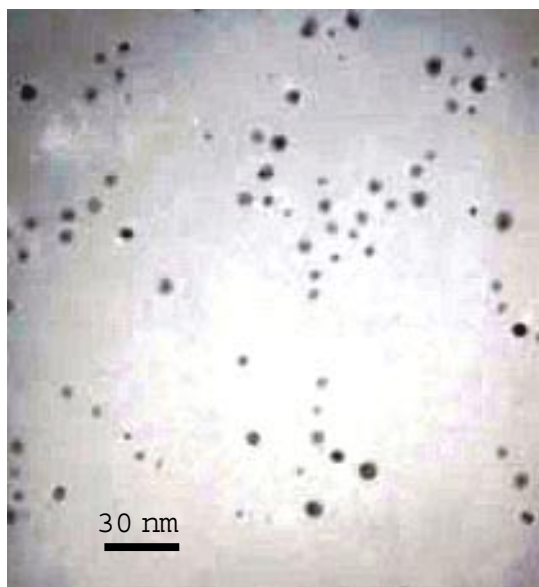


# Epitope Presentation on Monolayer-Protected Clusters for Multi-component Functional Nanostructures

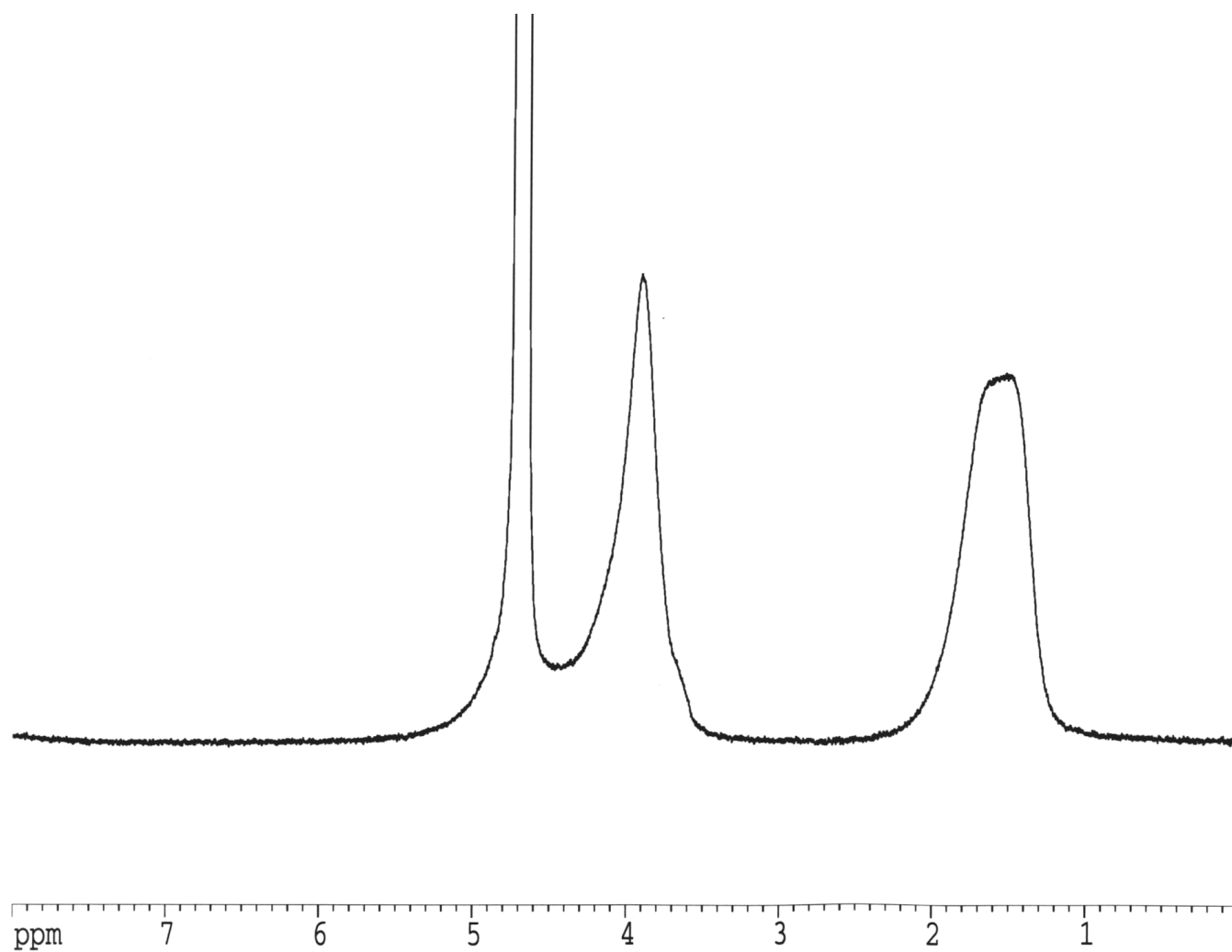
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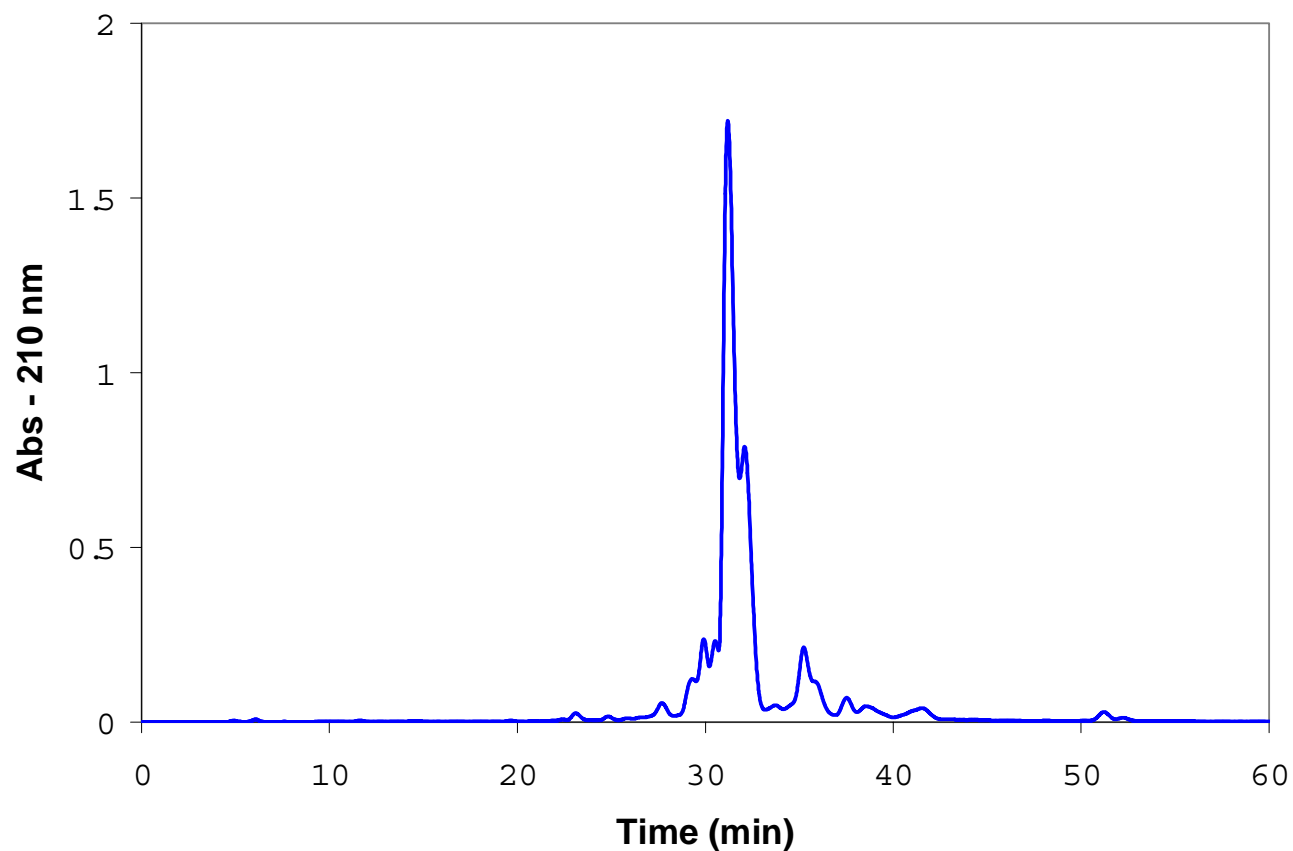
- S-1.** Title and Table of Contents
- S-2.** TEM image of Tiop-MPC, showing spherical cluster
- S-3.**  $^1\text{H}$  NMR of Tiop-MPC
- S-4.** HPLC trace of HA peptide
- S-5.** MALDI mass spectrum of HA peptide
- S-6.**  $^1\text{H}$  NMR functionalized HA-MPC



