

# ProtVista

Open-Source Protein Feature Visualisation with  
reusable Web Components

Aurélien Luciani



[www.uniprot.org](http://www.uniprot.org)



# UniProt

A comprehensive, high-quality and publicly accessible resource of protein sequence and functional information

It includes, among other things:

- Physiological protein function including subcellular location, pathways, reactions, interactions and involvement in disease
- Sequence annotation of domains, PTMs, mutations, disease variants and much more



European Bioinformatics Institute (EMBL-EBI),  
Hinxton, Cambridge, UK

Protein Information Resource (PIR),  
Washington DC and Delaware, USA

SIB Swiss Institute of Bioinformatics (SIB),  
Geneva, Switzerland

UniProt BLAST Align Peptide search ID mapping SPARQL Release 2026\_01 | Statistics Help

## Find your protein

UniProtKB  Advanced | List Search

Examples: Insulin, APP, Human, P05067, organism\_id:9606

UniProt is the world's leading high-quality, comprehensive and freely accessible resource of protein sequence and functional information. [Cite UniProt](#)

⚠ Our Proteomes and UniProtKB/TrEMBL resources are undergoing a significant transition. Please read our [help page](#), view [affected entries](#) and [proteomes](#), or contact us with any questions.

Proteins  
UniProt Knowledgebase

Reviewed  
(Swiss-Prot)  
211,477

Unreviewed  
(TrEMBL)  
2102,556,313

Species  
Proteomes

Protein sets for species with sequenced genomes from across the tree of life

Protein Clusters  
UniRef

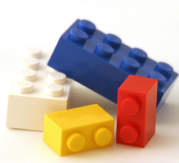
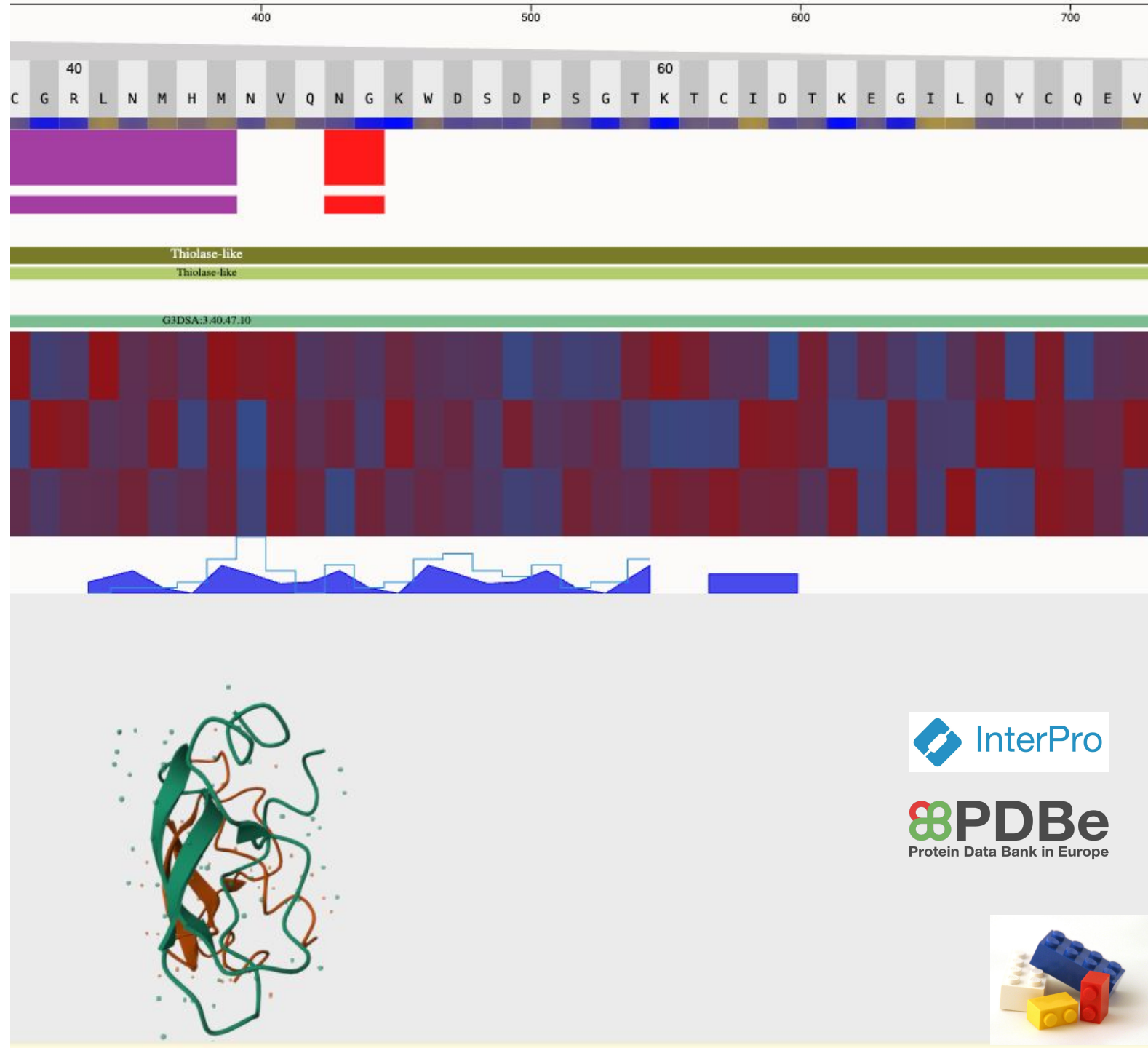
Clusters of protein sequences at 100%, 90% and 50% identity

Sequence archive  
UniParc

Non-redundant archive of publicly available protein sequences seen across different databases

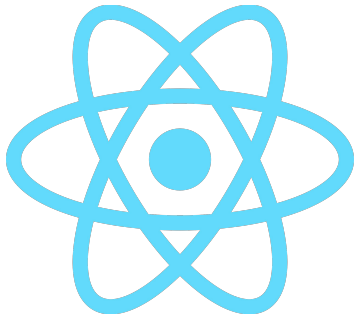
# Nightingale

- An **open-source** visualization library of **standard web components**
- Designed for representing protein-related data
- Composable** architecture facilitates vertical stacking of tracks, aiding visual comparison across datasets
- Interoperable** with other standard components, regardless of the underlying framework
- Compatible** with any component following the **Nightingale APIs**



# Building using the standards: Web Components

- Combination of standard APIs: **Custom elements** + **Shadow DOM** + **HTML templates**
- Not dependent** on any framework



React  
and related



Angular



Vue.js

...



