

A1	Analysis workflow for smallRNA-seq data <i>Sebastien Nin, Stéphanie Rialle, Emeric Dubois and Laurent Journot</i>
A2	Analyse du réseau moléculaire impliqué dans le remodelage ventriculaire gauche post-infarctus du myocarde <i>Marie Cuvelliez, Christophe Bauters, Thomas Kelder, Marijana Radonjic, Philippe Amouyel and Florence Pinet</i>
A3	Mitochondrial genome variability of 205 Arabian endurance horses <i>Alexandre Heurteau, Claire Hoede, Anne Ricard, Diane Esquerré, Morgenthaler Caroline, Nuria Mach, Céline Robert and Eric Barrey</i>
A4	Epigenetic heterogeneity in multiple myeloma <i>Jennifer Rondineau, Victor Gaborit, Catherine Guerin-Charbonnel, Philippe Moreau, Stéphane Minvielle and Florence Magrangeas</i>
A5	NF-kappaB Landscape in Multiple Myeloma by high-throughput sequencing analysis <i>Victor Gaborit, Jennifer Rondineau, Wilfried Gouraud, Jérémie Bourdon, Stéphane Minvielle and Florence Magrangeas</i>
A6	Efficient MinION data management <i>Laurent Jourden, Aurélien Birer, Lionel Ferrato-Berberian, Sophie Lemoine and Stéphane Le Crom</i>
A7	Mise en place d'un pipeline de contrôle de la qualité de runs Minlon. <i>Lionel Ferrato-Berberian, Aurélien Birer, Ammara Mohammad, Corrine Blugeon, Fanny Coulpier, Stéphane Le Crom, Laurent Jourden and Sophie Lemoine</i>
A8	Impact et évolution de la correction d'erreur sur des lectures longues issues de séquençage MinION Oxford Nanopore dans un contexte transcriptomique <i>Lionel Ferrato-Berberian, Aurélien Birer, Stéphane Le Crom, Laurent Jourden and Sophie Lemoine</i>
A9	Toullig: New pipeline for nanopore data analysis <i>Aurélien Birer, Lionel Ferrato-Berberian, Stéphane Le Crom, Sophie Lemoine and Laurent Jourden</i>
A10	Extreme phenotypes define epigenetic and metabolic myeloid signatures in cardiovascular diseases. <i>Denis Seyres, John Lambourne, Paul Kirk, Alessandra Cabassi, Frances Burden, Roman Kreuzhuber, Samantha Farrow, Carly Kempster, Harriet McKinney, David Savage, Jules Griffin, Sylvia Richardson, Kate Downes, Willem Ouwehand, Mattia Frontini, Adrian Park and Oliver Stegle</i>
A11	Analyse et co-développement d'outils de bioinformatique destinés au traitement de données NGS issues de métagénomique virale <i>Emilie Delpuech, Guillaume Croville, Jean-Luc Guerin, Christophe Klopp and Sarah Maman</i>
A12	3-SMART : Bioinformatic analysis of intronic polyadenylation regulation <i>Mandy Cadix, Iris Tanaka, Pierre Gestraud, Marine Séjourné, Stéphan Vagner, Nicolas Servant and Martin Dutertre</i>
A13	Developing and sharing reproducible bioinformatics pipelines: best practices <i>Yohann Lelievre, Audrey Bihouée, Eric Charpentier, Alban Gaignard, Simon Souchet and Damien Vintache</i>
A14	BIOSEPCIMENS v1.5: a web platform to facilitate collaborative research on infectious diseases <i>Karen Louis, Blandine Rimbault, Clément Delestre, Yoann Mouscaz, Marine Albrieux, Christelle Boisse, Jennifer Tambosco, Régis Villet and Guillaume Boissy</i>
A15	MICROSCOPE: an integrated platform for the Exploration and Curation of Microbial Genomes <i>David Vallenet, Alexandra Calteau, Stéphane Cruveiller, Mathieu Gachet, Guillaume Gautreau, Adrien Josso, Aurélie Lajus, Jordan Langlois, Jonathan Mercier, Hugo Pereira, Rémi Planel, Johan Rollin Rollin, David Roche, Zoé Rouy and Claudine Médigue</i>
