

# Structural Characterization to Identify and Resolve Aggregation in Protein Therapeutics

**Don't let aggregation ruin your discovery efforts!**

Protein structure, vs. sequence alone, is critical for understanding aggregation. Don't leave discovery and early development phase without investigating structural vulnerabilities of your candidate biologic.

**Catch aggregation while you can still resolve it**

Use Immuto's groundbreaking structural characterization platform to get actionable data on problematic residues – then fix the issue and save the day!

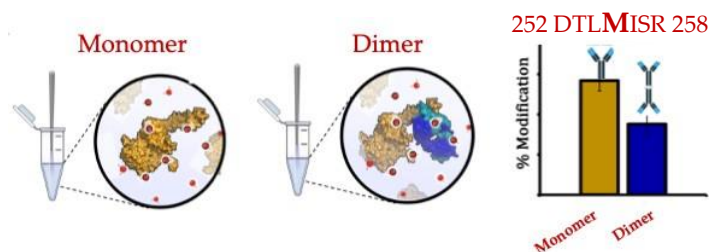
**Our proprietary approach gives guaranteed results**

Immuto has developed a mass spec-based Hydroxyl Radical Footprinting (HRF) approach for characterization of protein aggregates.

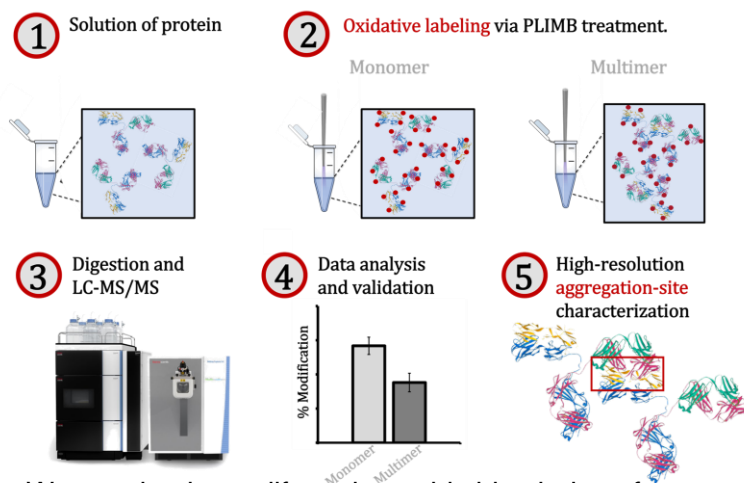
**How do we compare with other techniques?**

Technique	Cost	Resolution	Throughput
CryoEM	\$\$\$	High	Low
CD / SAXS	\$	Low	High
HRF	\$\$	High	High

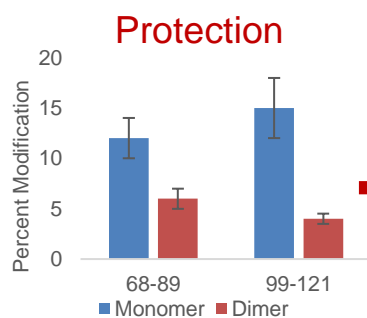
**What do the data look like?**



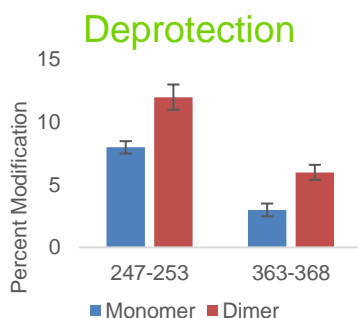
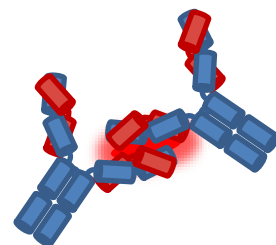
**Our Workflow – Novel, Yet Familiar**



We covalently modify amino acid side chains of proteins (1,2), enzymatically digest the sample (3), and analyze according to well established proteomic mass-spec techniques (4,5).



**Ab/Ab interactions**



**Unfolding**

