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Research Sequencing & Multiomics Services

A comprehensive service portfolio for life science, biomedical, veterinary, agricultural and environmental research.

GENOMICS • TRANSCRIPTOMICS • MICROBIOMICS
SINGLE-CELL • PROTEOMICS • METABOLOMICS • BIOINFORMATICS

ALUNA SCHRIFT / SERVICE PORTFOLIO / 01

Microbiome & Microbial Genomics

#	SERVICE / METHOD	RESEARCH APPLICATION
01	16S rRNA gene amplicon sequencing	Bacterial community composition and diversity
02	18S rRNA amplicon sequencing	Eukaryotic microbial diversity profiling
03	ITS amplicon sequencing	Fungal community characterization
04	Archaeal marker gene sequencing	Archaeal community profiling
05	Functional gene amplicon sequencing	Targeted ecological or functional genes
06	Multi-primer amplicon panels	Complementary taxonomic marker profiling
07	Full-length 16S / marker sequencing	Long-read marker sequencing with higher taxonomic resolution
08	Absolute quantitative 16S profiling	Abundance-adjusted microbiome characterization
09	Shotgun metagenomic sequencing	Microbial taxa, genes and functional potential
10	Oxford Nanopore metagenomics	Long-read microbial community characterization
11	Metagenome-assembled genomes (MAGs)	Genome binning and reconstruction from metagenomes
12	Microbial resistome analysis	Antimicrobial resistance gene profiles
13	Biogeochemical functional analysis	Potential roles in carbon, nitrogen and other cycles
14	Metatranscriptomic sequencing	Active RNA expression within communities
15	Metavirome sequencing	Characterization of viral sequence diversity
16	Microbial comparative genomics	Genome similarities, differences and phylogeny
17	Bacterial draft / complete genomes	Isolate genome assembly and gene annotation
18	Fungal draft / high-quality genomes	Fungal genomic assembly and analysis
19	Bacterial / fungal identification	Sequence-based taxonomic identification

Genome Sequencing & Genetic Variation

#	SERVICE / METHOD	RESEARCH APPLICATION
01	Standalone DNA sequencing	Sequencing of suitable DNA libraries or DNA inputs
02	Whole-genome sequencing / resequencing	Reference-based genome-wide variation
03	Disease-focused genome resequencing	Disease-related genome-wide research
04	Cancer whole-genome sequencing	Research characterization of tumor alterations
05	Whole-exome sequencing (WES)	Variant discovery in coding regions
06	Disease-focused whole-exome sequencing	Research on coding variation in disease
07	Cancer whole-exome sequencing	Tumor coding-variant analysis for research
08	Population genetics and evolution	Diversity, ancestry and population structure
09	Genome-wide association studies (GWAS)	Genotype association with measured traits
10	Genetic linkage map construction	Genetic markers and inheritance patterns
11	Bulked segregant analysis (BSA)	Trait-associated genomic region discovery
12	SNP / InDel / structural variant analysis	Variant calling and annotation as data permit

Transcriptomics & Regulatory RNA

#	SERVICE / METHOD	RESEARCH APPLICATION
01	Eukaryotic reference-based RNA-seq	Transcript abundance and differential expression
02	Eukaryotic de novo RNA-seq	Transcript assembly without a suitable reference
03	Disease-oriented RNA-seq workflows	Molecular expression in biomedical models
04	Host-pathogen interaction transcriptomics	Expression patterns across interacting species
05	Prokaryotic strand-specific RNA-seq	Bacterial transcripts with strand information
06	Whole-transcriptome sequencing	Joint coding and noncoding RNA characterization
07	Small RNA sequencing	Short regulatory RNA profiling
08	MicroRNA expression analysis	miRNA abundance and target-related analysis
09	Long noncoding RNA sequencing	lncRNA discovery and differential analysis
10	Circular RNA sequencing	circRNA identification and comparison
11	Full-length transcriptome sequencing	Transcript isoforms and splice structure
12	mRNA + lncRNA joint analysis	Coding and long noncoding RNA relationships
13	mRNA + lncRNA + miRNA analysis	Exploratory regulatory network analysis
14	mRNA + lncRNA + circRNA analysis	Integrated circular and coding RNA relationships

Single-Cell & Spatial Omics

#	SERVICE / METHOD	RESEARCH APPLICATION
01	Single-cell RNA sequencing (scRNA-seq)	Cell-type composition, states and heterogeneity
02	Single-cell immune repertoire + RNA	TCR/BCR sequences linked to cell states
03	Single-cell ATAC-seq	Accessible chromatin and regulatory activity
04	Joint single-cell mRNA + ATAC	Integrated transcriptional and chromatin profiles
05	Spatial transcriptomics	Spatially mapped gene expression in tissue
06	High-resolution spatial transcriptomics	Detailed spatial gene expression patterns
07	Fresh frozen / FFPE spatial workflows	Tissue-specific platform options, by compatibility
08	Microbial single-cell transcriptomics	Gene expression heterogeneity in individual bacteria
09	Single-cell whole-transcriptome analysis	Broad RNA features from compatible samples

