

Jobim 2022 Posters -- new numbers

EasyChair ID	New number	When ?	Title
64	T8.12	Wed-6th	What are the functions of the short open reading frame-encoded peptides in monocytes? An interactomic approach.
65	D.7	both	ASTERICS: A Tool for the ExploRation and Integration of omiCS data
66	T4.2	Wed-6th	A comprehensive map of preferentially located motifs reveals novel proximal cis-regulatory elements in plants
68	T3.5	Thu-7th	Comparative study of protein aggregation propensity and mutation tolerance between naked mole-rat and mouse
69	T4.3	Thu-7th	Long reads RNA sequencing analysis with Oxford Nanopore Technologies: comparison of different library protocols and bioinformatics processing
70	T3.6	Wed-6th	Yeast recombination specificity impact on demography inference
71	T3.28	Wed-6th	Impact of sequencing platforms on cgMLST and wgSNP analyses on species of <i>Listeria</i> and <i>Salmonella</i>
72	D.2	both	IMPatient: an integrated web application to digitize, process and explore multimodal patient data
73	N.1	both	Expé-1point5 : une expérimentation nationale unique pour faciliter et étudier la transition des labos de recherche vers une réduction de leurs émissions de gaz à effet de serre
74	T4.4	Wed-6th	MYC deficiency impairs the development of effector/memory T lymphocytes
75	D.6	both	RiboTaxa: Combined approaches for taxonomic resolution down to the species level from metagenomics data revealing novelties
76	T3.1	Thu-7th	Evaluation of word-based alignment-free methods for yeast genome comparison and taxonomy
77	T2.16	Wed-6th	In-silico genome-wide detection of common fragile sites in human cells using BrdU-seq data
78	T9.15	Thu-7th	scAN10 : A reproducible and modular Nextflow pipeline for processing 10X single cell RNAseq data
79	T3.23	Thu-7th	Exploration and modeling the evolution of metabolic networks in fungi
80	T5.11	Thu-7th	Characterising competition and cooperation potentials in microbial communities using discrete models of metabolism
81	T9.11	Thu-7th	Automated solutions for big genomic data treatment in the context of the medical diagnosis platform SeqOIA
82	T8.13	Thu-7th	A new <i>Penicillium chrysogenum</i> Genome Scale-Metabolic Network: reconciliation of previous data and focus on specialised metabolism
83	T7.7	Thu-7th	Generation of a genome-wide 3D RNA profile of the catshark <i>habenulae</i>
84	T6.11	Thu-7th	Structural prediction of macromolecular interactions using evolutionary information
85	T1.13	Thu-7th	MAM : Methylation Analysis of Microalgae.
86	T3.7	Thu-7th	Wood-decomposing fungi through the lens of genomes comparison
87	T9.16	Wed-6th	Single-cell Initiative of Institut Curie: presentation of technologies & bioinformatics resources
88	T8.14	Wed-6th	Met4J, a programmatic toolbox for graph-based analysis of metabolic networks
89	T4.5	Thu-7th	Analysis of single-cell RNA-seq human PBMC datasets
90	T7.9	Thu-7th	Developpement d'une methode quantitative d'analyse de donnees RNA-Seq pour l'etude des variations in vivo des états de phosphorylation en 5' des ARN et application chez <i>Staphylococcus aureus</i>
