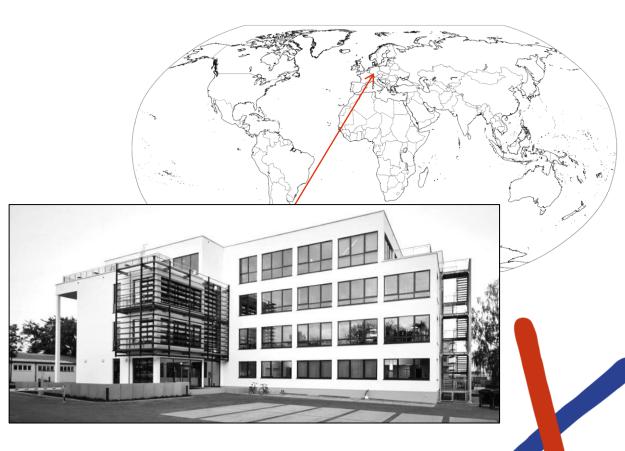
CENTER FOR GENOMICS AND TRANSCRIPTOMICS



Research & Pharma Solutions

Patrick Walter, PhD Sales Manager - RPS

Cosmin Pocanschi, PhD Head of Sales - RPS



OUR VISION





Our vision is to make CeGaT the partner of choice for research institutions and pharmaceutical companies around the globe.

We are committed to translate and further develop the extensive knowledge of genetics into real-life and practical applications for research and medicine.

INNOVATION OUT OF EXPERIENCE

CeGaT



GENETIC DIAGNOSTICS

RESEARCH & PHARMA SOLUTIONS

Experience & reliability

- > 10 years of experience in genetic diagnostics
- Privately owned
- 100 % of our services are performed in-house (made in Germany)

Consistent, high quality

- High degree of automatization, sample tracking
- Accredited ISO 15189, CAP, CLIA

Capacity

 Currently one of the largest NGS service providers in Europe (5 NovaSeq 6000 Systems)

NOVASEQ - HIGH CAPACITY - BRIEF TAT





ABOUT US

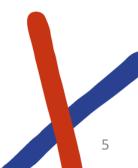


CeGaT Research & Pharma Solutions provide researchers and pharmaceutical companies with NGS analysis for medical innovation and clinical trials.

Our interdisciplinary team is composed of specialists of various disciplines, ready to bring in their specific know-how.



Together, we can create smart sequencing solutions to address your research questions.



WHY CHOOSE CEGAT FOR YOUR NGS PROJECTS

CeGaT

Discover our Research & Pharma Solutions Portfolio

SEQUENCING SERVICE

TRANSLATIONAL ONCOLOGY

Tumor Mutational Burden

Liquid Biopsy

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- Genome Sequencing
- Exome Sequencing
- Panel Sequencing
- Transcriptome Sequencing
- Small RNA Sequencing
- Single-Cell Sequencing
- Ready to Load Sequencing
- Methylation Sequencing

- IMMUNOLOGY
 - HLA Typing
 - T-Cell Receptor Sequencing

MICROBIOME ANALYSIS

- Bacterial Profiling (16S Sequencing)
- Metagenomic Profiling (Shotgun Metagenomics Classic)



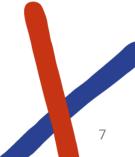
GENOME SEQUENCING





Get the most comprehensive collection of an individual's genetic information

- For a wide variety of organisms (human, animals, plants, microorganism)
- Available for different DNA quality
- Output: 90 Gb WGS Large Classic 2 Gb WGS Small Classic
- Protocol options: ± PCR
- Data supplied: FASTQ files
- Additional bioinformatic analysis available



EXOME SEQUENCING



Specifications

- For human and murine samples
- Available for different DNA quality
- Target enrichment:
 - Whole exomic regions plus mitochondrial genome (Twist): 37 Mb
 - Core exomic regions (Twist): 33 Mb
- Data supplied: FASTQ files
- Additional bioinformatic analysis available



Fast and precise, suited for your research



PANEL SEQUENCING





Examine a distinct set of regions within the genome

- Human or various species
- Target enrichment:
 - predesigned CeGaT panel (e.g. somatic Tumor Panel; produced by Twist Bioscience)
 - individual custom panel (produced by Twist Bioscience)
- Data supplied: FASTQ files and additional bioinformatics (BAM; VCF; TSV files)

TRANSCRIPTOME SEQUENCING

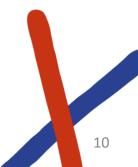


Specifications

- Human, mouse and other eukaryotes as well
- Different RNA quality and low input options
- Target enrichment:
 - Total RNA sequencing with rRNA depletion
 - mRNA enrichment
- Data delivery: FASTQ files
- Additional bioinformatic analysis available