A16	NETSYN : NETWORK SYNteny, a new tool to help functional annotation <i>Benjamin Viart, Karine Bastard, Guillaume Reboul, Hugo Pereira, Rémi Planel, Mark Stam, Claudine Médigue and David Vallenet</i>
A17	Stratégie d'assemblage de génomes en cellule unique de protistes marins dans le cadre du projet Tara Oceans <i>Léo d'Agata, Yoann Seeleuthner, Julie Poulain, Patrick Wincker and Jean-Marc Aury</i>
A18	Assessing the functional impact of genomic alterations using proteogenomics <i>Georges Bedran, Yves Vandenbrouck, Eric Bonnet, Jean-François Deleuze, Delphine Pflieger and Christophe Battail</i>
A19	Deciphering early cell fate decision by Single Cell RNA-Seq and DGE-Seq <i>Dimitri Meistermann, Yohann Lelièvre, Eric Charpentier, Stéphanie Kilens, Thomas Fréour, Jérémie Bourdon and Laurent David</i>
A20	In search of W sex chromosome-specific sequences in the genome of the isopod crustacean <i>Armadillidium vulgare</i> <i>Mohamed Amine Chebbi</i>
A21	Exome sequencing to identify the molecular mechanism underlying chordomas pathogenesis. <i>Zakia Tariq, Keltouma Driouch, Virginie Bernard, Ivan Bieche, Virginie Raynal, Sylvain Baulande, Hamid Mammam and Julien Masliah Planchon</i>
A22	Revisiting cell lineage specification during male sex determination with single-cell RNA sequencing <i>Isabelle Stévant, Yasmine Neirjinck, Christelle Borel, Jessica Escoffier, Lee B. Smith, Stylianos E. Antonarakis, Emmanouil T. Dermitzakis and Serge Nef</i>
A23	How to analyse human or mouse Genome-scale CRISPR Knock-Out (GeCKO) datasets ? <i>Marc Deloger, Pierre Gestraud, Raphaël Margueron and Nicolas Servant</i>
A24	Functional characterization of human epidermis co-expression modules <i>Gwenaëlle Lemoine, Marie Pier Scott-Boyer, Mickael Leclercq and Arnaud Droit</i>

A25	Integrated and flexible analysis of scRNA-seq data with Eoulsan scRNA-seq <i>Geoffray Brelurut, Nathalie Lehmann, Céline Hernandez, Morgane Thomas-Chollier, Denis Thieffry, Stéphane Le Crom and Laurent Jourden</i>
A26	Efficient data structure for indexing and similarity computation of nucleic sequences <i>Camille Marchet, Arnaud Meng, Lolita Lecompte, Antoine Limasset, Lucie Bittner and Pierre Peterlongo</i>
A27	Detection of poly-adenylation sites from RNA-Seq data <i>Cyril Fournier and Anamaria Necsulea</i>
A28	Développement d'une structure pour l'indexation et la compression de multi-génomés <i>Clément Agret, Manuel Ruiz and Alban Mancheron</i>
A29	Epigenetic marks and the human transcriptome diversity <i>Guillaume Devailly, Anna Mantsoki and Anagha Joshi</i>
A30	Microbial diversity and plant cell wall-degrading enzyme dynamics during dew-ripping of flax - one of the oldest applications of biotechnology to textile transformation <i>Christophe Djemiel, Sébastien Grec and Simon Hawkins</i>
A31	Splicing Lore: Speeding up the identifications of splicing factors regulating alternative exons across physiological and pathological conditions. <i>Hélène Polvêche, Nahed Bouchouicha and Didier Auboeuf</i>
A32	A method for DNA virus detection and quantification during pregnancy based on noninvasive prenatal testing whole genome sequencing results <i>Virginie Chesnais, Alban Ott, Emmanuel Chaplais, Samuel Gabillard, Christelle Vauloup-Fellous, Alexandra Benachi, Jean-Marc Costa and Eric Ginoux</i>
