Motivation: Sequence diagrams (SD) are a common way to visualize the amino acid sequence of proteins [1]. Additional rows in the SD can show attributes per amino acid like B-factor, hydrophobicity, binding sites, or secondary structure (typically by color-coding). SDs are often rendered only as static images.

Contribution: We present an interactive web-based SD that was implemented using the JavaScript library D3 [2]. Our enhanced SD visualizes not only the attributes stored in the RCSB Protein Data Bank [3], but also information provided by external analysis tools, such as the predicted intrinsic disorder by IUPred [4]. Furthermore, we enhanced the basic idea of SDs by adding per-atom information instead of showing only per-amino-acid attributes.

Outlook: Our prototypical visualization application is still work in progress, therefore, there are plenty of options for future work:

- Integrate more attributes to support a wider range of analysis tasks
- Explore additional visualizations to show more detailed information
- Display which residues are bonded or in contact to residues of another chain (e.g., hydrogen bonds or disulfide bridges)
- Link our interactive SD to a 3D molecular structure viewer such as Mol* [5]
- Comparative visualization of proteins using a multi-sequence alignment [6]
- Improve the user interface of our current prototype
- Evaluate our proposed per-atom visualization concepts with domain experts

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References: