

Posters

Affectation Number	Flash	Authors	Titles
1		Rim Zaag, Maxime Lienard, Sébastien Toffoli and Jean-François Laes	Multi-factor Data Normalization enables the detection of LOH in amplicon sequencing data
2		Christelle Hennequet-Antier, Aurélien Brionne and Amélie Juanchich	ViSEAGO: Easier data mining of biological functions organized into clusters using Gene Ontology and semantic similarity
3		Mathieu Bahin, Benoit F Noel, Valentine Murigneux, Charles Bernard, Leila Bastianelli, Hervé Le Hir, Alice Lebreton and Auguste Genovesio	ALFA: Annotation Landscape For Aligned reads
4		Céline Bougel, Sébastien Déjean, Caroline Giuliani, Philippe Saint-Pierre, Nicolas Savy and Sandrine Andrieu	Classification of evolutionary trajectories of cognitive functions
5		Céline Bougel, Sébastien Déjean, Caroline Giuliani, Philippe Saint-Pierre, Nicolas Savy and Sandrine Andrieu	Classification of the evolutionary trajectories of cognitive functions
6		Charlotte Berthelier, Bérengère Laffay, Sophie Lemoine and Laurent Jourden	A state-of-the-art analysis of innovation software tools for primary analysis for Oxford Nanopore sequence data
7		Laurent Jourden, Charlotte Berthelier, Corinne Blugeon, Fanny Couplier, Karine Dias, Bérengère Laffay, Sophie Lemoine and Stéphane Le Crom	IBENS Genomics core facility
8		Michaël Pierrelée, Laurent Tichit and Bianca Habermann	Pathway analysis from time course gene expression experiments to unveil the dynamic of cellular responses
9		Loan Vulliard, Michael Caldera and Jörg Menche	Understanding Chemical-Genetic Interactions
10		Martial Briand, Mariam Bouzid, Marc Legeay, Marion Fischer-Le Saux, Claire Lemaître, Gilles Hunault and Matthieu Barret	A tool for very fast taxonomic comparison of genomic sequences
11		Hélène Polvèche, Margot Jarrige, Didier Auboeuf, Cécile Martinat and Marc Peschanski	SIStemA : Gene expression database of human Stem Cell and their differentiated derivative,
12		Anna Tran, Sèverine Bérard and Anne-Muriel Arigon Chifolleau	Évaluation de la qualité et comparaison des assemblages des génomes
13		Xavier Mialhe, Stéphanie Rialle, Marine Pralong and Emeric Dubois	Analysis workflow for low frequency variant detection
14		Laffay Bérengère, Corinne Blugeon, Laurent Jourden and Sophie Lemoine	Evaluation d'outils de quantification des transcrits alternatifs à partir de données de séquençage longue lecture Nanopore
15		Virginie Lollier, Dominique Tessier, Mathieu Fanel and David Ropartz	mzLabelEditor: un outil pour annoter des spectres de masse
16		Abdenour Abbas, Karima Naciri, Geoffray Brelurut, Nils Collinet, Denis Thieffry, Elena Tomasello, Marco Pettini, Marc Dalod and Thien-Phong Vu Manh	Deciphering the activation states of plasmacytoid dendritic cells, their dynamical relationships and their molecular regulation
17		Claire Vincent, Laetitia Aznar-Cormano, Alexander Fedosov, Yuri Kantor, Maria-Vittoria Modica and Nicolas Puillandre	Identification des proies de gastéropodes venimeux (Conoidea) par approche de métabarcoding
18		Dominique Tessier, Matthieu David, Virginie Lollier, Guillaume Fertin and Hélène Rogniaux	SpecOMS: découverte des modifications portées par les protéines
19		Ariane Bassignani, Magali Berland, Sandra Plancade and Catherine Juste	ProteoCardis: an intestinal metaproteome-wide association study of coronary artery disease
20		Laureline Dejardin Bretones, Aubin Thomas and William Ritchie	Stratégie de compression de données de séquençage cliniques
21		Mokhtari Wafa, Khemili-Talbi Souad, Kwasigroch Jean Marc and Gilis Dimitri	Performance evaluation of bioinformatics tools for predicting allergenic proteins in food
22		Emeline Perthame and Natalia Pietrosemoli	Integration of transcriptomic and proteomic data for biomarker discovery in Lassa fever
23		Joanna Fourquet, Adeline Chaubet, Hélène Chiapello, Christine Gaspin, Marisa Haenni, Christophe Klopp, Agnese Lupo, Jean Mainguy, Céline Noirot, Tony Rochegue, Matthias Zytnicki, Tristan Ferry and Claire Hoede	MetagWGS: an automated Nextflow pipeline for metagenome
24		Ahmad Abdel Sater, Pierre-Julien Viailly, Thierry Lecroq, Élise Prieur-Gaston, Élodie Bohers, Mathieu Viennot, Vincianne Marchand, Philippe Ruminy, Hélène Dauchel, Martine Becker, Hervé Tilly, Pierre Vera and Fabrice Jardin	UMI-VarCal: a new UMI-based variant caller that efficiently improves low-frequency variant detection in paired-end sequencing NGS libraries
25		Elodie Persyn, Matthew Traylor, Hugh Markus and Cathryn Lewis	Exploring white matter hyperintensities genetic associations through the use of external transcriptomic data
