UD GENOMED
UD-GenoMed Medical Genomic Technologies Ltd.

UD-GenoMed Medical Genomic Technologies Ltd.
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About UD-GenoMed

UD-GenoMed Ltd. is an innovative R&D SME and service laboratory offering large scale clinical genomics studies, molecular testing, related consulting and training services to both Academy and Industry. UD-GenoMed's services are based on the unique know-how of the Department of Biochemistry and Molecular Biology, Faculty of Medicine, University of Debrecen. UD-GenoMed Ltd. was founded by University of Debrecen with the ultimate goal to commercialize its genomic technology base and additional services previously provided exclusively by the Clinical Genomic Center of the University. In 2010 the company's capital had been increased by the managing private individuals who acquired 50% as shareholders in the company.

UD-GenoMed acts as an integrated testing laboratory and clinical study provider with dedicated focus on patient recruitment and has references in the following fields:

I. **chronic inflammatory diseases e.g. COPD, rheumatoid arthritis, inflammatory bowel disease,**

II. **tumor diseases including lung cancers, colon cancers, lymphoid leukemia and**

III. **schizophrenia and other mental disorders.**

Using functional genomics applications, UD-GenoMed is developing novel diagnostics biomarkers on these fields.

You have a scientific problem – we give you the solution!

www.ud-genomed.com

Portfolio

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Patient recruitment

- Large number of patient groups at the University of Debrecen treating yearly 150 000 patients and more than 100 clinical studies managed yearly.

Biobanking

- Create biobanks by collecting, processing and archiving primer samples.
- Construction of clinical and molecular biology databases.
- Ensure access and provide consultation training in biobanking protocols.

Functional analysis services

Full processing of your samples

- Sample QC.
- Illumina next-generation sequencing.
- Affymetrix microarray services.
- Capillary sequencing and RT-qPCR applications.

Bioinformatics

- Primer analysis of NGS data and advanced services for data interpretation.
- Gene expression, genotyping, metagenomics and epigenetic data biostatistics.
- Customized data analysis (data formating, advanced statistics).

Genotyping

- Whole genome analysis to determine associations between genetic variablitiy, drug response and diseases.
- Variant discovery to identify genotype/ phenotype correlations.
- Targeted genotyping to analyze targeted SNPs of your choice.

RNA and smallRNA sequencing

- RNA sequencing: deep sequencing of RNA that delivers unbiased and unparalleled information about the transcriptome allowing identification of transcript or splice variant or differential expression revealing a snapshot of RNA present .
- SmallRNA sequencing: thousands of small RNA sequences with unprecedented sensitivity and dynamic range for both small RNA discovery and profiling applications, novel miRNAs and other small non-coding RNAs discovery, characterization of variations and analysis of differential expression of all small RNAs.

Metagenomic sequencing

- Metagenomic sequencing: analysis of microbial samples from different sources (e.g. human-, soil-, water-, and thermal water related samples).
- Revealing composition of microbial communities in several applications such as medicine, engineering, agriculture, and ecology.

ChIP/MethylCap Seq

- ChIP Seq: combination of chromatin immunoprecipitation with next-generation sequencing for genome-wide mapping of histone modifications and identifying consensus protein-binding sites in DNA.
- MethylCap Seq: Methyl Binding Domain (MBD) based enrichment followed by next-generation sequencing for genome-wide DNA-methylation profiling.

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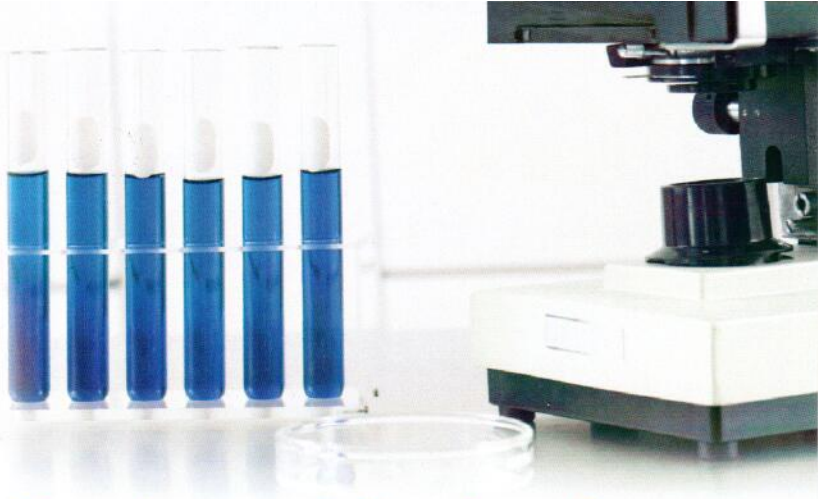
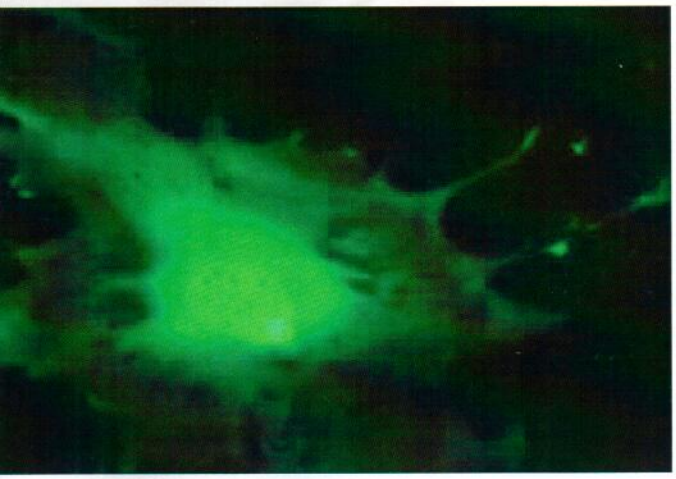