Quantitative Proteomics

#	SERVICE / METHOD	RESEARCH APPLICATION
01	DIA quantitative proteomics	Proteome-wide relative protein quantification
02	4D-DIA proteomics	Ion mobility-enhanced quantitative profiling
03	Astral-DIA proteomics	Deep protein profiling on compatible MS instrumentation
04	4D label-free proteomics	Protein quantification using 4D MS workflows
05	Label-free quantitative proteomics	Between-sample relative protein abundance
06	TMT multiplexed proteomics	Isobaric-label comparisons across sample groups
07	iTRAQ / TMT analysis workflows	Bioinformatics analysis of labeled proteomics data
08	Targeted PRM proteomics	Focused quantification of predefined protein targets
09	Deep plasma / serum proteomics	Protein biomarker discovery in blood specimens
10	Metaproteomics analysis	Protein signals from microbial communities

Specialized Proteomics & Drug Discovery

#	SERVICE / METHOD	RESEARCH APPLICATION
01	Phosphoproteomics	Protein phosphorylation sites and signaling pathways
02	Glycoproteomics	Protein glycosylation-associated modifications
03	Lactylation proteomics	Lysine lactylation modification profiling
04	Acylation proteomics	Selected novel acylation modifications
05	Acetylation proteomics	Protein acetylation profiles
06	Ubiquitination proteomics	Ubiquitination-related protein modification
07	SUMOylation proteomics	SUMO-associated protein modification
08	Limited proteolysis MS (LIP-MS)	Proteome structural changes and target exploration
09	Thermal proteome profiling (TPP)	Protein thermal stability changes after perturbation
10	Regional spatial proteomics	Protein signatures in selected tissue regions
11	Serial-section spatial proteomics	Protein patterns across spatially resolved tissue cuts
12	Single-cell proteomics	Protein profiling at individual cell level
13	Exosome / extracellular vesicle proteomics	Protein cargo in isolated vesicles
14	Immunopeptidomics	MHC-presented peptide identification
15	Biological peptidomics	Naturally occurring peptide identification and quantification

Metabolomics, Lipidomics & Targeted Panels

#	SERVICE / METHOD	RESEARCH APPLICATION
01	LC-MS untargeted metabolomics	Broad small-molecule detection and comparison
02	GC-MS untargeted metabolomics	Volatile and derivatized metabolite profiling
03	Targeted metabolomics	Preselected analyte panels and quantification
04	Untargeted lipidomics	Broad lipid-class characterization
05	Targeted lipid / lipid-class profiling	Focused lipid measurements where available
06	Spatial metabolomics	Spatial distribution of metabolites in tissue
07	Volatile metabolomics	Volatile compound signatures
08	Plant metabolomics	Metabolites related to plant biology
09	Bile acid profiling	Bile acid panels
10	Amino acid profiling	Free amino acid abundance
11	Short-chain fatty acid profiling	Microbiome-associated SCFA measurements
12	Long-chain fatty acid profiling	Selected fatty acid panels
13	Steroid hormone profiling	Selected steroid hormones
14	Ceramide and sphingolipid panels	Selected ceramide metabolites
15	Acylcarnitine profiling	Fatty-acid transport and oxidation markers
16	Catecholamine profiling	Selected catecholamine metabolites
17	TMAO-related metabolite profiling	Gut microbial metabolism-associated molecules
18	Organic acid profiling	Organic acid panels
19	Fat-soluble vitamin analysis	Lipophilic vitamin profiling
20	Water-soluble vitamin analysis	Hydrophilic vitamin profiling
21	Gut microbiota-related metabolite panels	Preselected microbial-associated metabolites
22	Flavonoid profiling	Selected plant secondary metabolites
23	Plant hormone profiling	Plant regulatory metabolites

Bioinformatics & Multiomics Integration

#	SERVICE / METHOD	RESEARCH APPLICATION
01	Read processing and quality control	Sequencing quality, filtering and QC reports
02	Reference alignment and de novo assembly	Genome / transcript assembly and mapping
03	Gene / variant functional annotation	Gene annotation, enrichment and variant reporting
04	Differential expression and pathway analysis	Gene sets, pathways and network interpretation
05	Microbiome composition and diversity	Alpha / beta diversity and taxon comparisons
06	Shotgun metagenomic pathway profiling	Functional potential and differential functions
07	Microbial MAG / resistome workflows	Assembly, binning and resistance analysis
08	Protein abundance and PTM analysis	Differential protein profiles and modification interpretation
09	Metabolomics statistics and annotation	Feature identification and multivariate analysis
10	Single-cell cell-state and trajectory analysis	Cell clustering and exploratory state changes
11	Spatial transcriptome analysis	Spatial clustering and gene feature patterns
12	Microbiome + metabolome integration	Associations between microbial and chemical profiles
13	Transcriptome + proteome integration	RNA and protein-level concordance
14	Transcriptome + metabolome integration	Gene expression–metabolite associations
15	Transcriptome + proteome + metabolome	Multi-layer integrated research interpretation
16	Customized data visualization and reports	Publication-oriented figures and clear summaries



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