Vanilla JS

- Limited** library dependencies
- Set of components, as **independent packages** under the `@nightingale-elements` scope on NPM

# Same blocks, different



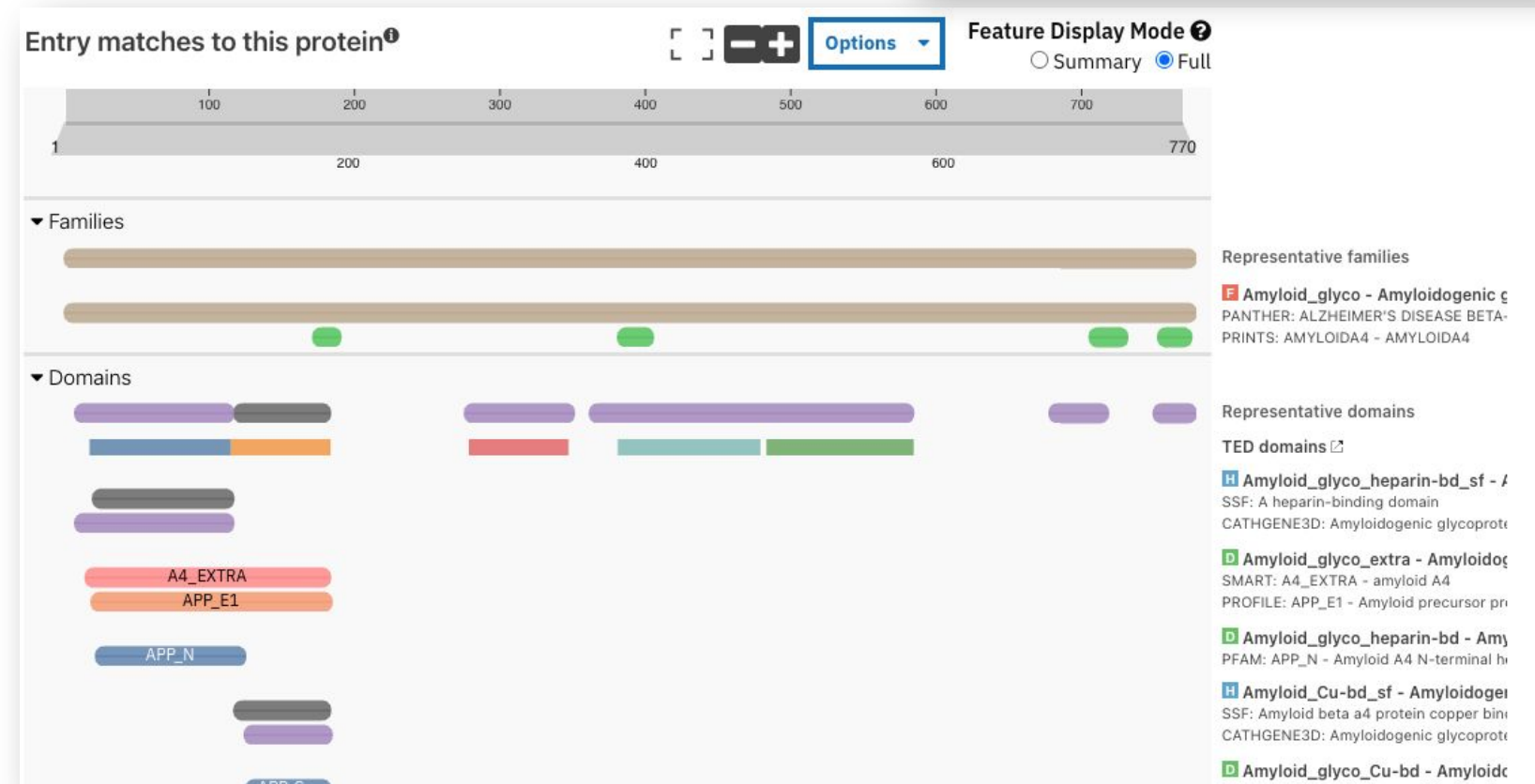
Visualization showing family and domains in UniProt's entry page of [P05067](#) using minimal number of tracks as needed



InterPro's protein viewer using Nightingale components for [P05067](#)



