CENTOGENE
THE RARE DISEASE COMPANY

Bioinformatic SaaS Platform

CentoCloud® Exome

In Collaboration With Twist Bioscience

CentoCloud® – The Decentralized Diagnostic Solution

Analyze, interpret, and report genomic variants no matter where you are located via our clinical decision support platform. With CentoCloud, we enable laboratories around the world to establish and run state-of-the-art genomic testing and deliver best diagnostic insights to local patients.

As a cloud-based Software as a Service (SaaS) platform, CentoCloud is specifically designed to support laboratories with the execution of superior Next Generation Sequencing (NGS)-based diagnostics. Our fully automated CE-marked bioinformatics pipeline analyzes NGS data based on CENTOGENE's validated testing products, annotated with data from the CENTOGENE Biodatabank.

The CentoCloud Advantage

What sets CentoCloud services apart from standard bioinformatic SaaS platforms?

End-to-end workflow from FASTQ files to expert medical report

Powered by the CENTOGENE Biodatabank

Best-in-class, CE-marked bioinformatics with superior variant annotation, classification, and prioritization

Best diagnostic reliability through superior, end-to-end validated gene panels and protocols

Outstanding Clinical Coverage and Diagnostic Power

CENTOGENE has partnered with Twist Biosciences to bring you the best quality in clinical coverage and diagnostic results. When choosing one of the Twist Alliance CNTG panels, you receive the highest quality, best-in-class design, and tailored bioinformatics – delivering enhanced performance from leaders and trusted partners in rare disease diagnostics. In choosing Twist Alliance CNTG Exome, which combines insights from our Biodatabank with superior omics technology, you benefit from a solution that delivers a higher diagnostic yield compared to standard WES.[1–10]

Key Features and Performance – Twist Alliance CNTG Exome

Broad and Uniform Exome & Mitochondrial Genome Coverage	• Highly uniform coverage of the entire exome (~20,000 genes), +/-10 bp exon-intron boundaries, and complete mitochondrial genome (37 genes) • ≥98 % target regions covered at ≥20 x
Enhanced Coverage of Clinically Relevant Regions	• Enhanced coverage of disease-associated genes (OMIM®, HGMD®, CENTOGENE Biodatabank), with ≥99 % target regions covered at ≥20 x • Coverage of known clinically relevant variants in coding and non-coding regions (HGMD®, ClinVar, CENTOGENE Biodatabank for rare and neurodegenerative diseases)
Variant Types	• Highly sensitive and specific detection of SNVs, InDels, CNVs of exon-level to cytogenomic-level changes, UPD*, and mtDNA with heteroplasmy ≥15 % • Sensitivity: - SNVs and InDels (≤50 bp) >99.6 % - CNVs >95 %** • Specificity of > 99.9 % is guaranteed for all reported variants, only when physical sample material is available***
Technical Details	• CentoCloud Exome requires the upload of two FASTQ files per sample as well as a description of the patient's phenotype using Human Phenotype Ontology (HPO) terms • For sequencing we recommend: Illumina paired-end (2 x 150 bp) NGS technology (e.g. NovaSeq™ 6000 and NextSeq 500 / 550 sequencing systems) • Twist Alliance CNTG Exome consists of exome capture with custom-designed reagents based on Twist® Human Core Exome, with an expected 18 – 20 Gb of sequencing data generated per patient • Reference genome used: - Nuclear genome aligned to GRCh37 / hg19 Human genome assembly - Mitochondrial genome aligned to Cambridge Reference Sequence of the Human Mitochondrial DNA (NC_012920)

SNVs: single nucleotide variants; **InDels:** small insertions/deletions; **CNVs:** copy number variations; **UPD:** uniparental disomy; **mtDNA:** mitochondrial DNA

* UPD screening is performed using an in-house algorithm for Mendelian Inheritance Errors (MIE) to detect Runs of Homozygosity (ROH) for the following well-known clinically relevant chromosomal regions: 6q24, 7, 11p15.5, 14q32, 15q11q13, 20q13 and 20

** CNV detection sensitivity is decreased for repetitive and homologous regions, such as pseudogenes

*** Only if physical sample material is provided via CentoCard, variants with low quality and/or unclear zygosity are confirmed by orthogonal methods (i.e., SNVs and InDels by Sanger sequencing; CNVs by Multiplex ligation-dependent probe amplification, MLPA; quantitative polymerase chain reaction, qPCR; or chromosomal microarray, CMA , and UDP internal confirmatory testing using CMA when necessary)

Tailored Testing and Life-Long Diagnostic Support

We offer flexible testing options and additional services, such as index and family analysis, to meet the individual needs of your patient. Committed to improving the lives of patients with rare diseases, CentoCloud Exome customers benefit from life-long diagnostic support via a free-of-charge and proactive reclassification program when choosing our medical evaluation service.

Options & Additional Services

Turnaround Time	• ≤ 5 business days • ≤ 12 business days (including medical report)
Testing Design	Solo, Duo, Trio, and Trio Plus
Raw Data	Result data files for download (BAM, VCF files) along with annotated variant table, sequencing statistics, gender and kinship check (XLS files) as well as coverage statistics
Medical Evaluation	Optional add-on: Comprehensive medical reports with extensive expert interpretation of clinical data, as well as differential diagnostic approaches, and detailed interpretation of key findings, including Carriership Findings*
Life-long Reclassification	Proactive variant-level re-evaluation and reclassification at no extra cost**

Solo: only the affected index patient is tested; **Duo:** index patient and affected or unaffected family member are tested; **Trio:** index patient and two family members, affected or unaffected are tested; **Trio Plus:** additional family members beyond Trio are tested

* For more infromation about our medical reporting at CENTOGENE, please visit centogene.com/reporting; for more details about our carriership findings centogene.com/carriership

** More details about Variant Reclassification Program centogene.com/diagnostics/benefits-of-genetic-testing/variant-reclassification-program

References

1 Cheema et al. 2020, PMID: 33083013
2 Clark et al. 2018, PMID: 30002876
3 Data on file at CENTOGENE
4 Gross et al. 2018, PMID: 30293986
5 Posey et al. 2019, PMID: 31234920
6 Schon et al. 2020, PMID: 32674947
7 Scuffins et al. 2021, PMID: 33495530
8 Stark et al. 2016, PMID: 26938784
9 Trujillano et al. 2017, PMID: 27848944
10 Wagner et al. 2019, PMID: 31059585

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