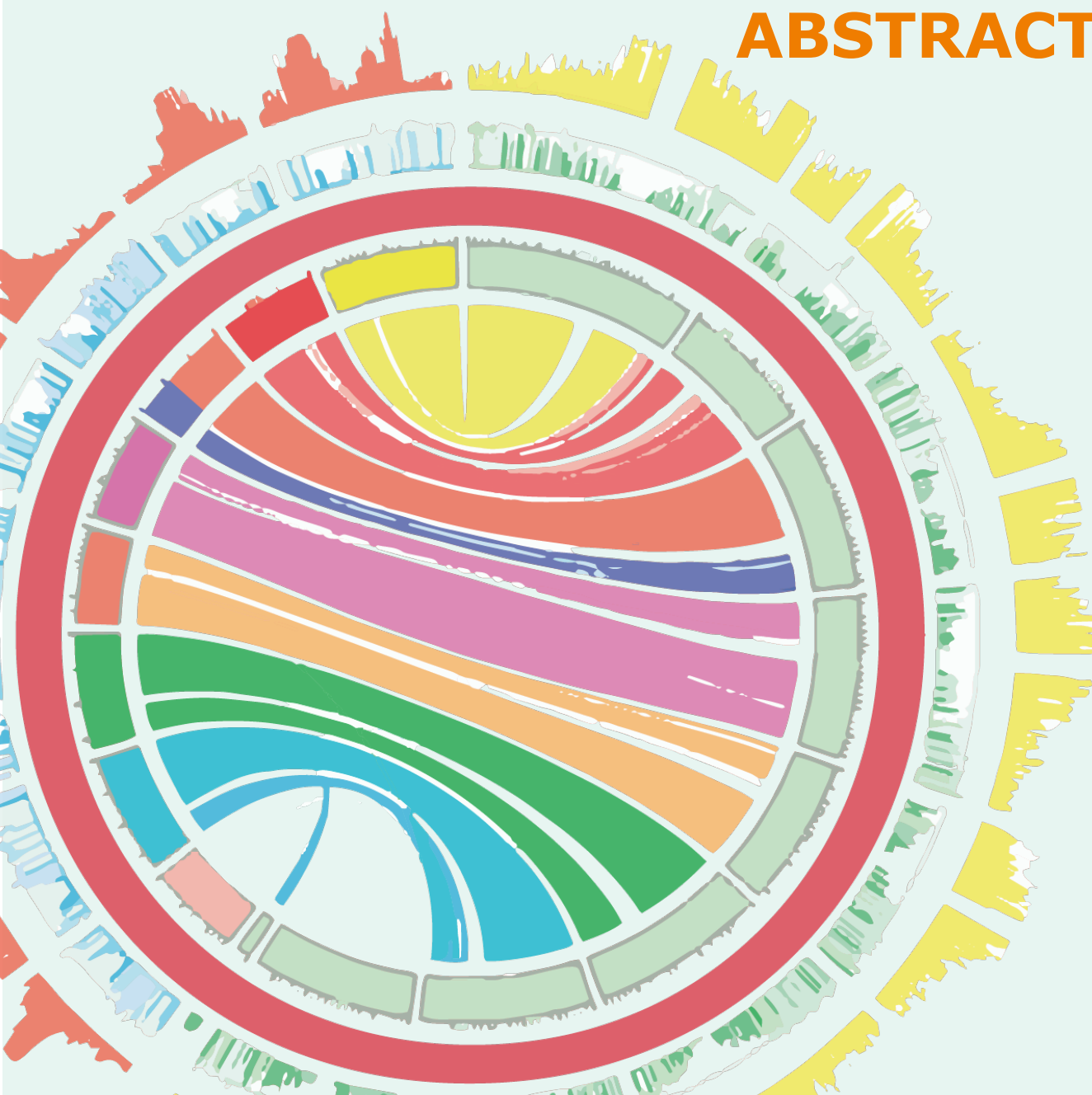


JOURNÉES OUVERTES DE BIOLOGIE INFORMATIQUE & MATHÉMATIQUES



03>06 JUIL
PALAIS DU PHARO | MARSEILLE

ABSTRACTS



Marseille, June 20, 2018

Welcome to the 480 attendees of the 2018 JOBIM edition!

Eleven years after the first JOBIM edition organized in Marseille, here we are again. Since then, the bioinformatics field and its community have notably grown up as reflected by the numbers of attendees and submissions: we have received 263 abstracts for communications that will be presented as 46 talks and 217 posters.

This year, the conference is divided in five main sessions, that will be all opened by a keynote talk by **Ludovic Orlando**, **Pierre-Antoine Gourraud**, **Eleftheria Zeggini**, **Edda Klipp**, **Emmanuel Levy** and **Elizabeth Purdom**, respectively. We tremendously thank them to have accepted to participate and to contribute to the success of this Marseilles edition.

In addition to the simplified submission format, the novelties this year lie in the diversity of the poster tracks to highlight and cover the work of the whole community (Research, Service and Platform activity, Thematic networks, Working groups and Associations) and in the return of the flash poster presentations.

We sincerely thank all the members of the Program Committee who helped us to set up such a great program and reviewed all submissions in time. This task would have been impossible without you!

We are indebted to the organizing institutions and all our partners and sponsors for their financial supports.

For their daily efforts for the past 18 months, we thank the local Inserm administration, and Christa Roqueblave Conseil and Myriam Ramadour for their unfailing professionalism and assistance...Finally, many thanks to the local organizing committee.

Enjoy JOBIM 2018!

Christine Brun & Benoit Ballester

ORGANIZED BY



PARTNERS & SPONSORS



Sponsors posters



Facilitating bioinformatics analyses by combining artificial and collective intelligence

Recent breakthroughs in biological technics have generated massive amounts of complex data in biology and health. Handling, processing and storing information

have become new challenges for biologists. Addressing the challenge of identifying the best resources to handle biological big data, we created a decision-making web platform for bioinformatics resources. To do so, we followed a three-fold approach:

First of all, we built a database for bioinformatics resources fed by manual curation. Its specificity lies in a categorization of resources by application and analysis step. Each tool possesses its own page featuring technical and scientific information as well as community feedback.

Then, we added a layer based on artificial intelligence to automatically display optimal pipelines of tools for any biological question asked via the integrated search engine. They are generated using a combination of machine learning, manual curation and community feedback. The sequence can evolve in real-time if suggested tools are switched or optional analysis steps added. We also implemented various filters to match the user IT skills level or favorite operating system for example.

Ultimately, we developed a feature to easily run analysis on a secured cloud from the generated pipelines. When uploaded, files are analyzed beforehand to ensure compatibility, then required software are installed on containers before being used for the analysis.

By bridging artificial and collective intelligence, we offer a solution to facilitate bioinformatics analyses in a rapidly evolving field.

<https://omictools.com/>



GenoScreen is a French biotech company that specializes in genomics and bioinformatics.

Since 2001, we have offered innovative services and solutions (Based on the characterization and exploitation of DNA/RNA) to research groups from the private and public sectors.

GenoScreen works on all kinds of genomes (Human, animal, plant and microbial genomes) and delivers solutions for human healthcare, the agrifood industry, the environmental sector, and the cosmetics industry.

Our R&D and Innovation department's highly qualified staff are committed in the development of dedicated molecular and analytical solutions in the field of microbial genomics. GenoScreen constantly interacts with top-level academic research teams, in order to maintain its cutting-edge expertise and offer high-quality services and products to its customers.

<https://www.genoscreen.fr/>

Table of contents

Bioinformatics for Bugs, Beasts and Greens	19
---	-----------

Oral Communications

The evolution of large and giant viruses and their relationships with Eukaryotes, Julien Guglielmini [et al.]	20
Co-option of complex molecular system in bacterial and archaeal membrane, Rémi Denise [et al.]	22
A new rapid, flexible and intuitive software to simulate phylogenies of infections, Gonché Danesh [et al.]	24
Combining eDNA metabarcoding and supervised machine learning for routine environmental applications: an example with marine aquaculture, Tristan Cordier	26
MACADAM a user-friendly MetAboliC pAthway DATabase for complex Microbial community function analysis, Malo Le Boulch [et al.]	27
Probabilistic PCA for count data in microbial ecology, Mahendra Mariadassou [et al.]	30
Single-cell genome study of marine protists in the framework of the Tara Oceans project, Léo D'agata [et al.]	33
PPanGGOLiN: Depicting microbial diversity via a Partitioned Pangenome Graph, Guillaume Gautreau [et al.]	35
Comparative metagenomics highlighted a core of metabolic capabilities in multiple serpentinizing ecosystems, Eléonore Frouin [et al.]	39
Assembling the genome of the desert ant and uncovering structural rearrangements with instaGRAAL, a fast and scalable scaffolder based on Hi-C data, Lyam Baudry [et al.]	42

	CARNAC-LR : Clustering coefficient-based Acquisition of RNA Communities in Long Reads, Camille Marchet [et al.]	43
Posters		
1	The genome assembly of a hot ammonia-oxidizing archaeon illuminates the origins of Thaumarchaeota's evolutionary success., Sophie Abby [et al.]	46
2	Metagenomic analysis of ancient DNA from dental calculus, Céline Bon [et al.] .	47
3	Gene expression analysis of duck liver steatosis from hybrid and parental species, Xi Liu [et al.]	50
4	Développement et optimisation d'un outil de simulation en C++ de données génomiques en populations spatialisées, Thimothée Virgoulay [et al.]	52
5	Discovering Millions of Plankton Genomic Markers from the Atlantic Ocean and Mediterranean Sea, Majda Arif	54
6	Introducing Metavariant Species for Reference-Free Population Genomics Analysis using Metagenomics, Laso-Jadart Romuald [et al.]	55
7	Bacterial genomes assembly using PacBio long read technologies, Sophia Achai-bou [et al.]	56
8	Data Integration and VISualization (DIVIS) : from large heterogeneous datasets to interpretable visualisations in plant science, Ophélie Thierry [et al.]	57
9	Detection and Characterization of Genomic Variations using Running Median and Mixture Models: application to CNV detection., Thomas Cokelaer [et al.] . .	60
10	TRANS-C3 - The Transcriptome of downy oak (<i>Quercus pubescens</i> Wild) in Response to Climate Change, Xi Liu [et al.]	63
11	PiRATE v2: detection, classification and annotation of transposable elements of non-model organisms, Jérémy Berthelie [et al.]	65
12	Metabarcoding on the deep seafloor: optimizing multigene approaches for large-scale biodiversity assessments, Caroline Dussart [et al.]	67
13	Building a Metatranscriptomics Strategy to explore Insect Vectors in Africa, Vanesa Assele Koghe [et al.]	71
14	Assessing the datation of gene duplication in vertebrates and its link with species diversification, Guillaume Louvel [et al.]	73

