

Supporting Information for

Increased β -Sheet Dynamics and D-E Loop Repositioning are Necessary for Cu(II)-Induced Amyloid Formation by β -2-Microglobulin

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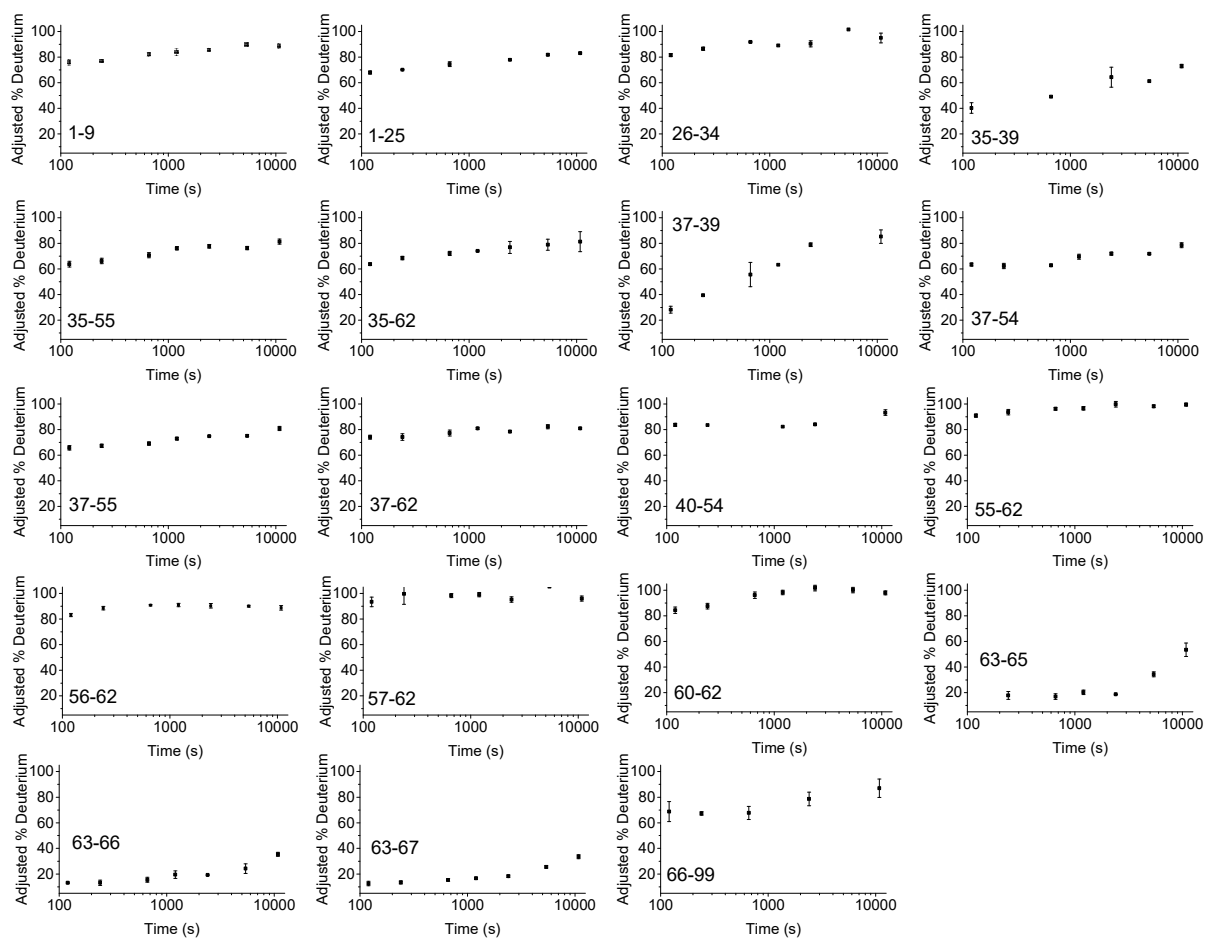


Figure S1: Extent of deuterium incorporation into measured peptide fragments of β 2m after HDX in the absence of metal. The numbers in the bottom left corner of each graph indicate the amino acid sequence numbers of the peptide. The sequence of the protein is indicated below.

