SARvision|Biologics

SARvision|Biologics is a desktop application designed to transform biologics informatics. With its intuitive smart spreadsheet interface, it enables users to read, organize, and analyse data on various biological polymers, including peptides, proteins, nucleic acids, chemically modified residues, and unnatural amino acids.

By identifying relationships between sequences and associated data, SARvision|Biologics enhances your research workflow, providing deeper insights and streamlining data management for more efficient and impactful discoveries.

Key Features and Benefits:

1. Import, Align, and Organize Biological Sequences:

- SARvision|Biologics allows users to import, align, and organize biological sequences from multiple formats, ensuring comprehensive data integration.

2. Flexible Sequence Analysis:

- The application supports the use of any number of chemically modified residues and unnatural monomers in sequence analysis, providing flexibility for complex biological research.

3. Smart Spreadsheet for Sequence Activity Analysis:

- Users can create a smart spreadsheet to highlight and analyze Sequence Activity Analysis, facilitating the identification of key patterns and relationships.

4. Advanced Visualization Tools:

- SARvision|Biologics enables the creation of mutation cliffs, sequence maps, and graphs, offering powerful visualization tools to enhance data interpretation.

5. Efficient Sequence Alignments:

- The application supports both automatic and manual sequence alignments for hundreds of sequences, streamlining the alignment process for large datasets.

6. Seamless Data Export:

- Users can seamlessly export their analysis to Excel, ensuring easy integration with other data management and reporting tools.

7. Advanced Search Capabilities:

- The tool allows for efficient searching of biological libraries with multiple queries at once, significantly speeding up the data retrieval process.

8. Active Data Filtering:

- SARvision|Biologics provides active data filtering based on chemotype, scaffold, data range, and properties, allowing users to quickly focus on the most relevant data.