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27		Thomas E, Ludwig, Reda Bellafqira, David Niyitegeka, Daniel Salas, Isabelle Perseil, Gouenou Coatrieux and Emmanuelle Génin	PrivAS: a tool to perform Privacy-Preserving Association Studies
28		Amandine Lecerf Defer, Laurent Mesnard, Pierre-Antoine Gourraud, Sophie Limou and Nicolas Vince	Development and validation of an alloscore in kidney transplantation



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29		Helene Arduin, Marcin Domagala, Mary Poupot and Vera Pancaldi	Modelling the differentiation dynamics of monocytes in contact with CLL B cells
30		Emmanuelle Morin, Shingo Miyauchi, Hélène San Clemente, Eric Chen, Alan Kuo, Igor Grigoriev, Bernard Henrissat, Christophe Roux, Nicolas Corradi and Francis Martin	Comparative genomics of <i>Rhizophagus irregularis</i> , <i>R. cerebriforme</i> , <i>R. diaphanus</i> and <i>Gigaspora rosea</i> highlights specific genetic features in Glomeromycotina,
31		Ayan Ianniello, Nicolas Vince, Pierre-Antoine Gourraud, Sophie Limou, Venceslas Douillard and Estelle Geffard	Development of a complete HLA analysis pipeline: HLA-Functional Immunogenomic eXploration (HLA-FIX)
32		Thomas Riquelme, Antoine Grigis, Cathy Philippe and Vincent Frouin	Polygenic Risk Scores for Autism spectrum disorder and Alzheimer's disease enable the identification of new white matter tract biomarkers
33		Estelle Geffard, Thomas Goronflot, Sophie Limou, Nicolas Vince, Matthieu Wargny and Pierre-Antoine Gourraud	Pioneer data-driven methods generating synthetic data: the HLA "avatars" are shifting paradigms in data sharing,
34		Léo Boussamet, Estelle Geffard, Alexandre Walencik, Sophie Limou, Pierre-Antoine Gourraud and Nicolas Vince	Easy-HLA web application: new tools for HLA genotypes studies
35		Hugo Talibert and François Coste	Using residues coevolution to search for protein homologs through alignment of Potts models
36		Sylvain Prigent, Olivier Fernandez, Stéphane Bernillon, Pierre Petriacq, Annick Moing, Thierry Berton, Llorenç Cabrera-Bosquet, Émilie Millet, Claude Welcker, François Tardieu and Yves Gibon	Using Metabolomic Data to Predict Maize Yields
37		Axelle Durand, Estelle Geffard, Rokhaya Ba, Sophie Limou, Sophie Brouard, Alexandre Loupy, Nicolas Vince and Pierre-Antoine Gourraud	De-centralized database: new challenges to design innovative contextualization algorithms
38		Sophie Limou, Axelle Durand, Nicolas Vince, Venceslas Douillard, Estelle Geffard, Pierre-Antoine Gourraud, Cheryl Winkler, Derek K, Ng, Bradley Warady, Susan Furth, Jeffrey B, Kopp and Frederick J, Kaskel	Statistical inference of immunogenetic parameters reveals an HLA allele associated with pediatric Focal Segmental Glomerulosclerosis
39		Guita Niang, Mark Hoebeke, Arnaud Meng, Xi Liu, Maxim Scheremetjew, Rob Finn, Eric Pelletier, Erwan Corre	METdb: A GENOMIC REFERENCE DATABASE FOR MARINE SPECIES
40		Jeff Mold, Laurent Modolo, Joanna Hård, Margherita Zamboni, Anton Larsson, Patrik Ståhl, Erik Borgström, Simone Picelli, Björn Reinius, Rickard Sandberg, Pedro Réu, Carlos Talavera-Lopez, Björn Andersson, Kim Blom, Johan Sandberg, Jakob Michaelsson, Franck Picard and Jonas Frisen	Divergent Clonal CD8+ T Cell Differentiation Establishes a Repertoire of Distinct Memory T Cell Clones Following Human Viral Infections
41		Nadège Guiguelmoni, Romain Koszul and Jean-François Flot	Benchmarking Hi-C scaffolders
42		Venceslas Douillard, Nicolas Vince, Sophie Limou and Pierre-Antoine Gourraud	Navigating the treacherous waters of HLA imputation with the SHLARC (SNP-HLA Reference Consortium)
43		Delphine Nègre, Arnaud BELCOUR, Meziane AITE, Anne SIEGEL, Erwan CORRE, Gabriel MARKOV	Genome-scale metabolic networks from two asian brown algae : integrating targeted pathways analyses and metabolomic data
44		Ludovic Cottret, Caroline Baroukh and Stéphane Genin	Comparaison des réseaux métaboliques de bactéries phytopathogènes
45		Sebastien Carrere, Thomas Garcia, Ludovic Legrand and Jérôme Gouzy	Structuration et consolidation de résultats d'analyses de RNAseq et Polymorphisme
46		Anne-Laure Abraham, Sandra Dérozier, Quentin Cavailé, Thibaut Guirimand, Solange Aka, Valentin Loux and Pierre Renault	Metagenomic analysis of an African beer ecosystem using FoodMicrobiomeTransfert application
47		Céline Gottin, Anne Diévar, Nathalie Chantret and Vincent Ranwez	Comment annoter et analyser les protéines à motifs répétés : Cas des protéines contenant des répétitions riches en leucine (LRR) chez le riz,
48		Abel Garnier, Nicolas Vince, George Nelson, Elizabeth Binns-Roemer, Victor David, Kevin Hoang, Pierre-Antoine Gourraud, James J, Goedert, Cheryl Winkler and Sophie Limou	Epigenome-wide association study reveals immunogenetic targets of DNA methylation modification by HIV-1