1	11	21	31	41	51
IQRTPKIQVY	SRHPAENGKS	NFLNCYVSGF	HPSDIEVDLL	KNGERIEKVE	HSDLSEFSKDW
61	71	81	91		
SFYLLYYTEF	TPTEKDEYAC	RVNHVTLSPQ	KIVKWDRDM		

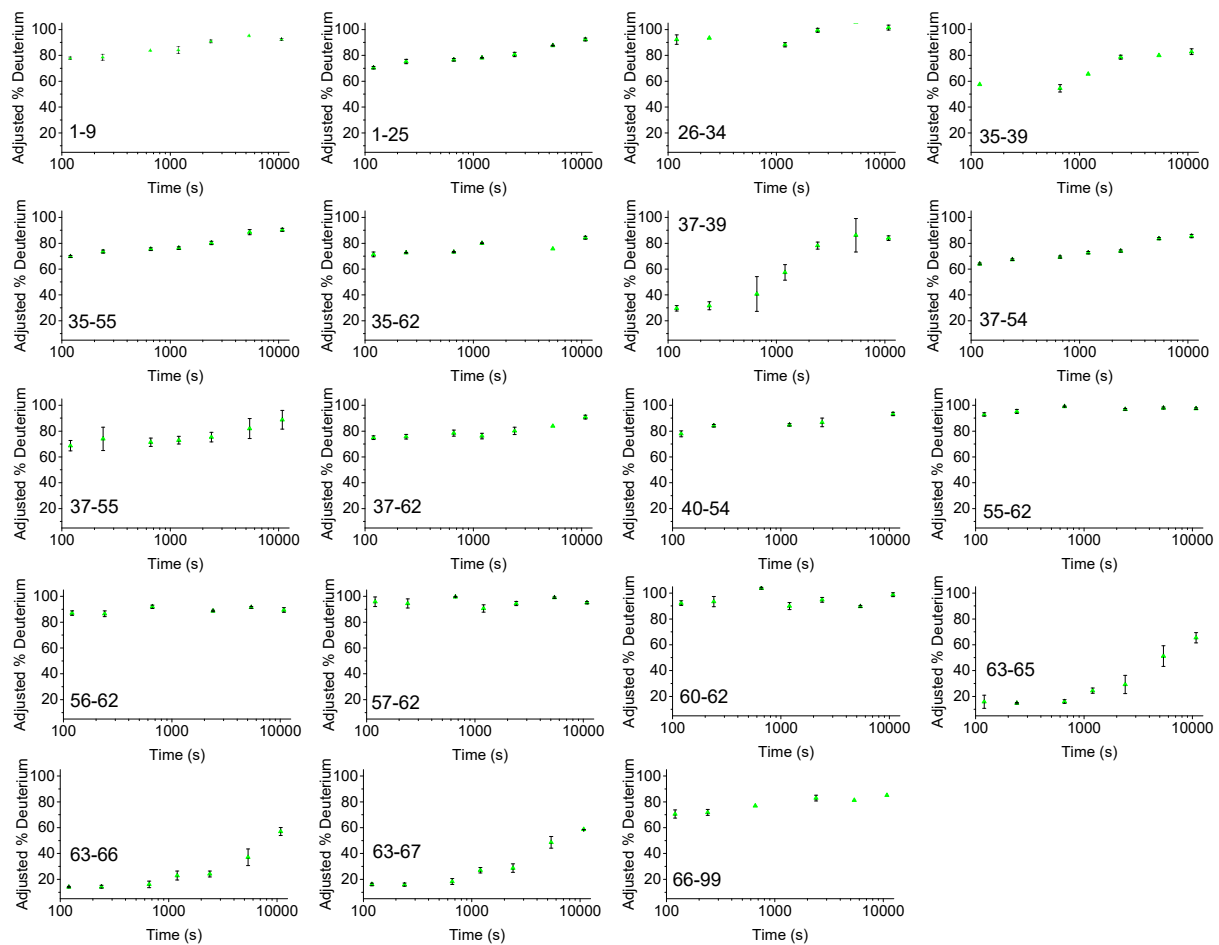


Figure S2: Extent of deuterium incorporation into measured peptide fragments of $\beta 2m$ after HDX in the presence of Cu(II). The numbers in the bottom left corner of each graph indicate the amino acid sequence numbers of the peptide.