91	D.3	both	FAIR-Checker: Checking and Inspecting metadata for FAIR bioinformatics resources.
92	T8.24	Wed-6th	Galaxy-SynBioCAD: tools and automated pipelines for Synthetic Biology Design and Metabolic Engineering
93	T6.1	Thu-7th	LibProtein: a rapid and versatile annotation library for protein post-translational annotations
94	T2.1	Thu-7th	MetExploreViz: Visualization tool for metabolic networks
95	T7.16	Wed-6th	Robust deconvolution of transcriptomic samples using the gene covariance structure
96	T9.17	Thu-7th	EDAM, life sciences ontology for data analysis and management.
97	T4.27	Thu-7th	QC impact on rare variant association results based on whole exome sequencing data

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98	T1.11	Thu-7th	AptaMat: a matrix-based algorithm to compare single-stranded oligonucleotides secondary structures
99	T8.6	Wed-6th	Prioritization of Master Regulators Through Influence Maximization
100	T1.1	Thu-7th	EstiAge: A tool to estimate the age of a variant
102	T4.28	Wed-6th	AskoR, an R package for easy RNA-Seq data analysis illustrated by the analysis of plant/pathogen/microbiote interactions
103	T7.8	Wed-6th	Novel adversarial autoencoders to simulate human genomic data for clinical research
104	T5.2	Wed-6th	Analyse de la diversité génétique des communautés planctoniques du Pacifique Sud-Ouest influencé par l'arc volcanique des Tonga
105	T4.6	Wed-6th	Impact of genomic variation on CTCF binding and 3D genome organization in breast cancer cells
106	D.5	both	Phylogenomics.fr : a user-friendly web interface to phylogenomic tools and reconciliation workflow
107	T4.29	Thu-7th	ReMap 2022: a database of Human, Mouse, Drosophila and Arabidopsis regulatory regions from an integrative analysis of DNA-binding sequencing experiments
109	T4.1	Thu-7th	Extensive Characterisation of Mitochondrial Genomes in Chemically Induced Mouse Liver Tumours
110	T5.1	Thu-7th	PANORAMA : comparative pangenomics tools to explore interspecies diversity of microbial genomes
111	T6.3	Thu-7th	Towards molecular understanding of the UbiJ-UbiK2 protein complex by multiscale molecular modelling studies
112	T1.12	Wed-6th	Interpreting mass spectra differing from their peptide models by several modifications
113	T3.4	Wed-6th	MicroScope: a web platform for microbial genome annotation through pangenomic and metabolic analysis
114	T1.2	Wed-6th	ROCK: digital normalization of whole genome sequencing data
115	T9.7	Thu-7th	The Assemblathon of the UAR 2AD, Data Acquisition and Analysis for Natural History
116	T9.10	Wed-6th	Montpellier GenomiX (MGX) : next-generation sequencing and data analysis service and expertise
117	T4.7	Thu-7th	GenomiqueENS, the IBENS Genomics core facility
118	T1.14	Wed-6th	ToulligQC 2: fast and comprehensive quality control for Oxford Nanopore sequencing data
119	T4.8	Wed-6th	Research and development at the I2BC Next-Generation Sequencing Facility: an overview
120	T8.15	Thu-7th	Modélisation du métabolisme de l'adénocarcinome pancréatique
121	D.8	both	Fantasio : Identifying rare recessive variants involved in multifactorial traits
122	T5.3	Thu-7th	FROGSFUNC: Smart integration of PICRUST2 software into FROGS pipeline
123	T3.8	Wed-6th	Caractérisation du contenu en gènes de l'espèce bactérienne Coxiella burnetii issue de différentes lignées en Europe
124	T5.9	Thu-7th	Deciphering molecular mechanisms governing malignant transformation in Neurofibromatosis Type 1 (NF1) from single cell transcriptomic
125	T2.2	Wed-6th	Improving attribute exploration for the detection and correction of anomalies in an agroecological knowledge base
126	T2.15	Thu-7th	Expanding FORVM Knowledge graph with link suggestion for under-studied compounds
127	T6.4	Wed-6th	Getting two birds with one stone: the Bios2cor R package for protein correlation analysis
128	T7.15	Thu-7th	Deep learning approaches as scoring methods for protein-protein rigid body docking.
129	T6.2	Wed-6th	An integrative bioinformatics approach to explore the biodiversity of enzyme families
130	T7.17	Thu-7th	AOP-helpFinder : a tool for exploration of the literature to support adverse outcome pathways development
131	T3.24	Wed-6th	DNA methylation patterns of transcription factor binding regions characterize their functional and evolutionary contexts
132	T8.2	Wed-6th	Nouvelle signature pour GSEA à partir des métabolites

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133	T3.25	Thu-7th	Evolution of promoter-centered 3D genome architecture across mammalian tissues
134	T4.9	Thu-7th	Predicting clinical response to immunotherapy in melanoma
135	T3.9	Thu-7th	The genomic basis of the <i>Streptococcus thermophilus</i> health-promoting properties
