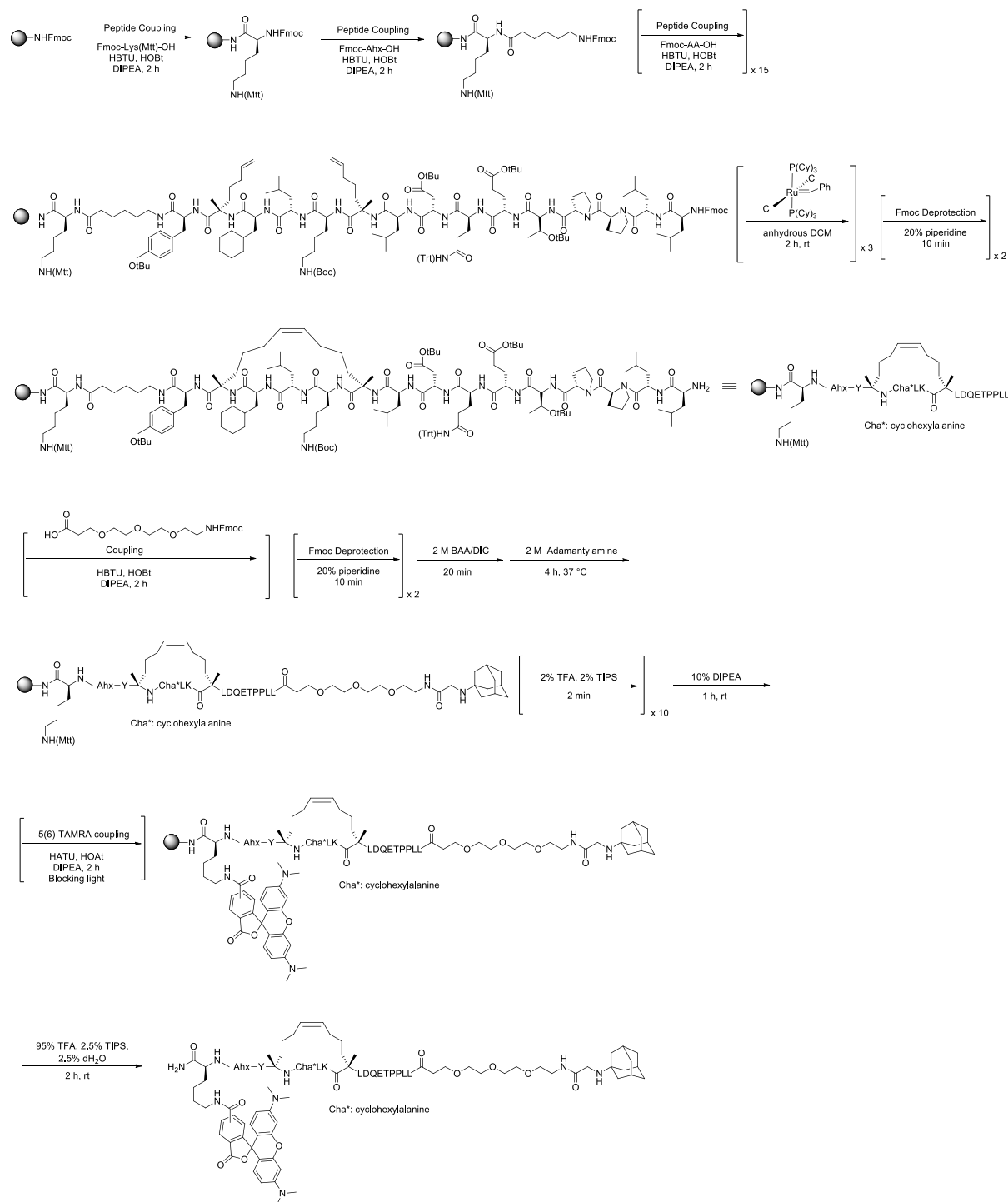


Figure S4. Quantitation of cellular levels of SRC-1 after incubation of MDA-MB-231 cells with indicated concentration of YL2-HyT6 for 18 h. The SRC-1 levels (%) were normalized to GAPDH and DMSO controls. Error bars in data represent standard deviation from three independent experiments.



Scheme S2. Synthesis of TAMRA-labeled YL2-HyT6 (TAMRA-YL2-HyT6).



Scheme S3. Synthesis of TAMRA-labeled ND1-YL2 (TAMRA-ND1-YL2).