A33	RINspector: a Cytoscape app that combines centrality analyses with DynaMine flexibility prediction <i>Guillaume Brysbaert, Kevin Lorgouilloux, Wim Vranken and Marc F. Lensink</i>
A34	Automated generation and analysis of parametric kinetic models obtained from biochemical interaction maps <i>Marion Buffard, Oscar O. Ortega, Carlos F. Lopez and Ovidiu Radulescu</i>
A35	Étude de processus de coalescence dans les paysages contemporains : bibliothèques template C++ pour le Calcul Bayésien Approché. <i>Arnaud Becheler, Camille Coron and Stéphane Dupas</i>
A36	PROqPCR : a Shiny web application for PROcessing of qRT-PCR data <i>Mathilde Sautreuil and Caroline Bérard</i>
A37	Bivariate Negative Binomial Mixture Model for the analysis of RNA-seq data <i>Mathilde Sautreuil, Nicolas Vergne, Antoine Channarond, Angelina Roche, Gaëlle Chagny and Caroline Bérard</i>
A38	Quality evaluation of the mapping of small RNA-footprinting reads <i>Pauline Fourgoux, Etienne Delannoy, Claire Lurin, Guillem Rigaiil and Véronique Brunaud</i>
A39	Medical diagnosis pipelines on the new AP-HP bioinformatics platform <i>Jocelyn Brayet, Camille Barette, Mathieu Barthelemy, Vivien Deshaies and Alban Lermine</i>
A40	Mathematical modeling of a genetic network controlling the regulation of Fe-S biogenesis <i>Firas Hammami, Frédéric Barras, Pierre Mandin and Elisabeth Remy</i>
A41	First gene-annotation enrichment analysis based on bacterial coregenome variants: Insights into mammalian and avian host adaptation of Salmonella serovars <i>Meryl Vila Nova, Kevin Durimel, Arnaud Felten, Laurent Guillier, Michel-Yves Mistou and Nicolas Radomski</i>
A42	A network approach to decipher bacterial adaptation through horizontal gene transfer <i>Damien Richard, Virginie Ravigné, Aude Chabirand, Olivier Pruvost and Pierre Lefeuvre</i>
A43	Méthodes et outils de construction de super-arbres en phylogénie <i>Morgan Soulié, Vincent Lefort and Anne-Muriel Arigon Chifolleau</i>
A44	Implémentation d'une interface pratique pour l'évaluation de stratégies d'exploration de la diversité moléculaire par protéogénomique <i>Yannick Cogne, Christine Almunia, Olivier Pible, Duarte Gouveia, Arnaud Chaumot, Olivier Geffard and Jean Armengaud</i>
A45	Pea genetic map enrichment with Genotyping By Sequencing markers <i>Ayité Kougbéadjo, Grégoire Aubert, Judith Burstin and Jonathan Kreplak</i>
A46	Développement d'une mesure du biais d'usage des codons : application aux virus humains <i>Jérôme Bourret, Ignacio G. Bravo and Samuel Alizon</i>
A47	Was the Chlamydial Adaptive Strategy to Tryptophan Starvation an Early Determinant of Plastid Endosymbiosis? <i>Ugo Cenci, Mathieu Ducatez, Derifa Kadouche, Christophe Colleoni and Steven Ball</i>
A48	OrthoInspector 3.0: orthology en route to big data <i>Yannis Nevers, Arnaud Kress, Raymond Ripp, Olivier Poch and Odile Lecompte</i>
A49	Déploiement automatique d'une infrastructure complexe pour le mapping des données de séquençage <i>Sandrine Perrin, Bryan Brancotte, Jonathan Lorenzo, Christophe Blanchet and Jean-François Gibrat</i>
A50	State of the art and comparison of long reads technologies <i>Anais Poiradeau, Maxime Manno, Céline Vandecasteele and Claire Kuchly</i>
