



CREATOR OF
THE **alamut** SOFTWARE SUITE

The lower half of the image has a solid red background. On the left side, there is a stylized graphic of a DNA double helix, rendered in a lighter shade of red. To the right of this graphic, the text 'CREATOR OF' is written in a white, uppercase sans-serif font. Below this, the phrase 'THE **alamut** SOFTWARE SUITE' is displayed. 'THE' and 'SOFTWARE SUITE' are in white uppercase sans-serif font, while 'alamut' is in a larger, bold, white lowercase sans-serif font.



► High-throughput
variant annotation

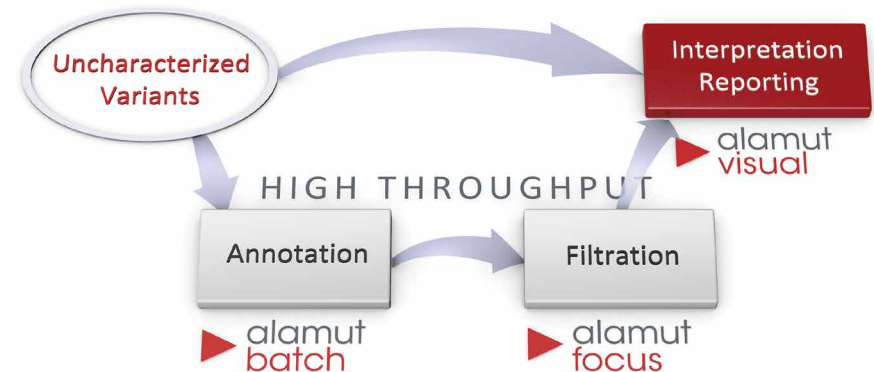
ALAMUT BATCH is a high-throughput variant annotation application for NGS analysis. Designed for intensive analysis workflows, Alamut Batch enriches raw NGS variants with a wealth of attributes including effects on human genes, allele frequencies, and missense and splicing predictions.

Rated as one of the most comprehensive NGS annotation tools, Alamut Batch is powerful, efficient and the industry leader in splicing predictions.

MAIN FEATURES

- Efficient high-throughput human variant annotation engine for studies ranging from gene panels to exome analyses
- Data enrichment based on the well-curated and clinically oriented Alamut database and on efficient prediction tools
- Annotation on coding and non-coding human genes, RefSeq transcripts, and LRG/RefSeqGene sequences
- Provides advanced splicing effects predictions
- Available on Linux (command-line) as a standalone installation, including the Alamut database, or in a client/server architecture. Available on Windows with a graphical user-interface.
- Easy to integrate into any analysis pipeline

instrumenting variant interpretation



► NGS variant filtration

ALAMUT FOCUS is an interactive variant filtration application for NGS analysis. Starting from annotated variant collections the software selects candidate variations based on user-defined or pre-configured criteria.

MAIN FEATURES

- Quickly design and apply simple to complex variant filtering strategies
- Apply pre-configured inheritance-based scenarios: autosomal recessive, autosomal dominant, X-linked recessive, *de novo*
- Fully compatible with **ALAMUT BATCH**



