XPLORER™ PROGRAM

Biomarker Xplorer™

Find the markers that separate two groups, and confirm them before you build on them.

Biomarker Xplorer™ reads DNA, RNA and proteins against the same question, from the isolation of biomolecules to a short list of candidates confirmed by targeted quantification. Designed by GENXMAP and run in our Marseille laboratories. Single-cell and spatial transcriptomics are available through Transcriptomics 360.

3
levels of analysis: DNA, RNA, proteins

>95%
alignment to the reference transcriptome

20k+
genes profiled per sample

WHAT THE PROGRAM ANSWERS The questions it answers

A single data layer, genomic, transcriptomic or proteomic, captures only part of a biological mechanism. Biomarker Xplorer combines them, so a candidate is supported by more than one measurement before it is confirmed on its own.

01 Discovery
Which molecular features separate your groups: patients and controls, responders and non-responders, treated and untreated?

02 Mechanism
Which pathways and cell programs sit behind the signature, and do DNA, RNA and protein point the same way?

03 Confirmation
Which candidates hold up when measured by a targeted assay on more samples, or on a cohort they were not derived from?

04 Decision
Which short list is worth developing, and which candidates should be dropped now, with the evidence to say why?

WHERE IT IS USED

Oncology and cancer · Rare and genetic diseases · Immunology and inflammation · Pharmacogenomics and treatment response · Experimental models and CRISPR validation · Translational research and precision medicine · Neurology and neurodegeneration · Environment and microbiota · Molecular toxicology

OMICS LAYERS Layers combined according to the question

Genomics (DNA)

Somatic and germline variants, copy number and mutational signatures, summarized per sample and per group.

- **WGS · WES** genome, exome
- **Targeted panels** amplicons
- **Copy number** signatures

Transcriptomics (RNA)

Bulk RNA-seq profiles more than 20,000 genes per sample, with more than 95% of reads aligned to the reference transcriptome.

- **Bulk RNA-seq** in-house
- **Single-cell and spatial** through Transcriptomics 360

Proteomics

Protein-level quantification by label-free LC-MS/MS, performed on site on a timsTOF Pro 2 (Bruker), matched against the transcriptomic result.

- **timsTOF Pro 2** on site
- **RNA–protein agreement** per candidate

Targeted confirmation

Selected candidates measured by targeted assays on the full sample set, following MIQE and dMIQE guidance.

- **RT-qPCR** expression
- **Digital PCR** absolute quantification
- **Amplicon panels** DNA markers

Single-cell and spatial transcriptomics are available through Transcriptomics 360.

WORKFLOW How a program runs

01
Question and design
Groups, sample size and the split between discovery and confirmation are set before a single sample is run.

02
Isolation and QC
DNA, RNA and proteins extracted from tissues, blood, cells or biofilms; purity, concentration and integrity (RIN, RQN) checked before anything is sequenced.

03
Discovery
Bulk RNA-seq in our laboratories for global expression profiles, with genomics and proteomics where the question needs them.

04
Bioinformatics and integration
Versioned pipelines, differential analysis, GO, KEGG and Reactome enrichment and multi-omics integration narrow thousands of features to a testable few.

05
Targeted confirmation
The short list is measured by qPCR or dPCR on the full sample set, and read against the question the study started from.

DELIVERABLES What you receive

Data	FASTQ, alignments, variant and expression matrices, quality-controlled and documented.
Analysis	Differential analysis, enrichment and integration results, with tool versions, parameters and thresholds for every step.
Candidates	A ranked short list, each candidate mapped to a confirmation assay, and a documented no-go on those that did not hold up.
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 · IMMUNO-ONCOLOGY
Finding, and confirming, markers of response to checkpoint blockade
Key result 7 confirmed markers combined in one locked score; held-out AUC 0.78 against 0.62 for PD-L1 IHC alone.
Illustrative scenario, not a client project
genxmap.com/resources/biomarker-xplorer-immuno-oncology.html

QUOTES AND PROJECTS
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