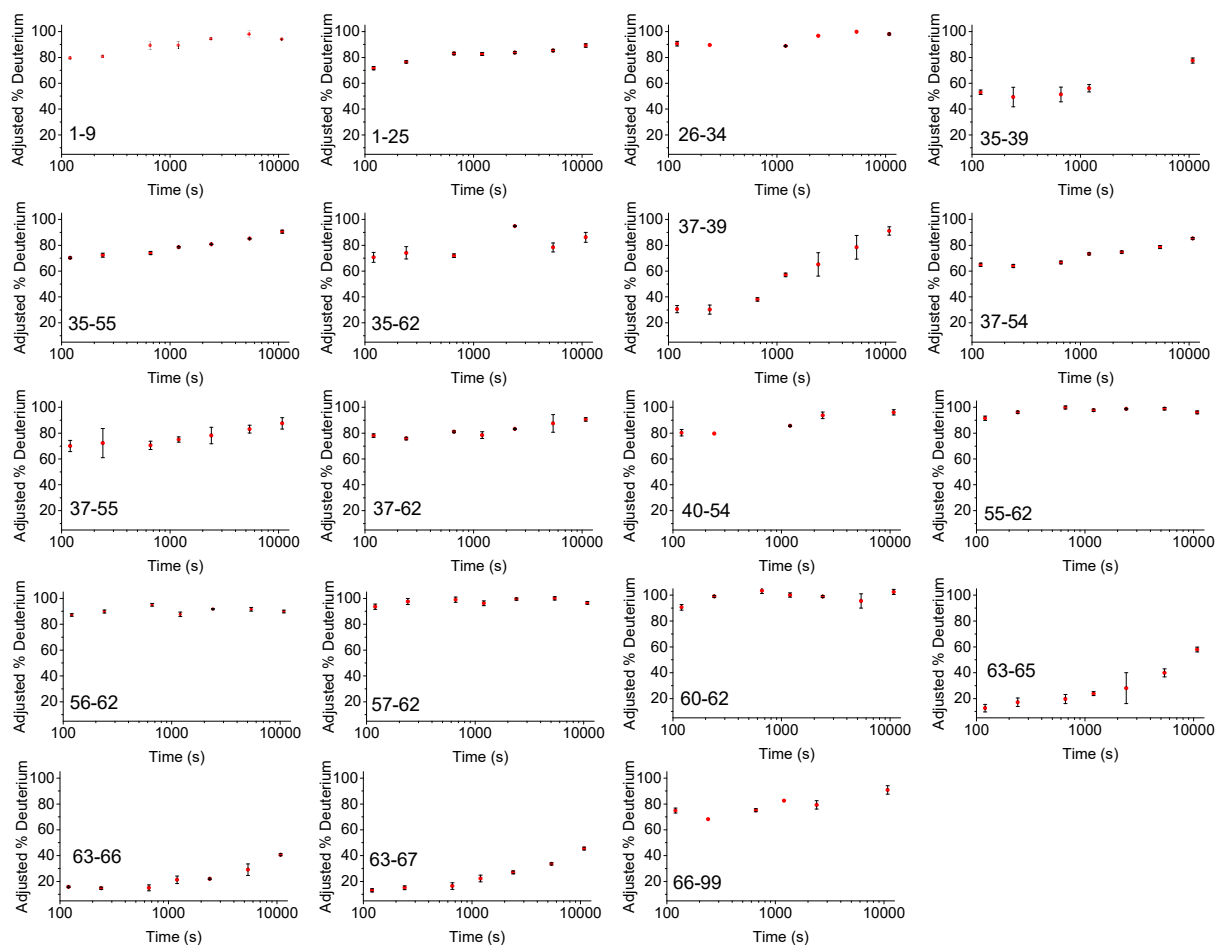


Figure S3: Extent of deuterium incorporation into measured peptide fragments of $\beta 2m$ after HDX in the presence of Ni(II). The numbers in the bottom left corner of each graph indicate the amino acid sequence numbers of the peptide.