Mammalian Stable Cell Line Development Services for Recombinant Protein Expression and Antibody Production

Mammalian stable cell lines are widely used in antibody production and recombinant protein production, drug screening, assay development, gene editing, functional studies and other applications. These cell lines can grow continuously over a prolonged period of time and stably carry a genetic modification and / or express a transgene without significant changes in expression levels. Overexpression of transgene proteins is critical for many applications, including large-scale antibody production, in vivo localization experiments, and purification for structure-function studies.

UD-GenoMed offers state-of-the art services for establishing stable cell lines can overexpress virtually any protein of interest in your cell line of choice for protein overexpression, gene knockdown or genome editing that meets your specific research needs. We offer an overall mammalian stable cell line development workflow.

Gene synthesis, Cloning process → Transfection → Expression, Validation → Stable cell line development → Cell cloning → Screening, Optomalization → Production in bioreactor → Final quality control



Host mammalian cell lines: CHO, HEK293T, 293T or client-specified cell line

Genes: enzymes, transmembrane and cytoplasmic proteins, antibodies, cytokines

Services: Efficient genome editing by the CRISPR-Cas and TALEN systems, Effective viral and non-viral transfection systems, Multiple rounds of cell subcloning, Optimized production in BD Cell Line, rolling flask and microbioreactor

Applications: monoclonal antibody production, protein production assays, fusion, tagging for different applications, reporter cell lines for bioassays

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Assay development and screening services

UD-GenoMed offers a variety of assay services that can be performed as additional characterization steps for your custom made mammalian stable cell line and product quality control or as stand-alone screening projects. We supply a complete biosimilarity validation platform according to the related FDA and EMA guidelines.

Protein purification
IEF / SDS-PAGE / Western blot
Immunoprecipitation
Flow Cytometry / Cell sorting
Epitope mapping
Sandwich and competition ELISA
Confocal microscopy
Variable region sequencing
Glycane analysis

Contacts:

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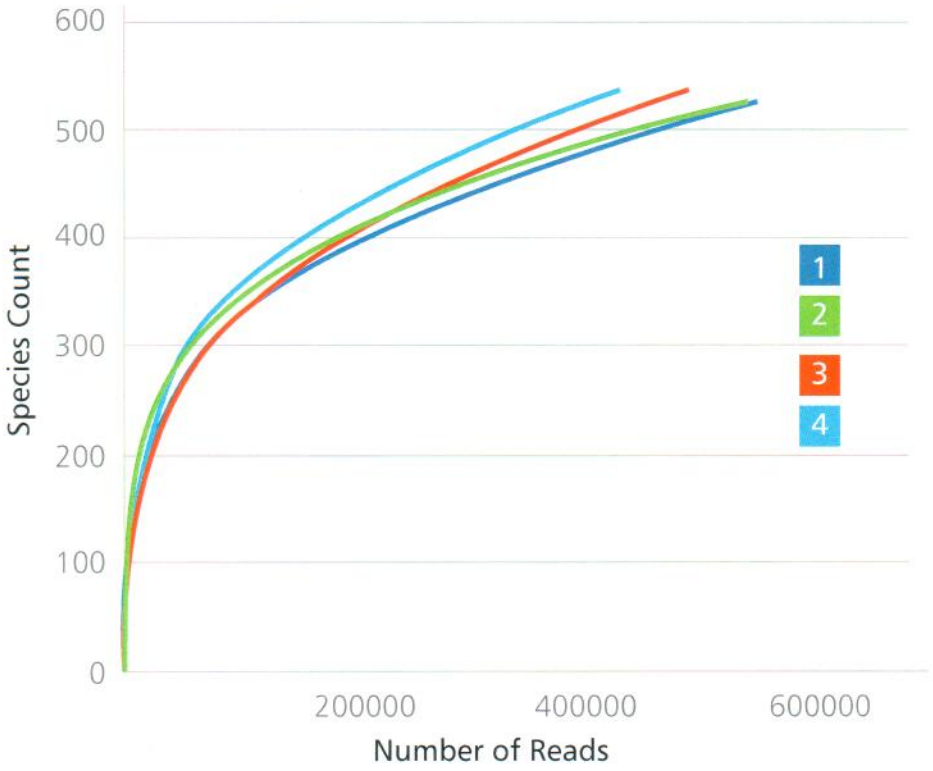
Metagenome Sequencing