A51	Genomic markers of species diversification in vertebrates <i>Guillaume Louvel, Eric Lewitus, Hélène Morlon and Hugues Roest Crollius</i>

A52	PREMS / ELVIS : A local plant biological resource management system <i>Fabrice Dupuis, Aurélie Lelièvre, Sandra Pelletier, Tatiana Thouroude, Julie Bourbeillon and Sylvain Gaillard</i>
A53	Découverte et analyse de polymorphismes SNPs issus de RNA-seq chez le peuplier noir <i>Odile Rogier, Souhila Amanzougarene, Marie-Claude Lesage-Descauses, Sandrine Balzergue, Véronique Brunaud, José Caius, Aurélien Chateigner, Ludivine Soubigou-Taconnat, Véronique Jorge and Vincent Segura</i>
A54	DiNAMO: Exact method for degenerate IUPAC motifs discovery: characterization of sequence-specific errors <i>Chadi Saad, Laurent Noé, Hugues Richard, Julie Leclerc, Marie-Pierre Buisine, Hélène Touzet and Martin Figeac</i>
A55	Evolutionary conservation of unusual N-glycosylation sites in the human glycosyltransferase B4GALNT2 <i>Virginie Cogez, Anaïs Barry, Jérôme de Ruyck, Sophie Groux-Degroote and Anne Harduin-Lepers</i>
A56	Comparison of statistical methods of inference of cooccurrence networks within microbial ecosystems from metagenomics data <i>Julie Lao, Mahendra Mariadassou and Sophie Schbath</i>
A57	ShRCAn: a user-friendly Shiny application for quantitative metagenomic analysis <i>Florence Thirion, Emmanuelle Le Chatelier, Nicolas Pons, Anne-Sophie Alvarez, Pierre Léonard and Dusko Ehrlich</i>
A58	Genetic diversity of <i>Anaplasma phagocytophilum</i> among ticks and roe deer in a fragmented agricultural landscape <i>Amelie Chastagner, Angélique Pion, Hélène Verheyden, Bruno Loutret, Bruno Cargnelutti, Denis Picot, Valérie Poux, Émilie Bard, Olivier Plantard, Karen D. McCoy, Agnes Leblond, Gwenaél Vourc'H and Xavier Bailly</i>
A59	A transcriptional study of five fungal <i>Mucor</i> strains <i>Annie Lebreton, Laurence Meslet-Cladière, Jean-Luc Jany, Georges Barbier and Erwan Corre</i>
A60	Multi-Cloud deployment for microbial genomes analysis <i>Jonathan Lorenzo, Bryan Brancotte, Thomas Lacroix, Christophe Blanchet, Jean-François Gibrat and Mohamed Bedri</i>
A61	Evaluation of 15 in silico prediction tools for the classification of MED13L missense variations <i>Thomas Smol, Caroline Thuillier, Sylvie Manouvrier-Hanu and Jamal Ghoumid</i>
A62	HiFit: robust data analysis method for High-throughput qPCR <i>Mathieu Bahin, Quentin Viautour, Elise Diaz, Bertrand Ducos and Auguste Genovesio</i>
A63	Is UniProtKB Missing Knowledgeable Proteins? <i>Benoit Bely, Sara Benmohammed, Guoying Qi, Nidhi Tyagi and Maria Martin</i>
A64	Co-option of complex molecular system in bacterial membrane <i>Remi Denise, Eduardo Rocha and Sophie Abby</i>
A65	High-quality, fast, and memory-efficient assembly of metagenomes and large genomes using Minia-pipeline <i>Rayan Chikhi, Charles Deltel, Guillaume Rizk, Claire Lemaitre, Pierre Peterlongo, Kristoffer Sahlin, Lars Arvestad, Paul Medvedev and Dominique Lavenier</i>
A66	Debugging long-read genome and metagenome assemblies using string graph analysis <i>Pierre Marijon, Jean Stéphane Varré and Rayan Chikhi</i>
A67	Labsquare une communauté de développeurs libres <i>Sacha Schutz and Pierre Marijon</i>