15	IDENTIFICATION OF CORE-GENOME OF ASIAN RICE AND THE IM- PACTS OF DOMESTICATION ON THIS CORE-GENOME, Nguyet Dang [et al.]	74
16	Evaluation of different approaches for plasmid detection from genome assem- blies, Brice Letcher [et al.]	76
17	ProkTE: A web server for large-scale analysis of genetic context associated to the insertion sequences and their putative roles, Sebastien Tempel [et al.]	79
18	A high-quality genomic database for clinical pathogens outbreak monitoring using NGS technology, Aurélien Griffon [et al.]	80
19	PathostDB - Base de donnée légère d'interactions hôtes-pathogènes de plantes, Maira Barca [et al.]	83
20	Using metabarcoding data to reveal the distribution and interactions of cyanobac- teria in the oceans, Ewen Corre [et al.]	86
21	High intraspecific genome diversity in the model arbuscular mycorrhizal symbiont Rhizophagus irregularis, Emmanuelle Morin	87
22	AquaPony: visualization of phylogeographic information on phylogenies, Bastien Cazaux [et al.]	88
23	Développement d'outils pour la détection de variants génomiques dans le cadre d'analyses de pan-génomés, Amad Diouf [et al.]	90
24	Mise au point d'approches d'analyses génomiques de novo avec la technologie long read Oxford Nanopore, Valentin Klein [et al.]	92
25	A new multiple nucleotide sequence exact search tool for performing fast core- genome Multi-Locus Sequence Typing, Yoann Dufresne [et al.]	94
26	Comparative study of RNA-Seq analyses based on the genome or transcriptome as reference, Florent Tessier [et al.]	97
27	How to improve genome assembly using repetitive elements., Quentin Delorme [et al.]	98
28	An -omics search for viruses infecting the phytoparasitic nematode <i>M. incog- nita</i> , Marc Bailly-Bechet [et al.]	100
29	Contribution of Oxford NanoPore technology for the de novo genome assembly of non-model species: the case of the Asian ladybird <i>Harmonia axyridis</i> , Jacques Lagnel [et al.]	101

30	Coevolution analysis finds amino-acids involved in immune evasion in Hepatitis B Virus., Elin Teppa [et al.]	103
31	Microbiote et santé : impact des nouveaux pipelines bio-informatiques en métagénomique ciblée, Benoit Goutorbe [et al.]	107
32	GENOTOUL BIOINFO PLATFORM, Claire Hoede [et al.]	110
33	Transcriptomics analysis using Long Read sequencing, Rachel Legendre [et al.]	112
34	The Migale bioinformatics platform, Valentin Loux [et al.]	113
35	BIPAA, Bioinformatics Platform for the Agroecosystems Arthropods., Stéphanie Robin [et al.]	115
36	Sequanix: a dynamic graphical interface for Snakemake workflows, Thomas Cocklaer [et al.]	117
37	Bioconvert: a collaborative bioinformatics format converter library., Anne Biton [et al.]	118
38	Novel approaches for phylogenetic analysis of NGS data, Yannick Antoine [et al.]	119

New challenges for bioinformatics in the personalized medicine era 121

Oral Communications

Identification de marques épigénétiques marqueurs de prédisposition aux maladies métaboliques, Jérémy Tournayre [et al.]	122
I-LowVarFreq : improving low-frequency variant detection using a new UMI-based variant calling approach for paired-end sequencing NGS libraries., Pierre-Julien Viailly [et al.]	126
Perturbed human sub-networks by <i>Fusobacterium nucleatum</i> candidate virulence proteins, Andreas Zanzoni [et al.]	128
Sarek, a portable workflow for WGS analysis of germline and somatic mutations, Maxime Garcia [et al.]	130
Proteomic and phosphoproteomic analysis of medulloblastoma reveals distinct activated pathways between subgroups, Loredana Martignetti [et al.]	132
From individual genetic variations towards haplotype: GEMPROT, a new way of reading VCF files, Tania Cuppens [et al.]	134

	Bayesian Genome-Wide Association Study to discover novel lifespan-associated loci, Ninon Mounier [et al.]	136
	Aggregation of rare family-specific variants associated with Rheumatoid Arthritis, Maëva Veyssiere [et al.]	138
	Unravelling human preimplantation development by single-cell RNA-Seq: from experiment design to cell fate trajectories., Dimitri Meistermann [et al.]	142
	Fine-scale genetic population structure in western France, Christian Dina [et al.]	145
Posters		
39	Exploring Chemical Space Using ChemMaps.com, Alexandre Borrel [et al.] . . .	149
40	Interpretation of mass spectrometry-based metaproteomics: how much can we trust the MetaHIT 9.9 catalog?, Ariane Bassignani [et al.]	151
41	Semantic lab. data interoperability: Encoding microbiology tests results using international biomedical onto-terminologies, Maël Le Gall [et al.]	152
42	AnnotSV: An integrated tool for Structural Variations annotation, Véronique Geoffroy [et al.]	154
43	A new protocol for sequencing and analysis of virus genomes in clinical context with amplicon-seq data., Florence Maurier [et al.]	156
44	Comparaison des approches d'étude du microbiote en contexte clinique : le séquençage 16S et le Whole Genome Sequencing, Aziza Caidi [et al.]	159
45	GDSCTools for mining pharmacogenomic interactions in cancer, Thomas Cokelaer	161
46	Multi-omics pan-cancer classification and biomarker design using machine learning, Aurélie Gabriel [et al.]	162
47	REGOVAR, logiciel libre pour l'analyse de données de séquençage haut débit pour les maladies génétiques rares, Anne-Sophie Denommé-Pichon [et al.]	165
48	Mutational landscape of synchronous and metachronous breast cancer metastases through whole exome sequencing, Zakia Tariq [et al.]	167
49	VarAFT : Un système d'annotation et de filtration pour les données issues de séquençage haut débit., Jean-Pierre Desvignes [et al.]	169
50	Deducing cellular composition of complex airway epithelia from single cell RNA-seq data phenotyping, Marin Truchi [et al.]	171

51	Skip-E : un système bioinformatique dédié au saut d'exon thérapeutique., David Salgado [et al.]	174
52	Inter-cellular gene coexpression between microglia and oligodendrocytes during microglia activation in the developing brain, Nour Touibi	176
53	BioInfuse v3, Ewen Corre [et al.]	179
54	Bioinformatics for diagnosis and clinical trials, Elodie Girard [et al.]	180
55	Molecular characterization of rhabdoid tumors based on highthroughput and multi- omics data analysis, Mamy Andrianteranagna	181
56	BaSaV: New Database for antibiotic resistance, Aurélien Birer [et al.]	183
57	Omics data analyses and integration for precision medicine applied to advanced cancers, Arnaud Guille [et al.]	185
58	MobiCNV : a simple and rapid method for detecting Copy Number Variants in Illumina gene panel, clinical exome and exome data, Henri Pégeot [et al.]	187
59	MPA, a free, accessible and efficient pipeline for SNV annotation and prioritization for NGS routine molecular diagnosis., Kevin Yauy [et al.]	189
60	Développement d'un pipeline bioinformatique en oncogénétique clinique: sélection des outils, validation de seuils et exigence des normes, Quentin Da Costa	191
61	Application pour une lecture et une gestion facilitées des données brutes générées lors de l'analyse d'un panel CFTR par NGS, Laetitia Gaston [et al.]	193
62	A centralized web interface for genomic medicine labs, Gaelle Vilchez [et al.] . . .	195
63	SHAMAN : a shiny application for quantitative metagenomic analysis, Amine Ghoulane [et al.]	197
64	FI-MICS test: innovative tool for Cardiac enriched lncRNAs measurement, Sami Ait Abbi Nazi [et al.]	198
65	RABIOPRED, an innovative theranostic tool to assist clinicians select an optimal anti-TNF alpha biological therapy for Rheumatoid Arthritis Patients, Eric Schordan [et al.]	200
66	Rencontre autour de l'Enseignement en BioInformatique en France (REBIF 2018), Morgane Thomas-Chollier [et al.]	202
67	JeBiF fête ses 10 ans !, Florence Jornod [et al.]	204

68	Association des Jeunes Bioinformaticiens de France, Florence Jornod [et al.] . . .	205
69	Taking genomics into the clinic: whole genome sequence of 13,000 patients with a rare disorder., Karyn Megy [et al.]	207

Systems Biology/Functional Genomics 209

Oral Communications

A map of direct TF – DNA interactions in the human genome, Marius Gheorghe [et al.]	210
---	-----

Multilevel logical modelling of the regulatory network governing dorsal-ventral axis specification in the sea urchin <i>P. lividus</i> ., Swann Floc'hlay [et al.]	215
--	-----

ReMap 2018: an updated atlas of regulatory regions from an integrative analysis of DNA-binding ChIP-seq experiments, Jeanne Chèneby [et al.]	217
--	-----

Logical modelling and analysis of cellular regulatory networks with GINsim 3.0, Aurélien Naldi [et al.]	220
---	-----

PhyloSofS: PHYLOgenies of Splicing isOForms Structures, Adel Ait-Hamlat [et al.]	222
--	-----

Prediction of new multiciliogenesis genes using a fine-grained comparative genomic approach, Audrey Defosset [et al.]	225
---	-----

RSAT 2018: regulatory sequence analysis tools 20th anniversary, Nga Thi Thuy Nguyen [et al.]	229
--	-----

Predicting 3'UTR's regulation of protein multifunctionality, Diogo Ribeiro [et al.]	231
---	-----

Enhancer-gene associations in complete genomes unravel ancestral vertebrate regulation and key principles of enhancer function, Yves Clement [et al.]	234
---	-----

Multiple probabilistic models resolve the functional organization of the cryptochrome/photolyase protein family, Riccardo Vicedomini [et al.]	236
---	-----

Statistical modeling of bacterial promoter sequences for regulatory motif discovery using expression data, Ibrahim Sultan [et al.]	240
--	-----

Mathematical modeling of Fe-S biogenesis shows strong links between iron homeostasis and oxidative stress response, Firas Hammami [et al.]	241
--	-----

Biocuration and rule-based modelling of protein interaction networks in KAMI, Sébastien Légaré [et al.]	243
---	-----

Build your own multi-omics website with BACNET, Christophe Becavin [et al.] . 248

Gigwa - Genotype Investigator for Genome-Wide Analyses, Guilhem Sempéré [et al.] 251

Posters

70 Molecular analysis and in silico research of expressed genes in relationship with salt stress tolerance in *Medicago truncatula* Gaertn., Adel Amar Amouri 253

71 A Novel Computational Approach for Global Alignment for Multiple Biological Networks, Warith-Eddine Djeddi [et al.] 254

72 The genome of the Microsporidia *Nosema granulosis*, an endosymbiotic feminizing parasite of amphipod crustaceans., Alexandre Cormier [et al.] 255

73 Characterization of the drug resistances in *Salmonella enterica* serovar Typhi isolated from Bangladesh, Emilie Westeel [et al.] 256

74 Pan-genomic analysis to redefine species and subspecies, Aurélia Caputo [et al.] . 258

75 ToulligQC: A MinION run data analysis tool, Berengere Laffay [et al.] 259

76 An evaluation of Oxford Nanopore data in RNASeq projects, Berengere Laffay [et al.] 261

77 Comprehensive repeatome annotation reveals strong potential impact of repetitive elements on tomato ripening, Ophélie Jouffroy [et al.] 263

78 A tool to genotype individuals and assemble allelic sequences at highly polymorphic loci from raw NGS reads data: application to the self-incompatibility locus of Brassicaceae, Mathieu Genete [et al.] 265

79 Extraction of biologically meaningful patterns from high-dimensional omics data, a platform based on Self-Organizing Maps, Shingo Miyauchi [et al.] 266

80 Deciphering the origins of enzymes substrate specificity using large-scale sequence analyses, Clothilde Chenal [et al.] 268

81 Genetic diversity of staphylococcal strains isolated from food and enterotoxin coding genes, Arnaud Felten [et al.] 270

82 A Multiplex Network approach to Premature Aging Diseases, Alberto Valdeolivas [et al.] 271

83 Integrative visual omics of the white-rot fungus *Polyporus brumalis* exposes the biotechnological potential of its oxidative enzymes for delignifying raw plant biomass., Elodie Drula [et al.] 273

84	Context-specific prioritization of non-coding variants implicated in human diseases, Lambert Moyon [et al.]	276
85	Characterization of Escherichia coli K-12 regulatory networks by bioinformatics integration of high-throughput data, Claire Rioualen [et al.]	277
86	Knowledge management and standard representation of causal statements: new resources for systems modelling, Vasundra Touré [et al.]	280
87	Dynamical modelling of T cell co-inhibitory pathways to predict anti-tumour responses to checkpoint inhibitors, Celine Hernandez [et al.]	282
88	The vanishing Gram-positives: a third lineage with outer membranes in the Firmicutes, Najwa Taib [et al.]	284
89	Characterization of mutations that dysregulate driver microRNAs in breast cancer, Jaime Castro-Mondragon [et al.]	286
90	The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks, Aurélien Naldi [et al.]	288
91	In-depth analysis of the impact of transposable elements on genome assembly quality, Rémy Costa [et al.]	290
92	A logical approach to identify Boolean Networks that model cell differentiation, Stéphanie Chevalier [et al.]	292
93	Alienness vs. Predictor (AvP): fast and robust detection of horizontal gene transfers across the tree of life, Corinne Rancurel [et al.]	296
94	bioLQM: a java library for the manipulation and conversion of logical qualitative models of biological networks, Aurélien Naldi	300
95	Modelling gene regulatory networks in oncogene-induced senescence, José Américo Nabuco Leva Ferreira De Freitas [et al.]	302
96	Allele-specific analysis of the effect of non-coding SNPs on gene expression during Drosophila embryonic development., Swann Floc'hlay [et al.]	305
97	Synteny-guided gene tree correction accounting for whole-genome duplication, Elise Parey [et al.]	308
98	Phylogenetic study of Macrophage Migration Inhibitory Factor (MIF) cytokines and analysis of their role in host - parasite interactions, Claire Michelet [et al.] .	310

99	New 10x Genomics and SMART-seq2 workflows for single-cell RNA-seq data analysis using Eoulsan, Geoffray Brelurut [et al.]	311
100	Transcriptomic analysis of the epipelagic copepod <i>Oithona nana</i> (Crustacea; Cyclopoida) developmental biology, Kevin Sugier [et al.]	314
101	Systems biology analysis of interaction and regulation networks in siRNA high throughput screenings., Claire Rioualen [et al.]	315
102	Search of therapeutic targets in metabolic pathways of TGF- β using graph coloring approaches, Maxime Folschette [et al.]	317
103	The reconstruction of the metabolic network of the <i>Tisochrysis lutea</i> microalgae thanks to the AuReMe workspace leads to analysis of carnosine and beta-carotene pathways, Jeanne Got [et al.]	319
104	PSSMSearch: discovery of protein motifs on a proteome-wide scale, Izabella Krystkowiak [et al.]	322
105	Gravity: a tool to analyze genetic variants in individuals using gene networks, Freddy Cliquet [et al.]	323
106	Optimization of RNA-seq differential expression analysis and transcriptome profiling of metabolism and triacylglycerol biosynthesis in a novel halotolerant <i>Chlorella</i> species, Michaël Pierrelée [et al.]	325
107	From gene expression to genomic networks : development of a user-friendly pipeline for the analysis and visualization of RNA-seq data, Ilana Lambert [et al.]	326
108	TOGGLE (Toolbox for Generic NGS Analyses) A framework to quickly build pipelines and to perform large-scale HTS analysis., Julie Orjuela [et al.]	330
109	Phage Remote Ortholog Groups (PhROG) : clustering phage proteins using remote homology, Paul Terzian [et al.]	332
110	CoRegCAD: leveraging networks for metabolic engineering, Pauline Trébulle [et al.]	333
111	Integrative analysis of genomic regulation combining cistrome, epigenome and transcriptome, Lucie Khamvongsa-Charbonnier	336
112	Building artificial genetical genomic datasets to optimize the choice of gene regulatory network inference methods., Lise Pomiès [et al.]	338
113	A Genetic Algorithm to identify biological processes deregulated in Progeria, Elva María Novoa Del Toro [et al.]	342

114	Studying tomato fruit development through reconstruction of stage specific genome scale metabolic models using proteomics and transcriptomics, Sylvain Prigent . .	344
115	IDENTIFICATION DES FACTEURS DE L'HÔTE FYN et PTPN11 IMPLIQUÉS DANS L'INFECTION PAR LE VIRUS DE L'HÉPATITE B., Mohcine Elmessaoudi-Idrissi [et al.]	345
116	Analyse du génome de tumeurs neuroendocrines par puces SNP, Mario Neou [et al.]	347
117	Integrating, visualising and jointly exploiting heteroclit knowledge to analyze omics data with NeOmics, Ludovic Léauté [et al.]	349
118	Bacterial genome mining for the discovery of new natural products, Faustine Durand [et al.]	353
119	Development of an automated pipeline to translate oligosaccharide sequences of glycosaminoglycans binding to proteins into 3D models., Olivier Clerc [et al.] . .	354
120	Measuring the expression of RNA sequences in hundreds of RNA-seq libraries at nucleotide resolution, Mariam Bouzid [et al.]	357
121	Characterization of mouse early hematopoiesis changes during aging with high throughput single-cell RNA-sequencing, Léonard Hérault [et al.]	359
122	Towards an integrated approach for the annotation of ICEs and IMEs in bacterial genomes, Julie Lao [et al.]	361
123	Characterizing transcription factor combinatorics in cis-regulatory regions with supervised classification and sparse encoding, Quentin Ferré [et al.]	363
124	CRISPR-Cas++, a webserver including tools for identification and analysis of CRISPR arrays and associated Cas proteins., David Couvin [et al.]	368
125	Understanding the gene regulatory network that directs human monocytes to dendritic cells differentiation, Karen Nuñez [et al.]	371
126	Deciphering functional annotation of multiple gene sets with MOTVIS., Aarón Ayllón-Benítez [et al.]	373
127	Identification of regulatory variants involved in the development of sepsis, Florian Rosier [et al.]	378
128	Simulation of RNA sequencIng with Oxford Nanopore Technologies, Camille Marchet [et al.]	379

129	Automatically identifying eu-hetero-chromatin boundaries through recombination rate estimates, Yasmine Mansour [et al.]	382
130	evoDRUM: a new framework to model the evolution of metabolic networks under non-balanced growth conditions, Ghjuvan Grimaud	384
131	Charting the functional regulatory landscape of human RBPs through protein-RNA interaction predictions., Andreas Zanzoni [et al.]	389
132	IBENS Genomics core facility, Laurent Jourden [et al.]	392
133	Enrichment analysis with EpiAnnotator., Yoann Pageaud [et al.]	395
134	FoodMicrobiome Transfert : Web based Metagenomic Analysis, Quentin Cavaillé [et al.]	396
135	ARTwork, a bioinformatics solution dedicated to bacterial WGS data management and analysis in the context of foodborne pathogens surveillance and outbreak investigations, Kevin Durimel [et al.]	398
136	Galaxy-based Interactive ANalysis of Transcriptomic data (GIANT): A modular Galaxy pipeline as an alternative to licenced softwares for analyzing transcriptomic data, Jimmy Vandel [et al.]	400
137	BIG: BioInformatics and Genomics platform at Institut Sophia Agrobiotech, Martine Da Rocha [et al.]	402
138	The Bioinformatics and Biostatistics Hub: first results and challenges, Damien Mornico [et al.]	405
139	The CRCM Integrative Bioinformatics (Cibi) platform, an offer of service in latest bioinformatics technologies for large scale data analysis in biology, Quentin Da Costa [et al.]	407
140	MicroScope: an integrated platform for the annotation and exploration of microbial gene functions through genomic and metabolic comparative analysis, David Vallenet [et al.]	410
141	Montpellier GenomiX (MGX) : next-generation sequencing and data analysis service and expertise, Stéphanie Rialle [et al.]	413
142	Community support for Systems Ecology, Marie Chevallier	415
143	South Green, une plateforme de bioinformatique tournée vers l'agriculture dans les pays du sud, Sébastien Ravel [et al.]	418

144	The Systems Biology Graphical Notation: a standardised representation of biological maps, Vasundra Touré [et al.]	421
145	The StatOmique group is ten years old, Marie-Agnès Dillies [et al.]	423
146	3'seq-RP : A low cost high throughput digital sequencing technique to evaluate gene expression profiles, Eric Charpentier [et al.]	424
147	Third Generation Sequencing Technologies to Decipher Genomic Structures of Recombinant-prone Viruses, Mathias Vandenberg [et al.]	428
148	Characterization of DNA replication plasticity among 12 human cell lines, Hadi Kabalane [et al.]	431

Structural Bioinformatics/Proteomics 436

Oral Communications

Assessing the functional impact of genomic alterations using proteogenomics, Georges Bedran [et al.]	437
Structural and dynamics studies of a potassium channel and disease-associated mutants, Charline Fagnen [et al.]	441
Protein interaction energy landscapes are shaped by functional and also non-functional partners, Hugo Schweke [et al.]	444
NR-DBIND : A database dedicated to nuclear receptor binding data including negative data and pharmacological profile, Manon Réau [et al.]	448
A hybrid combinatorial method for docking a single-stranded RNA in a protein pocket at the thermodynamic equilibrium, Chinmay Singhal [et al.]	450

Posters

149	Comparing protein structures with RINspector automation in Cytoscape, Guillaume Brysbaert [et al.]	455
150	Evaluation of the docking performance of open source algorithms on carbohydrate binding domains, Charlotte Brunel-Cadic [et al.]	458
151	Repository of Enriched Structures of Proteins Involved in the Red blood Cell Environment (RESPIRE), Stéphane Téletchéa [et al.]	459
152	Could MAPKs watch in the mirror? Exploring large-scale phosphoproteomics data to assess whether MAPKs could phosphorylate the Pro-(Ser/Thr) motif in addition to the canonical (Ser/Thr)-Pro motif., Emmanuelle Lastrucci [et al.] . . .	460
153	In silico protein digestion, Nicolas Maillet	465

154	ARIAEC: protein structure folding from evolutionary couplings and NMR restraints, Fabrice Allain [et al.]	468
155	MetaFoldScan: a pipeline to scan metagenomes and identify structural homologs using HMM, Sandra Dérozier [et al.]	470
156	Ligand-guided homology modelling of the GABAb2 subunit of the GABAb receptor, Thibaud Freyd [et al.]	472
157	Amino acid pair interactions in membrane proteins investigated with the statistical potential formalism, Mame Ndew Mbaye	474
158	Solubility-dependent statistical potentials to probe into the (in)solubilizing effect of residue-residue interactions in proteins, Hou Qingzhen [et al.]	478
159	Identification of additional Ser/Thr protein kinases in the genome of <i>Streptococcus thermophilus</i> using structural homology detection., Samantha Samson [et al.]	481
160	Involvement of 3D motifs in RNA secondary structure prediction, Phuong Chu [et al.]	483
161	Evaluation de l'assemblage de données Rna-seq et de la construction des bases de données protéomiques d'organismes non modèles, Yannick Cogne [et al.] . .	486
162	Analyzing RNA folding landscapes using non-redundant sampling, Juraj Michalik [et al.]	489
163	A voltage-gating mechanism in plant aquaporins, Robin Mom [et al.]	493
164	Proteins and their multiple interactions, Chloé Dequeker [et al.]	495
165	Promiscuous binding site: a frequent material of proteins, Natacha Cerisier [et al.]	498
166	Mass spectrometry data-independent acquisition (DIA/SWATH-MS) management and processing with myProMS web server, Marine Le Picard [et al.]	500
167	Advanced molecular dynamics simulations for understanding the functions and dysfunctions of the CFTR channel, Ahmad Elbahnsi [et al.]	503

Data Science	505
---------------------	------------

Oral Communications

mmquant and mmannot: How to handle multiple-mapping reads in (s)RNA-Seq, Matthias Zytnecki [et al.]	506
---	-----

RNA complex prediction as a constrained maximum clique problem, Audrey Legendre [et al.]	511
--	-----

Latent Tree based Inference of Ecological Network using the Poisson Log-Normal Model, Raphaëlle Momal [et al.]	515
--	-----

On improving the approximation ratio of the r-shortest common superstring problem, Tristan Braquelaire [et al.]	520
---	-----

Protein domain sequence analyses using Long-Short Term Memory Recurrent Neural Networks, Tristan Bitard Feildel [et al.]	524
--	-----

Posters

168 The Ocean Gene Atlas: exploring the biogeography of plankton genes online, Emilie Villar [et al.]	528
---	-----

169 How in vitro data can contribute to in vivo toxicity prediction using Machine Learning ?, Ingrid Grenet [et al.]	529
--	-----

170 Causal Mediation Analysis with Multiple Mediators, Allan Jérôlon [et al.]	533
---	-----

171 Easy16S: a user-friendly Shiny interface for analysis and visualization of metagenomic data., Cédric Midoux [et al.]	535
--	-----

172 Let-it-bin an optimised workflow for binning metagenomic short reads from multiple samples, Quentin Letourneur [et al.]	539
---	-----

173 Pixel : une solution Open Source pour l'annotation, le stockage, l'exploration et l'intégration des résultats d'analyses de données multi-omiques en biologie, Thomas Denecker [et al.]	540
---	-----

174 Agronomic Linked Data (AgroLD): a Knowledge-based System to Enable Integrative Biology in Agronomy, Pierre Larmande [et al.]	542
--	-----

175 On the use of interaction terms in GLMs to model complex experimental designs: the example of RNA-Seq data, Hugo Varet	544
--	-----

176 Investigation of differences between long read overlappers, Pierre Marijon [et al.]	545
---	-----

177 Full-length transcripts sequencing (Iso-Seq) : the Institut Curie feedback, Marc Deloger [et al.]	546
---	-----

178 PythieVar, a collaborative tool for integrating and analyzing genetic and clinical data of rare diseases, Mélissa N'debi [et al.]	548
---	-----

179 Systematic identification and characterization of non-coding RNAs associated with bladder cancer progression, Louis Chauvière [et al.]	551
--	-----

	The Role of User-Centred Design When Revisiting a Scientific Web Application	
180	: Redesign of iPPI-DB, a database for modulators of Protein-Protein Interactions, Rachel Torchet	554
181	HOMARD : High throughput Optical MApping of Replicating DNA, Nikita Menezes [et al.]	558
182	Calcul haute performance pour l'exploration de génomes obtenus par séquençage en cellule unique avec des données métagenomiques et métatranscriptomiques de Tara Oceans., Artem Kourlaiev [et al.]	561
183	Florilege: an integrative database using text mining and ontologies, Estelle Chaix [et al.]	563
184	A data science approach for exploring differential expression profiles of genes in transcriptomic studies – Application to the understanding of ageing in obese and lean rats in the FIGHT-HF project., Emmanuel Bresso [et al.]	565
185	ALFA: compute and display mapped reads distribution by genomic categories and biotypes, Mathieu Bahin [et al.]	569
186	Indexing de Bruijn graph with minimizers, Antoine Limasset [et al.]	571
187	TOGGLE, a framework for simple and fast building or reproducible parallel workflows for large scale analyses, Christine Tranchan-Dubreuil [et al.]	575
188	Recipes for a successful collaborative software development: the test-case of bioconda. Application to the bioconvert: a bioinformatics format converter library., Anne Biton [et al.]	581
189	Genome-wide supervised learning of non-coding loci associated to complex phenotypes, Aitor Gonzalez [et al.]	583
190	K-merator, an efficient design of highly specific k-mers for quantification of transcriptional signatures in large scale RNAseq cohorts., Sébastien Riquier [et al.]	584
191	ELECTOR: EvaLUation of Error Correction Tools for lOng Reads, Camille Marchet [et al.]	586
192	Stochastic optimization approach to large scale inferences of single molecule dynamics, François Laurent [et al.]	590
193	A first step toward the personalized interactome: predicting the impact of mutations on proteins interaction profiles, Zacharie Ménétrier [et al.]	592
194	ThaliaDB, a tool for data management and genetic diversity data exploration, Delphine Steinbach	596

195	Exploration of EDAM ontology and bioinformatics resources in a reusable web-visualization, Bryan Brancotte [et al.]	597
196	IMGT® genomic annotation of the dog (<i>Canis lupus familiaris</i>) seven immunoglobulin (IG) or antibody and T cell receptor (TR) loci, Imène Chentli [et al.]	600
197	<i>Capra hircus</i> and <i>Ovis aries</i> IGK loci simultaneous annotation in IMGT®, Viviane Nguefack Ngoune [et al.]	604
198	CeSGO : integrating data and project lifecycle on a bioinformatics facility, Cyril Monjeaud [et al.]	608
199	BD_NGS, a complete tool for management, analysis and visualisation of NGS data for diagnosis purposes, Julien Plenecassagnes [et al.]	610
200	The journey of a team of engineers in learning packaging technology, Valentin Marcon [et al.]	612
201	IMGT/mAb-DB and IMGT/2Dstructure-DB for IMGT standard definition of an antibody: from receptor to amino acid changes, Mélissa Cambon [et al.]	614
202	IMGT/HighV-QUEST statistical analysis of IMGT clonotypes (AA), novel interface and functionalities for NGS analysis of IG and TR, Marianne Lèbre [et al.]	618
203	JASS: visualising the results of a joint analysis in the context of GWAS, Pierre Lechat [et al.]	622
204	New selected set of species for the Quest for Orthologs Consortium, Alan Sousa Da Silva	623
205	AuBi platform for biologists and bioinformaticians at UCA Mesocentre, Nadia Goué [et al.]	625
206	Taking tools out of their laboratory: methods and practices to make bioinformatics tools accessible., Valentin Marcon [et al.]	626
207	Bioinformatics services provided at Institut Curie, Marc Deloger [et al.]	628
208	The bio.tools portal of bioinformatics tools and services, Piotr Chmura [et al.] . .	630
209	Framboisine mini-clusters for Southern countries, Ndomassi Tando [et al.]	632
210	ProteoRE, a Galaxy-based infrastructure for annotating and interpreting proteomics data, Florence Combes [et al.]	635

211	iCONICS: a bioinformatics/biostatistics core facility dedicated to the analysis and integration of biomedical multimodal data, Ivan Moszer [et al.]	637
212	pitfalls and tricks in data analysis, Samuel Granjeaud	639
213	Spark-ics, exploration de l'application de l'architecture Apache Spark à la bioinformatique, Axel Verdier [et al.]	641
214	Groupe de travail sur les Métiers de la Bioinformatique (MetBIF), Hélène Chiappello [et al.]	643
215	Straightforward finding of differential expressions through intensive randomization in transcriptomic studies, Dorota Desaulle [et al.]	644
216	A tool to interactively query, mine, and visualise Ribosome profiling data., Damien Paulet [et al.]	645
217	IRSOM, a reliable identifier of ncRNAs based on supervised Self-Organized maps with rejection, Ludovic Platon [et al.]	647
Author Index		652

Author Index

- Abby, Sophie, 5, 29, 251
ABDEL SATER, Ahmad, 109
Abou-Jaoudé, Wassim, 203, 265
Abraham, Anne-Laure, 379
Abulfaraj, A.Aala, 443
Achaibou, Sophia, 39
Adélaïde, José, 168
AH LONE, Sam, 96
Ait Abbi Nazi, Sami, 181, 183
Ait-hamlat, Adel, 205
Alarcon, Flora, 516
Alcala, Nicolas, 145
Alhoraibi, Hanna, 443
Alizon, Samuel, 7
Allain, Fabrice, 451
Almunia, Christine, 469
Ambroise, Christophe, 18, 498
Amouri, Adel Amar, 236
André-Leroux, Gwenaëlle, 453, 464
ANDRIANTERANAGNA, Mamy, 164
Angel, Eric, 466, 494
Anne, Jouinot, 330
ANTOINE, Yannick, 102
ARDIN, Maude, 611
Ardouin, Olivier, 170
Argoul, Françoise, 414
Arif, Majda, 37, 38, 297
Armengaud, Jean, 469
Armougom, Fabrice, 22
Arnaud-Haond, Sophie, 50
Arneodo, Alain, 414
Arold, Stefan T, 443
Aron, Serge, 25
Arras, Guillaume, 483
Artufel, Marie, 200, 566
ARVEILER, Benoit, 176
Aschard, Hugues, 605
ASSELE KOGHE, Vanesa, 54
Assenov, Yassen, 378
Assié, Guillaume, 330
Atkinson, Alexandre, 325
AUBERT, Julie, 406
Audit, Benjamin, 414
AUDOUX, Jérôme, 340, 567
Auguin, Daniel, 476
Aure, Miriam, 269
Aury, Jean-Marc, 16, 26, 544
Averous, Julien, 105
Ayllón-Benítez, Aarón, 356
Badawi, Myriam, 48
Badel, Anne, 481
Baglietto, Laura, 516
Bahin, Mathieu, 212, 552
Bailly-Bechet, Marc, 83
BAKKALI KASSIMI, Labib, 411
BALIERE, Charlotte, 411
Ballester, Benoit, 193, 200
Barbe, Valérie, 541
Barbry, Pascal, 154
BARCA, Maira, 66
Bardel, Claire, 178
Bardiaux, Benjamin, 451
Barillot, Emmanuel, 115, 483, 534, 611
Barras, Frédéric, 224
Bartoli, Marc, 152
BASSIGNANI, Ariane, 134
Bastianelli, Leila, 552
BATEJAT, Christophe, 411
Battail, Christophe, 420
Baudot, Anaïs, 254, 325
Baudry, Lyam, 25
BAULANDE, Sylvain, 529
Baulande, Sylvain, 150
Baux, David, 170, 172
Bayard, Quentin, 481
BEAUDONNET, Guillemette, 531
Becavin, Christophe, 231
BEDO, Justin, 62
Bedran, Georges, 420
Bei, Wanying, 427
Belliardo, Carole, 83
Belmudes, Lucid, 420
Beloïn, Christophe, 267
Ben Yahia, Sadok, 237
Bendezu Sarmiento, Julio, 30
Benhamo, Vanessa, 150
Benjelloun, Soumaya, 328
Benoist, Camille, 163
Benvegna-Sallou, Benvegna, 188, 189
Bergsten, Emma, 142
BERLAND, Magali, 134
Bernard, Charles, 552
Bernard, Maria, 595
Bendhamane, Abdelhafid, 647

Bernard, Virginie, 150, 163
 Bernheim, Aude, 351
 BEROUD, Christophe, 157
 Beroud, Christophe, 152
 Berrabah, Wahiba, 541
 Berthelier, Jérémy, 48
 Berthelot, Camille, 259, 291
 bertherat, Jerome, 330
 Berthet, Nicolas, 54
 Bertignac, Morgane, 587
 Bertrand, Baussart, 330
 Bertucci, François, 168
 BEURY, Delphine, 139
 Beuvin, Mylène, 393
 Bièche, Ivan, 150
 Bidard, François-Clément, 150
 Bidaut, Ghislain, 90, 298, 390
 Bieche, Ivan, 163
 Bigeard, Jean, 443
 Bigey, Pascal, 627
 Bihouee, Audrey, 407
 Birer, Aurélien, 166
 Birnbaum, Daniel, 168
 Bischof, Oliver, 285
 Bitard Feildel, Tristan, 507
 Biton, Anne, 101, 564
 Bize, Ariane, 518
 BLAISE-BOISSEAU, Sandra, 411
 Blanc, Pierre, 178
 Blanchet, Christophe, 580
 BLUGEON, Corinne, 242, 375
 Bocs, Stéphanie, 401
 BOHERS, Elodie, 109
 Bohuon, Jean-Baptiste, 546
 Bojarski, Andrzej, 455
 Boland, Anne, 121
 Bon, Céline, 30
 Bonne, Gisèle, 172
 Bonneau, Dominique, 148
 Bonnet, Eric, 420
 Bonnet, Richard, 166
 Borrel, Alexandre, 132, 187
 Borrel, Guillaume, 267, 522
 Borresen-Dale, Anne-Lise, 269
 Borry, Maxime, 30
 Bossy, Robert, 546
 Bouchez, Théodore, 518
 bouchez, valérie, 77
 Boudet, Matéo, 591
 Bougé, Anne-Laure, 567
 BOULIGAND, Jérôme, 531
 Bouly, Jean-Pierre, 219
 Boumaza, Rachid, 40
 Bourbeillon, Julie, 40
 Bourdon, Jérémie, 125
 Boureux, Anthony, 567
 Bourgeas, Raphaël, 461
 Bourgeron, Thomas, 306
 Bourqui, Romain, 356
 Bouzid, Mariam, 340
 Braham, Shérazade, 111
 Brancotte, Bryan, 101, 564, 580
 Brandt, Miriam, 50
 BRANGER, Maxime, 96
 Braquelaire, Tristan, 503
 Brelurut, Geoffray, 294
 Bresso, Emmanuel, 548
 Breteau, Anthony, 98
 Bretherick, Andrew, 119
 Bretin, Betty, 125
 Briand, Martial, 624
 BRITO, Isabel, 611
 Brousseau, Louise, 401
 Bruhat, Alain, 105
 Brun, C., 372, 575
 Brun, Christine, 111, 214
 Brun, Virginie, 618
 brunel-cadic, charlotte, 441
 Brysbaert, Guillaume, 438
 Buitink, Julia, 40
 Cabanettes, Floreal, 93
 Caboche, Ségolène, 139
 CAFFARRI, Stefano, 46
 CAIDI, AZIZA, 142
 Callebaut, Isabelle, 486
 Callens, Celine, 163
 Caloustian, Christophe, 121
 Calteau, Alexandra, 393
 Calzone, Laurence, 115, 271
 Camadro, Jean-Michel, 523
 Cambon, Mélissa, 597
 Campait, Raphaëlle, 176
 Camproux, Anne-Claude, 481
 Capponi, Cécile, 346, 575
 Caputo, Aurélia, 241
 Carbone, Alessandra, 86, 219, 478, 507
 Carbuccia, Nadine, 168
 CARO, Valérie, 411
 Carrère, Sébastien, 624
 Carraro, Valerie, 105
 Carrier, Grégory, 48
 CARRIER, Gregory, 302
 Casse, Nathalie, 48

Cassou, Manon, 593
 CASTEL, Guillaume, 71
 CASTRIC, Vincent, 248
 Castro-Mondragon, Jaime, 212, 269
 Cau, Pierre, 254
 Cavaillé, Quentin, 379
 Cazaux, Bastien, 71
 CERISIER, Natacha, 481
 Chèneby, Jeanne, 193, 200
 Chaffanet, Max, 168
 Chaix, Estelle, 546
 CHANAS, Laetitia, 611
 Chanas, Laetitia, 163
 CHANDLER, Mike, 62
 Chaouiya, Claudine, 203, 271
 CHAPEL, Margaux, 63
 Chapleur, Olivier, 518
 Charafe-Jauffret, Emmanuelle, 298
 Charpentier, Eric, 407
 CHATEAU, Annie, 365
 Chateau, Annie, 81, 273
 Chatel, Jean-Marc, 453
 Chatel, Stéphanie, 128
 Chatron, Nicolas, 178
 Chaudru, Valérie, 121
 Chaumot, Arnaud, 469
 Chauvière, Louis, 534
 Chauvot de Beauchêne, Isaure, 433
 Chebbi, Mohamed Amine, 238
 CHENAL, Clothilde, 251
 Chentli, Imène, 583
 Cherouali, Karima, 597
 Chetrit, Bernard, 298
 chevalier, celine, 393
 Chevalier, Stéphanie, 188, 189, 275
 Chevallier, Marie, 398
 Chiapello, Hélène, 96, 344, 626
 Chibon, Frédéric, 414
 Chikhi, Rayan, 340, 528, 554
 Chiquet, Julien, 13
 Chmura, Piotr, 613
 Christiany, David, 96
 Chu, Phuong, 466
 Clark, David, 119
 Claustres, Mireille, 170
 CLEMENT, Yves, 217
 Clerc, Olivier, 337
 Cliquet, Freddy, 306
 cogne, yannick, 469
 Cohen-Boulakia, Sarah, 271
 cokelaer, thomas, 39, 43, 54, 95, 100, 101, 144, 564
 Colella, Stefano, 309
 Collado Vides, Julio, 260
 Collin, François David, 35
 Collin, Olivier, 591
 Collombet, Samuel, 212
 Combes, Florence, 618
 Combes, Sylvie, 10
 Comet, Jean-Paul, 512
 Commes, Thérèse, 567
 Contreras-Moreira, Bruno, 212
 Coq, Matthieu, 183
 Cordaux, Richard, 238
 Cordier, Tristan, 9
 Cormier, Alexandre, 238
 Cornec, Marine, 407
 Cornelis, François, 121
 CORRE, Erwan, 33, 46
 Corre, Ewen, 69, 162
 Cossée, Mireille, 170, 172
 Costa, Rémy, 273
 Cottu, Paul, 150
 Culpier, Fanny, 242, 375
 Coustau, Christine, 293
 Couvin, David, 351
 Criscuolo, Alexis, 77
 Croce, Olivier, 80
 Cruaud, Corinne, 26
 Cruveiller, Stéphane, 18
 Cruveiller, Stephane, 393
 CUNNAC, Sébastien, 75
 Cuppens, Tania, 117
 d'Agata, Léo, 16, 544
 Díaz De Ståhl, Teresita, 113
 Dérozier, Sandra, 453, 546
 Da Costa, Quentin, 168, 174, 298, 390
 DA ROCHA, MARTINE, 385
 Da Rocha, Martine, 624
 Da Silva, Corinne, 26
 Danchin, Etienne G J., 279
 danchin, Etienne G.J, 385
 DANESH, Gonché, 7
 DANG, NGUYET, 57
 Danilin, Sabrina, 181, 183
 Darras, Hugo, 25
 DAUCHEL, Hélène, 109
 Dauga, Catherine, 54
 Davey, Norman, 305
 David, Alexandre, 628
 David, Laurent, 125, 407
 De Araujo, Aline, 424
 De Bruyne, Katrien, 239

De Carli, Francesco, 541
 de Givry, Simon, 321
 De Lamotte, Frédéric, 401
 DE SOYRES, Henri, 611
 de Vargas, Colomban, 69
 De-Sandre-Giovannoli, Annachiara, 325
 DECOUT, Jean-Luc, 486
 Deevi, Sri, 190
 Defosset, Audrey, 208
 Dehais, Patrice, 10
 Dehne-Garcia, Alexandre, 35, 624
 Deléger, Louise, 546
 Delague, Valérie, 152
 DELATTRE, Olivier, 529
 Deleuze, Jean-François, 121, 420
 DELOGER, Marc, 529, 611
 Delorme, Quentin, 81
 Delorme, Richard, 306
 Denecker, Thomas, 523
 Denise, Rémi, 5
 Denommé-Pichon, Anne-Sophie, 148
 Dequeker, Chloé, 478
 Dereeper, Alexis, 234, 313, 401, 558, 609
 Derozier, Sandra, 96, 379
 DESAULLE, Dorota, 627
 DESVIGNES, Jean-Pierre, 152
 Desvignes, Jean-Pierre, 157
 DESVILLECHABROL, Dimitri, 43, 100, 611
 Devignes, Marie-Dominique, 548
 Di-Filippo, Mathilde, 178
 DIALLO, Abdoulaye, 558
 DIANCOURT, Laure, 411
 Dillies, Marie-Agnès, 388, 406
 DiLorenzo, Sebastian, 113
 Dina, Christian, 128
 Dingli, Florent, 483
 Diot, Christian, 33
 Diouf, Amad, 73
 DJEDDI, Warith-Eddine, 237
 Do Souto Ferreira, Laura, 593
 Dogrusoz, Ugur, 404
 Dollfus, Hélène, 137
 Donnadieu, Cécile, 84
 Donnart, Audrey, 407
 Doré, Gregory, 285
 Dorkeld, Franck, 624
 Douge, Aurore, 105
 Dräger, Andreas, 404
 Drevet, Patricia, 476
 Dridi, Bedis, 379
 Drillon, Guenola, 414
 Driouch, Keltouma, 150
 Droc, Gaëtan, 401
 DRULA, ELODIE, 256
 Dubois, Emeric, 396
 Dubois, Mathieu, 393
 Dubois-Chevalier, Julie, 383
 Dubos, Paul, 332
 Dubreuil-Tranchant, Christine, 615
 dufayard, Jean-François, 401
 Dufresne, Yoann, 77, 101, 564
 Dumas, Guillaume, 306
 Dumont, Solenne, 407
 Duprez, Estelle, 342
 Durand, Faustine, 336
 Durand, William, 523
 Durimel, Kevin, 381
 Duroux, Patrice, 583, 597, 601
 Durrleman, Stanley, 620
 Dussart, Caroline, 50, 595
 Eeckhoute, Jérôme, 383
 Eisfeldt, Jesper, 113
 El Hassouni, Nordine, 525
 EL Jazouli, Hatim, 294
 Elati, Mohamed, 316
 ELBAHNSI, Ahmad, 486
 ELMESSAOUDI-IDRISSI, Mohcine, 328
 Enault, François, 315
 Endtz, Hubert, 239
 Erauso, Gaël, 22
 Escudié, Frédéric, 593
 Esko, Tõnu, 119
 Estoup, Arnaud, 84
 ETCHEBEST, Catherine, 442
 Etienne, Danchin, 83
 Ewels, Phil, 113
 Ezzikouri, Sayeh, 328
 FÉREC, Claude, 128
 Fafournoux, Pierre, 105
 FAGNEN, Charline, 424
 Falciatore, Angela, 219
 Falentin, Hélène, 546
 Fatemeh, Fatemeh, 554
 Felten, Arnaud, 253, 381
 Feng, Xiao, 119
 FERGELOT, Patricia, 176
 Fernández-Breis, Jesualdo Tomas, 356
 Fernandez-Cuesta, Lynnette, 145
 Ferré, Quentin, 346, 575
 Filangi, Olivier, 624
 Firat, Hueseyin, 181, 183
 Firmin, Julie, 125

Fischer, Krista, 119
 Fiston-Lavier, Anna-Sophie, 81, 273, 365
 Flippe, Léa, 407
 Flobak, Åsmund, 263
 FLOC'HLAY, Swann, 198
 Floc'hlay, Swann, 288
 Flot, Jean-Francois, 25
 Folch, Géraldine, 583, 587
 Foll, Matthieu, 145
 Folschette, Maxime, 300
 Forest, Eric, 424
 Forterre, Patrick, 3
 Fourches, Denis, 132
 FOUSSIER, Loic, 531
 Fréour, Thomas, 125
 François-Campion, Valentin, 125
 Frances, Tristan, 48
 FRANCOU, Bruno, 531
 Frankel, Diane, 325
 Freyd, Thibaud, 455
 Froidevaux, Christine, 275
 Frouin, Eléonore, 22
 Fumanal, Boris, 476
 Fumey, Julien, 162, 187–189, 306
 Fund, Cédric, 414
 Furlong, Eileen, 288

 GABRIEL, Aurélie, 145
 Gabrielsen, Mari, 455
 Gachet, Mathieu, 393
 Gaia, Morgan, 3
 Galiez, Clovis, 315
 Gallina, Sophie, 248
 Gansel, Xavier, 135
 Garcia, Maxime, 113
 Garcia-Garcia, Gema, 170
 Gareau, Thomas, 620
 Garfield, David, 288
 GARIBAL, Marc, 157
 Garnier, Séverine, 168
 Garnier, Xavier, 624
 Gasparoux, Marie, 503
 Gaspin, Christine, 93, 489
 Gaston, Laetitia, 176
 Gaudriault, Georges, 336
 GAUTHERET, Daniel, 340, 567
 Gautheret, Daniel, 351
 Gautier, Mathieu, 84
 Gautreau, Guillaume, 18, 393
 Geffard, Olivier, 469
 GENETE, Mathieu, 248
 Genin, Emmanuelle, 117, 128

 Genovesio, Auguste, 541, 552
 GEOFFROY, Véronique, 137
 GESTRAUD, Pierre, 611
 Gheeraert, Céline, 383
 Gheorghe, Marius, 193, 200
 Ghozlane, Amine, 180, 522
 Giemza, Joanna, 128
 Gilardi-Hebenstreit, Pascale, 217
 Ginestier, Christophe, 298
 GIRARD, Elodie, 163, 611
 Giraud, Isabelle, 238
 Giudicelli, Véronique, 583, 597, 601
 Gody, Louise, 321
 Goffard, Anne, 139
 Gonçalves, Anthony, 168
 Gonzala, Luiz, 239
 Gonzalez, Aitor, 566
 Gonzalez, Pablo, 354
 Goris, Johan, 239
 GOT, Jeanne, 302
 Goué, Nadia, 608
 goudenège, david, 148
 Gousset, Aurélie, 476
 Goutorbe, Benoit, 90
 Gouveia, Duarte, 469
 Gouzy, Jérôme, 624
 Grandjean, Cyrille, 441
 Granjeaud, Samuel, 390, 622
 Granjeon-Noriot, Solène, 279
 Grenet, Ingrid, 512
 Grentzinger, Victor, 188, 189
 Gribaldo, Simonetta, 267
 Griffon, Aurélien, 59, 63
 Grigoriev, Igor V., 256
 Grimaud, Ghjuvan, 367
 Grimbichler, David, 608
 Gschloessl, Bernhard, 624
 Guédon, Gérard, 344
 Guégan, Justine, 620
 Gueudelot, Olivier, 148
 Guglielmini, Julien, 3
 GUIBERT, BENOIT, 567
 Guignard, Thomas, 172
 Guignon, Valentin, 401
 Guigon, Ghislaine, 59, 63
 Guille, Arnaud, 168
 guillemot, vincent, 605
 Guirimand, Thibaut, 379
 Gutierrez, Darely, 354
 Guziolowski, Carito, 300
 Guzman, F. Javier, 443
 György, Beáta, 620

Hébert, Charles, 523
 Hérault, Frédéric, 33
 Hérault, Léonard, 342
 Habib, Christophe, 531, 593
 Hainque, Bernard, 627
 Halfon, Philippe, 90
 Haller, Lucia, 464
 Hamelin, Chantal, 401
 Hammami, Firas, 224
 Harmer, Russel, 226
 Heinaut, Matthieu, 256
 Helikar, Tomáš, 271
 Helou, Laura, 558
 Hennekinne, Jacques-Antoine, 253
 Hennequet-Antier, Christelle, 406
 Henrissat, Bernard, 256
 Henry, Nicolas, 69
 Herenger, Yvan, 137
 Hernandez, Céline, 198, 203, 294
 Hernandez, Celine, 265, 271
 Herpoël-Gimbert, Isabelle, 256
 Hillion, Kenzo-Hugo, 101, 564, 613
 Hingamp, Pascal, 511
 Hirt, Heribert, 443
 Hoede, Claire, 93
 HOFFMANN, Brice, 486
 Hoffmann, Céline, 627
 Hot, David, 139
 HOURDEL, Véronique, 411
 HUPE, Philippe, 611
 Hupe, Philippe, 163
 Hyrien, Olivier, 414, 541

 Inizan, Olivier, 96, 595, 609
 Ishi, Leandro, 362
 Ison, Jon, 613

 Jérolon, Allan, 516
 Jaillon, Olivier, 16, 544
 Jamet, Jean-Louis, 297
 Jamilloux, Véronique, 48
 JARDIN, Fabrice, 109
 JARLIER, Frédéric, 611
 Jaszczyszyn, Yan, 414
 Jeanne, Nicolas, 593
 Jonquet, Clement, 525
 Jornod, Florence, 162, 187–189
 Joshi, Peter, 119
 Jouffroy, Ophélie, 246
 Jouneau, Luc, 609
 JOURDREN, Laurent, 242, 244, 294, 375
 Jousse, Celine, 105

 Julienne, Hanna, 605
 JUNIER, Ivan, 251
 Juntas Morales, Raul, 172
 Juste, Catherine, 134

 Käller, Max, 113
 kabalane, hadi, 414
 Kahli, Malik, 414
 Kalyan, Karthik, 601
 Kamal, Maud, 163
 KAMOUN, Choumouss, 611
 Kamoun, Choumouss, 163
 KANEKO, Gaël, 63
 Karakachoff, Matilde, 128
 Keller, Harald, 293
 Kennedy, Sean, 54
 Kergrohen, Thomas, 306
 Kerou, Melina, 29
 KETTANI, Anass, 328
 Khamvongsa-Charbonnier, Lucie, 319
 Khan, Aziz, 193
 Kilens, Stéphanie, 125, 407
 Kim, Hee-Sik, 308
 KLEIN, Valentin, 75
 Kleinstreuer, Nicole, 132
 Klopp, Christophe, 93
 Koenig, Michel, 170, 172
 Komurian-Pradel, Florence, 239
 Kornobis, Etienne, 101, 564
 Kossida, Sofia, 583, 587, 597, 601
 Koszul, Romain, 25
 Kourlaiev, Artem, 16, 544
 Koutsovoulos, Georgios D., 279
 Krahm, Martin, 152, 172
 Kress, Arnaud, 137, 208
 Kristensen, Vessela, 269
 Krystkowiak, Izabella, 305
 Kuiper, Martin, 263
 Kushwaha, Anjana, 597
 Kutalik, Zoltán, 119
 KWASIBORSKI, Aurélia, 411

 Läll, Kristi, 119
 Léauté, Ludovic, 332
 Légaré, Sébastien, 226
 Léonard, Sylvain, 188, 189
 Lèbre, Marianne, 601
 Lægreid, Astrid, 263
 LA ROSA, Philippe, 611
 Labadie, Karine, 297
 Labalme, Audrey, 178
 Label, Philippe, 476

Laborie, Didier, 93
 Labrador, Boris, 620
 LACOMBE, Maud, 618
 Lacomblez, Claire, 548
 Lacourt, Delphine, 170, 172
 Lacroix, Thomas, 344
 LAFFAY, Berengere, 242, 244, 375
 Lagnel, Jacques, 84
 Laine, Élodie, 205
 Laine, Elodie, 478
 Lajus, Aurélie, 393
 Lambert, Ilana, 309
 LAMEIRAS, Sonia, 529
 Landès, Claudine, 40
 Langella, Olivier, 134
 Langerod, Anita, 269
 Langlade, Nicolas, 321
 Langlois, Jordan, 393
 Lao, Julie, 344
 Lapalu, Nicolas, 624
 Laperrousaz, Bastien, 414
 Larmande, Pierre, 234, 401, 525
 Larsson, Malin, 113
 Lastrucci, Emmanuelle, 443
 Laurent, François, 573
 laville, vincent, 605
 Le Boulch, Malo, 10
 LE CROM, Stéphane, 185
 Le Crom, Stéphane, 242, 244, 294, 375
 Le Gall, Maël, 135
 Le Hir, Herve, 552
 Le Marec, Hervé, 128
 Le Novère, Nicolas, 404
 Le Picard, Marine, 483
 Le Quere, Antoine, 309
 Le Tourneau, Christophe, 163
 Leblois, Raphael, 35
 Leblond-bourget, Nathalie, 344
 Lebreton, Alice, 552
 Lechat, Pierre, 101, 231, 564, 605
 Lecompte, Lolita, 26, 569
 Lecompte, Odile, 208
 LECROQ, Thierry, 109
 Lecroq, Thierry, 569
 Lefebvre, Arnaud, 569
 Lefebvre, Philippe, 383
 Lefranc, Marie-Paule, 583, 587, 597, 601
 Legagneux, Vincent, 300
 Legeai, Fabrice, 98
 Legendre, Audrey, 466, 494
 LEGENDRE, Rachel, 95
 Legendre, Rachel, 101, 564
 Legrand, Ludovic, 624
 Lehmann, Nathalie, 294
 Lehn, Pierre, 486
 Lehtokari, Vilma, 172
 Lejeune, François-Xavier, 620
 Lelandais, Gaëlle, 523
 Lemoine, Frédéric, 101, 564
 Lemoine, Sophie, 242, 244, 375
 Lensink, Marc, 438
 LEONARD, Sylvain, 442
 LEPAGE, Thierry, 198
 Lepetit, Marc, 309
 Leprince, Olivier, 40
 Lescot, Magali, 511
 Letcher, Brice, 59
 Letellier, Guillaume, 336
 Letourneur, Quentin, 522
 Levy, Nicolas, 271
 Li, Blaise, 101, 564
 Lidereau, Rosette, 150
 Lima, Nicholas, 239
 Limansky, Grégoire, 620
 Limasset, Antoine, 554, 569
 LINARD, Benjamin, 102
 Lindholm, Evita, 269
 Lingjaerde, Ole Christian, 269
 LINGLART, Agnès, 531
 Lisacek, Frederique, 337
 LIU, Xi, 33, 46
 LIVA, Stéphane, 611
 Liva, Stéphane, 115, 483
 Liyakat Ali, Tharvesh Moideen, 534
 Loew, Damarys, 483
 Loiseau, Anne, 84
 Lombard, Bérangère, 483
 Lopes, Anne, 427
 Lopez-Roques, Céline, 84
 LORIOD, Beatrice, 46
 Lossouarn, Julien, 315
 Loubersac, Sophie, 125
 Louvel, Guillaume, 56
 Loux, Valentin, 96, 379, 453, 518, 546, 595, 618
 LUCOTTE, Georges, 611
 Ludwig, Thomas, 117
 Luna, Augustin, 404
 Médigue, Claudine, 18, 393
 Ménétrier, Zacharie, 575
 Ménager, Hervé, 580, 613
 Madoui, Mohammed-Amin, 38, 297
 Maguer-Satta, Véronique, 414
 Mahé, Frédéric, 401

Mahul, Antoine, 608
 Maillet, Nicolas, 101, 231, 448, 564
 Malabat, Christophe, 388
 Malissen, Bernard, 265
 Maman, Sarah, 609
 Mandin, Pierre, 224
 Mangin, Brigitte, 321
 Manguy, Jean, 305
 Manno, Maxime, 84
 MANSOUR, Yasmine, 81, 365
 Mansour, Yasmine, 273
 Manuguerra, Jean-Claude, 411
 Mapeta, Rutendo, 190
 Marbouty, Martial, 25
 Marchet, Camille, 26, 362, 569
 Marcon, Valentin, 96, 595, 609
 Mariadassou, Mahendra, 13, 518
 Mariethoz, Julien, 337
 Mariette, Jérôme, 93
 Marijon, Pierre, 528
 Martínez-Zamudio, Ricardo Iván, 285
 Martignetti, Loredana, 115
 Martin, Guillaume, 401
 Martin, Marcel, 113
 Martin, Véronique, 96, 453, 464
 Martin-Magniette, Marie-Laure, 309
 Mashkour, Marjan, 30
 Masliah-Planchon, Julien, 163
 Masson, Jean-Baptiste, 573
 Masson, Vanessa, 483
 Mathelier, Anthony, 193, 200, 269
 Mathieu, Alexandre, 306
 Mathieu, Charly, 172
 Matias, Catherine, 18
 Maumus, Florian, 246
 Maupetit, Julien, 523
 Mauri, Théo, 438
 Maurier, Florence, 139
 Maurin, Anne-Catherine, 105
 Mazein, Alexander, 404
 Mbaye, Mame Ndew, 457
 McKay, James, 145
 Medina Rivera, Alejandra, 212
 Medina-Rivera, Alejandra, 354
 Megy, Karyn, 190
 Mehdi, Madah, 183
 Meistermann, Dimitri, 125, 407
 Menager, herve, 605
 Menezes, Nikita, 541
 MEPHU NGUIFO, Engelbert, 237
 Merda, Déborah, 253
 Mestivier, Denis, 142
 MEVY, Jean-Philippe, 46
 Meyer, Vincent, 121
 Mezura-Montes, Efrén, 325
 Mhoumadi, Yasmina, 424
 Michalik, Juraj, 351, 472
 Michaloud, Joumana, 583, 587
 Michaut, Magali, 187
 MICHELET, CLAIRE, 293
 Michou, Laetitia, 121
 Midoux, Cédric, 96, 518
 MIRANDE, Caroline, 63
 Mistou, Michel-Yves, 253, 381
 Miyauchi, Shingo, 249, 256
 Mohammad, Ammara, 242, 375
 Molina, Christian, 354
 Mom, Robin, 315, 476
 Momal, Raphaëlle, 498
 Momin, Afaque Ahmad, 443
 Monat, Cecile, 558
 Mondy, Samuel, 626
 MONJEAUD, Cyril, 591
 Monnet, Véronique, 464
 Montagud, Arnau, 115
 Montaudon, Eric, 96
 Monteiro, Pedro, 203, 271
 Montes, Matthieu, 431
 Mordalski, Stefan, 455
 Morel, Claire, 163
 morin, emmanuelle, 70
 Morisse, Pierre, 569
 MORNICO, Damien, 388
 Mornon, Jean-Paul, 486
 Moszer, Ivan, 620
 Mougin, Fleur, 356
 Mounier, Ninon, 119
 Moyon, Lambert, 259
 Mucchielli-Giorgi, Marie-Hélène, 427
 Mueller, Lukas, 246
 MULLER, Bruno, 63
 Muller, Jean, 137
 Murigneux, Valentine, 552
 N'DEBI, Mélissa, 531
 Nédellec, Claire, 546
 Néron, Bertrand, 101, 351, 564
 Nabuco Leva Ferreira de Freitas, José Américo, 285
 Nadalin, Francesca, 86
 Naldi, Aurélien, 203, 265, 271, 283, 354
 Navarro, Claire, 254
 Navarro, David, 256
 Neou, Mario, 330

Nevers, Yannis, 208
 Nguefack Ngoune, Viviane, 587
 Nguyen, Lien, 618
 Nguyen, Nga Thi Thuy, 212
 Nguyen, Thi-Phuong-Lien, 96
 Nguyen, Vy, 567
 Nicaud, Jean-Marc, 316
 Nicolas, Jacques, 26
 Nicolas, Lévy, 325
 Nicolas, Pierre, 223
 Nicolini, Frank-Emmanuel, 414
 Nilges, Mickael, 451
 Ning, Zheng, 119
 Nister, Monica, 113
 Noel, Benjamin, 16, 544
 Noel, Benoit, 552
 Noirot, Céline, 93, 624
 NOVOA DEL TORO, Elva María, 325
 Nuñez, Karen, 354
 Nystedt, Björn, 113

 Olaso, Robert, 121
 Olason, Pall, 113
 ORJUELA, Julie, 313
 ORJUELA-BOUNIOL, Julie, 558
 Orjuela-Bouniol, Julie, 401
 Orsel, Mathilde, 40
 Oshurko, Ievgeniia, 226
 Ossio, Raul, 212
 Oubella, Iman, 424
 Ouwehand, Willem, 190

 Pégeot, Henri, 170, 172
 Pégorier, Perrine, 583
 Pérez, Serge, 337
 Pétel, Gilles, 476
 Padilla, Monica, 354
 Padua, Agilio, 476
 Pageaud, Yoann, 378
 Paquet, Agnès, 154
 PARDI, Fabio, 102
 Parey, Elise, 291
 Parry, Laurent, 105
 Pascal, Géraldine, 10, 595
 Patrick, Durand, 595
 Patro, Rob, 554
 Paulet, Damien, 628
 Paulevé, Loïc, 271, 275
 Payen, Thibaut, 188, 189
 Paysant - Le Roux, Christine, 309
 Pelletier, Eric, 69
 PELOSI, Ludovic, 251

 Penkett, Christopher, 190
 Penouilh-Suzette, Charlottte, 321
 Perahia, David, 424
 Perduca, Vittorio, 516
 Perea, Javier, 121
 Pereira, Hugo, 188, 189
 Perlberg, Vincent, 620
 Perlemoine, Karine, 330
 Perrin, Amandine, 18, 101, 564
 Perrin, Sophie, 254
 Perus, Lisa, 618
 Pervent, Marjorie, 309
 Petel, Adrien, 234
 PETERA, Mélanie, 609
 Peterlongo, Pierre, 26, 38, 569
 Petit, Emmanuelle, 297
 Petit, Marie-Agnès, 315
 Petit-Teixeira, Elisabeth, 121
 Petitjean, Michel, 481
 Petryk, Nataliya, 414
 Pflieger, Delphine, 420, 443
 Pible, Olivier, 469
 Picard, Sylvain, 178
 PIERREL, Fabien, 251
 Pierrelée, Michaël, 308
 Pierron, Gaelle, 163
 Pietrucci, Fabio, 486
 Pineau, Pascal, 328
 PIPOLI DA FONSECA, Juliana, 529
 Pipoli da Fonseca, Juliana, 95
 Pitollat, Bertrand, 401
 Piton, Amélie, 137
 Pizard, Anne, 548
 PLANCADE, Sandra, 134
 Planel, Rémi, 18, 393
 Plass, Christoph, 378
 Platet, Nadine, 342
 Plauzolles, Anne, 90
 Plenecassagnes, Julien, 593
 Poch, Olivier, 208
 Polit, Lélia, 205
 Pomiès, Lise, 321
 Ponty, Yann, 433, 472
 Poplineau, Mathilde, 342
 Poppleton, Daniel, 267
 POULAIN, Julie, 16, 297
 Poulain, Pierre, 523
 POULLET, Patrick, 611
 Poullet, Patrick, 115, 483
 Pourcel, Christine, 351
 Pozos, Paulina, 354
 Pradel, Lydie, 361
 Platon, Ludovic, 647

Pratlong, Marine, 396
 Prigent, Sylvain, 327
 PROUST, Alexis, 531
 PRUD'HOMME, François, 529
 Pucci, Fabrizio, 461
 Puthier, Denis, 346

 Qingzhen, Hou, 461
 Quesada-Martínez, Manuel, 356
 Quesneville, Hadi, 246
 Quintric, Laure, 595

 Réau, Manon, 431, 481
 Radvanyi, François, 534
 Raffinot, Mathieu, 503
 Rajoharison, Alain, 239
 Rama Rao, Nalini, 453
 Rancon, Anaïs, 256
 Rancurel, Corinne, 279, 385, 624
 Raouche, Sana, 256
 Raoult, Didier, 241
 RAVEL, Sébastien, 313, 401, 558
 Rayapuram, Naganand, 443
 Raymond, Lucy, 190
 Raynal, Virginie, 150
 REBOUL, Marie-Pierre, 176
 Redon, Richard, 128, 407
 Regad, Leslie, 481
 Regovar, Consortium, 148
 Remy, Elisabeth, 224, 325, 342
 Renault, Pierre, 379
 Rialle, Stéphanie, 396
 Ribeiro, Diogo, 214, 372, 575
 Ricard-Blum, Sylvie, 337
 Richard, Hugues, 205
 Rigaud, Thierry, 238
 Rihet, Pascal, 361, 566
 Rioualen, Claire, 260, 298
 Ripp, Raymond, 208
 RIQUIER, Sébastien, 567
 Rivals, Eric, 71, 628
 Rivet, Alain, 337
 Robert, Aude, 414
 Robin, Stéphane, 13, 498
 Robin, Stéphanie, 98
 Robinson, Lucas, 285
 Robles-Espinoza, Carla Daniela, 212
 Rocha, Eduardo, 5, 18, 351
 Roche, David, 393
 Roest Crollius, Hugues, 217
 Roest-Crollius, Hugues, 56, 259, 291
 Rohmer, Marine, 336

 Roll, Patrice, 325
 Rolland, Thomas, 306
 Rollat-Farnier, Pierre-Antoine, 178
 rollin, johan, 393
 ROMEJON, Julien, 611
 Romejon, Julien, 163
 Romuald, Laso-Jadart, 38, 297
 Roncagalli, Romain, 265
 Rooman, Marianne, 461
 Roquet, Jérémie, 148
 Rosier, Florian, 361
 Rossignol, Patrick, 548
 Rosso, Marie-Noëlle, 249
 Rosso, Marie-Noëlle, 256
 ROTHENBUHLER, Anya, 531
 Rouard, Mathieu, 401
 Rouault, Karen, 128
 Rougeulle, Claire, 534
 Rougny, Adrien, 404
 Roux, Anne-Françoise, 170
 Roux, Pierre-François, 285
 Rouy, Zoe, 393
 Rovetta, Christelle, 472
 Rozenblum, Nir, 285
 Rozenholc, Yves, 627
 Rué, Olivier, 96, 518
 Rubinat, Laura, 69
 Ruiz, Manuel, 234, 401, 525
 Ruiz-Deñas, Francisco, 256
 RUMIGNY PIERROT, Marilyne, 63
 Ruohong, Xia, 414

 Sabatet, Valentin, 18, 393
 SABOT, François, 66, 73, 75, 313, 558, 615
 Sabot, François, 401
 SABOT, FRANCOIS, 57
 Sacquin-Mora, Sophie, 427
 Saha, Samir, 239
 Saha, Surya, 246
 Saint-Jean, Bruno, 48
 SALGADO, David, 157
 Salgado, David, 152
 Saljoqi, Saïda, 583
 Sallet, Erika, 624
 Samson, Samantha, 464
 Sandgren, Johanna, 113
 Sandve, Geir Kjetil, 193
 Sanlaville, Damien, 178
 Santagostini, Pierre, 40
 Santana, M., 354
 Santana-Garcia, Walter, 212
 SANTIAGO ALLEXANT, Emmanuelle, 63

Santuz, Hubert, 442
 SARAH, Gautier, 401, 558
 Saulnier, Emma, 7
 SAULNIER, Olivier, 529
 Savel, Caroline, 476
 Schbath, Sophie, 96, 223
 Schleper, Christa, 29
 Schordan, Eric, 181, 183
 Schott, Jean-Jacques, 128
 Schweke, Hugo, 427
 Schwikowski, Benno, 285, 306
 Seeleuthner, Yoann, 16, 544
 Sempéré, Guilhem, 234, 401
 Servant, Nicolas, 163, 529, 611
 Shamardina, Olga, 190
 Shen, Xia, 119
 Sicard, Delphine, 546
 Siegel, Anne, 300, 302
 Sigal, Brigitte, 150
 SIMONET, Floriane, 128
 Simonet, Thomas, 178
 Singhal, Chinmay, 433
 Smaïl-Tabbone, Malika, 548
 SOBHANI, IRADJ, 142
 Sotelo, Jesús, 354
 Sousa da Silva, Alan, 606
 Spicuglia, Salvatore, 346, 354
 Spinelli, Lionel, 111, 214, 372, 575
 Stéphan, Gaillard, 330
 STA, Alexandre, 611
 Sta, Alexandre, 115, 483
 Staels, Bart, 383
 Stark, Hannah, 190
 STEINBACH, delphine, 579
 Stirrups, Kathleen, 190
 Stoetzel, Corinne, 137
 Stoll, Gautier, 271
 Sugier, Kevin, 297
 Sultan, Ibrahim, 223
 Summo, Maryline, 401
 SWENSON, Krister, 102
 Sylte, Ingebrigt, 455
 Szilveszter, Juhos, 113

 Téletchéa, Stéphane, 441, 442
 TAHI, Fariza, 494
 Tahi, Fariza, 466
 Taib, Najwa, 267
 TALLA, Emmanuel, 62
 TANDO, Ndomassi, 313, 401, 558, 615
 Tanmoy, Arif, 239
 Tariq, Zakia, 150
 Tahi, Fariza, 647

 Tartaglia, Gian Gaetano, 372
 Tauzin, Marc, 309
 Teixeira, Adrien, 214
 Teixeira, Maria, 238
 Tempel, Sebastien, 62
 Tenenhaus, Arthur, 620
 Teppa, Elin, 86
 Terzian, Paul, 315
 Tessier, Florent, 80
 Thébault, Patricia, 332
 Thérét, Nathalie, 300
 Thebault, Patricia, 356
 Thieffry, Denis, 198, 203, 212, 265, 271, 288, 294, 354
 Thierry, Ophélie, 40
 Thomas, Morgane, 354
 Thomas-Cholier, Morgane, 294
 Thomas-Chollier, Morgane, 185, 198, 212, 265, 288, 626
 Tichit, Laurent, 325
 Timmers, Paul, 119
 TINAT, Julie, 176
 Toffano-Nioche, Claire, 351
 Torbey, Patrick, 217
 TORCHET, Rachel, 537
 Torchét, Rachel, 101, 564
 Touchon, Marie, 18, 351
 Touibi, Nour, 159
 Touré, Vasundra, 263, 404
 Tournayre, Jérémy, 105
 Toussaint, Ariane, 315
 Touzet, Hélène, 472
 Trébulle, Pauline, 316
 TRANCHAN-DUBREUIL, Christine, 558
 TRANCHANT-DUBREUIL, Christine, 73, 313, 401
 Traut, Nicolas, 101, 564
 Tremblay-Franco, Marie, 609
 Trotard, Marie-Stephane, 93
 Trouvé, Pascal, 117
 Truchi, Marin, 154
 Tuffery-Giraud, Sylvie, 172
 Tuna, Salih, 190

 Ulveling, Damien, 620
 Uricaru, Raluca, 332, 503
 USARDI, Alessia, 531

 Vénien-Bryan, Catherine, 424
 Vachon, René, 135
 Vaginay, Athénaïs, 188, 189
 Valdeolivas, Alberto, 254

Vallenet, David, 18, 393
 Vallot, Céline, 534
 Van Belkum, Alex, 239
 Van Goethem, Charles, 170, 172
 van Helden, Jacques, 185, 212, 260, 346
 Vandame, Marc, 476
 Vandel, Jimmy, 383
 Vandenbogaert, Mathias, 411
 Vandenbrouck, Yves, 420, 618
 Vannier, Thomas, 511
 Varet, Hugo, 54, 527
 Varré, Jean Stéphane, 528
 Vasconcelos, Ana Tereza R., 239
 Vekemans, Xavier, 248
 Venisse, Jean-Stéphane, 476
 Venkatesan, Aravind, 525
 VERA, Pierre, 109
 Verdier, Axel, 624
 Vergnaud, Gilles, 351
 Verjus Lisfranc, Victoria, 330
 Vernet, Caroline, 511
 Veyssiere, Maëva, 121
 VIAILLY, Pierre-Julien, 109
 Vicedomini, Riccardo, 219
 Vidal, Valérie, 96
 VIENNOT, Mathieu, 109
 Vignes, Matthieu, 325
 Vilchez, Gaelle, 178
 vilhjalmsson, bjarni, 605
 Villa , Chiara, 330
 Villar, Emilie, 511
 Vincens, Pierre, 212
 Vingadassalon, Noémie, 253
 Virgoulay, Thimothée, 35
 Vituret, Cyrielle, 105
 Voisinne, Guillaume, 265
 Volant, Stevann, 180
 Volz, Ronny, 443

 Warszycki, Dawid, 455
 Wattier, Rémi, 238
 Wessener, Marc, 297
 Wessner, Marc, 16, 544
 Westeel, Emilie, 239
 Wiels, Joëlle, 414
 Wilson, James, 119
 Wincker, Patrick, 16, 38, 297, 544
 Wong, Emily, 288
 Wu, Xia, 414

 Yaury, Kevin, 172
 YOUNG, Jacques, 531

 Yun, Jin Ho, 308

 Zannad, Faiez, 548
 Zanzoni, Andreas, 111, 214, 372, 575
 Zareb, Anissa, 620
 Zea, Diego Javier, 205
 Zenagui, Reda, 170
 Zhao, Bingqing, 288
 Zhou, Simeng, 256
 Zhukova, Anna, 101, 564
 ZIENTARA, Stephan, 411
 Zinovyev, Andrei, 271, 275
 Zytnicki, Matthias, 489
 Zehraoui, Farida, 647

ORGANIZED BY



PARTNERS & SPONSORS

