SUPPORTING INFORMATION

Structural Characterization of Native Proteins and Protein Complexes by Electron Ionization Dissociation-Mass Spectrometry

Huilin Li,[†*] Yuewei Sheng,[#] William McGee,[‡] Michael Cammarata,[‡] Dustin Holden,[‡] and Joseph A. Loo[†#*]

[†]Department of Biological Chemistry, David Geffen School of Medicine, University of California, Los Angeles, CA, 90095, United States

[#]Department of Chemistry and Biochemistry, UCLA/DOE Institute of Genomics and Proteomics, and UCLA Molecular Biology Institute, University of California, Los Angeles, CA, 90095, United States

[‡]Department of Chemistry, The University of Texas at Austin, Austin, Texas 78712, United States

Corresponding Authors

*E-mail: lihuilin@gmail.com

*E-mail: JLoo@chem.ucla.edu

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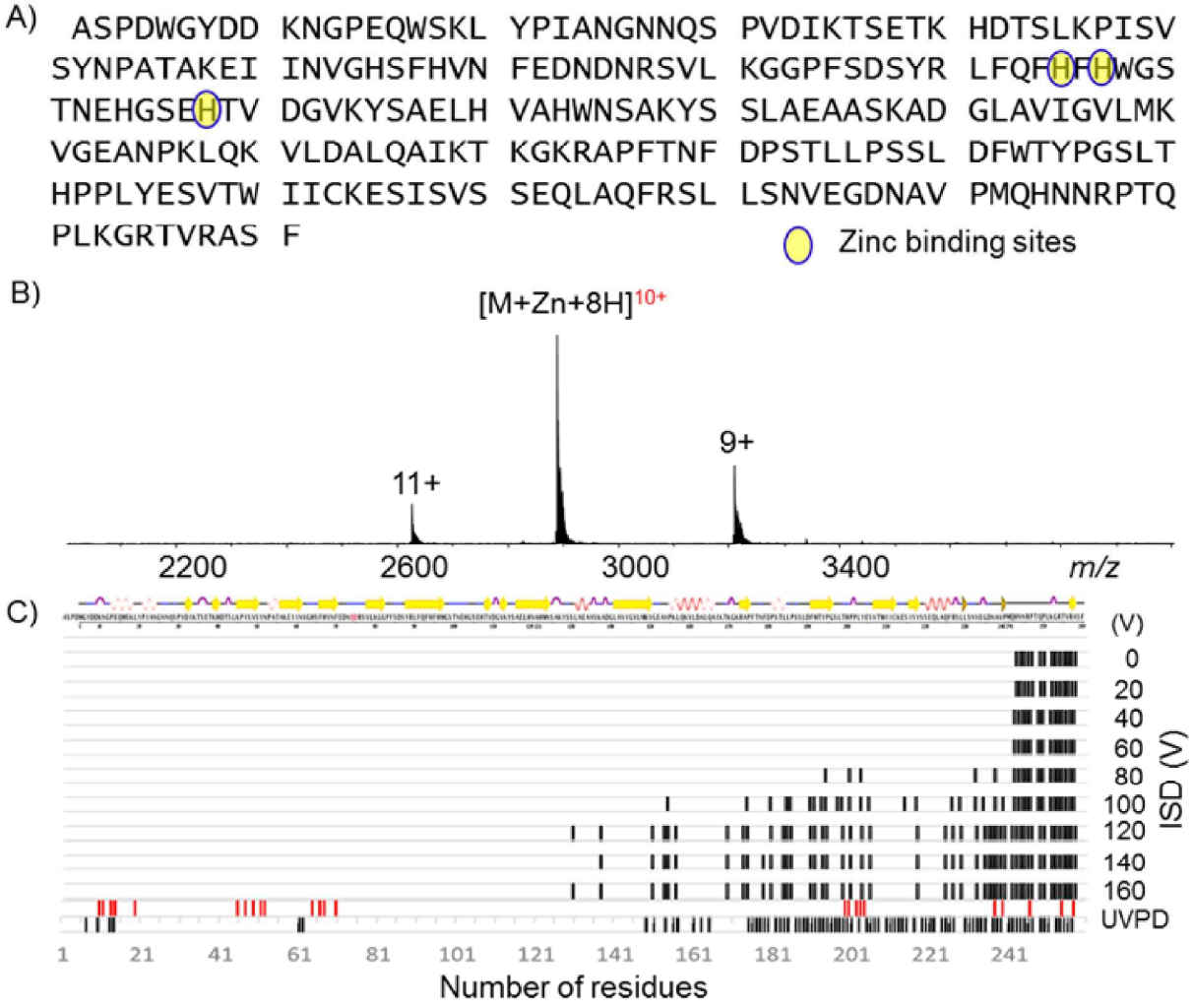

