XPLORER™ PROGRAM

Microbiome Xplorer™

Know how a treatment, a diet or a product reshapes a microbial community, and how the host responds.

From sampling to interpretation, Microbiome Xplorer™ shows which communities change, which functions they carry and which host signals follow, all measured on one collection. Gut, skin, oral, respiratory and environmental matrices.

4
molecular layers on the same samples

2
metagenomic routes: 16S and shotgun

In-house · on site
metatranscriptomics in-house, metabolomics on site

WHAT THE PROGRAM ANSWERS The questions it answers

Species names say who is there, functions say what they can do, host markers say whether it matters. Microbiome Xplorer reads the three on the same samples, so the chain from intervention to host is tested link by link rather than assumed.

01 Communities
Which communities change with the treatment, the diet, the product or the infection, and by how much?

02 Functions
Which functions do they carry, and are those functions actually expressed?

03 Host
Which microbial products reach the host, and which host signals respond?

04 Persistence
Does a strain engraft, for how long, and does the effect last once intake stops?

WHERE IT IS USED

Nutrition and probiotics · Gut–brain axis · Skin microbiome and cosmetics · Oral and respiratory microbiome · Infectious diseases and antimicrobial resistance · Host–pathogen interactions · Environmental and biofilm samples

OMICS LAYERS Layers combined according to the question

Metagenomics

Composition, diversity and differential abundance with 16S; functional potential, strains and resistance genes with shotgun. Depth is set by the question.

- **16S** composition
- **Shotgun** functions · strains
- **Resistome** resistance genes

Metatranscriptomics

Which microbial pathways are actually expressed, and the host's response read from the same material.

- **Expressed functions** RNA
- **Host and microbes** one sample
- **Curated modules** e.g. gut–brain

Metabolomics

Microbial products measured in stool and plasma, such as short-chain fatty acids and tryptophan metabolites.

- **Stool metabolome** community output
- **Plasma metabolome** what reaches the host
- **Targeted metabolites** e.g. butyrate, indoles

Host markers

Host transcriptome by bulk RNA-seq, proteins by label-free LC-MS/MS performed on site on a timsTOF Pro 2, and inflammation or stress markers chosen with you.

- **Host transcriptome** bulk RNA-seq
- **Proteomics** timsTOF Pro 2 · on site
- **Targeted markers** qPCR · dPCR

Sampling is standardized with you before the first sample is collected: matrices, timepoints, collection and storage protocols.

WORKFLOW How a program runs

01
Design and sampling
Matrices, timepoints and collection protocols chosen for the question.

02
Extraction and QC
Protocols chosen per matrix, including low-biomass samples where a standard extraction loses the signal.

03
Profiling
16S or shotgun metagenomics and metatranscriptomics run in-house, metabolomics on site, with host markers on the same participants and timepoints.

04
Integration
Taxa, functions, metabolites and host markers linked by sample and timepoint, and set against the clinical or product context.

05
Interpretation
A mechanism map stating which links of the chain are supported, partial or not shown.

DELIVERABLES What you receive

Data	Raw data (FASTQ, MS files) and taxonomic, strain, functional, metabolite and host-marker tables linked by sample and timepoint.
Analysis	Diversity, differential abundance and functional analyses, with tool versions, parameters and thresholds for every step.
Mechanism	A mechanism map and, where relevant, a strain-tracking report on engraftment and persistence.
Report	Interpretation written against your question, with publication-ready figures, delivered as a signed, time-stamped PDF.

PRACTICAL TERMS

Signature	Signed and time-stamped PDF
Data	Data is hosted in the EU, with backups in France, a separate space per team
Confidentiality	Mutual NDA available before any detail is shared, at no charge
AI	Models on our servers, no data sent to an external AI

TURNAROUND Turnaround, in working days from GO

STANDARD PROJECT
4–6 weeks
The usual pace for a project, confirmed in the quote.

PRIORITY
2–4 weeks
When your schedule requires it, agreed at scoping and confirmed in the quote.

Counted in working days from GO, given once samples have passed visual QC on receipt. Larger programs are planned in milestones, each with its own date.

ILLUSTRATED CASE STUDY See the program at work

CASE STUDY · GUT–BRAIN AXIS

Following the gut–brain chain: what a probiotic changes, and how the host responds

Key result Transient engraftment; butyrate, GABA and indole functions up; tryptophan shifted towards indoles; no change in inflammation or cortisol.

Illustrative scenario, not a client project

genxmap.com/resources/microbiome-xplorer-gut-brain.html

QUOTES AND PROJECTS
sales@genxmap.com
+33 7 69 44 16 18

SAMPLES, PROTOCOLS, QC
lab@genxmap.com
+33 4 13 73 24 81

LABORATORY
GENXMAP, IHU Méditerranée Infection
19-21 boulevard Jean Moulin
13005 Marseille, France