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BaseSpace® Variant Interpreter (Beta)

Rapidly extract and report biological insight from genomic data

The newest member of the BaseSpace Informatics Suite, BaseSpace Variant Interpreter (Beta) integrates with BaseSpace Sequence Hub and leverages the Illumina Annotation Engine to enable quick identification and classification of disease-relevant variants on a single scalable platform

Rapid, rich, and accurate annotation

- Extensive annotation of genomic data from a broad range of sources
- No need for manual assembly of variant information from disparate sources

Comprehensive filtering tools

- Quick isolation of relevant variants based on user-defined selections
- Intuitive, user-friendly interface and variant review grid

Streamlined and accelerated variant interpretation with BaseSpace Knowledge Network

- Integrated knowledge base containing genotype/phenotype associations
- Seamless integration with BaseSpace Sequence Hub
- Pathogenicity autoscoring and interpretation classification review

Customizable reporting

- Flexible templates to report on select variants of interest, including evidence-based variant associations

Operational efficiency and scalability

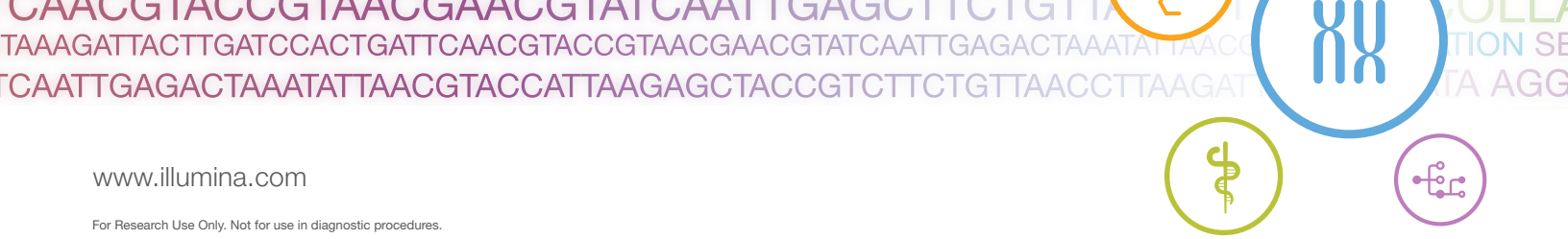
- Workflows designed for all assay types, from targeted sequencing to high-throughput whole-genome sequencing
- Ability to build and apply customized annotations, gene list, and region lists
- Customizable filters, views, and workflows

Compliance for laboratory testing

- Authentication for access control
- Traceability and ability to generate an audit log

As your trusted partner in informatics solutions, we are committed to meeting your data analysis needs. BaseSpace Variant Interpreter (Beta) uses Amazon Web Services that are ISO 27001 certified.

Try it out free for a limited time.
Visit https://variantinterpreter.informatics.illumina.com



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