A68	Influence of SNP coding on the analysis of disease risk <i>Hélène Sarter, Corinne Gower-Rousseau and Guillemette Marot</i>
A69	Ultra High throughput, single molecule mapping of replicating DNA <i>Nikita Menezes Braganca, Francesco De Carli, Wahiba Berrabah, Valérie Barbe, Auguste Genovesio and Olivier Hyrien</i>
A70	Data updates on Norine, the reference Non-Ribosomal Peptide knowledge base <i>Yoann Dufresne, Juraj Michalik, Areski Flissi, Valerie Leclere and Maude Pupin</i>
A71	NRPro: a Bioinformatics Tool for Nonribosomal Peptides Identification by Tandem Mass Spectrometry <i>Emma Ricart, Mickael Chevalier, Maude Pupin, Valerie Leclere, Christophe Flahaut and Frederique Lisacek</i>
A72	Multi-scale characterization of symbiont diversity in the pea aphid complex through metagenomic approaches <i>Cervin Guyomar, Fabrice Legeai, Christophe Mougél, Claire Lemaitre and Jean-Christophe Simon</i>
A73	iMOMi: a database dedicated to integration and exploration of multi-omic data. <i>Nicolas Pons, Jean-Michel Batto, Amine Ghozlane, Kévin Weiszer, Pierre Léonard, Emmanuelle Le Chatelier, Pierre Renault and S. Dusko Ehrlich</i>
A74	Sequence composition-based read binning and taxonomic profiling in infectious metagenomics diversity analyses <i>Mathias Vandenbergert, Charlotte Balière and Valérie Caro</i>
A75	REGOVAR, logiciel libre pour l'analyse de données de séquençage haut débit pour les maladies génétiques rares <i>Anne-Sophie Denommé-Pichon, Olivier Gueudelot, Jérémie Roquet, June Sallou and David Goudenège</i>
A76	Alignement à grande échelle pour une approche métagénomique dans le cadre du projet Tara Oceans <i>Artem Kourlaiev, Corinne Da Silva, Stefan Engelen, Alexis Bertrand, Aimeric Bruno, Eric Pelletier, Patrick Wincker and Jean-Marc Aury</i>
A77	Seqenv: linking sequences to environments through text mining <i>Lucas Sinclair, Umer Z Ijaz, Lars Juhl Jensen, Marco Coolen, Cecile Gubry-Rangin, Alica Chrokov, Anastasis Oulas, Christina Pavloudi, Julia Schnetzer, Aaron Weimann, Ali Zeeshan Ijaz, Alexander Eiler, Christopher Quince and Evangelos Pafilis</i>

A78	Predicting the ecological quality status of marine environments from eDNA metabarcoding data using supervised machine learning <i>Tristan Cordier, Philippe Esling, Franck Lejzerowicz, Joana Visco, Amine Ouadahi, Catarina Martins, Tomas Cedhagen and Jan Pawlowski</i>
A79	Extended HLA haplotypes in Membranous Nephropathy <i>Louis Édouard Chauvière, Pierre Ronco and Hanna Debiec</i>
A80	RSAT matrix-clustering: dynamic exploration and redundancy reduction of transcription factor binding motif collections <i>Jaime Castro-Mondragon, Sébastien Jaeger, Denis Thieffry, Morgane Thomas-Chollier and Jacques van Helden</i>
A81	Assemblage de novo de quasi-espèces virales basé sur un graphe de chevauchements <i>Jasmijn Baaijens, Amal Zine El Aabidine, Eric Rivals and Alexander Schoenhuth</i>
A82	Characterization of biological data <i>Arthur Chambon, Frederic Lardeux, Frédéric Saubion and Tristan Boureau</i>
A83	Conservation of interaction energy landscapes across structural homologs through cross-docking calculations <i>Hugo Schweke, Sophie Sacquin-Mora, Marie-Hélène Mucchielli and Anne Lopes</i>