49		Nils Giordano and Samuel Chaffron	Co-activity networks reveal the structure of planktonic symbioses in the global ocean
50		Hélène Kabbech, Eduardo Gade Gusmao and Argyris Papantonis	An Integrative Deep-Learning Framework for Analyzing Native Spatial Chromatin Dynamics
51		David Vallenet, Alexandra Calteau, Mathieu Dubois, Mylène Beuvin, Laura Burlot, Xavier Bussel, Stéphanie Fouteau, Guillaume Gautreau, Aurélie Lajus, Jordan Langlois, Rémi Planel, David Roche, Johan Rollin, Zoé Rouy and Claudine Médigue	MicroScope: an integrated platform for the annotation and exploration of microbial gene functions through genomic and metabolic comparative analysis

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52		Rémi Guimon, Nicolas Vince, Fabienne Haspot, Nicolas Poirier, Gilles Blanco, Sophie Limou and Pierre-Antoine Gourraud	The SIRP gene family: widespread conservation in animals, haplotypic polymorphisms in humans and its therapeutic consequences for monoclonal antibody reactivity,
53		Caroline Peltier, François-Xavier Lejeune, Ivan Moszer and Arthur Tenenhaus	RGCCA with block-wise missing structure
54		Celine Le Beguec, Vincent Anquetil, Ivan Moszer, Isabelle Le Ber, Olivier Colliot, Pierre Perterlongo and Dominique Lavenier	Biomarkers for neurodegenerative diseases
55		Margot Correa, Cécile Guichard, Julien Roziere, Marie-Laure Martin-Magniette and Véronique Brunaud	Detection of transcriptional regulatory motifs specific to plant gene responses in stress conditions
56		Christophe Le Priol, Chloé-Agathe Azencott and Xavier Gidrol	Large-scale RNA-seq datasets enable the detection of genes with a differential expression dispersion in cancer
57		Sophie Lemoine, Ammara Mohammad, Corinne Blugeon, Bérengère Laffay and Laurent Jourdren	cDNA length improvement is essential to allow better isoform characterization for long read RNA sequencing
58		Nicolas Guillaudeux, Catherine Belleannée, Samuel Blanquart and Jean-Stéphane Varré	Predicting isoform transcripts: lessons from human, mouse and dog
59		Marjorie Couton, Aurélien Baud, Claire Daguin-Thiébaud, Thierry Comtet and Frédérique Viard	High-Throughput Sequencing from preservative ethanol and bulk of specimens to jointly assess species and population genetic diversity of colonial ascidians
60		Toni Paternina, Auguste Genovesio and Hervé Le Hir	Unraveling the rules of the Exon Junction Complex deposition with CLIP-seq
61		Galadriel Briere, Ludovic Léauté, Raluca Uricaru and Patricia Thebault	Development of a novel multi-scale integrative computational method dedicated to the analysis of heterogeneous omics data,
62		Gwendal Virlet, Erwan Corlouer, Alexandre Termier, Anne Laperche, Nathalie Nesi and Dominique Lavenier	Interactions de SNPs d'ordre N par pattern mining
63		Aimeric Dabin, Thomas Goronflot, Benoît Tessoulin, David Chiron, Anne Monlien, Steven Le Gouill, Pierre-Antoine Gourraud and Matilde Karakachoff	Refract-Lyma and CHU hub: from a research cohort to a regional electronic medical record system and back
64		Nicolas Maillet	RPG: fast and efficient in silico protein digestion
65		Stevann Volant, Aroldo Ayub Dargél and Chantal Henry	Chronic mood instability, cardiometabolic risk and functional impairment in bipolar patients: relevance of a multidimensional approach
66		Fanny Casse, Emmanuelle Becker, Susete Alves-Carvalho, Violette Thermes, Fabrice Legeai and Julien Bobe	Régulation par les miARN des gènes régulant la fécondité et le développement embryonnaire précoce chez le poisson medaka (<i>Oryzias latipes</i>)
67		Rokhaya Ba, Nicolas Vince, Estelle Geffard, Dorian Malguid, Marie Lanza, Pierre-Antoine Gourraud and Sophie Limou	Burrowing functional and immunogenetic information through the 1000 Genomes Project with Ferret v.3,0
68		Ting Xie and Vera Pancaldi	A novel DNA methylation signature for cell-type deconvolution in immuno-oncology
69		Jocelyn Brayet, Camille Barette, Vivien Deshaies, Alban Lermine, Mathieu Barthelemy and Laurent Frobert	Industrial NGS analysis processes from sequencing to variant interpretation on MOABI platform
70		Adelme Bazin, Guillaume Gautreau, Claudine Medigue, Alexandra Calteau and David Vallenet	Comparative microbial pangenomics to explore mobilome dynamics
71		Jean Fabre-Monplaisir, Brigitte Mossé and Élisabeth Remy	Symmetries of the hypercube : a tool for regulatory networks analysis
72		Paul Terzian, Céline Vandecasteele, Alice Guidot, Ludovic Legrand and Christophe Klopp	Can we detect DNA methylation with Oxford Nanopore reads ?
73		Alexia Alfaro, Mélanie Guyot, Clara Panzolini, Philippe Blancou, Agnès Paquet and Julie Cazareth	Mise en place d'un pipeline automatisé d'analyses multivariées pour la cytométrie en flux multi-couleurs
74		Miguel Madrid Mencía and Vera Pancaldi	GARDEN-NET: a tool for chromatin 3D interaction network visualization
75		Julie Lao, Thomas Lacroix, Gérard Guédon, Nathalie Leblond-Bourget and Hélène Chiapello	The SeCoNeMo approach and its application to ICE annotation in Firmicutes
76		Cédric Midoux, Mahendra Mariadassou, Olivier Rué, Olivier Chapleur, Valentin Loux and Ariane Bize	Easy16S : a user-friendly Shiny interface for analysis and visualization of metagenomic data
77		Florian Thonier, Mathieu Giraud and Mikaël Salson	Vidjil, une plateforme pour l'analyse des répertoires immunitaires
78		Hadrien Regue, Nicolas Vince, Pierre-Antoine Gourraud and David Laplaud	Exploring relationship between to neuro-inflammatory diseases
79		Julien Saint-Vanne, Romain Dallet, Erwan Corre, Yann Guitton and Gildas Le Corguillé	LC-MS/MS tool and interactive visualizations integration on Galaxy Workflow4Metabolomics infrastructure
80		Guillaume Gricourt, Mélissa N'Debi, Vanessa Demontant, Anais Nguyen-Goument, Abdelrazak Aissat, Paul-Louis Woerther and Christophe Rodriguez	RandomRead : a sequence-read simulator program for metagenomic shotgun

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81		Lobna Oueslati and Vera Pancaldi	Bioinformatic characterization of the role of TRIP12 in pancreatic adenocarcinoma
82		Laura Conde-Canencia, Belaid Hamoum, Emeline Roux and Dominique Lavenier	Error Correction Schemes for DNA Storage with Nanopore Sequencing
83		Mélissa N'Debi, Guillaume Gricourt, Vanessa Demontant, Anais Nguyen-Goument, Abdelrazak Aissat, Paul-Louis Woerther and Christophe Rodriguez	Hermès : a management tool for Next-Generation Sequencing analysis on a genomic platform
84		Jean Mainguy, Géraldine Pascal, Olivier Bouchez, Adrien Castinel, Sylvie Combes and Claire Hoede	Identification of genomic regions for high-resolution taxonomic profiling using long-read sequencing technology
85		Cédric Midoux, Tiago Delforno, Thais Macedo, Gileno Lacerda, Olivier Rué, Mahendra Mariadassou, Maria Bernadete A, Varesche, Théodore Bouchez, Ariane Bize, Valéria Maria Oliveira and Valentin Loux	Feedback on a comparative metatranscriptomic analysis
86		Benoit Valot, Charlotte Couchoud, Daniel Martak, Anais Potron, Xavier Bertrand and Didier Hocquet	Flexible analysis of WGS of bacterial genomes using wgMLST approach,
87		Valentin Loux, Sam Ah Lone, Hélène Chiapello, David Christiany, Sandra Derozier, Olivier Inizan, Véronique Martin, Mahendra Mariadassou, Cédric Midoux, Olivier Rué, Sophie Schbath and Valérie Vidal	The Migale bioinformatics platform
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89		Claire Leman, Raphael Gaisne, Axelle Durand, Matilde Karakachoff, Romain Bourcier, Lucile Figueres, Nicolas Vince, Richard Redon, Hubert Desal, Pierre-Antoine Gourraud, Maryvonne Hourmant and Limou Sophie	Genetic determinants of intracranial aneurism in autosomal dominant polycystic kidney disease
90		Felipe Lira, Gilles Hunault, Martial Briand, Perrine Portier, Claudine Landes and Marion Fischer-Le Saux	PREDIdicting bacterial PATHogenicity on plant: PREDIPATH
91		Florian Berger, Eros Marin, Cynthia Fourgeux, Amandine Even, Laurence Bouchet-Delbos, Alice Mollé, Maria-Cristina Cuturi, Jeremie Poschmann and Aurélie Moreau	Comparison of tolerogenic dendritic cells used in clinic with other in vitro-derived myeloid cells by epigenetic and transcriptomic analyses
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93		Violaine Saint-André, Vincent Rouilly, Bruno Charbit, Matthew Albert, Lluís Quintana-Murci and Darragh Duffy	Inter-individual variability in healthy human cytokine responses
94		Valentin François - - Campion and Jerome Jullien	Study of sperm epigenetic contribution for the regulation of embryonic gene transcription in early development
95		Kévin Da Silva, Nicolas Pons, Magali Berland, Florian Plaza-Oñate, Mathieu Almeida and Pierre Peterlongo	From genomics to metagenomics: benchmark of variation graphs
96		Sam Ah-Lone, Sandra Dérozier, Valentin Loux and Hélène Chiapello	A workflow to build a relevant bacterial genome sub-dataset from public databases
97		Johanna Zoppi and Samuel Chaffron	MiBiOmics, a shiny application for graph-based multi-omics analysis
98		Stefano Caruso, Calatayud, Pilet, Rekik, La Bella, Imbeaud, Letouzé, Meunier, Bayard, Rohr-Udilova, Péneau, Grasl-Kraupp, de Koning, Ouine, Bioulac-Sage, Couchy, Calderaro, Nault, Jessica Zucman-Rossi and Sandra Rebouissou	Multi-omics approach to predict drug response in liver cancer cell lines