Figure S-1. (A) Sequence of HCA-1. (B) Full ESI mass spectrum of HCA-1. (C) Plot of backbone cleavage sites of HCA-I with different dissociation conditions; the plots for ISD-EID are shown at the top and the plot for UVPD shown at the bottom. Black bars show ions from the C-terminal region (x, y, and z) and red bars represent ions from the N-terminal region (a, b, and c).

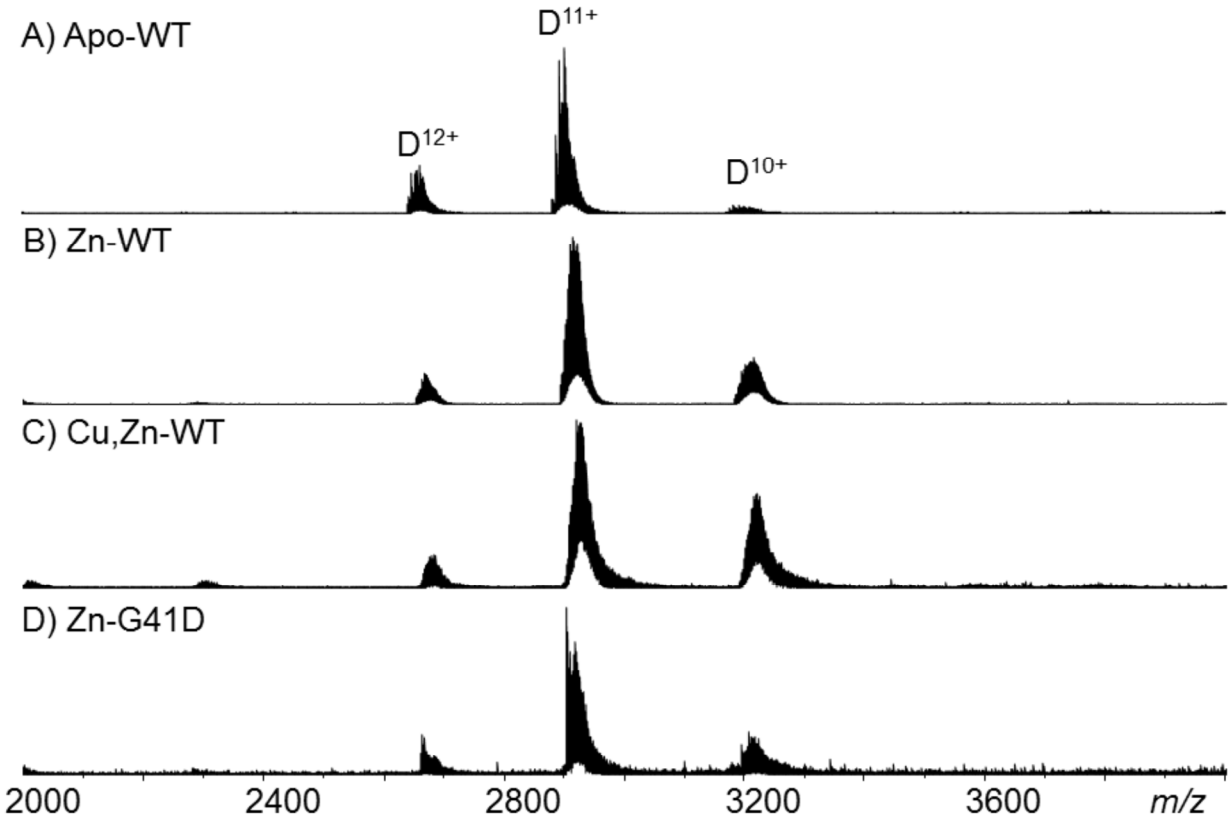

Figure S-2. Full ESI mass spectra of SOD1 dimers. (A) apo-WT, (B) Zn-WT, (C) Cu,Zn-WT, and (D) Zn-G41D.

