

**Ben Neely, PhD**  
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Dr. Benjamin Neely is a research chemist with the National Institute of Standards and Technology in Charleston, SC (NIST-Charleston). His diverse background includes microbiology, wildlife disease, cancer biology, biomarker discovery and validation (protein and glycan) and bioinformatics. He leads the Comparative Mammalian Proteome Aggregator Resource (CoMPARe) Program, generating standardized proteomic data across non-model species. Although non-human, much of his mammalian serum/plasma work, from method development to data analysis, borrows from and advances human proteomic techniques. For instance, improved proteomic analysis of undepleted cheetah serum is directly applicable to analysis of undepleted human serum. He also works with stakeholders to optimize and standardize methods for data-independent acquisition and metaproteomic analysis, with the overarching goal of accelerating research capabilities and supporting commerce by advancing and harmonizing measurement science.

Specific to his interest of serving on the US HUPO Board, Ben is enthusiastic about strengthening, engaging, and growing the US (and global) proteomics community, and the size, scope, and support of US HUPO aligns perfectly with these goals. He is already serving various roles with US HUPO such as co-organizing the 2022 conference in Charleston, currently chairing the VMO, and co-hosting a soon to be released US HUPO-sponsored podcast series promoting the 2023 Chicago meeting.