PDBe is an other user of Nightingale components

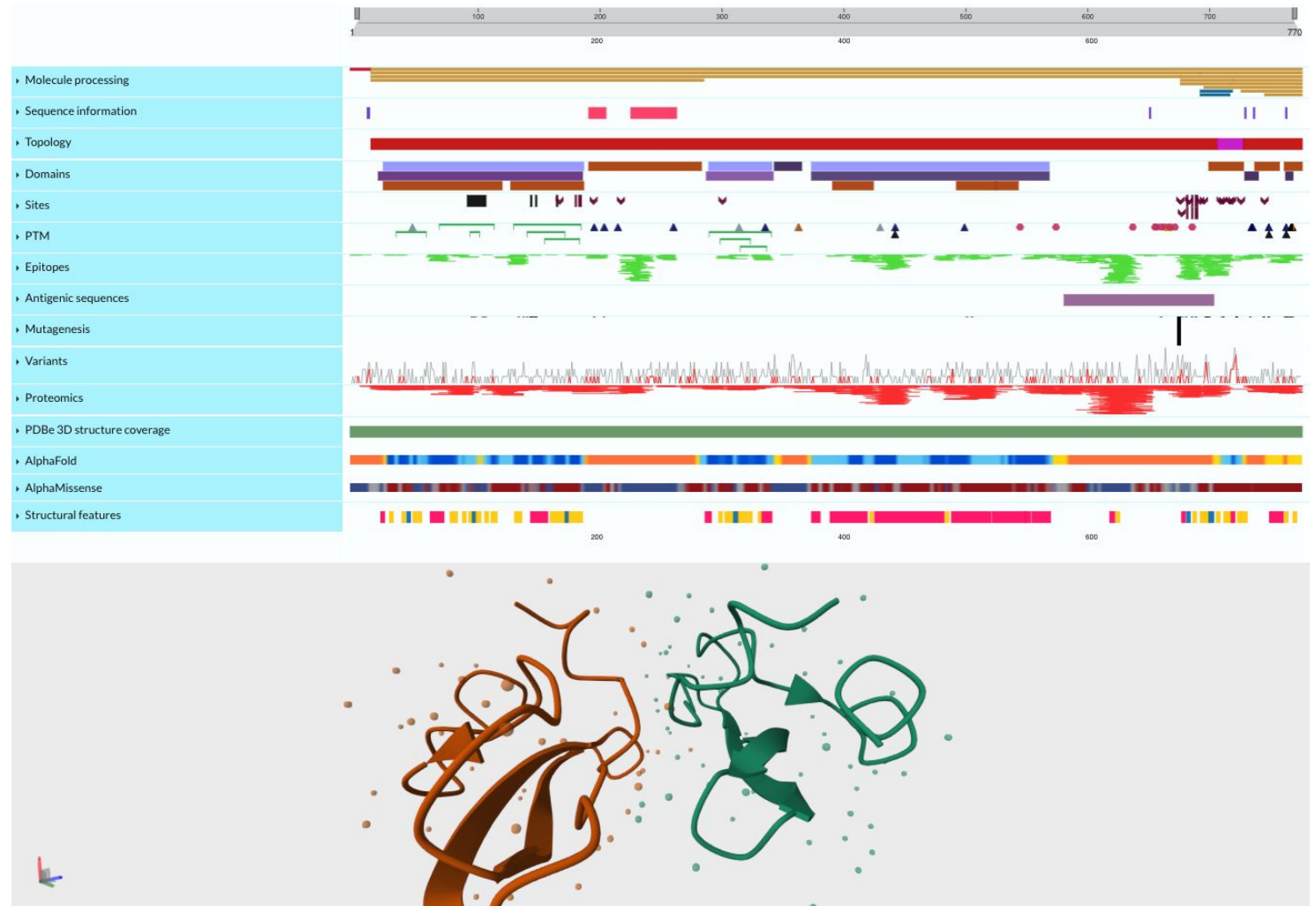




# UniProt's ProtVista visualization

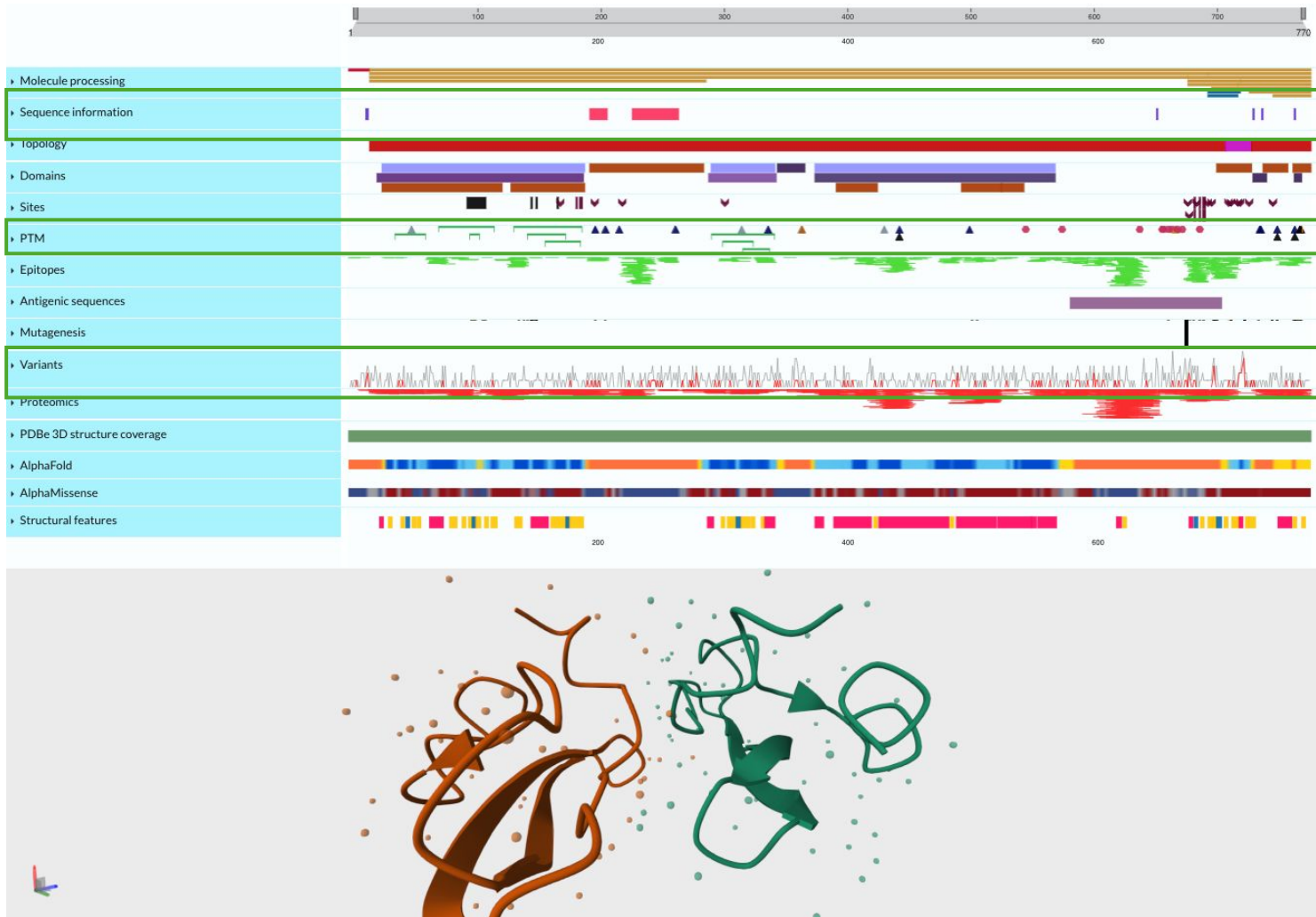


- **Turnkey** combination of tracks
- **Chooses** and aligns various tracks to best fit our needs
- Uses **different components** of Nightingale
- Uses UniProt's **data source**
- **Customizes** tooltips as needed
- Is itself a **Web Component**



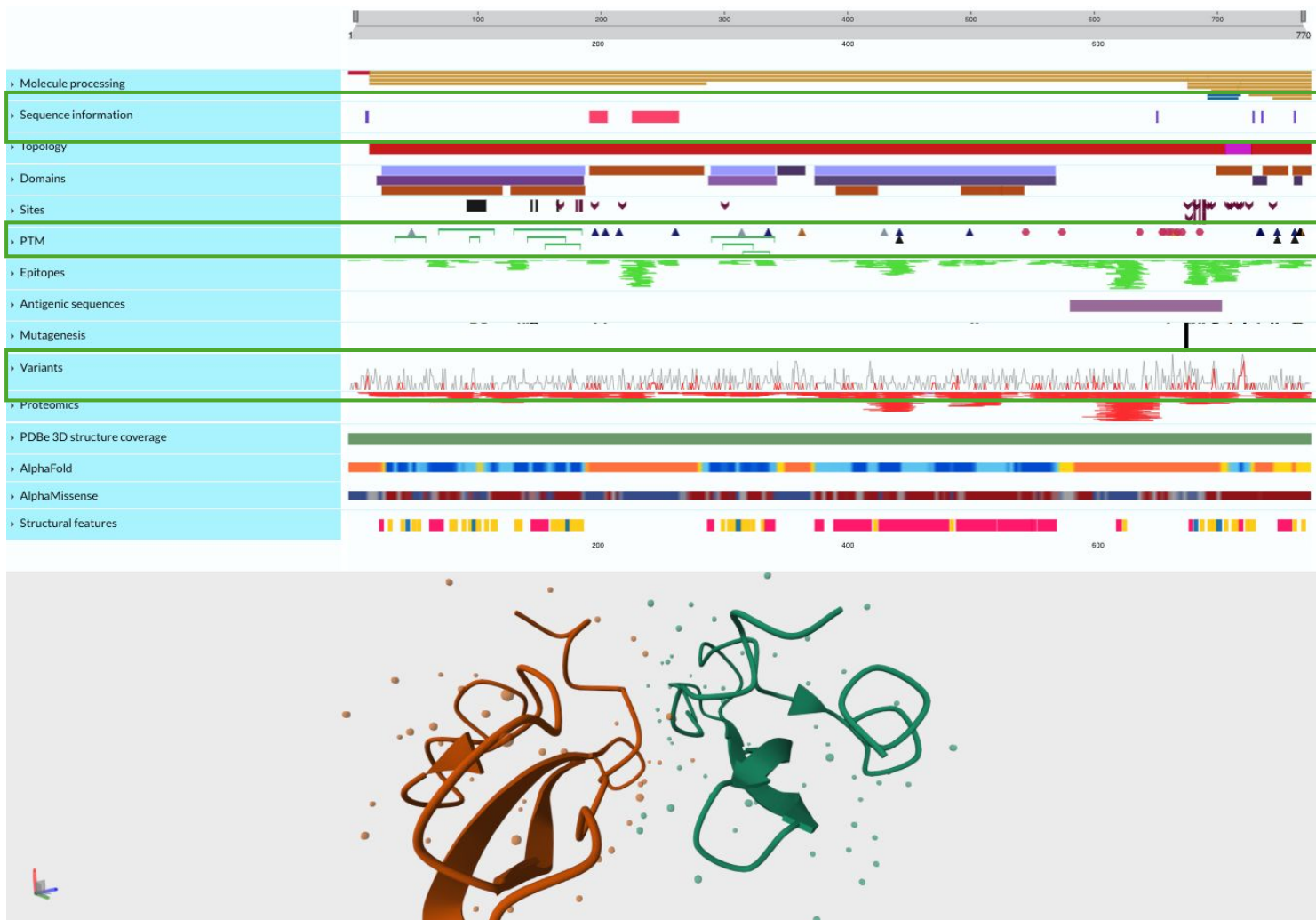
*Human Amyloid-beta precursor protein in UniProt's ProtVista visualization*