► Interactive graphical variant interpretation

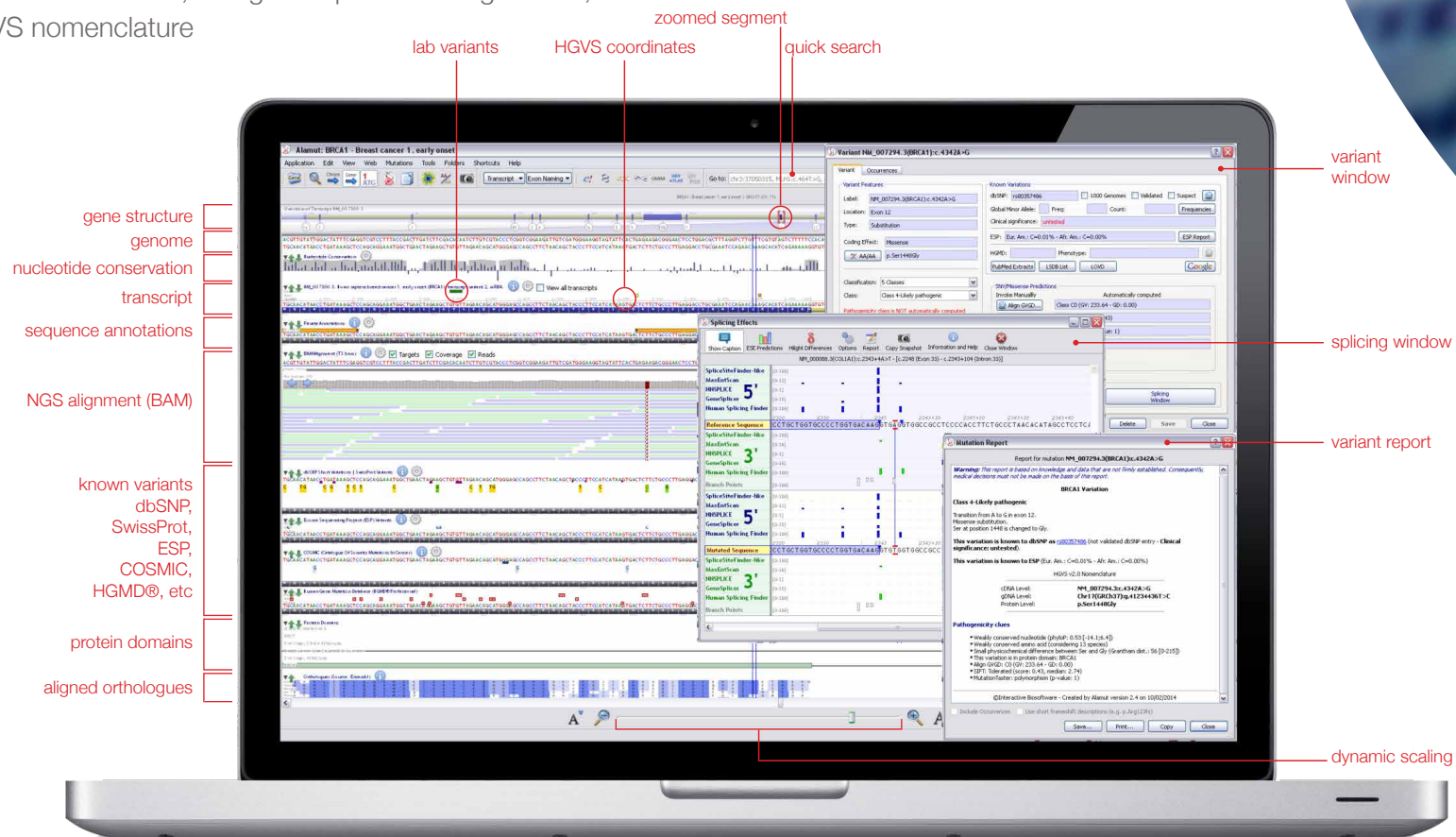
ALAMUT VISUAL helps scientists assess the pathogenic status of human genome variations in clinical and research settings.

- Save time with an all-in-one software portal designed for diagnostic testing
- Increase productivity with an intuitive and easy-to-use graphical user interface
- Improve quality with curated data, recognized prediction algorithms, and accurate HGVS nomenclature

MAIN FEATURES

- Gene browser supporting coding and non-coding human genes
- Unique interface with relevant annotations gathered from public databases
- HGVS nomenclature compliant software
- Variant reporting with pathogenicity clues
- Integrated prediction tools
- Advanced BAM NGS alignments viewer

THE REFERENCE
SOFTWARE
FOR HUMAN
VARIATION
INTERPRETATION




MAKING SENSE OF GENOMIC VARIATION

Interactive Biosoftware was founded in April 2007 in Rouen, France by a group of medical and computer scientists focusing on practical software applications for health care and life sciences, particularly in the field of molecular genetics.

Its mission is to provide geneticists and researchers with the most sophisticated, easy to use and reliable software to help them make appropriate diagnostics and share information between and across all tiers of human genome research.



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