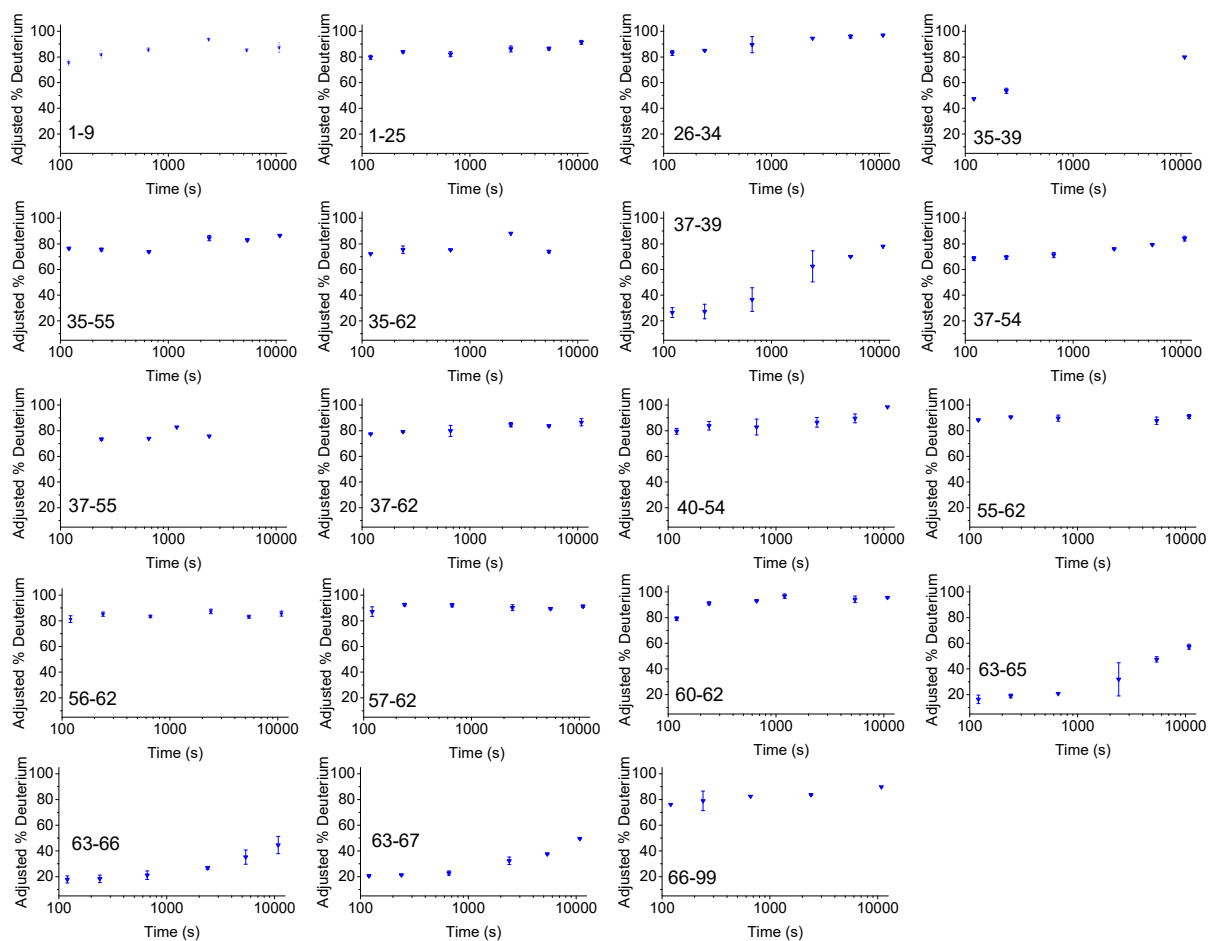


Figure S4: Extent of deuterium incorporation into measured peptide fragments of $\beta 2m$ after HDX in the presence of Zn(II). The numbers in the bottom left corner of each graph indicate the amino acid sequence numbers of the peptide.