A84	Dynamic model of Central Carbon Metabolism and electrochemical reactions of the cell. <i>Cécile Moulin, Jorgelindo Da Veiga Moreira, Erwan Bigan, Laurent Schwartz, Mario Jolicoeur, Laurent Tournier and Sabine Peres</i>
A85	Proposition d'un workflow d'analyse QIIME dans Galaxy et évaluation de trois techniques d'extraction d'ADN pour l'analyse du microbiote intestinal 16S <i>Sylvie Buffet-Bataillon, Marouane Ben Abdallah, Philippe Bordron, Erwan Corre and Samer Kayal</i>
A86	BIOSPECIMENS 1.5: a web platform to facilitate collaborative research on infectious diseases <i>Karen Louis, Blandine Rimbault, Clément Delestre, Yoann Mouscaz, Marine Albrieux, Christelle Boisse, Régis Villet and Guillaume Boissy</i>
A87	Host tropism and host-pathogen interplay of typhoidal Salmonella enterica <i>Ludovic Mallet, Claire Hoede, Franck Cerutti, Annick Moisan, Christine Gaspin, Isabelle Virlogeux-Payant, Inna Shomer, Ohad Gal-Mor, Thomas Schiex and Hélène Chiapello</i>
A88	Towards a new heuristics to compute Consensus Ranking of Big Biological datasets <i>Pierre Andrieu, Laurent Bulteau, Sarah Cohen-Boulakia, Alain Denise, Anthony Labarre, Adeline Pierrot and Stéphane Vialette</i>
A89	Comparaison de pipelines pour la découverte de signatures métagénomiques à partir de séquençage 16S en contexte clinique <i>Caidi Aziza, Mestivier Denis, Bergsten Emma and Sobhani Iradj</i>
A90	Horizontal gene transfer from viruses in the genomes of plant-parasitic nematodes <i>Carole Belliaro, Corinne Rancurel, Etienne Danchin and Marc Bailly-Bechet</i>
A91	Mutation of Tyr137 of the universal Escherichia coli fimbrial adhesin FimH relaxes the tyrosine gate prior to mannose binding <i>Eva-Maria Krammer, Goedeke Roos, Martine Prévost, Julie Bouckaert and Marc Lensink</i>
A92	Collapsing reads while maintaining qualities : srnaCollapser <i>Walid Ben Saoud Benjerri, Christine Gaspin and Matthias Zytnicki</i>

B1	BioManTM: a user-friendly interface for targeted metagenomic data visualization and analysis <i>Pauline Vaissé, Christophe Camus, Yao Amouzou, Thomas Carton, Sophie Le Fresne-Languille, Françoise Le Vacon, Murielle Cazaubiel and Sébastien Leuillet</i>
B2	WHORMSS : un nouvel outil pour l'exploration taxonomique et fonctionnelle sans a priori des métagénomomes <i>Yannick Laurent, Jérémie Denonfoux, Antoine Bodein and Stéphanie Ferreira</i>
B3	CRISPR LifePipe®: tools for the design of gRNAs and donor sequence required for genome editing using CRISPR/Cas9 system <i>Virginie Chesnais, Emmanuel Chaplais, Alban Ott and Eric Ginoux</i>
B4	Bioinfo-fr.net : présentation du blog communautaire scientifique francophone par les Geekus biologicus <i>Geekus Biologicus and Isabelle Stévant</i>
B5	Association des Jeunes Bioinformaticiens de France (RSG France - JeBiF) <i>Léopold Carron, Gwenaëlle Lemoine, Alexandre Nicaise, Aurélien Béliard, June Benvegna-Sallou, Rémi Denise, Florence Jornod, Hugo Pereira, Pauline Pommeret, Aubin Thomas, Athénaïs Vaginay and Julien Fumey</i>
B6	BioInfuse v2 <i>Nolwenn Lavielle, Léopold Carron, Gwenaëlle Lemoine, Alexandre Nicaise, Aurélien Béliard, June Benvegna-Sallou, Remi Denise, Florence Jornod, Hugo Pereira, Pauline Pommeret, Aubin Thomas, Athénaïs Vaginay and Julien Fumey</i>
B7	Association MyDisease2EZ <i>Aurélié Martin and Sébastien Tourlet</i>