Denis Bertrand

List of Publications by Year
in descending order

31	6,456	304743 22	434195 31
papers	citations	h-index	g-index

35	35	35	14553
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Critical Assessment of Metagenome Interpretation: the second round of challenges. Nature Methods, 2022, 19, 429-440.	19.0	133
2	Evaluating the accuracy of Listeria monocytogenes assemblies from quasimetagenomic samples using long and short reads. BMC Genomics, 2021, 22, 389.	2.8	9
3	Stool metagenome analysis of patients with Klebsiella pneumoniae liver abscess and their domestic partners. International Journal of Infectious Diseases, 2021, 107, 1-4.	3.3	4
4	A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 2021, 184, 3376-3393.e17.	28.9	164
5	Duration of Carbapenemase-Producing <i>Enterobacteriaceae</i> Carriage in Hospital Patients. Emerging Infectious Diseases, 2020, 26, 2182-2185.	4.3	13
6	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. Nature Medicine, 2020, 26, 941-951.	30.7	130
7	Hybrid metagenomic assembly enables high-resolution analysis of resistance determinants and mobile elements in human microbiomes. Nature Biotechnology, 2019, 37, 937-944.	17.5	216
8	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
9	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
10	ConsensusDriver Improves upon Individual Algorithms for Predicting Driver Alterations in Different Cancer Types and Individual Patients. Cancer Research, 2018, 78, 290-301.	0.9	20
11	Predicting Cancer Drug Response using a Recommender System. Bioinformatics, 2018, 34, 3907-3914.	4.1	101
12	Phenotype-driven precision oncology as a guide for clinical decisions one patient at a time. Nature Communications, 2017, 8, 435.	12.8	75
13	Tissue Microbiome Profiling Identifies an Enrichment of Specific Enteric Bacteria in Opisthorchis viverrini Associated Cholangiocarcinoma. EBioMedicine, 2016, 8, 195-202.	6.1	94
14	OPERA-LG: efficient and exact scaffolding of large, repeat-rich eukaryotic genomes with performance guarantees. Genome Biology, 2016, 17, 102.	8.8	77
15	Mutational spectrum of Barrettâ€™s stem cells suggests paths to initiation of a precancerous lesion. Nature Communications, 2016, 7, 10380.	12.8	57
16	Cloning and variation of ground state intestinal stem cells. Nature, 2015, 522, 173-178.	27.8	156
17	Recurrent Fusion Genes in Gastric Cancer: CLDN18-ARHGAP26 Induces Loss of Epithelial Integrity. Cell Reports, 2015, 12, 272-285.	6.4	112
18	Patient-specific driver gene prediction and risk assessment through integrated network analysis of cancer omics profiles. Nucleic Acids Research, 2015, 43, e44-e44.	14.5	111

#	Article	IF	Citations
19	The Opisthorchis viverrini genome provides insights into life in the bile duct. Nature Communications, 2014, 5, 4378.	12.8	144
20	The draft genome of sweet orange (Citrus sinensis). Nature Genetics, 2013, 45, 59-66.	21.4	837
21	LoFreq: a sequence-quality aware, ultra-sensitive variant caller for uncovering cell-population heterogeneity from high-throughput sequencing datasets. Nucleic Acids Research, 2012, 40, 11189-11201.	14.5	1,074
22	Exome sequencing of gastric adenocarcinoma identifies recurrent somatic mutations in cell adhesion and chromatin remodeling genes. Nature Genetics, 2012, 44, 570-574.	21.4	560
23	FinIS: Improved in silico Finishing Using an Exact Quadratic Programming Formulation. Lecture Notes in Computer Science, 2012, , 314-325.	1.3	20
24	Whole-genome reconstruction and mutational signatures in gastric cancer. Genome Biology, 2012, 13, R115.	9.6	116
25	Evolution of orthologous tandemly arrayed gene clusters. BMC Bioinformatics, 2011, 12, S2.	2.6	40
26	Inferring the Evolutionary History of Gene Clusters from Phylogenetic and Gene Order Data. Molecular Biology and Evolution, 2010, 27, 761-772.	8.9	14
27	The artiodactyl APOBEC3 innate immune repertoire shows evidence for a multi-functional domain organization that existed in the ancestor of placental mammals. BMC Molecular Biology, 2008, 9, 104.	3.0	169
28	Inferring Ancestral Gene Orders for a Family of Tandemly Arrayed Genes. Journal of Computational Biology, 2008, 15, 1063-1077.	1.6	15
29	Duplication and Inversion History of a Tandemly Repeated Genes Family. Journal of Computational Biology, 2007, 14, 462-478.	1.6	26
30	Evolution of Tandemly Arrayed Genes in Multiple Species. Lecture Notes in Computer Science, 2007, , 96-109.	1.3	1
31	Topological Rearrangements and Local Search Method for Tandem Duplication Trees. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 15-28.	3.0	16