

Segolene Caboche

List of Publications by Year in descending order

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Version: 2024-02-01

11
papers

293
citations

1163117

8
h-index

1199594

12
g-index

14
all docs

14
docs citations

14
times ranked

679
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparison of mapping algorithms used in high-throughput sequencing: application to Ion Torrent data. BMC Genomics, 2014, 15, 264.	2.8	83
2	Assessment of Common and Emerging Bioinformatics Pipelines for Targeted Metagenomics. PLoS ONE, 2017, 12, e0169563.	2.5	80
3	A complete protocol for whole-genome sequencing of virus from clinical samples: Application to coronavirus OC43. Virology, 2019, 531, 141-148.	2.4	28
4	High-Throughput Sequencing, a Versatile Weapon to Support Genome-Based Diagnosis in Infectious Diseases: Applications to Clinical Bacteriology. Pathogens, 2014, 3, 258-279.	2.8	22
5	The Impact of Bioinformatics Pipelines on Microbiota Studies: Does the Analytical "Microscope" Affect the Biological Interpretation?. Microorganisms, 2019, 7, 393.	3.6	17
6	LeView: automatic and interactive generation of 2D diagrams for biomacromolecule/ligand interactions. Journal of Cheminformatics, 2013, 5, 40.	6.1	14
7	MICRA: an automatic pipeline for fast characterization of microbial genomes from high-throughput sequencing data. Genome Biology, 2017, 18, 233.	8.8	10
8	Genetic basis for virulence differences of various Cryptosporidium parvum carcinogenic isolates. Scientific Reports, 2020, 10, 7316.	3.3	10
9	Targeted metagenomic sequencing data of human gut microbiota associated with Blastocystis colonization. Scientific Data, 2017, 4, 170081.	5.3	8
10	Modelling the Impact of Chronic Cigarette Smoke Exposure in Obese Mice: Metabolic, Pulmonary, Intestinal, and Cardiac Issues. Nutrients, 2020, 12, 827.	4.1	6
11	Use of whole-genome sequencing in the molecular investigation of care-associated HCoV-OC43 infections in a hematopoietic stem cell transplant unit. Journal of Clinical Virology, 2020, 122, 104206.	3.1	5