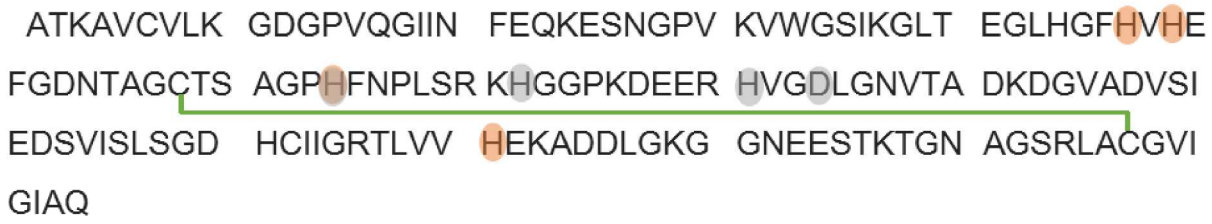

Figure S-3. Sequence of human SOD1. Copper-binding sites are indicated in orange, zinc-binding sites are in grey, and the disulfide bond is in green.

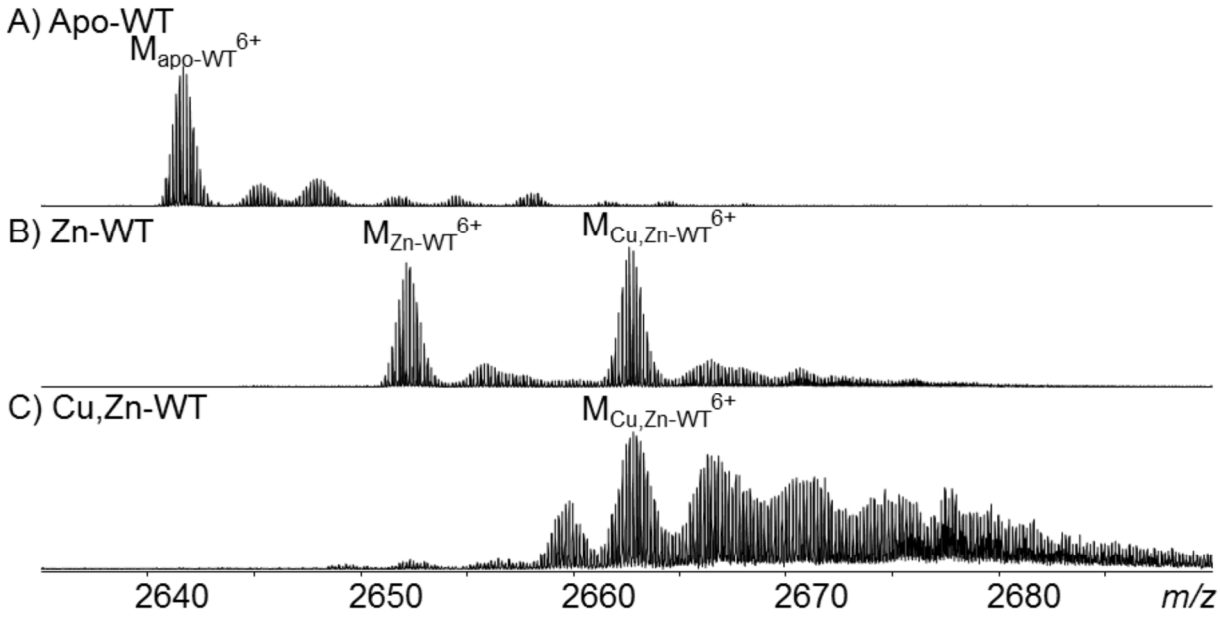

Figure S-4. The metal-binding states of SOD1s; (A) apo-WT, (B) Zn-WT, and (C) Cu,Zn-WT. M represents SOD1 monomer. ISD was applied to remove salt adducts and to dissociate dimers into monomers for a clearer view of the metal-binding states.