Analysis of all RNA molecules of a biological sample



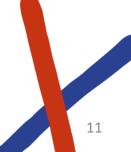
SMALL RNA SEQUENCING





Discover small RNA molecules in your biological sample

- Human, mouse and other eukaryotes
- Different RNA quality and low input options
- Target enrichment:
 - NEXTflex Small RNA-Seq kit (Bioo Scientific)
- Output: >10 Mio Cluster, flexible
- Data delivery: FASTQ files
- Additional bioinformatic analysis available



READY TO LOAD SEQUENCING



Specifications

- For all Illumina compatible Sequencing libraries
- Available Flow Cells:
 - MiSeq: nano Flow Cell, micro Flow Cell, V2 and V3 Flow Cell
 - NovaSeq: SP Flow Cell, S1 Flow Cell, S2 and S4 Flow Cell
- Different read length options
- Data supplied: FASTQ files



Flexible sequencing options, including different flow cells and read modes

METHYLATION SEQUENCING

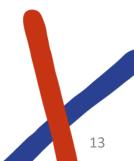


Specifications

- All Species
- Different DNA quality
- Cytosine Conversion Method
- Output: 90 Gb, flexible
- Data delivery: FASTQ files
- Additional bioinformatic analysis available



Explore the Epigenome – Methylation Matters!



TUMOR MUTATIONAL BURDEN





Measurement of the biomarker TMB

- Analysis of tumor and normal tissue or only tumor
- Sequencing Panel:
 - Somatic Tumor Panel (CeGaT GmbH), 2,2 Mb, >766 genes
 - Whole exome sequencing (Twist Bioscience), 37 Mb, ~ 20,000 genes
 - TruSight Oncology 500 (Illumina) 1,94 Mb, 523 genes
- Data delivery: of FASTQ files,TMB, MSI, alignment, variant calling (SNVs/InDels), annotation and filtering

LIQUID BIOPSY



Specifications

- cfDNA isolation from whole blood (e.g. Streck[®] tubes), plasma, other body fluids and cells
- Available workflows:
 - ddPCR analysis commercially available assays
 - NGS analysis whole exome sequencing, or panel enrichment
- Data delivery: FASTQ files
- Additional bioinfomatic analysis available



Isolation and analysis of cell-free DNA in the blood

HLA TYPING





Reliable and accurate insights into HLA types

- For analysing HLA Class I or HLA Class I and II
- Available workflows:
 - Whole Exome Sequencing (Twist Bioscience) 50x mean coverage
 - TruSight HLA Sequencing Panel (Illumina): 150x mean coverage
- Data delivery: FASTQ and additional bioinformatic analysis (XLS, PDF, TXT files)

T-CELL RECEPTOR SEQUENCING



Specifications

- For human DNA and RNA
- DNA isolation from sorted cells, PBMCs, Whole blood, fresh frozen tissue, FFPE tissue
- Target chain:
 - Beta (CDR3)
- Output: 2 Mio Cluster
- Data delivery: FASTQ and additional bioinformatic analysis (reconstructed TCR clones with frequencies)



Investigate diversity, clonality and changes in the T-cell repertoire or single TCR clones

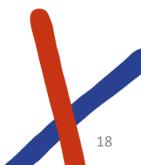
SHOTGUN METAGENOMICS CLASSIC





Accurate detection of all microbes

- Detection of Bacteria, Archaea, Fungi, Protozoa, Viruses down to species level
- Stool sampling kit available
- Target: whole genomes via shotgun sequencing.
- Output: 2 Gb or variable output options
- Data delivery: FASTQ files
- Additional bioinformatic analysis available



16S SEQUENCING

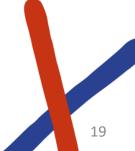


Specifications

- Detection of Bacteria and Archaea down to genus level
- Stool sampling kit available
- Target gene:
 - 16S rRNA gene (V3-V4)
- Output: >25 000 cluster per sample
- Data delivery: FASTQ files
- Additional bioinformatic analysis available



Highly Accurate detection of Bacteria and Archaea



CONTACT US

Let us know your project ideas and questions.

SALES



Cosmin Pocanschi

Patrick Walter





Nicole Weiblen





Anja Grohmann



Sonja Sändig



Alexander Fuchs



Carolin Thöm



Manuel Kreutzer

20





Elisabeth Maritschnegg Dorothea Kemmler

Karolin Birkle



Your Research & Pharma Solutions Team

cosmin.pocanschi@cegat.de

patrick.walter@cegat.de

rps@cegat.com +49 (0) 7071 565 44 333



THANK YOU FOR YOUR ATTENTION

CeGaT GmbH

Paul-Ehrlich-Str. 23 D-72076 Tübingen

info@cegat.com www.cegat.com