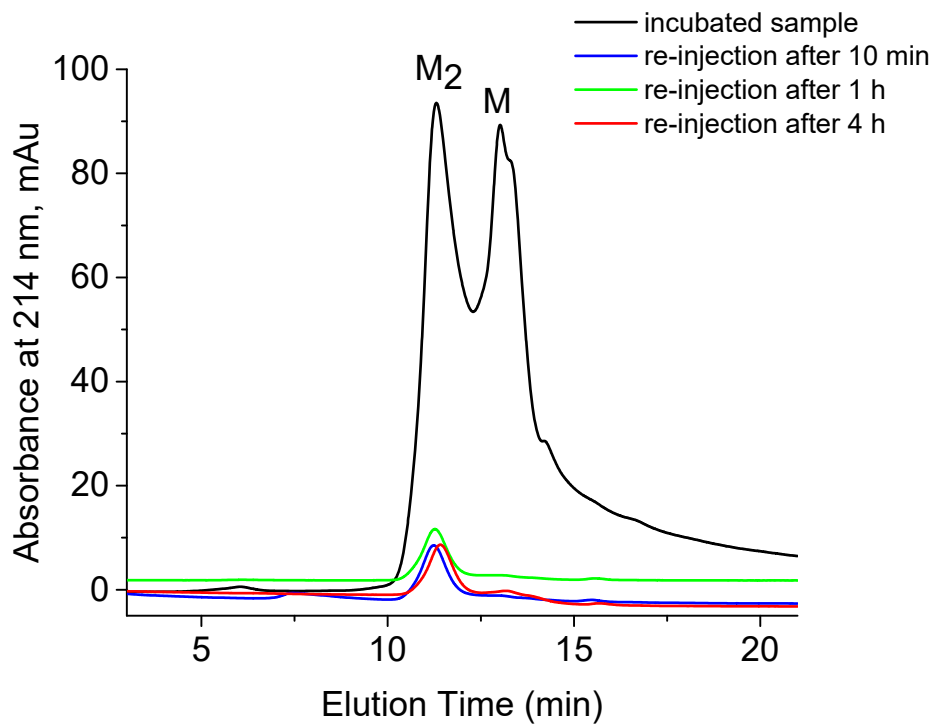


Figure S5: Size-exclusion chromatogram of $\beta 2m$ sample incubated for 3 days (black). A 300 μ L fraction of the dimer (M_2) was collected and then re-injected into the SEC column 10 min (blue), 1 h (green), and 4 h (red) later. In all cases, the sample elutes at the same time as the original dimer, indicating that the dimer does not dissociate measurably for up to 4 h.

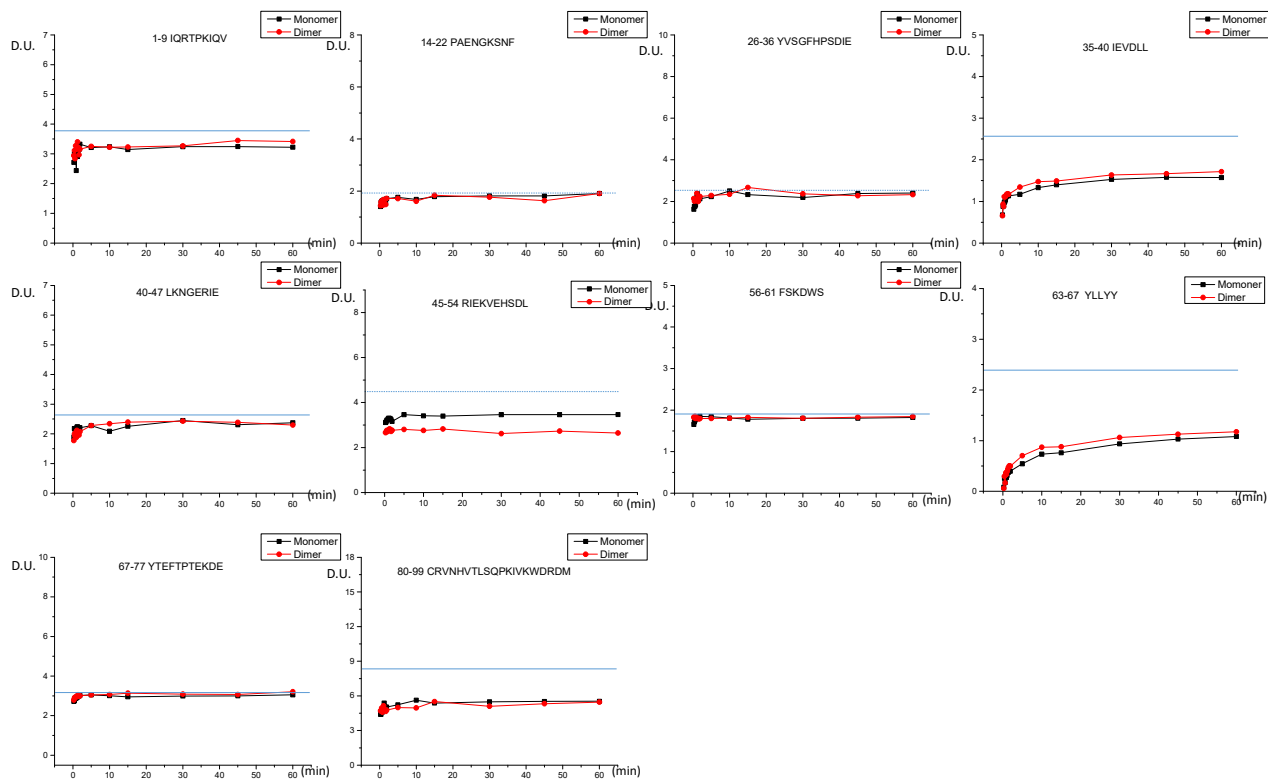


Figure S6: Extent of deuterium incorporation into measured peptide fragments after HDX of monomer (black) and dimer (red) protein fractions collected from SEC separation of $\beta 2m$ incubated in the presence of $Zn(II)$.