

Heavy chain (51.15 kDa)

MDRLTSS~~FLLIVPAYVLS~~QVQLQQPGAELVKPGASVKLSCKSSGYHFTSYWMHWVKQRPQGQLEWIGVIHPNSGSIN
 YNEKFESKATLTVDKSSSTAYMQLSSLTSEDSAVYYCAGERDSTEVLPMDYWGQGTSTVTVSSAKTTPPSVYPLAPGSAA
 QTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLES~~DLYTLSSSVTPSSPRPSETVTCNVAHPASSTKVDKKI~~
 VPRDCGCKPCICTVPEVSSVFIFPPKPKDVLITITLTPKVTCTVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTF
 RSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVE
 WQWNGQPAENYKNTQPIMNTNGSYFVYSKLNQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK

Light chain (25.92 kDa)

MRFQVQVLG~~LLLLWISGAQC~~DVQITQSPSYLAASPGETITINCRASKSINKYLAWYQEKP~~GKTNKLLI~~YSGSTLQSGIPSR
 FSGSGSGTDFTLT~~ISSLEPEDFAMYYCQQHNEYPLTFGAGTKLELKRADAAPT~~VSIFPPSSEQLTSGGASVVCFLNNFY~~PK~~
 DINVKWKIDG~~SERQNGVLNSWTDQDSK~~STYSMSSTLT~~LTKDEYERHNSYTCEATHKTST~~SPIVKSFNRNEC

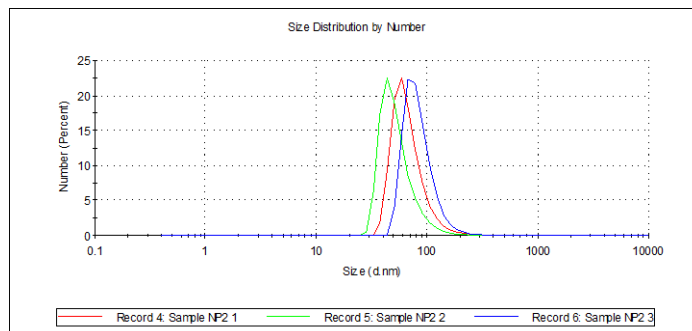
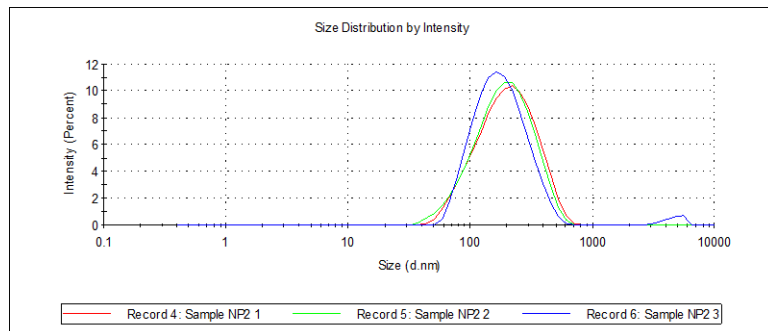
Supplementary Figure S1. Schematic representation and amino acid sequence of the mAbs ANX-M1. The selected peptide sequence for the quantitative LC-MS/MS analysis of ANX-M1 is indicated in green.

F4. TMC-B1R-DS-TPP (mAb + B2R agonist)

Z-ave = 165.6 ± 5.5 nm

PdI = 0.213 ± 0.004

Dh (number mean) = 69.4 ± 15.3 nm

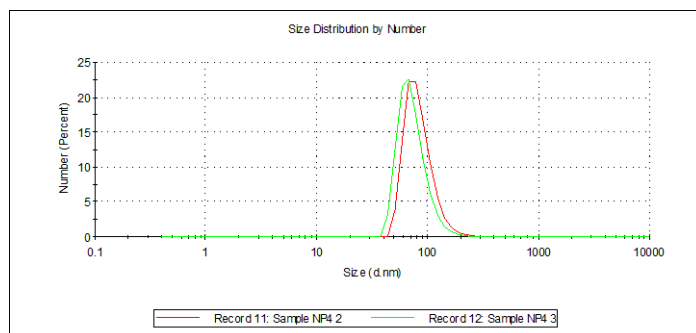
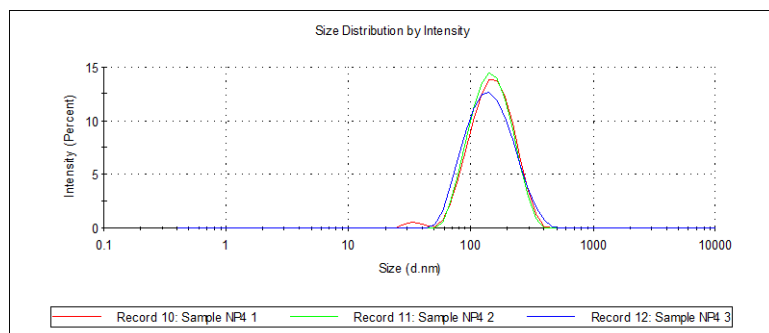


F6. TMC-DS-TPP (mAb + B1R + B2R)

Z-ave = 132.4 ± 2.3 nm

PdI = 0.144 ± 0.006

Dh (number mean) = 79.2 ± 7.3 nm



Supplementary Figure S2. Representative DLS graphs for the nanoformulations F4 and F6.