INVITAE®

Definitive answers for more patients

Expert-driven, AI-enabled

Invitae strikes a balance between a comprehensive team of genetics experts and new technologies, including artificial intelligence (AI). This allows our team of highly experienced genetic counselors, scientists and lab directors to make the most impact.

More than 300,000+ patients have received a definitively classified result thanks to these 7 new technologies[1]

1. **Invitae Population Frequency Modeling™:** This Invitae developed, machine learning algorithm estimates the probability of a variant's pathogenicity based on information from the gnomAD population database.[3,4]
2. **SpliceAI:** An open-source deep learning splicing predictor developed by Illumina5 that has higher accuracy than Alamut splicing predictors.[1]
3. **Large-scale functional/experimental datasets:** We rigorously assessed 5 datasets (BRCA1, BRCA2, TP53, MSH2, SCN5A) generated by academic labs to determine how much weight to give functional evidence and have integrated this data into variant classification.[6-12]
4. **Cellular evidence modeling:** Invitae has generated large-scale functional/experimental datasets for 19 genes using single-cell RNA expression profiling.[13]
5. **Evolutionary model of variant effect (EVE)**: Developed by researchers at Harvard Medical School and Oxford University,[14] the EVE deep learning algorithm uses evolutionary sequence conservation to predict variant pathogenicity with high accuracy.
6. **AlphaFold protein structures:** The AlphaFold database, developed by DeepMind and EMBL-EBI,[15] uses AI to predict the 3D structure of proteins. These predictions are incorporated into in-silico models developed by Invitae that predict the functional effect of missense variants.
7. **Invitae Evidence Modeling™ Platform:** A machine-learning platform developed at Invitae and designed for generating, validating and standardizing new types of evidence for variant classification. To date, this platform includes evidence for more than 10 million unique variants from more than 3,000 genes.[1]

We're the company that:

- tested over 4 million patients[1]
- classified over 2 million unique variants[1]
- submitted >1,300,000 variants to ClinVar[2]
- implemented 7 new technologies in the last 2 years[1]
- led and collaborated on more than 100 research publications[4]

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Disrupting the status quo

Innovation timeline

2014

- Developed Sherloc variant interpretation framework
- First launch with features at no added cost:
  - Fully customizable
  - Re-requisition
  - Family variant testing
  - Exon copy number variants (CNVs) on next-generation sequencing (NGS)
  - Post-test counseling

2015

- Implemented natural language processing to mine all publications where a variant is mentioned
- Launched scalable approach to full *PMS2* gene (pseudogene issues)[16]

2016

- Incorporated structured framework for highly predictive phenotype evidence into variant interpretation[17]

2017

- Launched first sponsored testing program for epilepsy
- Published Sherloc variant interpretation framework[18]
- Launched scalable next-generation sequencing method with sensitive copy number detection for *SMN1/2*[16]

2018

- Published prevalence of small copy number variations (CNVs) in >143k cohort[19]
- Launched comprehensive carrier screening

2019

- Launched Invitae's Functional Modeling™ Platform

2020

- Initiated routine case-level re-analysis for exome

2021

- Launched RNA analysis for hereditary cancer
- Implemented scalable approach to *RPGR* gene (low complexity issues)

2022

- Received ISO 15819 accreditation
- Incorporated saturation large scale functional/experimental datasets for *BRCA1, BRCA2, TP53, MSH2, SCN5A*
- Launched Invitae Population Frequency Modeling
- Implemented scalable approach to *C9orf72* gene (hexanucleotide repeat issue)
- Migrated exome sequencing over to genome sequencing assay to minimize bias in the data
- Started automated clinical information extraction
- Expanded functional modeling platform to 3,000 genes

2023

- Invitae Evidence Modeling Platform combines functional, population frequency, and cellular evidence modeling

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