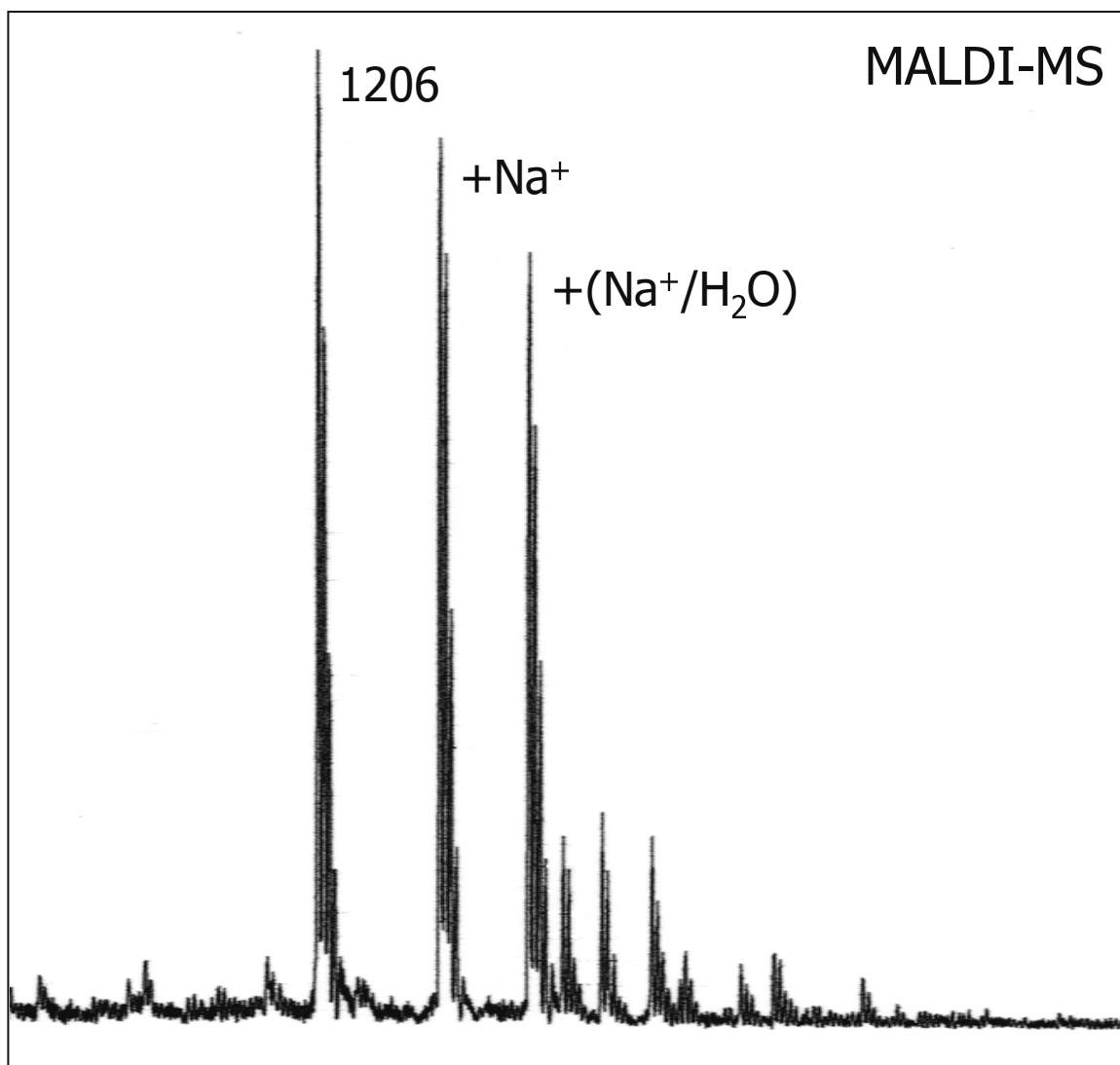
**S-2.** TEM image of Tiop-MPC, showing spherical cluster.



