MOLECULAR HEALTH

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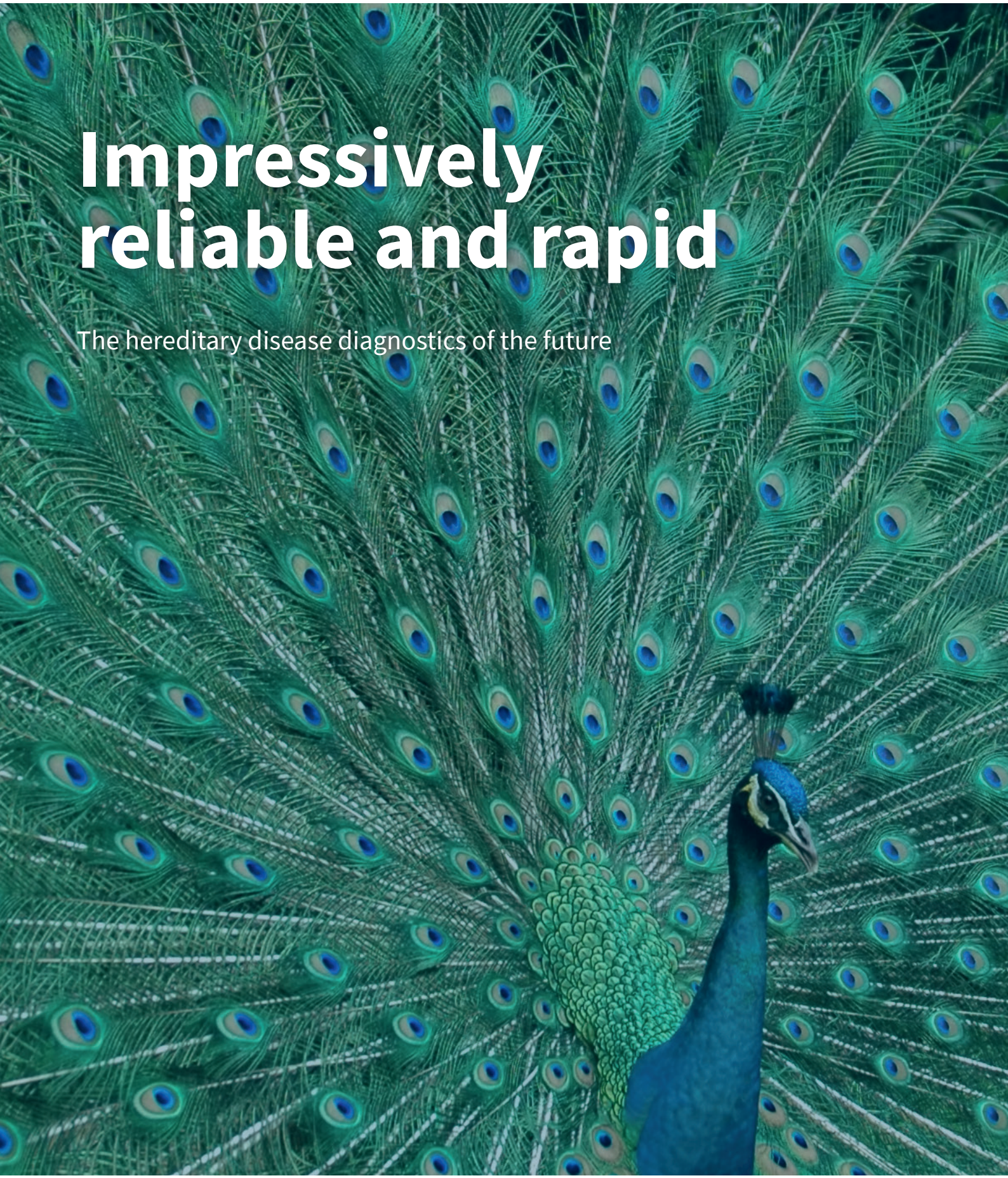
Impressively reliable and rapid