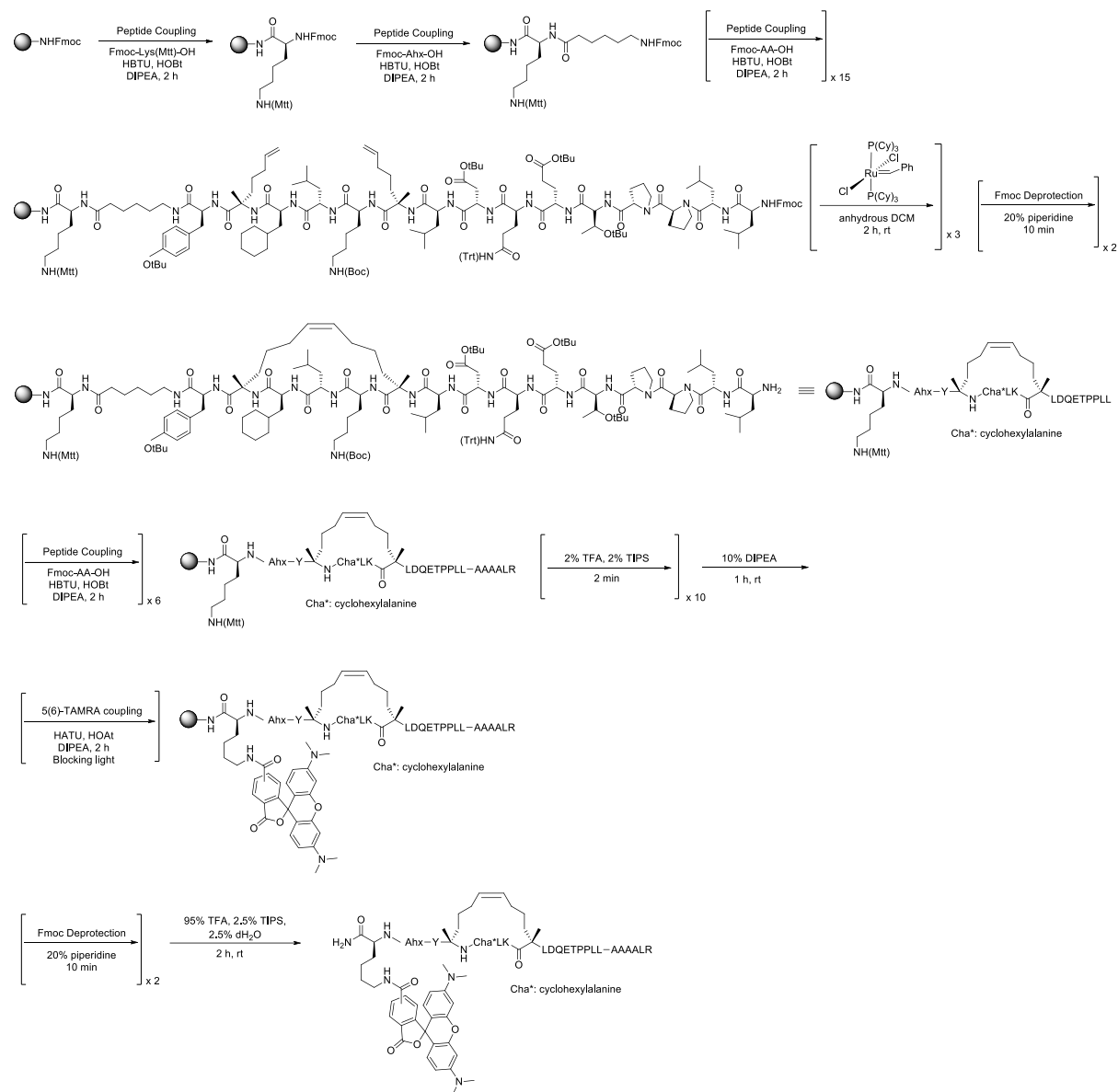
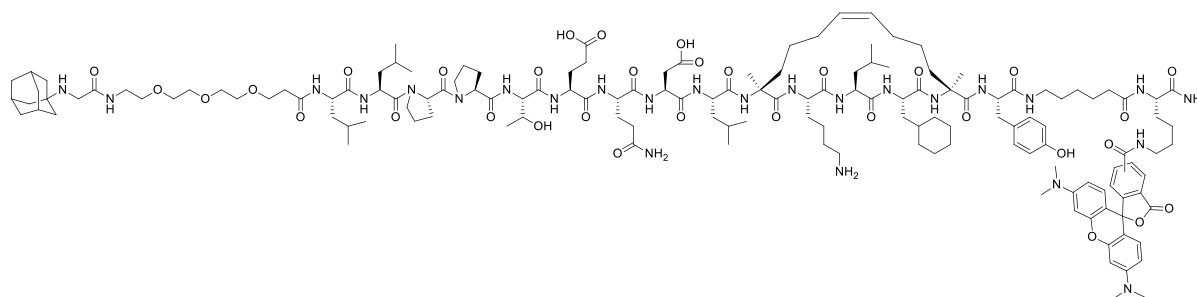