136	T3.2	Wed-6th	MPS Sampling : a novel method allowing the reliable selection of representative genomes to infer large-scale phylogenies
137	T8.16	Wed-6th	Improving the analysis of toxicants Mechanisms of Action with condition-specific models and network analysis
138	T3.26	Wed-6th	Multispecies comparison of fruit development through mRNA quantification analysis
139	T9.8	Wed-6th	Team efforts of the Bioinformatics and Biostatistics Hub of Institut Pasteur in response to the COVID-19 pandemic
140	T5.4	Wed-6th	metagWGS: a workflow to analyse short and long HiFi metagenomic reads
141	T5.12	Wed-6th	Analyzing and modelling functions carried by key species in minimal microbial communities
142	T3.10	Wed-6th	Evolution is not uniform along coding sequences
143	T9.2	Wed-6th	EMERGEN-DB : The French database for SARS-CoV-2 genomic surveillance and research
144	T3.11	Thu-7th	Most of the genetic diversity of the <i>Wolbachia</i> infecting <i>Culex pipiens</i> lies in the prophage regions
145	T9.18	Wed-6th	REPET evolutions: faster and easier
146	T4.10	Wed-6th	Automated identification of a cancer patient treatment: from sequencing to treatment prioritization
147	T2.9	Thu-7th	Cirscan: a shiny application to decipher circRNA-miRNA-mRNA networks from multi-level transcriptomic data
148	T9.3	Thu-7th	Omics Data Analysis Facilities in a Biomedical Research Institute
150	T7.10	Wed-6th	Predicting gene regulation through co-occurrence and evolutionary conservation of transcription factor binding sites
151	N.3	both	ABRomics - a digital platform on antimicrobial resistance to store, integrate, analyze and share multi-omics data
152	N.5	both	Green-BIM: a study to make young bioinformaticians aware of the carbon footprint of bioinformatics
153	T2.13	Thu-7th	PGxCorpus and PGxLOD, two shared resources for knowledge management in pharmacogenomics
154	T7.18	Wed-6th	Feature selection in longitudinal microbiome data via the analysis of random projections
155	T1.3	Thu-7th	msscaf: a multiple source genome scaffolder
156	T4.11	Thu-7th	RiboMethSeq platform at CRCL/CLB to profile ribosomal RNA 2'O-ribose methylation
157	T6.5	Thu-7th	A new way for finding drugs target protein and discover new protein complex in CETSA experiment
158	T9.19	Thu-7th	Comparison of Stacks and a custom pipeline for RADseq analysis
159	T2.11	Thu-7th	Revisiting iPPI-DB as a tool to navigate the pocketome protein-protein interactions
160	T3.12	Wed-6th	Characterization of the genomic diversity of <i>S. Typhimurium</i> and its monophasic variant in France in pig herds
161	T8.5	Thu-7th	Modelling the dynamics of <i>Salmonella</i> infection in the gut at the bacterial and host levels
162	T9.13	Thu-7th	ABiMS: Analysis and Bioinformatics for Marine Science
163	T2.3	Thu-7th	MyGOD : Interface de visualisation et d'analyse de données provenant des observatoires génomiques marins
164	T9.20	Wed-6th	ePeak: from replicated chromatin profiling data to epigenomic dynamics
165	T6.6	Wed-6th	Molecular modeling of plasmodesm organization by MCTP proteins
166	T5.5	Thu-7th	Eco-evolutionary diversity of the global ocean microbiome across plankton size fraction

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167	T6.7	Thu-7th	Reduced structural flexibility of eplet amino acids in HLA proteins
168	T7.19	Thu-7th	Axonal Delay Learning: from biology to computational neuroscience
169	T8.17	Thu-7th	The UNTWIST project: Network analysis and performance modelling of <i>Camelina sativa</i> under thermal and water stress
170	N.2	both	KATY european consortium: supporting the AI revolution in precision oncology
171	T5.6	Wed-6th	Construction of a reference genome catalog to decipher shared strains along an agrifood chain with shotgun metagenomic data
172	T1.15	Thu-7th	Benchmark of Nvidia Clara Parabricks suite for GPU-accelerated bioinformatic processing of raw RNA-seq data
173	T7.20	Wed-6th	Machine learning analysis on transcriptomic data reveals novel target genes of the WNT/ β -catenin pathway in colorectal cancer
174	T7.4	Wed-6th	Prediction of tumor microenvironment heterogeneity in kidney cancers by cell deconvolution
176	T3.13	Thu-7th	Deciphering the distribution of quinone biosynthetic pathways across Proteobacteria
177	T7.5	Thu-7th	Statistical approach for the detection of transposable element insertion bias in <i>Drosophila melanogaster</i>
179	T8.18	Wed-6th	Logical Modeling of Dysferlinopathies
180	T7.21	Thu-7th	SciGeneX: an unsupervised method to naturally discover cell types or cell states based on patterns of co-expressed genes in single-cell RNA-sequencing data
181	T7.22	Wed-6th	Bioinformatics integration of regulatory regions and variants in immune cells
182	T1.4	Wed-6th	Évaluation comparative des méthodes d'alignement multiple de séquences appliquées au séquençage de troisième génération
