

Visualizing Protein Residue Chemical Modifications

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Summary:

A key goal in the analysis of proteomic data is to identify and compare the frequency and types of chemical modifications occurring on different residues in a protein sequence. Depicting these data in an uncluttered but informative way is a significant challenge in visualizing these data. For this year's Bio+MedVis Protein Beasts Challenge, we propose a redesign of the existing visualization that reduces visual clutter and facilitates identification and comparison of modifications per site in a given protein. Our design consists of three linked views that facilitate the identification of sites with high modification diversity and which break down the frequency of each type of modification for each residue site in a protein sequence. Highlight and view subset interactions manage visual complexity and focus user attention.