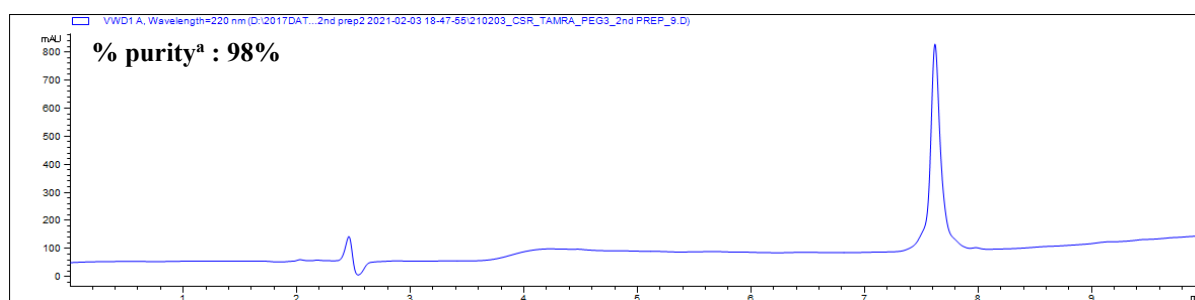
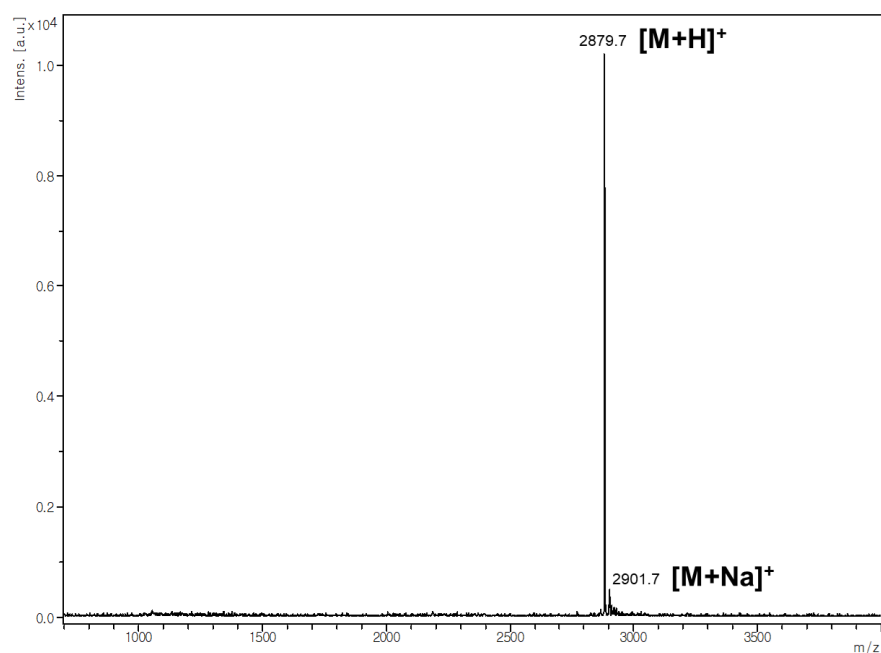


Figure S5. MALDI-TOF MS and LC data for purified TAMRA-YL2-HyT6 and TAMRA-ND1-YL2.

TAMRA-YL2-HyT6



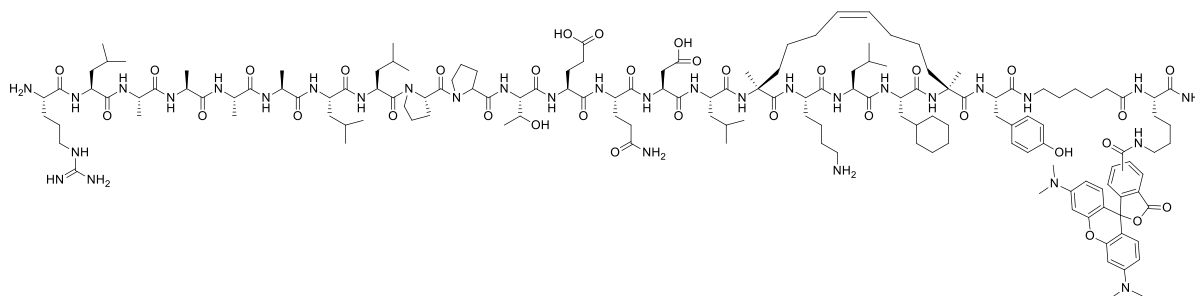
Calculated mass: 2878.65



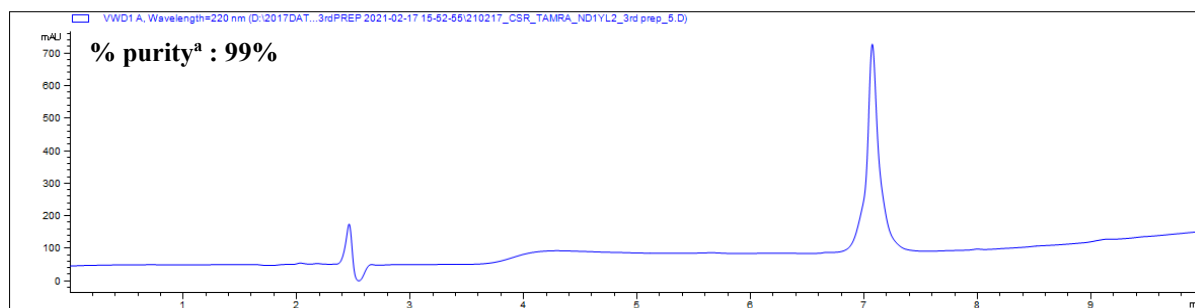
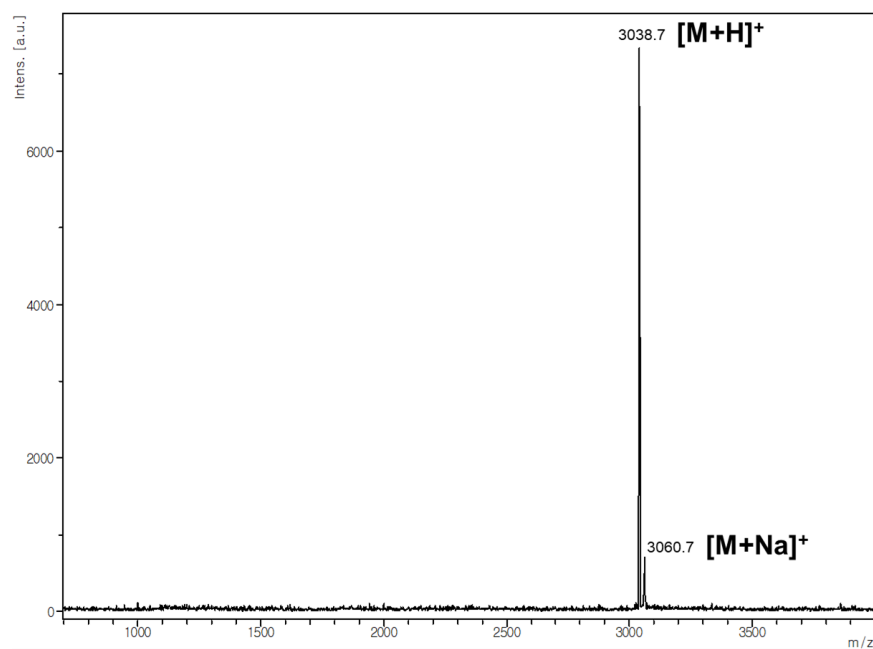
^a Determined by analytical reversed-phase HPLC of a product

Figure S5. (Cont'd)

TAMRA-ND1-YL2



Calculated mass: 3037.74



^a Determined by analytical reversed-phase HPLC of a product

Figure S6. Representative image from wound healing assay showing changes in MDA-MB-231 cell migration after treatment with ND1-YL2 (20 μ M). Images of wounds gap were taken at 0 h and 72 h.

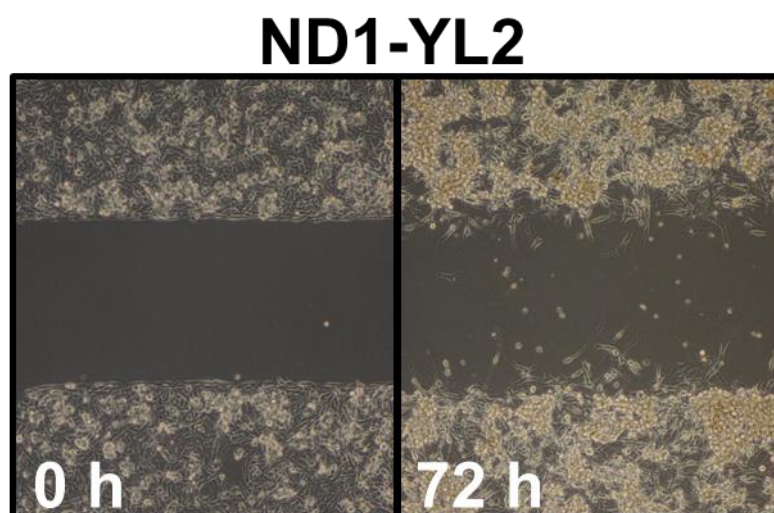


Figure S7. Representative image of transwell invasion assay of MDA-MB-231 cells after treatment with ND1-YL2 (20 μ M) for 24 h.