183	T6.12	Wed-6th	Modeling of NK-cell immunosurveillance in normal and pathological BM microenvironment
184	T8.3	Thu-7th	DNA methylation profiling of ATM-deficient breast tumours
185	T9.21	Thu-7th	CEA JupyterHub platform for multi-omics data analysis
186	D.9	both	Snakemake RNAseq workflow including repeat expression analysis
187	T8.7	Thu-7th	Using machine-learning on metabolomics data to predict complex phenotypes
188	T3.14	Wed-6th	Bacterial J-Domain Proteins and Partners Identification and Classification
189	T9.14	Wed-6th	The Migale bioinformatics core facility
191	T1.9	Thu-7th	Identifying Copy Number Variations in exome data – applications to infertility.
192	T2.12	Wed-6th	APPINetwork : an R package for building and computational analysis of protein-protein interaction networks
193	T9.4	Wed-6th	The IFB Catalogue
194	T7.23	Thu-7th	Bulk RNA-Seq deconvolution for the study of hemorrhagic fever
195	T6.8	Wed-6th	Investigating structural and sequence determinants of regioselectivity and substrate specificity in a family of enzymes: the case study of ubiquinone biosynthesis hydroxylases
196	T4.12	Wed-6th	<i>Rattus norvegicus</i> reference genome evaluation for hippocampus RNA-seq data analysis: a glimpse into spatial transcriptomics
197	T8.20	Wed-6th	An agent-based model of tumor-associated macrophage differentiation in chronic lymphocytic leukemia
198	T8.19	Thu-7th	Towards a data-driven network inference of interactions between immune and cancer cells in Chronic Lymphocytic Leukemia
199	T4.13	Thu-7th	TnSeek : analysing Tn-seq data for multiple conditions and multiple species
200	T9.22	Wed-6th	Creation of an integrated molecular dynamics workflow on the Galaxy platform : Characterization of aquaporin pores
201	T6.9	Thu-7th	BioacPepFinder: Discovery of bioactive peptides from protein digestion
202	T4.30	Wed-6th	Pipeline d'identification extensive de Variations Structurales dans du reséquençage nanopore de génome complet pour l'identification de mutations dans des maladies rares

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203	T7.11	Thu-7th	Identification of epimutations in rare diseases from a single patient perspective.
204	T3.3	Thu-7th	Alternative splicing modulates the number and composition of similar exonic regions
205	T7.32	Wed-6th	Latent Dirichlet Allocation for Double Clustering (LDA-DC): Discovering patients phenotypes and cell populations within a single Bayesian framework
206	T9.23	Thu-7th	Supports for imaging projects toward Open Science at AuBi platform
207	T4.31	Thu-7th	Harnessing gene expression profiling to infer the activation states of dendritic cell types, their dynamical relationships and their molecular regulation
208	T2.4	Wed-6th	The Phaeoexplorer Database: a Multi-Scale Genomic and Transcriptomic Data Resource for the Brown Algae
209	T9.1	Thu-7th	Impact environnementaux et sociaux du numérique
210	T3.29	Thu-7th	Automatization and optimization of TEFLoN, an accurate tool for detecting insertions of transposable elements
211	T9.24	Wed-6th	Development of a pipeline integrating single-cell omic sequencing and phenotypic imaging analyses
212	D.4	both	Openlink, a data management dashboard for research teams
213	N.4	both	Montpellier Omics Days: An annual bioinformatics and biostatistics conference organised by Bioinformatics students
214	T9.25	Thu-7th	Assemblage hybride d'un transcriptome de novo de Solanum nigrum
215	T9.26	Wed-6th	PitViper: a software for comparative meta-analysis and annotation of functional screening data
216	T2.10	Wed-6th	Heterogeneous biological data integration with Semantic Web technologies using RDF or RDF-Star formalisms generate topologically different graphs
217	T3.15	Thu-7th	Identification of conserved Regulatory Sequences in Ray-finned Fishes
218	T3.16	Wed-6th	MacSyFinder v2: An improved search engine to model and identify molecular systems in genomes
219	T3.17	Thu-7th	Structural variation involving transposable elements associated with grain width in cultivated rice
220	T9.5	Thu-7th	IFB training activities and resources
221	T9.9	Thu-7th	Bioinformatics and Genomics platform at Institut Sophia Agrobiotech
222	T9.27	Thu-7th	Poster UseGalaxy.fr: a Galaxy server for the French bioinformatics community
223	T8.1	Thu-7th	Chemomaps: Exploring the chimiodiversity of the living organisms
224	T7.12	Wed-6th	Dynamic genes network inference and very short time series. How repeated acoustic stimuli affect plant immunity?