The hereditary disease diagnostics of the future



GUIDE/MENDEL

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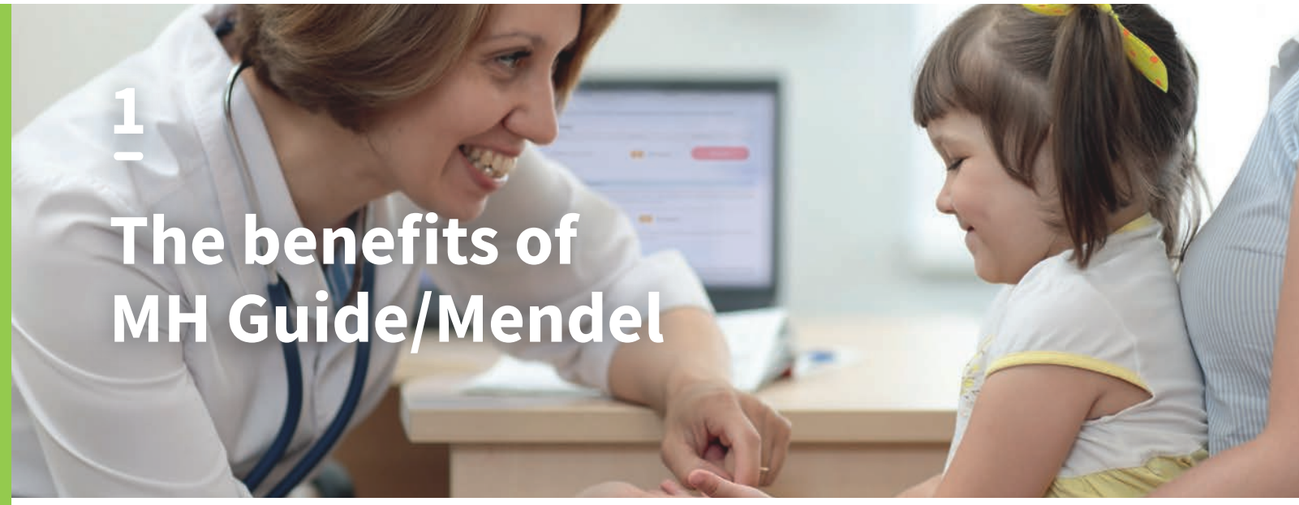
This might interest you:



1

The benefits of MH Guide/Mendel

Fast, precise evaluation of germline variants

MH Guide/Mendel is optimized for evaluating germline variants associated with hereditary diseases. The software application is a module of MH Guide and supports human genetics laboratories in next-generation sequencing (NGS)-based assessment of germline variants.

How human genetics laboratories benefit from MH Guide/Mendel:

- **Approved for diagnostic use**
  MH Guide/Mendel is a module of MH Guide, which is approved as an IVD medical device according to the EU regulation 2017/746 (IVDR).
- **Faster results**
  By automatically accessing relevant databases and pre-classifying variants according to ACMG criteria, MH Guide/Mendel quickly and accurately identifies and annotates gene variants associated with hereditary diseases.
- **Easy to integrate**
  Flexible interfaces make it possible to analyze standard data formats from the sequencing of commercially-available or proprietary gene panels, independent of the platform used.
- **Customizable evaluation**
  The filtering and editing options within the software allow quick access to the most important information. Users can store their own variant classifications in the protected area of their account.
- **Scalable analysis process**
  MH Guide/Mendel's optimized workflow allows a high sample throughput.
- **Audited quality**
  Molecular Health is certified to EN ISO 13485:2016. Users benefit from the safety and reliability of MH software applications.

2

The MH Guide/Mendel process

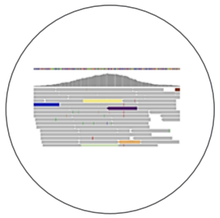
Use global knowledge to reliably determine the risk of genetic diseases

MH Guide/Mendel identifies and classifies variants for hereditary diseases. The software automatically matches these with data based on the comprehensive, regularly updated, and quality controlled Dataome database. This contains, among other things, the currently published biomedical knowledge on relevant hereditary diseases and pathogenic gene variants.

You can use any commercial or proprietary gene panel and have the data analyzed in VCF format with MH Guide/Mendel.