The viewer is composed of tracks – the fundamental building blocks.



*Human Amyloid-beta precursor protein in UniProt's ProtVista visualization*





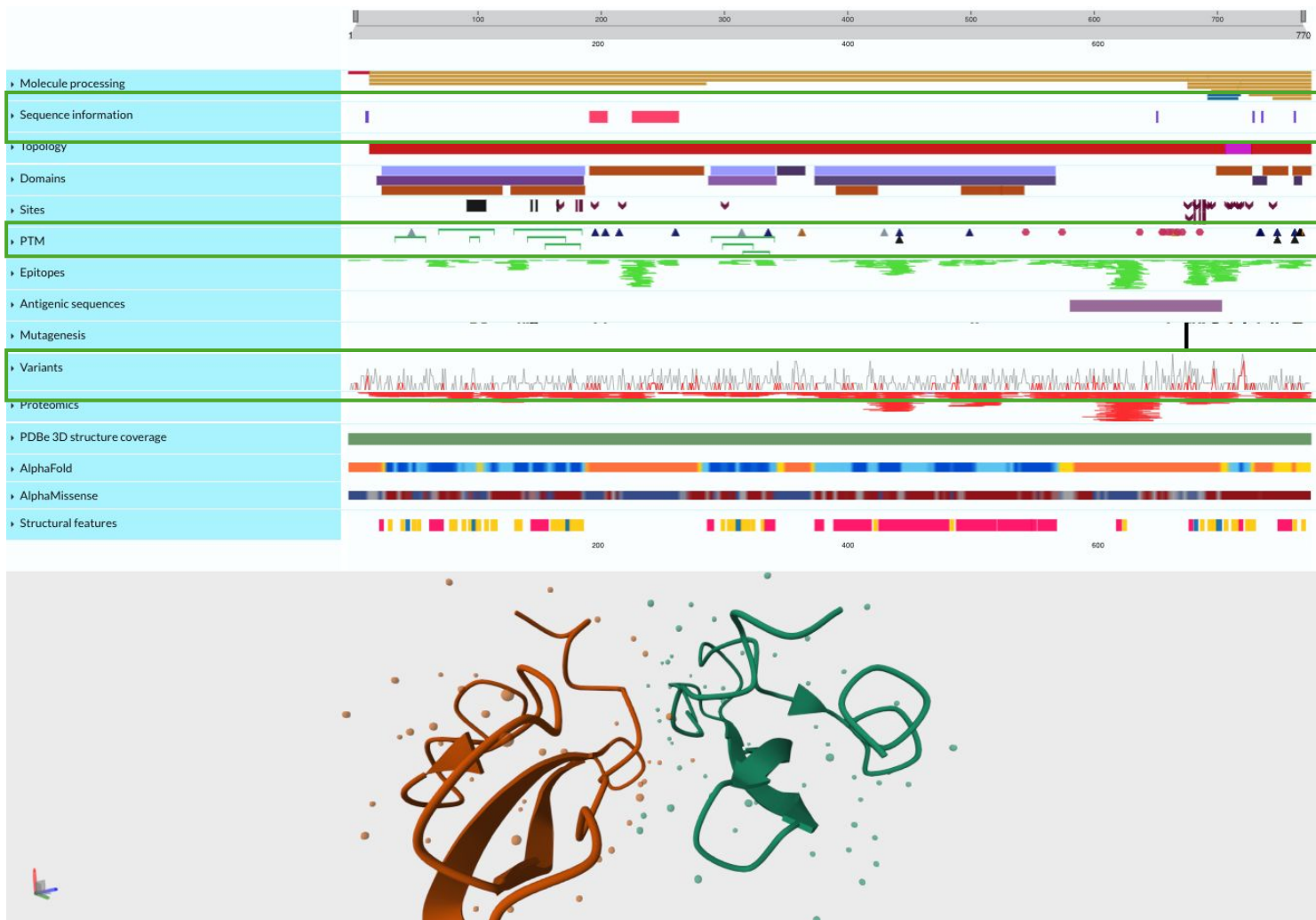
Human Amyloid-beta precursor protein in UniProt's ProtVista visualization

The viewer is composed of tracks – the fundamental building blocks.