225	T4.32	Wed-6th	scrNA-seq with Nanopore sequencing: benchmark of approaches based on hybrid sequencing
226	T9.28	Wed-6th	SCHNAPPs - Single Cell sHiNy APPLication(s)
227	T4.14	Wed-6th	PDXploR, a transcriptomic comparison methodology for PDX models and matched Patient samples, a case study on osteosarcoma.
228	T8.21	Thu-7th	Probing SARS-CoV-2 RNA interactome to identify post-transcriptional dysregulation associated with COVID-19
229	T4.15	Thu-7th	Prediction of pediatric cancer patient progression with non-invasive procedures: Pipeline to automatize liquid biopsy analysis
230	T5.13	Thu-7th	Construction of ASVs networks to monitor the temporal dynamics of bacterial communities - Application to public datasets on vegetable fermentations
231	T5.10	Wed-6th	Towards omics-based distribution modelling of marine plankton associations at global scale
232	T9.12	Wed-6th	A collaborative methodology for MULTI-OMIC analysis
233	T2.5	Thu-7th	Accessibilité des modèles pharmacocinétiques physiologiques
234	T9.29	Thu-7th	The IFB Core Cluster : an open HPC resource for all biologists and the breeding ground of the IFB National Network of Computational Resources (NNCR)
235	T4.16	Wed-6th	Chromatin meta-profiling of healthy and cancer cells using publicly available datasets

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236	T7.24	Wed-6th	DetecTree, from freehand drawing to digital patient care in genomic medicine
237	T3.30	Wed-6th	Fast Construction and Extension of Gene Families
238	D.1	both	Comptage massif et distribué de k-mers
240	T9.31	Thu-7th	A new bioinformatics pipeline for the analysis of hepatitis B virus transcriptome by Nanopore sequencing coupled to 5'RACE
241	T7.25	Thu-7th	Wasserstein regularisation for multidataset PCA
242	T7.1	Thu-7th	Investigation of neural population-based optimization
243	T9.30	Wed-6th	Automatization of Quality Data Workflows at a Genomic Platform: the GeT-PlaGe Solution
244	T1.5	Thu-7th	Preliminary Results from Nanopore Q20+ sequencing
245	T3.27	Thu-7th	MockVirus: expanding viral phylogenetic trees by protein sequence simulation
246	T7.13	Thu-7th	A general framework for classifying genomic sequences with Transformers: Application to gene annotation.
247	T4.17	Thu-7th	Single-cell deconvolution model predictive of patient survival in clear cell Renal Cell Carcinoma (ccRCC)
248	T3.18	Wed-6th	Evolution of Tandemly Arrayed Genes in Rosaceae
249	T3.31	Thu-7th	Caulifinder : a pipeline for automatic detection and annotation of endogenous viral sequences of Caulimoviridae
250	T8.8	Wed-6th	Multi-omic integration: adding network topology to study axial spondyloarthritis
251	T7.26	Wed-6th	Predicting the tissue or origin from circulating DNA fragments: Biological lessons learned from a comprehensive analysis of genetic, functional and computational features to increase the accuracy of a statistical model
252	T8.9	Thu-7th	Metamodelling of Dynamic Flux Balance Analysis
253	T3.32	Wed-6th	Screening of the natural two-component systems repertoire to establish guidelines for the construction of synthetic chimeras
254	T4.18	Wed-6th	Multi-omics and multi-tissues data to improve the understanding of heat stress adaptation mechanisms
255	T8.22	Wed-6th	A secondary analysis of the ASSESS cohort data: the role of IFN α on genes in Primary Sjögren's Syndrome