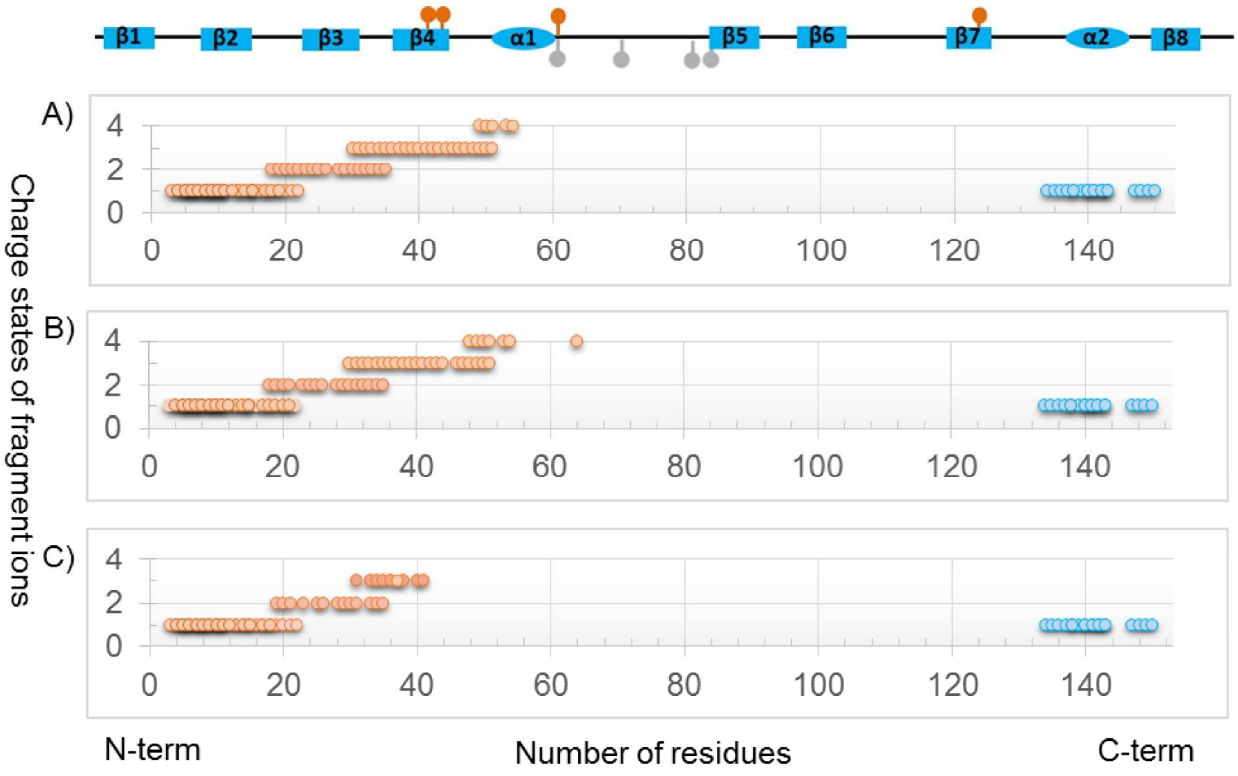

Figure S-5. Plot of backbone cleavage sites with respect to the charge states of fragment ions for different forms of WT-SOD1 dimer: (A) apo-WT, (B) Zn-WT, and (C) Cu/Zn-WT. The fragment ions from the N-terminal region are labelled in orange dots and the fragments from the C-terminal region are in cyan dots.