Each track can be used individually or combined as shown here







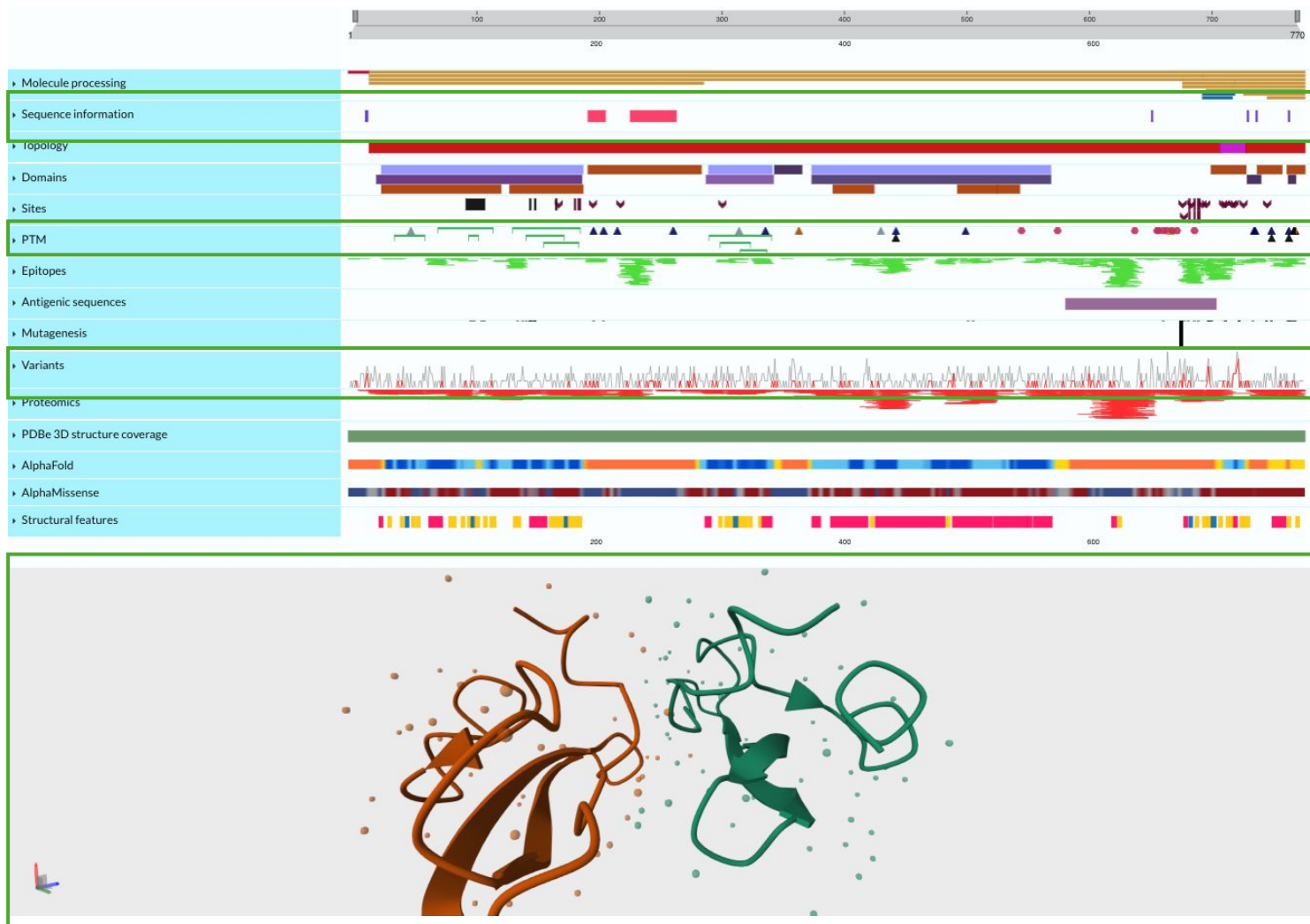
Human Amyloid-beta precursor protein in UniProt's ProtVista visualization

The viewer is composed of tracks – the fundamental building blocks.

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ProtVista fetches all the data and each track is responsible for representing its own data.





Human Amyloid-beta precursor protein in UniProt's ProtVista visualization

The viewer is composed of tracks – the fundamental building blocks.

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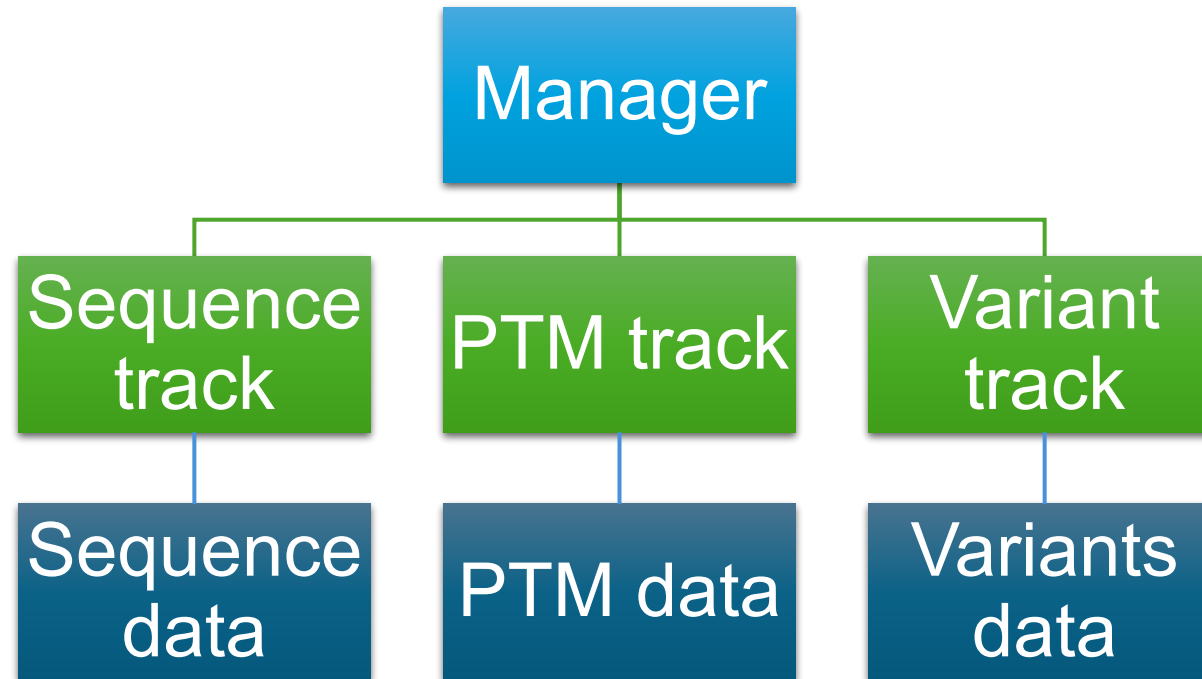
ProtVista fetches all the data and each track is responsible for representing its own data.

The structure viewer is also treated as a track that render data in 3D context



# Architecture

The manager serves as a container for all the tracks, handling events from its descendants and ensuring **synchronized** behavior across tracks.



