Feature Viewer in UniProt: Visualizing protein sequence features and variants

The challenge
As biological data continues to grow at exponential rates, visualization and integration become necessary to interpret data. Co-localization of features can have important biological significance (e.g., variants at the positions of active sites changing enzyme function) and these patterns can be difficult to spot in raw data.

Feature Viewer in UniProt
A new visual approach by UniProt presents protein sequence features using a highly interactive BioJS component. The viewer presents features like domains, sites, PTMs and variants from multiple sources in one compact view.

Expandable feature tracks
Features are organized in categorized tracks which are collapsed by default to provide an overview. Expanding the tracks displays the constituent feature types within.

Integrating data sources
The Variants track shows UniProt annotated variants as well as variants from large scale genomics studies like COSMIC, ExAC, ESP and 1000 Genomes.

Protein seq feature REST services
UniProt provides sequence feature data services to accompany the UniProt Feature Viewer. The services support three data formats, JSON, XML and GFF. http://www.ebi.ac.uk/uniprot/services/docs/index.html.