MH Guide/Mendel summarizes all of the relevant results in individual reports that provide users with clear, specific information on genetic mutations associated with hereditary diseases.

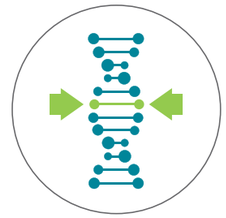
Genomic data from a blood sample



Technology-independent data upload

- VCF, FASTQ files
- Commercial panels
- Proprietary panels

Interpretation of genetic variants



Automated database comparison and classification

- Public databases
- MH database
- ACMG classification
- Automated CVI variant narratives

MH Guide/Mendel report

Standardized, customizable report

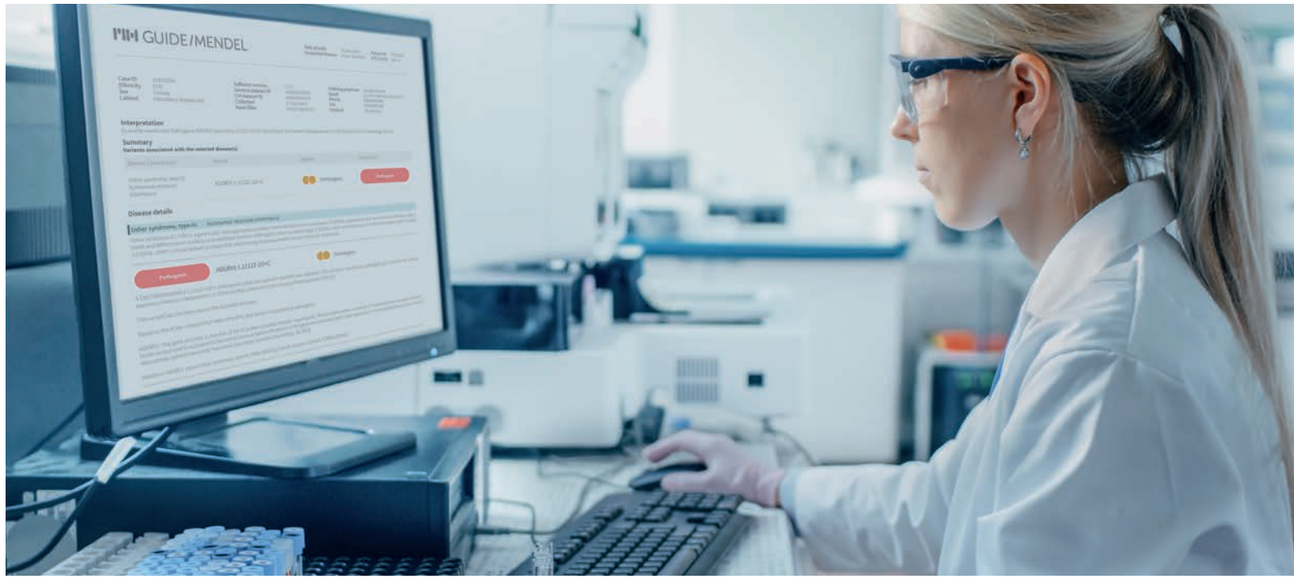
- Variant classification
- Functional effects

3

Integration in lab workflows

Flexibility and data security in one

The web-based software application can be easily integrated in the laboratory. It enables the annotation and interpretation of genetic variants from common NGS or other analysis platforms.



Approved for clinical use
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SaaS – individually scalable
MH Guide/Mendel is offered as scalable SaaS (Software as a Service) to suit small and large institutions alike.

Customizable patient reports
The design, content, and format of analysis reports can be adapted to individual needs on request.

Flexible input and output formats
MH Guide/Mendel can process the standard data formats VCF and FASTQ. Output formats are PDF, JSON, and XML.

Secure data transmission
MH Guide/Mendel provides secure transmission of patient data through advanced encryption standards (SSL/TLS, AES-256) and storage of patient data with controlled access authorization.

Data center architecture
All services are housed in data centers that are Trusted Site Infrastructure (TSI) or ISO 27001 certified and meet the highest industry standards.