99		Clément Frainay, Maxime Chazalviel and Fabien Jourdan	Recommendation system embedded in metabolic network visualization: a new way of looking at metabolomics results,
100		Justine Guegan, Aurélien Beliard, Mathilde Bertrand, Thomas Gareau, Beáta György, François-Xavier Lejeune and Ivan Moszer	Omics Data Analysis Facilities in a Biomedical Research Institute
101		Raphaël Gaisne, Lucile Figueres, Pascal Houillier, Rosa Vargas-Poussou, Sandrine Lemoine, Claire Leman, Nicolas Vince, Pierre-Antoine Gourraud and Sophie Limou	Exome sequencing in Hereditary Hypophosphatemic Rickets with Hypercalciuria
102		Maëlle Daunesse, Rachel Legendre, Hugo Varet, Thomas Cokelaer and Claudia Chica	ChIPuana: from raw data to epigenomic dynamics
103		Kirsley Chennen, Maxime Folschette, Alban Gaignard, Richard Redon, Hala Skaf-Molli, Olivier Poch, Jocelyn Laporte and Julie Thompson	INEX-MED: INtegration and EXploration of heterogeneous bio-MEDical data
104		Phillippe Noel, Emmanuel Bresso, Dave Ritchie, Bernard Maigret and Marie-Dominique Devignes	A workflow based on self-organizing map for clustering stable structures of proteins from molecular dynamics simulations
105		Méline Wery, Emmanuelle Becker, Franck Auge, Charles Bettenbourg, Olivier Dameron and Anne Siegel	Identification of causal signature from omics data integration and network reasoning-based analysis

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106		Dimitri Meistermann, Loubersac Sophie, Arnaud Reignier, Valentin François - - Champion, Thomas Fréour, Jeremie Bourdon and Laurent David	The limit of cell specification concept: a lesson from scRNA-Seq on early human development,
107		Claire-Cécile Barrot, Jean-Baptiste Woillard and Nicolas Picard	Cypascan: an online tool for star allele calling in pharmacogenetics
108		Justine Pollet, Jean-Baptiste Woillard and Claire-Cécile Barrot	Recherche par clustering de gènes impliqués dans le syndrome PTLD
109		Franck Bonardi, Loïc Couderc, Isabelle Guigon, Jean-Pascal Meneboo, Pierre Pericard and Hélène Touzet	Which genome browser to use for my data ?
110		Gautier Stoll, Aurélien Naldi, Vincent Noël, Eric Viara, Emmanuel Barillot, Guido Kroemer, Denis Thieffry and Laurence Calzone	Dynamic cell population modeling with UpPMaBoSS
111		Theo Hirsch, Jayendra Shinde, Benedict Monteiro, Quentin Bayard, Sandrine Imbeaud, Feng Liu, Victor Renault, Jessica Zucman-Rossi and Eric Letouzé	Palimpsest: an R package for studying mutational and structural variants signatures along clonal evolution in cancer from single or multiple samples sequencing
112		Yoann Pageaud	Advanced Visualization of Data Comparisons with BiocompR,
113		Walter Santana Garcia, Maria Rocha-Acevedo, Yvon Mbouamboua, Bruno Contreras-Moreira, Denis Thieffry, Morgane Thomas-Chollier, Jacques van-Helden and Alejandra Medina-Rivera	RSAT var-tools: an accessible and flexible framework to predict the impact of regulatory variants on transcription factor binding
114		Wesley Delage, Julien Thevenon and Claire Lemaitre	Comparison of large insertion variant callers on whole exome sequencing
115		Tanguy Lallemand, Sylvain Gaillard, Sandra Pelletier, Claudine Landès, Sébastien Aubourg and Julie Bourbeillon	Visualizing metadata change in networks and / or clusters
116		Amazigh Mokhtari, Bruno Etain, Ipek Yalcin, Cynthia Marie-Claire, El Chérif Ibrahim, Raoul Belzeaux, Pierre-Eric Lutz and Andrée Delahaye-Duriez	Transcriptome analysis to identify co-expressed gene networks as a molecular signature for childhood trauma-related mood disorders,
117		Lysiane Hauguel, Fabrice Dupuis, Sylvain Gaillard, Julie Bourbeillon, Claudine Landès and Sandra Pelletier	Mise en place d'un LIMS enrichi par une organisation harmonisée des métadonnées
118		Rémy Costa, Quentin Delorme, Yasmine Mansour, Anna-Sophie Fiston-Lavier and Annie Chateau	How to involve repetitive regions in scaffolding improvement
119		Maëlle Daunesse, Vincent Guillemot and Natalia Pietrosemoli	Analysis of multi-omics data: a comparison of correlation and functional integrative approaches on a cancer dataset
120		Maureen Muscat, Giancarlo Croce, Edoardo Sarti and Martin Weigt	Supervised contact prediction in proteins
121		Lea Bellenger, Mirca Saurty, Ghislaine Morvan-Dubois, Hervé Chneiweiss, Marie-Pierre Junier and Christophe Antoniewski	A workflow to analyse single-cell transcriptomes from heterogeneous tumors
122		Natacha Koenig, Chritine Almunia, Arnaud Chaumot, Jean Armengaud, Olivier Geffard and Davide Degli Esposti	Réseaux de co-expression pour l'analyse de données de protéomique pour la compréhension des mécanismes d'action de contaminants chez une espèce non-modèle, Gammarus fossarum,
123		Geoffray Brelurut, Nathalie Lehmann, Hatim El Jazouli, Céline Hernandez, Morgane Thomas-Chollier, Denis Thieffry, Stéphane Le Crom and Laurent Jourden	Eoulsan workflows for tag-based and full-transcript single-cell RNA-seq protocols