256	T7.14	Wed-6th	Using contrast to study RNA transcripts co-maturations
257	T9.6	Wed-6th	Towards open science for deep sea sponge microbiomes
258	T2.6	Wed-6th	Omnicrobe, an open-access database of microbial habitats, phenotypes and uses extracted from text
259	T7.27	Thu-7th	Computational study of chemical-induced liver injury using high-content imaging phenotypes
260	N.6	both	MaDMP4Is, or how to better manage bioinformatics projects with MY
261	T7.28	Wed-6th	Predicting adverse drug reactions on organs using sequential neural network models.
262	T2.14	Wed-6th	Computational analysis of molecules, olfactory receptors, odors and their interactions
264	T8.10	Wed-6th	Logic programs to infer computational models of the human embryonic development
265	T5.14	Wed-6th	An eucaryote-friendly set of python scripts for multi-sample shotgun metagenomics and its associated Shiny application for microbiota exploration
266	T7.2	Wed-6th	Integrated Analyses of Large Scale RNAseq Data in Acute Myeloid Leukemia
267	T8.23	Thu-7th	A Design of Experiment strategy for GRN selection and refinement
268	T7.29	Thu-7th	EnzBert : Transformer pour la caractérisation d'enzyme
271	T4.19	Thu-7th	Single-cell ATAC-seq integration highlight epigenetics remodeling within HSC quiescence signaling.
272	T3.19	Thu-7th	Alpha-solenoid proteins for the regulation of organellar gene expression: evolutionary history and conformation studies in photosynthetic model species

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273	T4.20	Wed-6th	Investigating the resistance to mDH inhibitors in Acute Myeloid Leukemia integrating multiple regulatory layers
274	T1.6	Wed-6th	SVJedi-graph: genotyping close and overlapping structural variants with a variation graph and long-reads
275	T3.20	Wed-6th	Telomere-to-telomere genome assembly of the phytoparasitic nematode and virus vector <i>Xiphinema</i> index
278	T7.3	Thu-7th	A novel method to identify and score clusters of motifs of protein sequences (CLUMPs) based on amino acids physicochemical properties.
279	N.7	both	JeBiF - Association for the Young Bioinformaticians of France
280	T5.7	Thu-7th	Full-length 16S rRNA gene MiniION™ sequencing characterizing bacterial microbiota at species-level?
281	T7.6	Wed-6th	Implementing a Text Mining Service Offer on the Migale Bioinformatics Platform
282	T1.8	Wed-6th	A novel weight-based approach to determine cell type specificity from single cell datasets
284	T4.21	Thu-7th	Detection of nucleotide repeat expansions by exome sequencing of Parkinson's disease patients using ExpansionHunter
285	T1.10	Wed-6th	Memory efficient subsampling strategy for large scale analysis of sequencing data
286	T6.10	Wed-6th	Towards the potentiation of selective inhibition of Mfd nanomachine
287	T7.30	Wed-6th	Exploring cell morphological profile information for the de-risking of small molecules.
288	T4.22	Wed-6th	Computational deconvolution of transcriptomics data reveals immune cell landscape of inflammatory infiltrates in giant cell arteritis
289	T1.16	Wed-6th	A nextflow workflow for peptide sequence design in a targeted proteomic approach
290	T7.31	Thu-7th	Automatic Empirical Segmentation of the Peritumoral Area in Lung Cancer Computed Tomography, Locating the Non-anatomical
291	T8.4	Wed-6th	Deciphering the molecular network controlling the biology of the pig blastocyst and its cellular interactions
292	T4.23	Thu-7th	Integration analysis for AAV-based gene therapy vectors with linked-read sequencing
294	T4.24	Wed-6th	interaction dynamics comparison of the models of Omicron BA.1 and BA.2 variants of SARS-CoV-2 Spike RBD in complex with human ACE2 through MD simulations and MM-PBSA calculations
295	T2.7	Thu-7th	IDy-Path : Identification Dynamique des épidémies de Pathogènes
296	T2.8	Wed-6th	The advantage of having a web dedicated group in a Bioinformatic team
297	T4.25	Thu-7th	Atlas and biological significance of transcribed non-coding regions of the human genome
298	T3.21	Thu-7th	Gene orthology detection for Long Non Coding RNA (LncRNA)
299	T8.25	Thu-7th	RFLOMICS : R package and Shiny interface for Integrative analysis of omics data.
300	T4.26	Wed-6th	Identification of molecular subtypes from Triple-negative breast cancer tumors
301	T5.8	Wed-6th	A metapangenomic approach for the association of prokaryotic genes to given phenotypic traits
302	T1.7	Thu-7th	Breakpoint detection in shallow and targeted panel in Rhabdomyosarcomas
305	T8.11	Thu-7th	Machine Learning classification performance on mechanistic representations of the gut microbiota built from abundance profiles
306	T3.22	Wed-6th	The effect of chromosomal rearrangements on base composition evolution in mammals