Guaranteed security of patient data
MH Guide/Mendel complies with GDPR in Europe, GenDG in Germany, and the Health Insurance Portability and Accountability Act (HIPAA) in the USA.

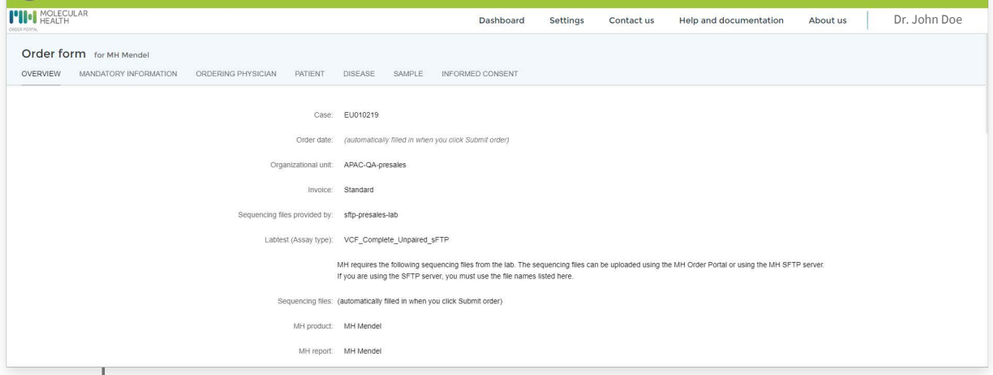
Efficient workflows in your lab
MH Guide/Mendel lets you optimize your everyday processes. The cloud-based software automates the interpretation of germline variants and delivers high-quality analyses.

4

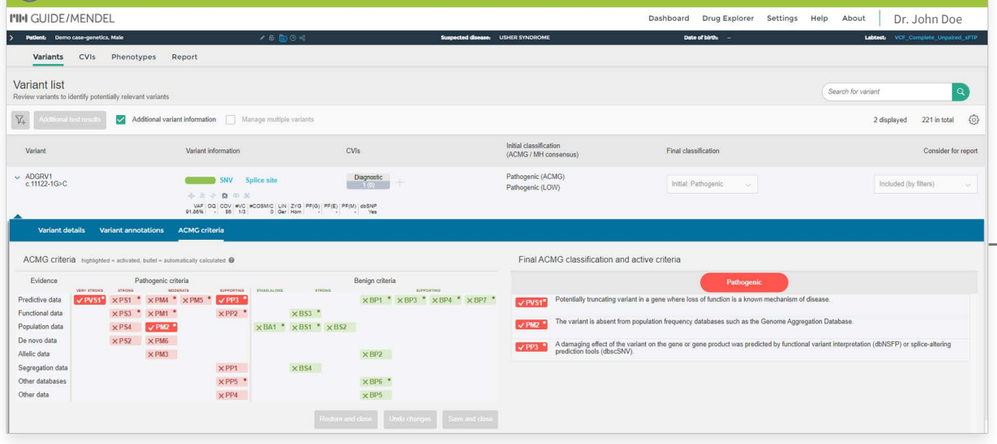
Generate the report: just a few, intuitive steps