124		Pierre Vignet, Anne Siegel, Nathalie Théret and Jean Coquet	CADBIOM – Un logiciel de modélisation des réseaux de signalisation
125		Elie Arnaud and Yvan Le Bras	R: Ecology Met A Data Language
126		Pierre Justeau, Simão Moreira Rodriguez and Martin Brian Richards	A graph theoretical approach to depicting sex-biased dispersal in ancient populations: mitochondrial DNA vs, Y-chromosome variation
127		Lucas Bourneuf and Sacha Schutz	Biseau: A declarative environment for high-level specification and visualization of graph theory
128		Elin Teppa and Alessandra Carbone	A web server for identification and analysis of coevolution in overlapping proteins
129		Leila Khajavi, Matthias Zytnicki and Roland Liblau	Transcriptomics Signature of Type I Narcolepsy (T1N)
130		Sabrina Lakoum, Andrée Delahaye-Duriez, Nour Touibi, Juliette Van-Steenwinckel, Bobbi Fleiss, Claire-Marie Rangon and Pierre Gressens	Sex-specific differences in microglia inflammatory response during brain development
131		Céline Sérazin, Léa Flippe, Dimitri Meistermann, Severine Bezie, Laurent David and Carole Guillonnet	Single cell transcriptomic analysis for a better understanding of human CD8 regulatory T cells
132		Matthias Zytnicki and Christine Gaspin	smaMapper: a mapping tool for short RNA reads
133		Thomas Laurent and Jeremie Poschmann	Longitudinal analysis of immune cells in kidney transplantation rejection by single-cell RNA-seq

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134		Sacha Schutz, Lucas Bourneuf and Pierre Vignet	CuteVariant: Un visualisateur de variants génétiques pour le diagnostic médical
135		Enora Geslain, Julien Robert, Jacky Ame and Erwan Corre	Bioanalysis activities on the ABiMS (Analysis and Bioinformatic for Marine Science) platform
136		Diego Zea, Hugues Richard and Elodie Laine	Transcript-aware Clustering of Orthologous Exons Shed Light on Alternative Splicing Evolution
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138		Vincent Henry, Giulia Bassignana, Violetta Zujovic, Fabrizio De Vico Fallani, Olivier Dameron, Ivan Moszer and Olivier Colliot	Conciliation of process description and molecular interaction networks using logical properties of ontology
139		Jelena Vucinic, David Simoncini, Manon Ruffini, Sophie Barbe and Thomas Schiex	Positive Multistate Protein Design
140		Quentin Ferré, Guillaume Charbonnier, Nori Sadouni, Fabrice Lopez, Yasmina Kermezli, Salvatore Spicuglia, Cécile Capponi, Badih Ghattas and Denis Puthier	OLOGRAM : Modeling the distribution of overlap length between genomic regions sets
141		Guillaume Reboul, David Moreira, Paola Bertolino, Luis J, Galindo, Natasha V, Annenkova and Purificacion Lopez-Garcia	Microbial communities from deep-lake sediments of Lake Baikal, Siberia
142		Marilyne Aza-Gnandji, Yves Prin, Estelle Tournier, Amadou Dien, Ézekiel Baudoin, Hervé Sanguin, Saliou Fall and Frédéric Mahé	Analyse du métagénome microbien fonctionnel des sols de parcelles paysannes en zone subsaharienne (Burkina Faso)
143		Axel Cournac	Apollo method: statistical inference to reveal hidden data in chromosome contact maps
144		Elisabeth Quellery, Charlotte Berhellier, Christian Dina and Isabel Alves	Population demographic estimation using simulated data
145		Marinna Gaudin, Floriane Simonet and Christian Dina	Etude de la trajectoire de fréquences alléliques pathogènes à travers le temps et l'espace
146		Mathieu Genete	Reducing your NGS dataset using a set of targets : how to optimize storage space, compute time and analysis accuracy
147		Thomas Obadia, Michael White, Narimane Nekkab and Ivo Mueller	Simulating the impact of Serological-Test-and-Treat measures to target the hidden P, vivax reservoir: public health impact and primaquine overtreatment
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149		Ségolène Diry and Virginie Chesnais	Comment prédire un gRNA efficace dans des contextes expérimentaux variés ? En apprenant des gRNA publiés
150		Emmanuel Gilson, Ségolène Diry, Pierre Sujobert, Kaddour Chabane, Alban Ott, Eric Ginoux and Virginie Chesnais	Stratégie de priorisation de variants après séquençage ciblé de l'ADN
151		Ségolène Diry, Alban Ott, Léo D'Agata, Eric Ginoux and Virginie Chesnais	Séquençage d'ADN natif dédié à l'étude du microbiome sur le MinION® : retour d'expérience de la paillasse à l'assignation taxonomique
152		Romuald Laso-Jadart, Kevin Sugier, Karine Labadie, Emmanuelle Petit, Christophe Ambroise, Pierre Peterlongo, Patrick Wincker, Jean-Louis Jamet and Mohammed-Amin Madoui	Linking Allele-Specific Expression And Natural Selection In Wild Populations
