

# Dive Deep into Genomic Variants

## HIGHLIGHTS

- Achieve advanced analyses of complex genomic variants on a full-genome level.
- Benefit from comprehensive variant annotation from a broad range of sources and up-to-date guidelines, and numerous bioinformatics file viewing tools.
- Gain time with efficient workflows and customizable reporting in a user-friendly interface.

## Alamut™ Visual Plus Advanced Features

### CUSTOMER EXPERIENCE

- User-friendly interface
- Private data management
- Customizable reporting



### VISUALIZATION OF VARIANTS

- Full-genome browser
- BAM, VCF, BED Sanger files viewer
- HGVS nomenclature



### DATA SOURCES

- ClinVar, dbSNP, COSMIC, MedGen, Orphanet, dbVAR, DGV
- Mastermind, Pubmed®
- ACMG guidelines



### SPLICING & MISSENSE PREDICTORS



alamut™  
VISUAL PLUS is a comprehensive genome browser that simplifies variant exploration.

The software includes genomic and literature databases, missense and splicing predictors, and guidelines in an intuitive interface.

Together with advanced visualization, customizable reporting, and local data management, Alamut™ Visual Plus increases operational efficiency by accelerating complex variant assessment.

## Simplified tertiary analyses

Customizable view

Gene structure

Genome sequence

Nucleotide conservation

Transcript

Lab variants

Known variants: dbSNP, COSMIC, Uniprot, ClinVar, etc.

Aligned orthologs, protein domains, dynamic scaling

Quick search

Genome view

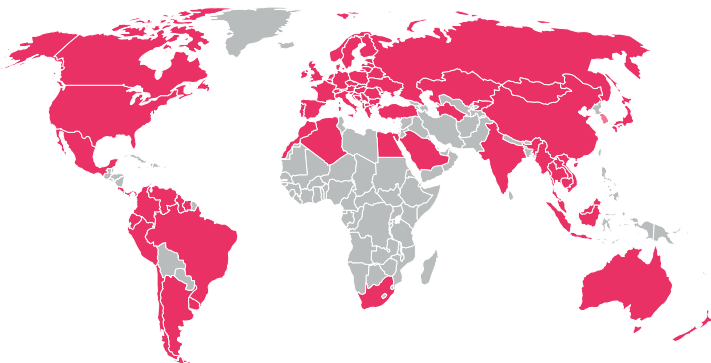
Customizable report

Sanger view

Variant panel

ACMG guidelines

## Global adoption



*“The previous AlamuT™ Visual software was a powerful tool widely used by our teams at CHU of Lille for research decisions in oncogenetics, rare diseases and pharmacogenetics. The new AlamuT™ Visual Plus is a step forward, allowing investigation of deep intronic sequences, the possibility to overlap Sanger sequences with NGS BAMs and obtain data quickly. Among other features, the variant report is further made easy by including ACMG guidelines.”*

**Tonio Lovecchio, MSc, Engineer | Cell and Molecular Biology Engineering, CHU of Lille, France**

*“I am honored to test AlamuT™ Visual Plus. I have witnessed the improvements made to AlamuT™ Visual and I particularly like the following:*

- Visualization of GRCh37, GRCh38, or mitochondrial genome, conveniently displaying regions close to the genes of interest and the option to see overlapping genes.
- Option of knowing the impact of a variant on the overlapping gene as the software enables analyses of several genes' BAM sequences simultaneously.
- Possibility of loading BAM and AB1 files in the same track Automatic suggestion of variant outcome according to the ACMG classification, and showing the guidelines.
- Customizable final report.”

**Agnes Bourillon, BA, Engineer | Hôpital Universitaire Robert Debré, Paris, France**

### Want to know more?

Contact us at: [alamut@sophiagenetics.com](mailto:alamut@sophiagenetics.com)

## Benefits

Save time

Increase productivity

Improve quality

### ABOUT US

SOPHIA GENETICS (Nasdaq: SOPH) is a software company dedicated to establishing the practice of data-driven medicine as the standard of care and for life sciences research. We are the creator of the SOPHIA DDM™ Platform, a cloud-native platform capable of analyzing data and generating insights from complex multimodal data sets and different diagnostic modalities. The SOPHIA DDM™ Platform and related applications, modules, and services are currently used by a broad network of hospital, laboratory, and biopharma institutions globally. Where others see data, we see answers.