How it looks on your screen: from raw data upload to final patient report

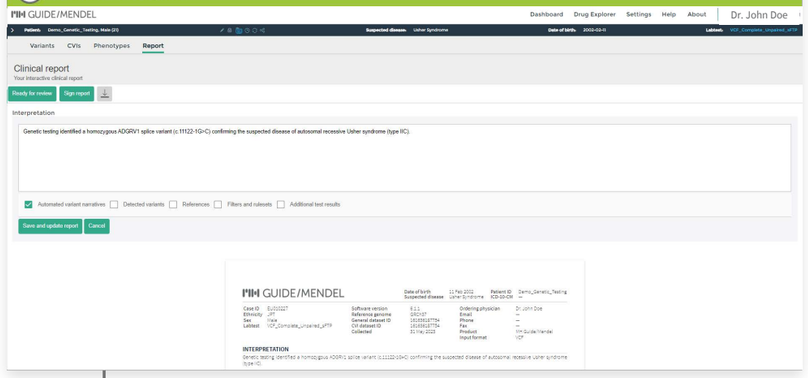
1 Upload sequence data



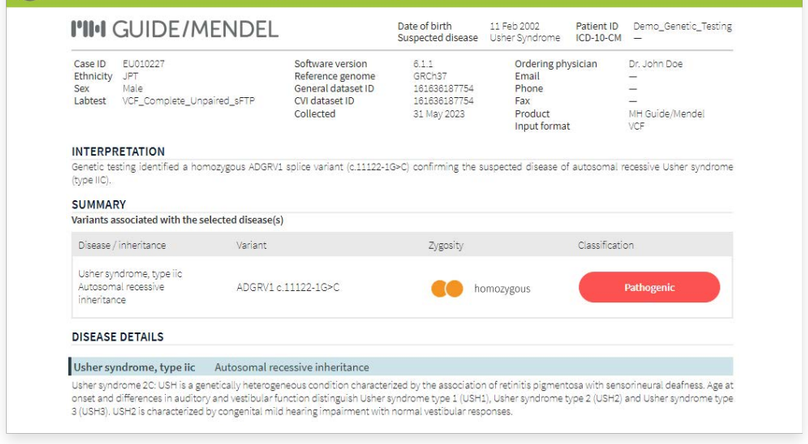
2 Automatic variant



3 Generate the report



4 Export the report (detailed description on following page)



GUIDE/MENDEL

		Date of birth	11 Feb 2002	Patient ID	Demo_Genetic_Testing
		Suspected disease	Usher Syndrome	ICD-10-CM	—
Case ID	EU010227	Software version	6.1.1	Ordering physician	Dr. John Doe
Ethnicity	JPT	Reference genome	GRCh37	Email	—
Sex	Male	General dataset ID	161636187754	Phone	—
Labtest	VCF_Complete_Unpaired_sFTP	CVI dataset ID	161636187754	Fax	—
		Collected	31 May 2023	Product	MH Guide/Mendel
				Input format	VCF

INTERPRETATION

Genetic testing identified a homozygous ADGRV1 splice variant (c.11122-1G>C) confirming the suspected disease of autosomal recessive Usher syndrome (type IIC).

SUMMARY

Variants associated with the selected disease(s)

Disease / inheritance	Variant	Zygosity	Classification
Usher syndrome, type IIc Autosomal recessive inheritance	ADGRV1 c.11122-1G>C	homozygous	Pathogenic

DISEASE DETAILS

Usher syndrome, type iic Autosomal recessive inheritance

Usher syndrome 2C: USH is a genetically heterogeneous condition characterized by the association of retinitis pigmentosa with sensorineural deafness. Age at onset and differences in auditory and vestibular function distinguish Usher syndrome type 1 (USH1), Usher syndrome type 2 (USH2) and Usher syndrome type 3 (USH3). USH2 is characterized by congenital mild hearing impairment with normal vestibular responses.