User clicks on a variant in the Variant track



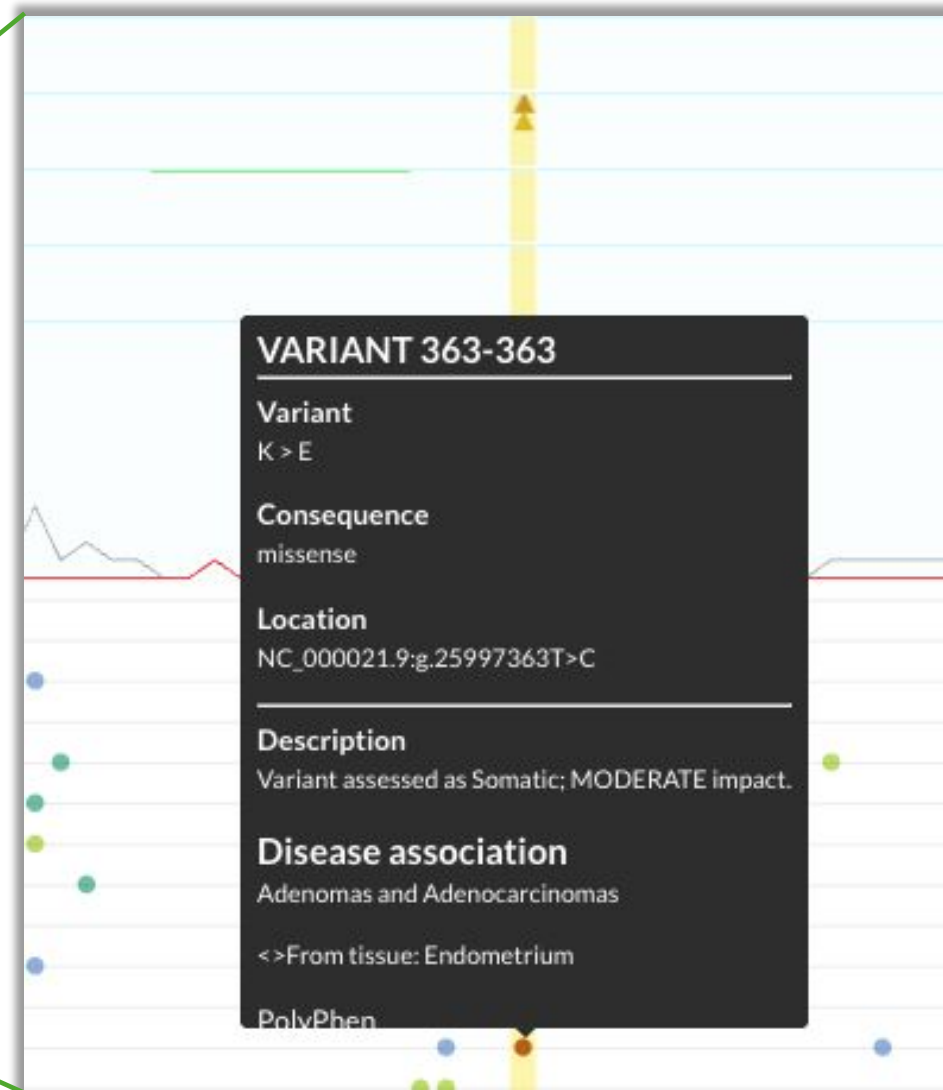
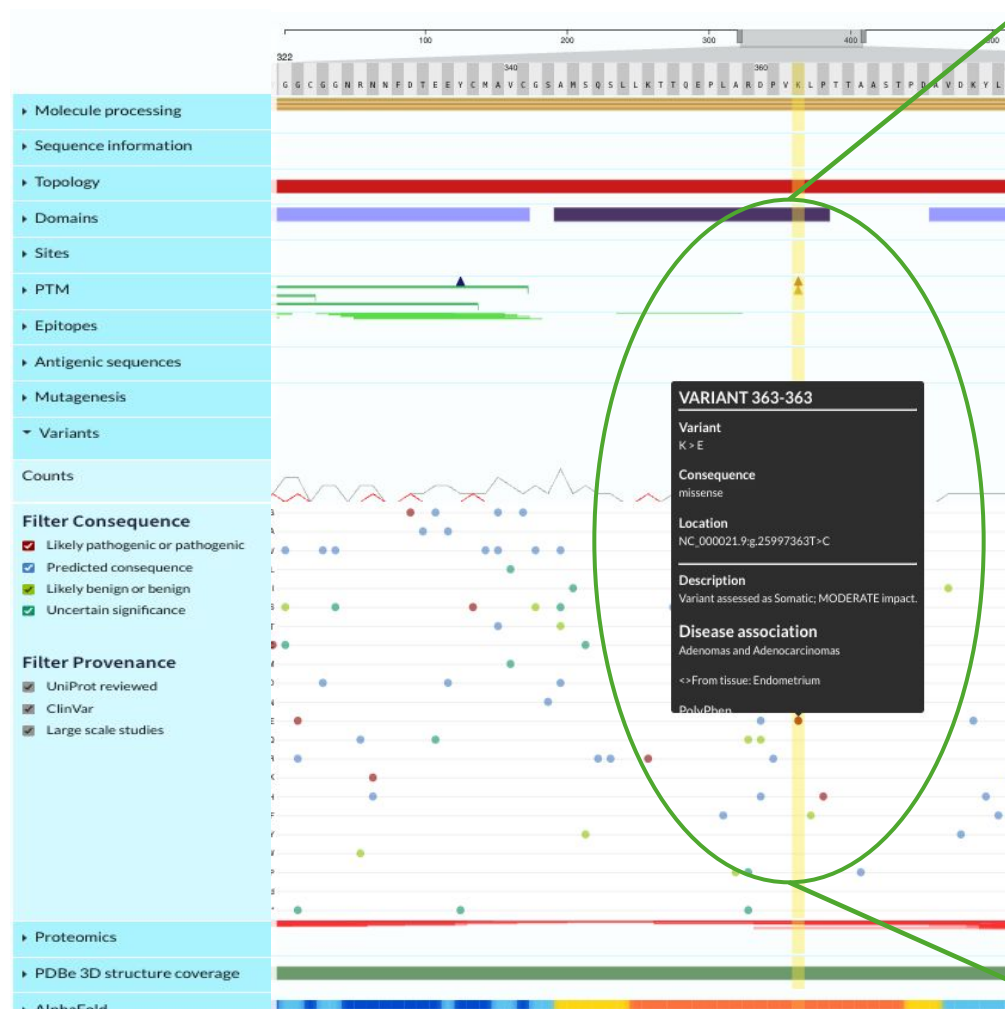
Track emits a 'highlight' event with the selected coordinates



