

Some features of Acobiom services

Transcriptomics - Gene expression

- RNA-seq
- qRT-PCR
- DGE / SAGE-like method
- Small RNA, miRNA, coding and non coding RNA

Sequencing - NGS

- Whole Human Genome Sequencing
- De Novo Sequencing
- Targeted Resequencing
- SNPs analysis
- ChIP-seq analysis
- EST library construction

Bioinformatics - Biostatistics

- Treatment and analysis of transcriptomic data
- Biostatistical analyses through customized algorithms
- In-silico investigations for targets and biomarkers discovery
- Biomarker validation through the MaRS database (27,000 human RNA-Seq)

Over 18 years Experience
combined with
A Customized Approach

The Objective:
Making Sense to Biological Data

For any query or demand concerning:

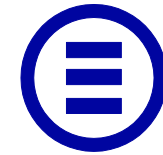
- ☞ **Genomics**
- ☞ **Transcriptomics**
- ☞ **Sequencing**
- ☞ **Bioinformatics**
- ☞ **Biostatistics**
- ☞ **Omics Big Data analyses**

Please contact:



Acobiom has obtained the label
"organisme agréé CREDIT IMPÔT RECHERCHE"
from the French Ministry of Research & Technology

Tel: +33 (0)467 419 748
Email: info@acobiom.com
Web: www.acobiom.com
Address: 1682, rue de la Valsière - CS77394
Cap Delta - Biopole Euromédecine II
34184 Montpellier Cedex 4 - France



ACOBBIOM

Omics Expertise
dedicated to
High Added Value
Services



ACOBBIOM

Tel: +33 (0)467 419 748
Email: info@acobiom.com
Web: www.acobiom.com

References: Partners & Clients

Antidoping agencies (AMA, USADA, AFLD): Discovery & validation of blood biomarkers (EPO drug abuse)

Aveyron Labo: Development of a qPCR diagnostic

CEA Cadarache: Arabidopsis thaliana genome annotation

Centre Européen du Cheval de Mont le Soie: Discovery & clinical validation of blood biomarkers for early detection of osteochondrosis disease

Inserm: Identification of MicroRNAs associated with the regulation of the human cumulus-oocyte complex

CIRAD-EMVT: Discovery of biomarkers of resistance in trypanosoma infection

CIRAD/COFEDIT: Bioinformatic developments for target sequences identification in coffee genome editing

CIRAD/UMR DAP: Tagging of small RNA libraries

CRIOBE: analysis of taxonomic diversity of bacterial communities associated with corals

IFREMER: Discovery & validation of transcriptomic biomarkers in infectiology/immunology & biomineralization process of prism & nacre deposition of the pearl oyster shell

INRA/UMR BDR 1198: qPCR analyses to evaluate blood transcriptomic biomarkers in osteochondrosis

IRD/UR121 GDP/UMR5096 LGDP: Transcriptomic analyses of host pathogen interaction

ISEM/UMR 5554: Fish genome sequencing & transcriptomic analysis

IRD/MIVEGEC: Transcriptomic analysis in malaria

Laboratoire des Courses Hippiques: Discovery & clinical validation of blood biomarkers (EPO drug abuse)

Regentis International: Toxicogenomics in skin study

University of Bern (Institute of Ecology and Evolution): Analysis of EST libraries & transcriptomic libraries

University of Western Cape (SANBI): RNA-Seq libraries construction on Illumina platform

University of Heidelberg (Medical Faculty Mannheim): Bioinformatic analysis of stems cells model

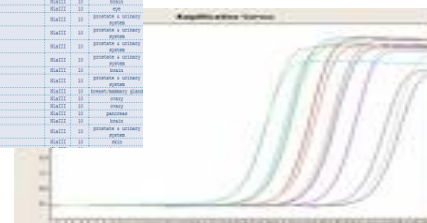
Examples of biological data processing, of genomics & bioinformatics data analysis

Sequencing of RNA-Seq, micro RNA and DGE libraries, treatment and analysis of the results, and setting-up of a customized web access tool to manage the data.



Performing of **qRT-PCR** experiences and analysis of the results by bioinformatics and biostatistical tools.

Library ID	Accession	FPKM	CPM	CPM
SIAS_2110_076	SIAC11	10	10	10
SIAS_2110_078	SIAC11	10	10	10
SIAS_2110_079	SIAC11	10	10	10
SIAS_2110_080	SIAC11	10	10	10
SIAS_2110_081	SIAC11	10	10	10
SIAS_2110_082	SIAC11	10	10	10
SIAS_2110_083	SIAC11	10	10	10
SIAS_2110_084	SIAC11	10	10	10
SIAS_2110_085	SIAC11	10	10	10
SIAS_2110_086	SIAC11	10	10	10
SIAS_2110_087	SIAC11	10	10	10
SIAS_2110_088	SIAC11	10	10	10
SIAS_2110_089	SIAC11	10	10	10
SIAS_2110_090	SIAC11	10	10	10
SIAS_2110_091	SIAC11	10	10	10
SIAS_2110_092	SIAC11	10	10	10
SIAS_2110_093	SIAC11	10	10	10
SIAS_2110_094	SIAC11	10	10	10
SIAS_2110_095	SIAC11	10	10	10
SIAS_2110_096	SIAC11	10	10	10
SIAS_2110_097	SIAC11	10	10	10
SIAS_2110_098	SIAC11	10	10	10
SIAS_2110_099	SIAC11	10	10	10
SIAS_2110_100	SIAC11	10	10	10



Development of a chain of **bioinformatics** treatments, algorithms, databases and web access tools to process data obtained by different high throughput sequencer systems.

Publications

PLoS One 2016: *Lipid Droplet Formation, Their Localization and Dynamics during Leishmania major Macrophage Infection.* Rabhi et al.

Ann Oncol. 2015: *A randomized, placebo-controlled phase III trial of masitinib plus gemcitabine in the treatment of advanced pancreatic cancer.* Deplanque et al.

BMC Genomics 2013: *Comparative analysis of resistant and susceptible macrophage gene expression response to Leishmania major parasite.* Rabhi et al.

PLoS Negl Trop Dis. 2013: *MicroRNA expression profile in human macrophages in response to Leishmania major infection.* Lemaire et al.

Hum Reprod. 2013: *MicroRNAs: new candidates for the regulation of the human cumulus-oocyte complex.* Assou et al.

Eur J Hum Genet. 2013: *The intellectual disability of trisomy 21: differences in gene expression in a case series of patients with lower and higher IQ.* Megarbane et al.

Proc Natl Acad Sci U S A. 2012: *Different secretory repertoires control the biomineralization processes of prism and nacre deposition of the pearl oyster shell.* Marie et al.

PLoS One 2012: *Of mice and men: divergence of gene expression patterns in kidney.* Cheval et al.

PLoS Negl Trop Dis. 2012: *Transcriptomic signature of leishmania infected mice macrophages: a metabolic point of view.* Rabhi et al.

BMC Genomics 2012: *A hemocyte gene expression signature correlated with predictive capacity of oysters to survive Vibrio infections.* Rosa et al.

J Proteomics 2012: *Large-scale discovery of conopeptides and conoproteins in the injectable venom of a fish-hunting cone snail using a combined proteomic and transcriptomic approach.* Violette et al.

Br J Haematol. 2012: *New prognostic markers, determined using gene expression analyses, reveal two distinct subtypes of chronic myelomonocytic leukaemia patients.* Bou Samra et al.