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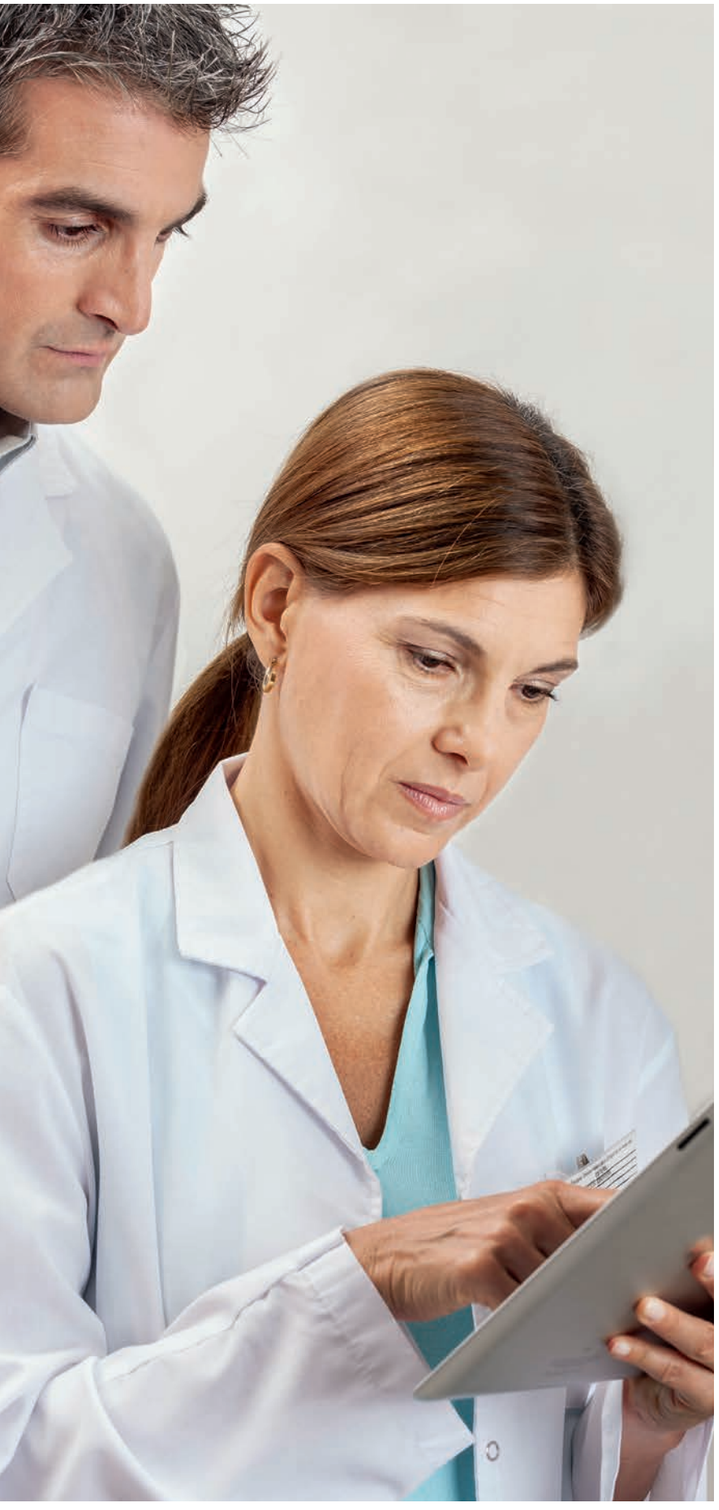


Everything at a glance:

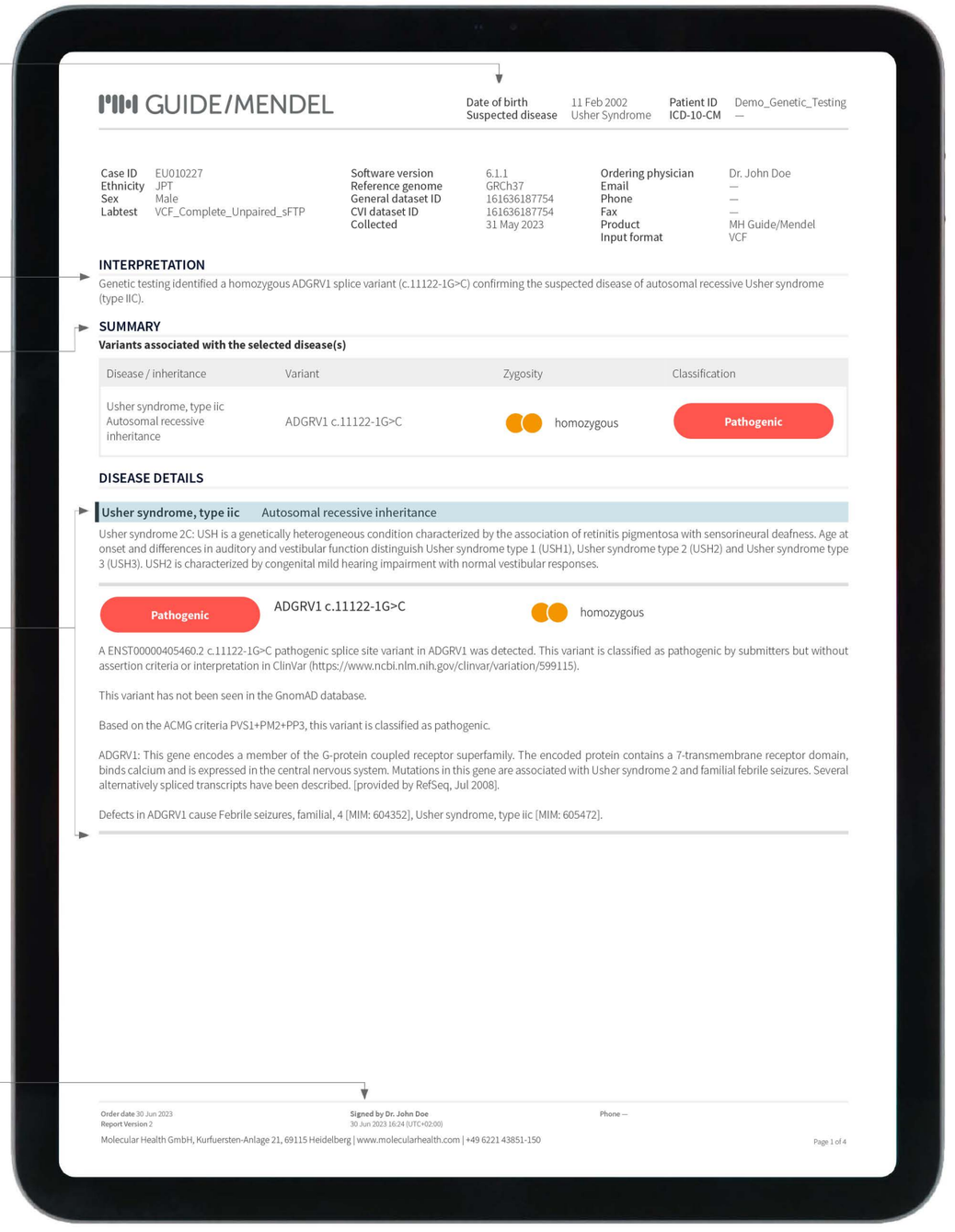
Patient data and suspected diagnosis

Your interpretation of findings and comments for colleagues and patients

Overview of detected variants and phenotype, including zygosity and classification

Detailed information on the disease, mode of inheritance, information on the source of genotype-phenotype correlation, and PubMed references

Electronic signature of the human geneticist in charge



GUIDE/MENDEL

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Pathogenic ADGRV1 c.11122-1G>C homozygous

A ENST00000405460.2 c.11122-1G>C pathogenic splice site variant in ADGRV1 was detected. This variant is classified as pathogenic by submitters but without assertion criteria or interpretation in ClinVar (https://www.ncbi.nlm.nih.gov/clinvar/variation/599115).

This variant has not been seen in the GnomAD database.

Based on the ACMG criteria PVS1+PM2+PP3, this variant is classified as pathogenic.

ADGRV1: This gene encodes a member of the G-protein coupled receptor superfamily. The encoded protein contains a 7-transmembrane receptor domain, binds calcium and is expressed in the central nervous system. Mutations in this gene are associated with Usher syndrome 2 and familial febrile seizures. Several alternatively spliced transcripts have been described. [provided by RefSeq, Jul 2008].

Defects in ADGRV1 cause Febrile seizures, familial, 4 [MIM: 604352], Usher syndrome, type iic [MIM: 605472].

Order date 30 Jun 2023	**Signed by Dr. John Doe**	**Phone** —
Report Version 2	30 Jun 2023 16:24 (UTC+02:00)	

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How to reach Molecular Health

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We develop and deliver innovative technologies for in silico medicine and precision medicine

Our solutions enable the conversion of large amounts of data into evidence-based, medically relevant results for the actors in the healthcare sector. Therewith, we provide molecular pathologists, geneticists, physicians, and patients with better information on diagnoses and therapy options. We support pharmaceutical and health organizations by optimizing clinical studies in the development of promising active ingredients and meaningful disease models.