The manager detects the event



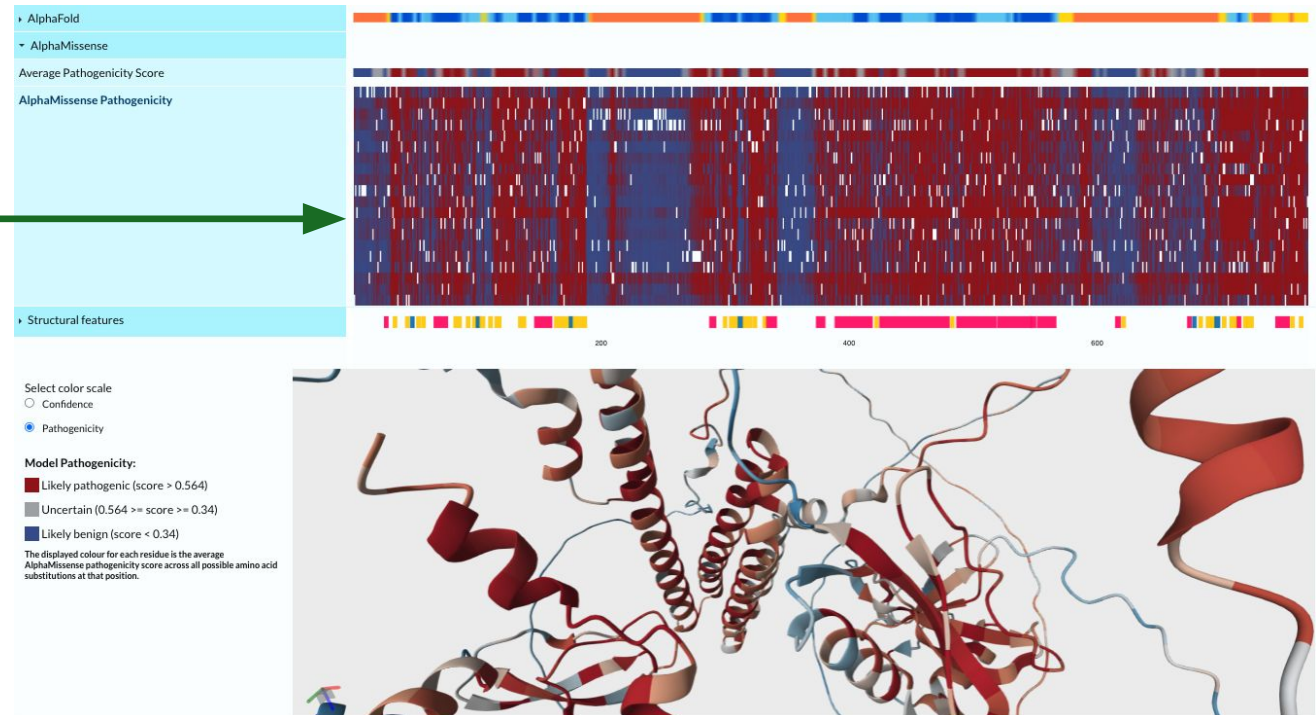
The manager sets the value to all the other tracks' highlight attribute



# Under the hood

- **Lit** - for building reusable Web Components
- **D3.js** - for data-driven rendering via SVG and Canvas
- **HTML5 Canvas** – leveraged for high performance rendering in heavily used tracks
- **SVG overlay** – enables interactivity on top of Canvas for minimal performance impact

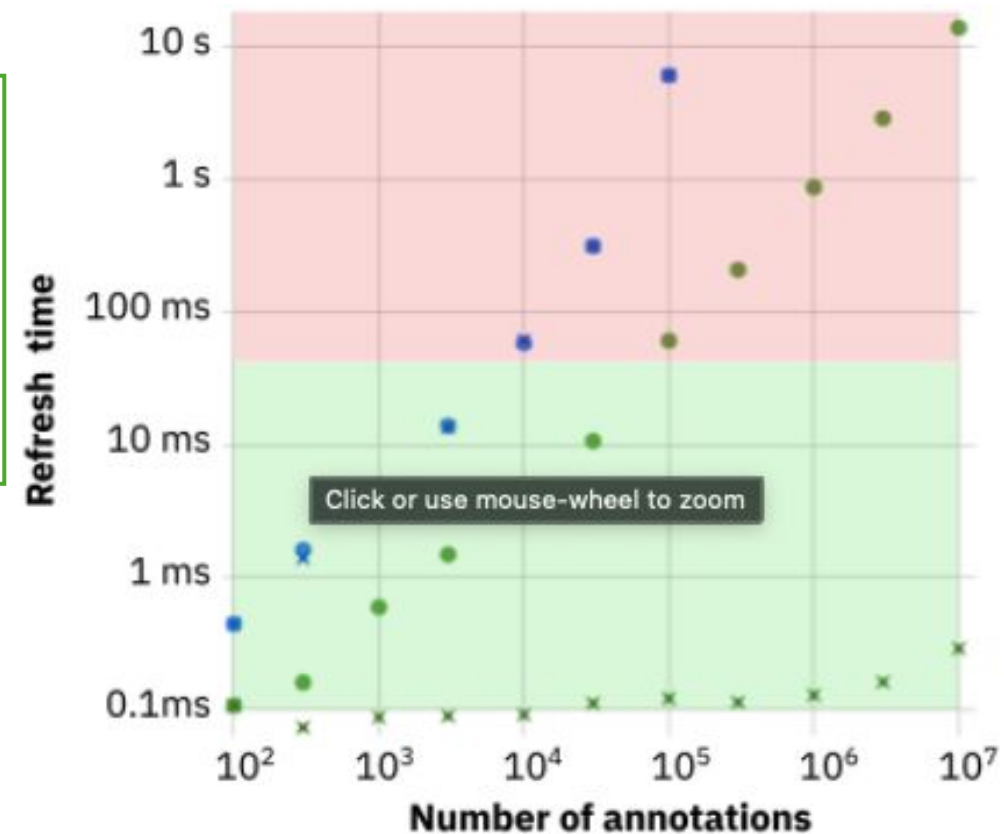
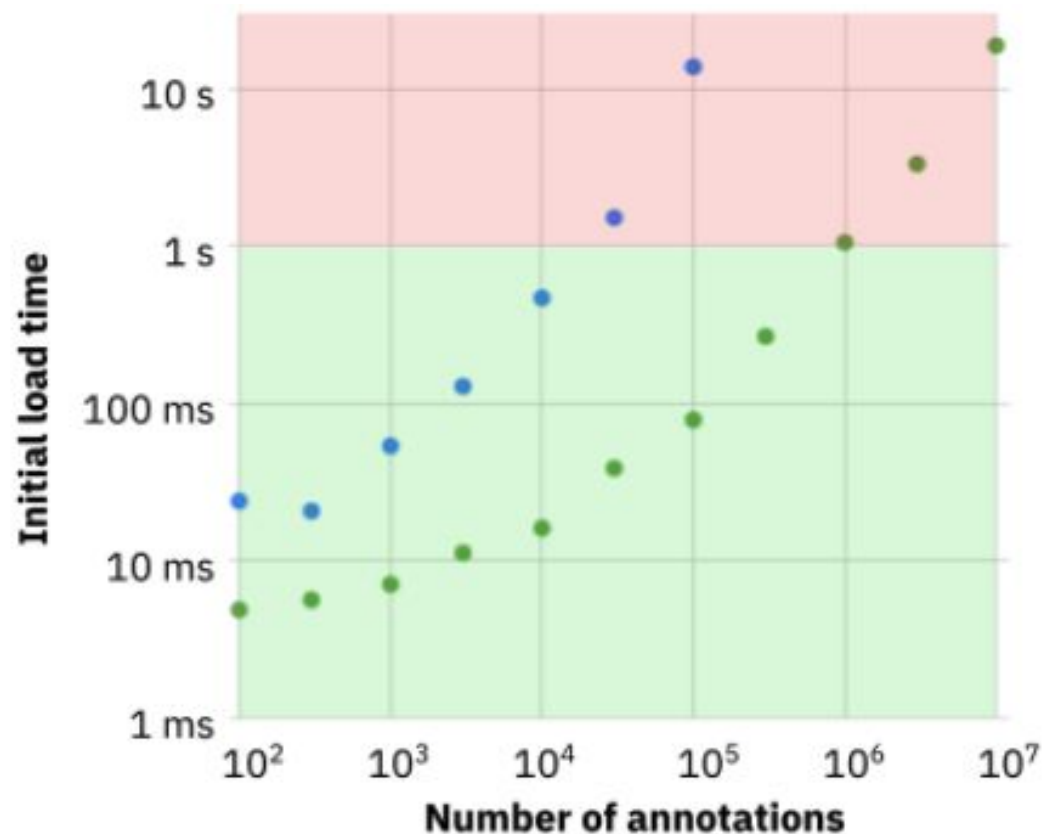
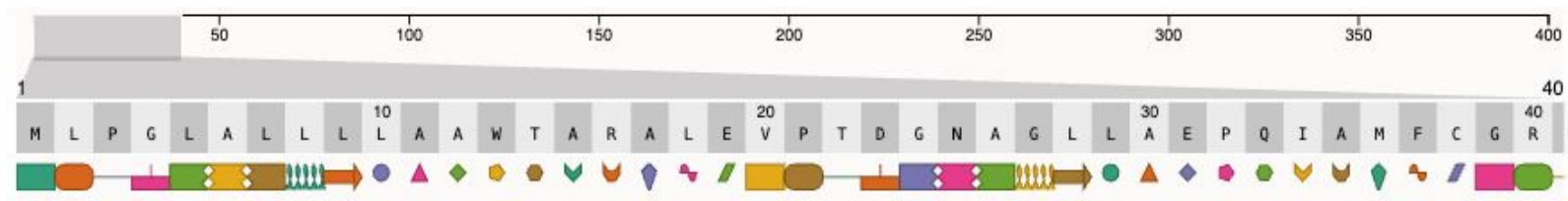
- Rendered using Canvas
- Pixels drawn directly onto the screen
- Doesn't retain all the elements in the DOM like SVG
- Reduces memory overhead