Metagenomics is the study of the collective genomes of microbes in a microbial community. Analysis is performed by utilizing sequencing of 16S ribosomal RNA gene or fragments of the whole genome without culturing the organisms from the sample. UD-Genomed provides solution for both cases. Shotgun sequencing provides a valuable tool for whole metagenome profiling of a microbial community while 16S rRNA or SSU (small subunit) sequencing enables comparative analysis between the relative abundance of species of interest by amplicon sequencing to specific hypervariable regions.



Dilution curves of samples from four different donors. The curve is a plot of the number of species as a function of the number of reads. On the left, the steep slope indicates that a large fraction of the species diversity remains to be discovered. If the curve becomes flatter to the right, a reasonable number of individual samples have been taken: more intensive sampling is likely to yield only few additional species.

Analyses based on the total gut microbiota provide a phylogenetic picture of the community, but do not reflect the viable microorganisms. Viable community analysis is based on RNA and includes only metabolically active microorganisms. Structure of DNA is more stable and easier to handle while isolation of RNA is more difficult and requires greater experience, due to the ubiquitous presence of ribonucleases in cells and their environment.

DNA isolation → **Library preparation** → **16S sequencing** → **Data analysis**

RNA isolation + RT → **Library preparation** → **16S sequencing** → **Data analysis**

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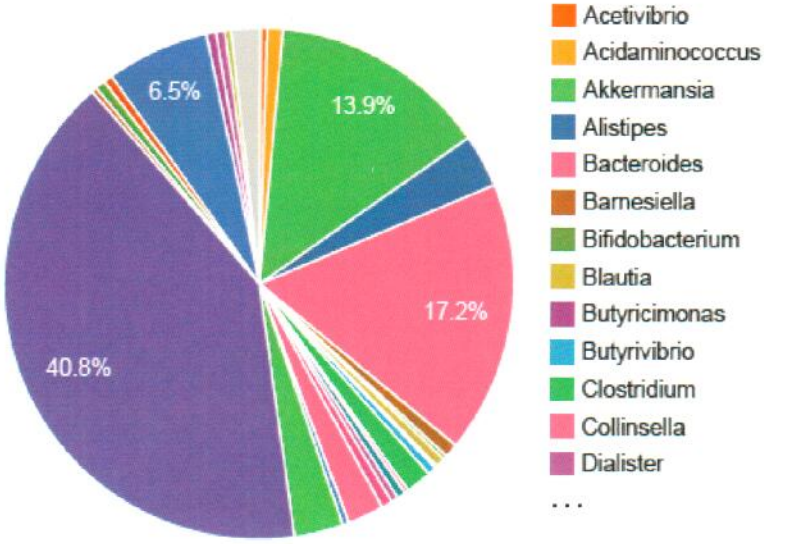
Metagenome Sequencing

Workflow starts with purifying genomic DNA or RNA. RNA samples are reverse transcribed to cDNA. Target region of 16S rRNA gene is amplified indexed with barcodes. Samples are pooled into a single library. Fragment length is 2×250 base pairs. Raw data are generated in fast-q files and visualized by our pipeline.

Shotgun sequencing

Shotgun sequencing refers to DNA that has been extracted and randomly sheared into smaller fragments before sequencing. It enables researchers to detect new members, new genes, and resolve complex taxonomies of the communities.



Distribution of microbiota from a human feces sample. The pie chart illustrates the distribution of annotated taxonomic generi. Each slice indicates the percentage of reads with predicted proteins and ribosomal RNA genes annotated to genus level. This information is based on all the annotation source databases used by MG-RAST.

Metagenome sequencing can detect the members of the microbial community with low occurrence since many samples can be combined in a single sequencing run and provides high coverage per sample.

Based on our expertise using Illumina sequencing technologies UD-GenoMed can be your perfect partner on your metagenomic studies!

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