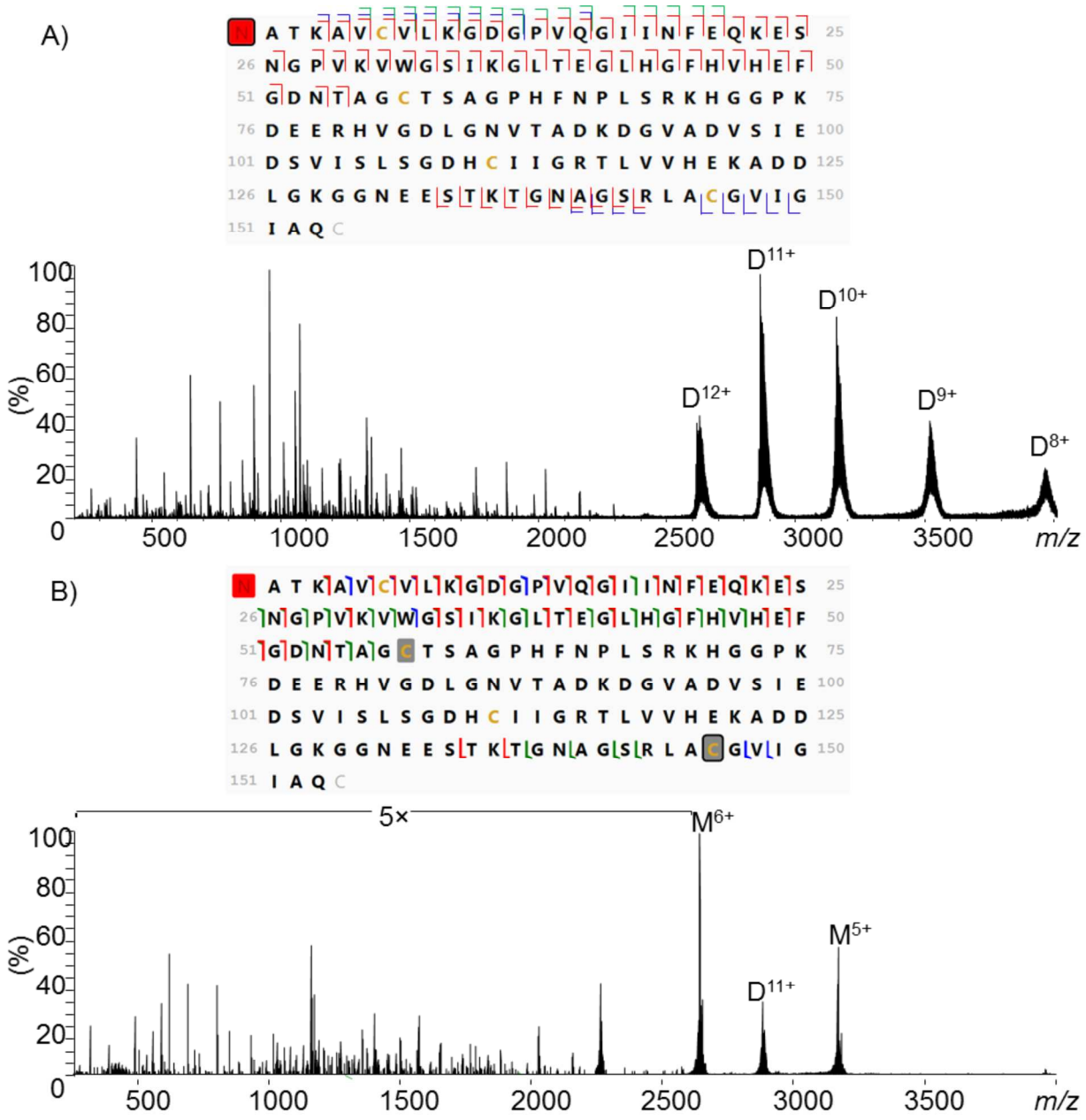

Figure S-6. (A) EID spectrum of apo-WT SOD1 dimer with the backbone cleavage map shown at the top. (B) UVPD spectrum of apo-WT SOD1 dimer with the backbone cleavage map shown at the top. The c/z-type ions are in red, b/y-type ions in blue, and a/x-type ions in green.