HybridSTAT

Your partner in
Biological Big Data Analytics

Bioinformatics made simple

Genomics Data Analytics services

High-throughput biological data analysis for research and clinical applications

- Next Generation Sequencing
  - RNA-Seq, ChIP-Seq, Whole Exome and Genome Sequencing, X-Seq* complete data analysis (from raw short sequences to biologically comprehensive results)
  - De novo genome/transcriptome assembly
- Microarrays
  - DNA and Genotype array data analysis and reporting
- Data mining and pattern discovery in high throughput genomics data (clusters, motifs, networks)
- Analysis of gene regulatory regions and elements
- Functional enrichment analysis (Gene Ontology, Biochemical pathways)

Next generation personalized medical decision support

Geniasis

Geniasis is a clinical genomics decision support system, harnessing the power of open biological data. Variant detection from exome sequencing data, variant filtering and prioritization. Rich variant reports including comprehensive annotations by intelligent integration of open data sources. Rich reports of gene-disease associations. Proprietary variant annotation engine and impact scoring workflows for genes and variants.

Learn more at https://geniasis.com

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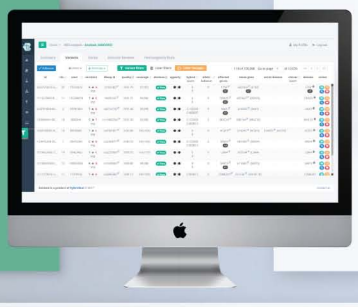
Geniasis

Robust, Flexible, Versatile

Geniasis provides a one-stop shop clinical genomics data analysis and management system. Cloud-based or on premises, Geniasis computational pipeline transforms your raw data to annotated, meaningful interpretation-ready DNA variations and gene-symptom-disease associations.

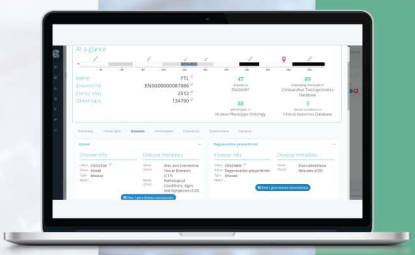


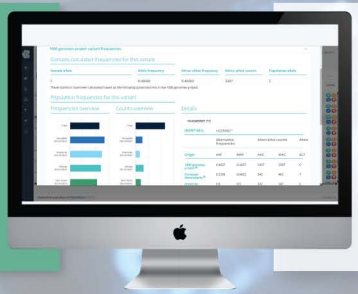
Outstanding variant annotation engine

Geniasis offers increased accuracy of reported data and diagnostic criteria, minimizing the risk of filtering wrong variations. The high-performance Geniasis annotation engine ensures that no previously known variations are missed due to dubious variant calls, through its unique identification algorithm for mutation equivalents.

Unprecedented levels of clinical information in one place

With Geniasis you can speed up your diagnostic work by orders of magnitude with access to the results of major population genetic studies (1000 Genomes Project, ExAC and gnomAD) and up-to-date gene-phenotype-disease associations (DisGeNET, HPO, CGD, CTD, Biochemical Pathways, Gene interactions).





Curated variant frequencies from major population studies

With Geniasis, you will never miss again a rare pathogenic variant because of poor annotation of known variants in major population studies including the 1000 Genomes Project, ExAC and gnomAD.

Improved productivity, unprecedented control

In Geniasis you will find the richest toolbox for the clinical geneticist including the greatest collection of pathogenic filters, algorithmic prioritization of mutation-associated genes and transcripts for each mutation and combined disease-symptom keyword filtering.

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Contact us at info@hybridstat.gr