153		Cedric Mendoza, Léa Bellenger, Naïra Naouar and Christophe Antoniewski	Metavisitor-2, a suite of Galaxy tools for simple and rapid detection and discovery of viruses in Deep Sequence Data
154		Loredana Martignetti, Akira Cortal, Steicy Sobrino, Emmanuelle Six, Marina Cavazzana and Antonio Rausell	A clinical bioinformatics framework for single-cell profiling of rare diseases
155		Zakia Tariq, Florian Bonin, Claire Fayard, Ivan Bièche, Virginie Raynal, Sylvain Baulande, Rosette Lidereau and Keltouma Driouch	Genomic evolution of contralateral breast cancer revealed from whole exome sequencing
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157		Sami Ait Abbi Nazi and Eric Schordan	Assessment of inflammatory and immune pathways in Rheumatoid Arthritis patients using BIOPRED kit
158		Jocelyn De Goër De Herve, Myoung-Ah Kang and Engelbert Mephu-Nguifo	PSH, une fonction de hachage issue du domaine du traitement d'images, permettant l'indexation et la comparaison de séquences ADN
159		Quentin Miagoux, Maëva Veysiere, Anna Niarakis, Elisabeth Petit-Teixeira and Valérie Chaudru	Caractérisation de CNV (variants de nombre de copies) à partir de données de séquences exoniques simulées
160		Maëva Veysiere, Fayrouz Hammal, Laetitia Michou, Jean-François Deleuze, François Cornelis, Elisabeth Petit-Teixeira and Valérie Chaudru	Etude de la composante auto-immune de la Polyarthrite Rhumatoïde
161		Christophe Djemiel, Corentin Journay, Battle Karimi, Samuel Dequiedt, Walid Horrigue, Pierre-Alain Maron, Nicolas Chemidlin-Prevost Boure, Lionel Ranjard and Sébastien Terrat	ReClustOR, a Re-Clustering tool using an Open-Reference method that improves OTU definition

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162		Elise Loffet, Nicole Brown, Nambirajan Sundaram, Carine Bouffi, Holly M Poling, Michel Neunlist, Michael A Helmuth and Maxime M Mahe	Single-cell analysis of human intestinal organoids reveals the ENS progenitor cells contribution on the gut mesoderm development
163		Guillaume Gautreau, Adelme Bazin, Rémi Planel, Mathieu Gachet, Mathieu Dubois, Laura Burlot, Amandine Perrin, Marie Touchon, Eduardo Rocha, Christophe Ambroise, Catherine Matias, Claudine Médigue and David Vallenet	PanGBank: depicting microbial species diversity via PPanGGOLiN
164		Brahim Mania, Joseph Tran, Eulalie Lefevre, Fabien Marcel, Marion Dalmais and Abdelhafid Bendahmane	Fast neutron variants detection in TILLING crop populations
165		Quentin Bonenfant, Laurent Noé and Hélène Touzet	Analyse de longs reads Nanopore avec des k-mers à erreurs
166		Julie Hurel, Mathieu Rolland, Sophie Schbath, Stéphanie Bougeard, Mauro Petrillo and Fabrice Touzain	Detection of unknown genetically modified organisms (GMO) by statistical analysis of high-throughput sequencing data
167		Agnes Basseville, Fabien Panloup, Bertrand Michel and Philippe Juin	Identifying predictive biomarkers for breast cancer treatment using an integrative transcriptomic analysis
168		Camille Peneau, Sandrine Imbeaud, Tiziana La Bella, Iadh Mami and Jessica Zucman-Rossi	Characterization of Hepatitis B Virus genomes identified by viral capture in Hepatocellular Carcinomas from European and African patients
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170		Marie Jeammet, Jordi Estellé, Nicolas Pons and Fanny Calenge	MetaChick: assembly and analysis of chicken cecal microbiome reveals wide variations according to the production methods
171		Alice Mollé, Cynthia Fourgeux and Jérémie Poshmann	CD4 T cell reprogramming in brain-injured patients
172		Véronique Hourdel, Mathias Vandenbogaert, Valérie Caro, Charlotte Balière, Laetitia Bremand, Bhetty Labeau, David Moua, Aurelia Kwasiborski, Jean-Michel Thiberge, Claire Mayence, Dominique Rousset, Didier Hommel, Jean-Claude Manuguerra, Hatem Kallel and Severine Matheus	French Guiana Severe Syndromes, a metagenomics analysis of unknown dark clinical samples
173		Stefani Dritsa, Thibaud Martinez, Weiyi Zhang, Chloé-Agathe Azencott and Antonio Rausell	Prediction of candidate disease genes through deep learning on multiplex biological networks
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175		Lise Pomiès, Celine Brouard, Brigitte Mangin, Nicolas Langlade and Simon De Givry	Comparison of efficiency of gene regulatory network inference algorithms on genomic and transcriptomic data
176		Alfred Goumou, Coralie Rohmer, Marie Grison, Marie-Anne Le Moigne, Thomas Guillemette, Valérie Grimault, Claudine Landès and Sylvain Gaillard	MYC-MACS (MYCètes pour une Meilleure Acquisition des Connaissances Scientifiques)
177		Pierre-Antoine Rollat-Farnier, Flavie Diguët, Thomas Simonet, Nicolas Chatron, Damien Sanlaville, Claire Bardel and Caroline Schluth-Bolard	Formatage et annotation des variants structuraux - Présentation du logiciel Svagga