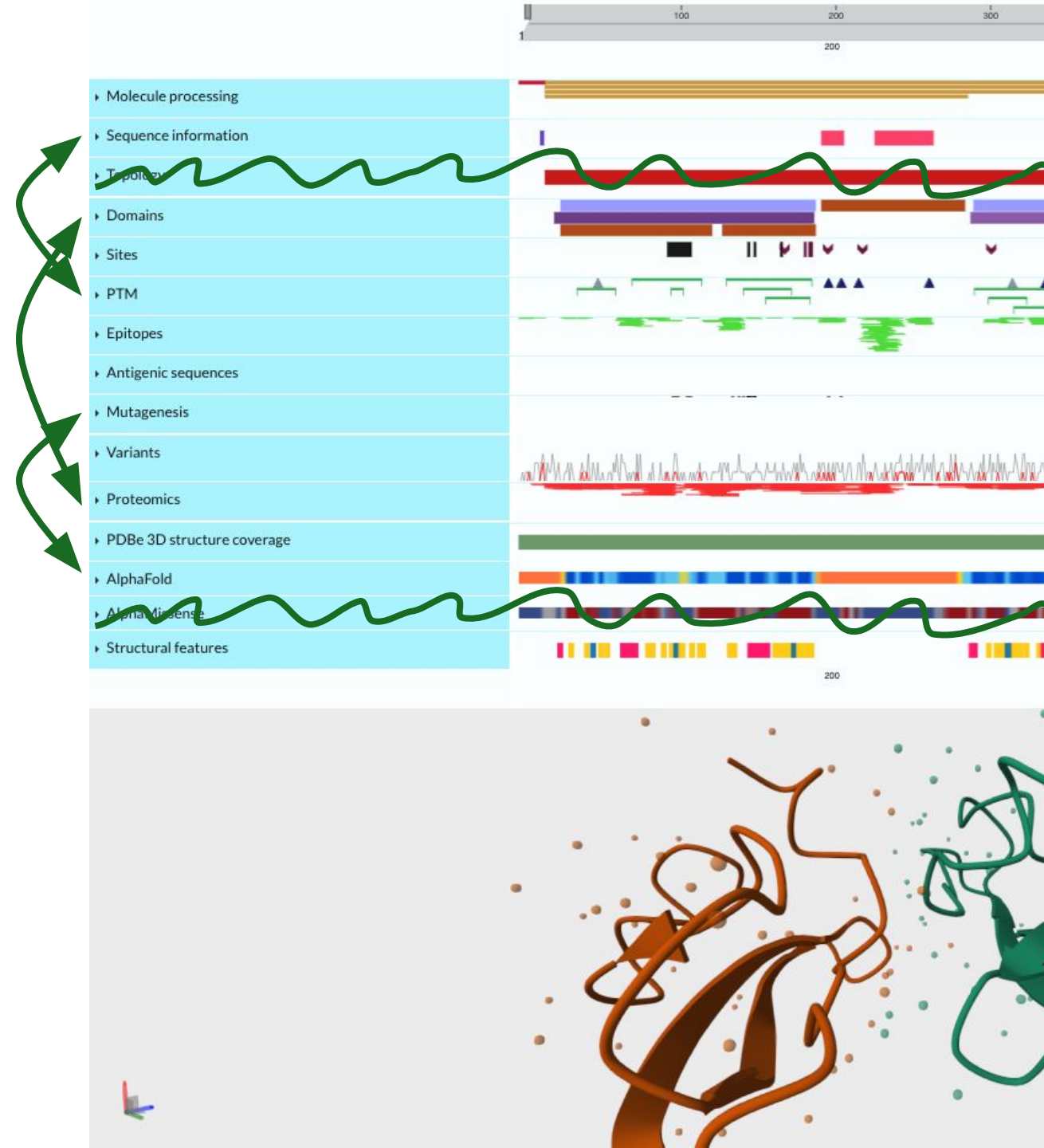
# Performance optimization

# Performance comparison between SVG and Canvas when visualizing the same dataset



# Challenges and future

- **From no dependency, to minimum dependencies**
  - Avoiding footguns
  - Embracing TypeScript
- **Package publication best practices**
  - Managing monorepos & bundles
- **Performance improvements**
  - Full transition to Canvas
  - Explore WebGL
- **Improve developer and user experiences**
- **Engaging a wider community**



# Funding



It is a collaboration with InterPro and PDBe and licensed under the MIT License.

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Nightingale monorepo

<https://github.com/ebi-webcomponents/nightingale>

Nightingale Example pages

<https://ebi-webcomponents.github.io/nightingale>

ProtVista repo

<https://github.com/ebi-webcomponents/protvista-uniprot>

Any questions? 