



Demonstrations			
Affectation Numbers	Flash	Authors	Titles
1		Estelle Geffard, Alexandre Walencik, Sophie Limou, Anne Cesbron, Nicolas Vince and Pierre-Antoine Gourraud	EasyMatch-R: a web application to facilitate donor query in Hematopoietic Stem Cell Transplantation (HSCT)
2		Estelle Geffard, Pauline Scherdel, Sophie Limou, Sophie Brouard, Magali Giral, Nicolas Vince and Pierre-Antoine Gourraud	A precision medicine application: personalized contextualization of patients after kidney transplantation,
3		Vivien Deshaies, Mathieu Barthelemy and Alban Lermine	Leaves : Application d'aide à l'interprétation de variants
4		Éloi Durant, François Sabot, Matthieu Conte and Mathieu Rouard	Panache: a visualization tool for the exploration of plant pangenomes
5		Wilfrid Richer, Jimena Tosello, Solène Brohard, Joshua Waterfall and Eliane Piaggio	scViz: a Rshiny app to easily explore scRNAseq data
6		Marc Legeay, Nadezhda T, Doncheva, John H, Morris and Lars J, Jensen	Omics Visualizer: a Cytoscape App to visualize omics data
7		Nicolas Tourasse and Fabien Darfeuille	TITAdb: the database of Type I Toxin-Antitoxin systems
8		Maxime Folschette, Kirsley Chennen, Alban Gaignard, Richard Redon, Hala Skaf-Molli, Poch Olivier, Jocelyn Laporte and Julie Thompson	INEX-MED: a Knowledge Graph to explore and link heterogeneous bio-medical data
9		Rachel Torchet, Alexandra Moine-Franel, Hélène Borges, Bryan Brancotte, Olivia Doppelt-Azzeroual, Fabien Mareuil, Hervé Ménager and Olivier Sperandio	Redesign of iPPI-DB, a database for modulators of Protein-Protein Interactions
10		Antoine Labeuw, Diego Zea, Elodie Laine and Hugues Richard	Reconstruction of Transcript phylogenies using PhyloSofS
11		Diego Zea	Linking structural and evolutionary information using MIToS.jl
12		Florence Combes, David Christiany, Virginie Brun, Christophe Caron, Valentin Loux and Yves Vandenbrouck	"ProteoRE, a Galaxy-based platform for the annotation and the interpretation of proteomics data in biomedical research",
13		Laurent David, Riccardo Vicedomini, Hugues Richard and Alessandra Carbone	S3A: A Scalable and Accurate Annotated Assembly Tool for Gene Assembly
14		Robert Clerc, Laurent Mesnard and Hugues Richard	Allogenomics – pipeline: prediction of the immune response from genetic variants during transplantation
15		Alexandre Renaux, Rabie Saidi and Maria Martin	UniFIRE: the UniProt Functional annotation Inference Rule Engine