178		Athénaïs Vaginay, Malika Smail and Taha Boukhobza	Conversion from quantitative model in sbml core to qualitative model in sbml qual
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180		Antoine Menard, Pascale Vonaesch, Emna Achouri, Hervé Abdi and Vincent Guillemot	Joint analysis of multiple compositional data
181		Maxime Delmas	A set of methods to study three classes of non-coding RNAs
182		David Baux, Michel Koenig and Anne-Françoise Roux	BamCramConverter: Utility for Easy Alignment/Map Data Storage
183		Thomas Cokelaer	Bioconvert, a common bioinformatics format converter library: status and perspectives,
184		Hugo Varet	checkMyIndex: a web-based R/Shiny interface for choosing compatible sequencing indexes
185		Nicolas Soirat, Anne-Laure Bouge, Jérôme Audoux, Sacha Beaumeunier, Charles Van Goethem, Julie Vendrell, Jérôme Solassol, Nicolas Philippe	Développement et validation de pipelines pour l'analyse de données NGS dans le cadre du diagnostic en oncogénétique somatique
186		Asma Tiss	Evolution of the angiotensin II receptors AT1 and AT2: Insights from molecular dynamics simulations
187		Théo Mauri	From primary to tertiary structure analyses of experimentally proven O-GlcNAcylated sites for an optimised prediction
188		Aarón Ayllón-Benítez, Patricia Thébault and Fleur Mougín	GSAn : Une alternative aux analyses statistiques des groupes de gènes
189		Florian Dubois, Sophie Limou, Mélanie Chesneau, Sophie Brouard and Richard Danger	Identification of a common transcriptional signature for regulatory B cells in Humans and Mice
190		Pablo Rodriguez-Mier, Nathalie Poupin and Fabien Jourdan	Ignoring the optimal set of tissue-specific metabolic networks can bias the interpretation of data

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191		Coralie Gimonnet	Impact de la manipulation thermique embryonnaire sur le méthylome de caille japonaise
192		Léonard Dubois, Magali Berland and Mahendra Mariadassou	In-silico benchmark of methods for detecting differentially abundant features between metagenomics samples
193		Sébastien Ravel	LeAFtool: Lesion Area Finding tool
194		Thomas Cokelaer	Long-read pacbio amplicon analysis From raw data to final results
195		Rym Ben Boubaker	Mechanism of mechanosensation mediated by the angiotensin II receptor 1: a molecular dynamics approach
196		David Baux, Nicolas Soirat, Kevin Yaou, Thomas Guignard, Henri Pégeot, Olivier Ardouin, Charles Van Goethem, Michel Koenig and Anne-Françoise Roux	MobiDL: next generation family of WDL DNA-NGS pipelines
197		Afaf Mikou a , Alexandre Cabayé a,b , Anne Goupil b , Hugues-Olivier Bertrand b , Jean-Pierre Mothet c, Francine Acher	Molecular Modeling of the Asc-1 Transporter: Insights into the first steps of the transport mechanism
198		Francine Acher	Recurrent deletions of 3q13,31 in human osteosarcoma commonly affect TUSC7 and LINC00901,
199		Hugues Ripoché	REGULOUT software identifies regulatory outliers, that have unexpected transcription profile inside a group of ortholog genes
200		Hugo Varet	repeatsFinder: a web-based R/Shiny interface for visualizing and characterize genomic repeated regions
201		Ahmed Keceli and Natalia Pietrosemoli	The extra mile of Gene Set Enrichment Analysis: seeing the data
202		Aurélien Chateigner	The relationship between gene co-expression network connectivity and phenotypic prediction sheds light at the core of the omnigenic theory
203		Kevin Sugier	The role of the LNR domain-containing protein explosion in Oithona nana male differentiation (Crustacea; Cyclopoida)
204		Julie Lê-Hoang	Transcriptional and functional analyzes of symbiotic coral micro-algae in the framework of Tara Pacific expedition
205		Hélène Mayeur	Transcriptomic analysis of habenular asymmetries in the catshark S. canicula
206		Pierre Lindenbaum, Matilde Karakachoff and Richard Redon	VCF2Table : a VCF prettifier for the command line,
207		Jonathan Cruard, Mathias Bagueneau and Jean-Baptiste Alberge	Pipeline d'analyse et de visualisation avancés de single cell RNAseq (SChnurR)
208		Jennifer Del Guidice	LENA Enancio
209		Bénédicte Condamine, Antoine Bridier-Nahmias, Hervé Le Nagard, Johann Beghain, Erick Denamur and Olivier Clermont	The ClermonTyper: an easy-to-use and accurate in silico tool for Escherichia genus strain phylotyping
210		Florence Jornod, Julien Fumey, Slim El Khiari, Victor Grentzinger, Xavier Bussell and Athénaïs Vaginay	Association des Jeunes Bioinformaticiens de France (RSG France - JeBiF)
211		Audrey Bioteau, Pierre-Étienne Jacques and Vincent Burrus	Study of the conservation and diversity of Mobile Genomic Islands (MGI) in Vibrionaceae : characterisation, detection and classification
212		Bryan Brancotte, Thomas Menard and Hervé Menager	DevOps bioinformatics services with Docker, GitLab CI, and Kubernetes