

THE WORLD'S LARGEST MUTATION DATABASE OF RARE GENETIC DISEASES

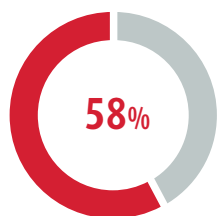
CentoMD® is your virtual encyclopedia. Search, select, and filter through genes, transcripts, and variants and end up with a detailed description including all associated data tailored to your needs. CentoMD® allows you to diagnose and treat rare diseases in a much more efficient, speedy and targeted manner. CentoMD® offers advanced **Genotype-Phenotype**, **Phenotype-Genotype**, and **vcf-upload modules**. Data can be retrieved at four different levels:

1. Variant rationale
2. Positive individuals
3. Statistics
4. Individual view

You can see the reasons behind the variant classification, view statistics and detailed individual related data.

A SIGNIFICANT NUMBER OF UNPUBLISHED VARIANTS

CentoMD® is evidence-based: behind every reported variant there is a clinical case analyzed at CENTOGENE by following a standardized medical workflow with accredited quality.



CentoMD® 58%
Published 42%

Ratio of newly detected
vs. previously published
clinically relevant and
uncertain variants



~ 180,000

ANALYZED
INDIVIDUALS



> 3,400

ASSOCIATED
PHENOTYPES



> 1.3 B

IDENTIFIED
ALLELES



> 6.7 M

UNIQUE
VARIANTS

Schedule your individual and free demo today

www.centogene.com/CentoMD-free-demo



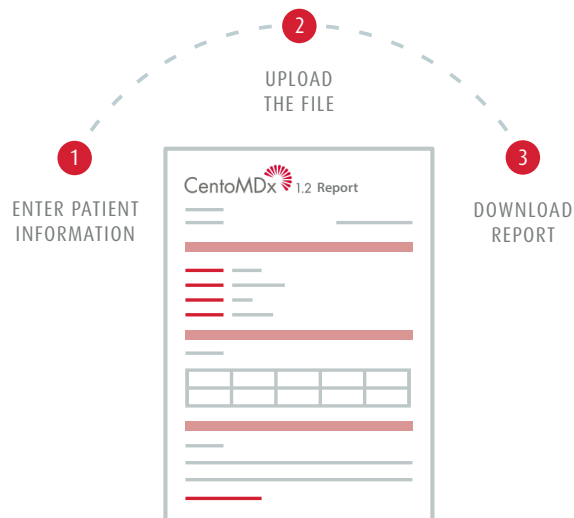
FOLLOWING THE ACMG GUIDELINES AND INDEPENDENT CURATION PROCESS

		ANNOTATION IN CentoMD®		
		(LIKELY) PATHOGENIC	VUS	(LIKELY) NEUTRAL
ANNOTATION IN PUBLIC SOURCES	(LIKELY) PATHOGENIC	Confirmation “(Likely) Pathogenic”		Re-classification “(Likely) Neutral”, but published as “(Likely) Pathogenic”
	VUS	Re-classification VUS to “(Likely) Pathogenic”	Additional info for re-evaluation	Re-classification VUS to “(Likely) Neutral”
	(LIKELY) NEUTRAL	Re-classification “(Likely) Pathogenic”, but published as “(Likely) Neutral”		Confirmation “(Likely) Neutral”
	NEW UNPUBLISHED VARIANT	New classification “(Likely) Pathogenic”	New classification “VUS”	New classification “(Likely) Neutral”

CentoMDx™ 1.2: DIAGNOSTIC SERVICE KEY FEATURES*

CentoMDx™ evaluates genetic data and provides a diagnostic report in three steps:

- Annotation of the variants from the uploaded VCF file
- Clear diagnostic statement based on detected pathogenic and likely pathogenic variants
- Extended individual variant interpretation, including software predictions, allele frequencies in various databases, reference to publications, related disease description and information about positive diagnosed patients analyzed at CENTOGENE
- Report storage and export functions
- User notification about any reclassified reported variants in the future



*Not yet offered in the US.

> Contact Details

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