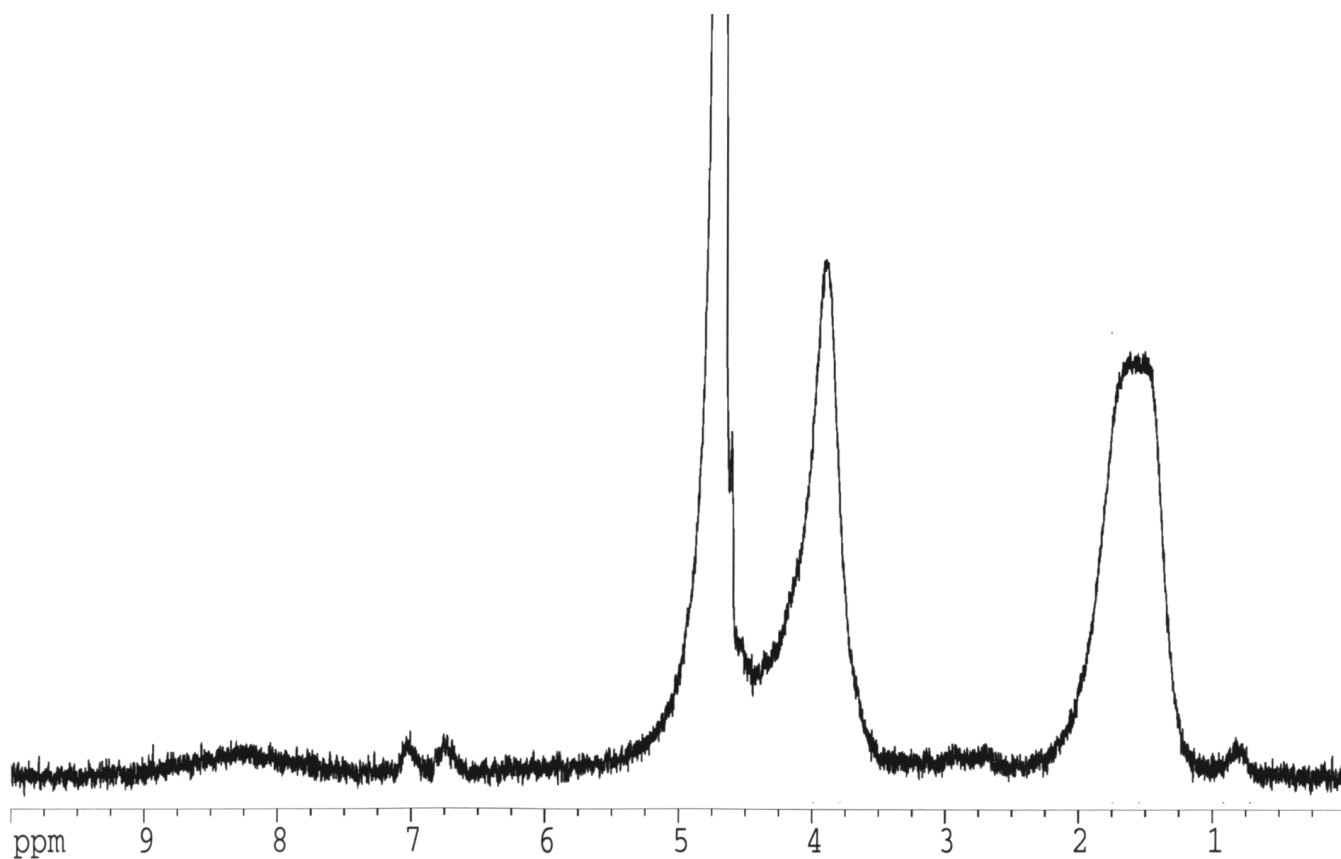
**S-3.**  $^1\text{H}$  NMR of Tiopronin MPC. Broad peaks are indicative of nanocluster formation. A lack of sharp peaks indicates purity.



**S-4.** Chromatogram from the purification of the crude HA peptide using semi-preparative HPLC. The relatively sharp peak and lack of other major peaks indicates a homogenous sample.



**S-5.** MALDI-MS of HA peptide collected from the major peak of HPLC (**S-4**). Major peak (1206) is indicative of the pure peptide + H<sup>+</sup>. Other peaks are listed according to their adducts.



**S-6.**  $^1\text{H}$  NMR of tiopronin-MPC after place exchange with HA peptide epitope. Tiopronin peaks are still present. Peptide peaks are visible at approximately 0.8, 2.8, 6.8, and 7.0 ppm. The number of peptides per cluster is determined through NMR integration values and the following equation:

$$[\text{Normalized Peak Area}]_{\text{Tiop}}/[\text{H per Ligand}]_{\text{Tiop}} : [\text{Normalized Peak Area}]_{\text{peptide}}/[\text{H per ligand}]_{\text{peptide}}$$