# Denis Bertrand

List of Publications by Year
in descending order

| 31 papers | 6,456 citations | 304743 22 h-index | 434195 31 g-index |
|---|---|---|---|
| 35 all docs | 35 docs citations | 35 times ranked | 14553 citing authors |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 1 | Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18. | 28.9 | 1,670 |
| 2 | 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 |
| 3 | The draft genome of sweet orange (Citrus sinensis). Nature Genetics, 2013, 45, 59-66. | 21.4 | 837 |
| 4 | 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 |
| 5 | Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10. | 28.9 | 272 |
| 6 | 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 |
| 7 | 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 |
| 8 | A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 2021, 184, 3376-3393.e17. | 28.9 | 164 |
| 9 | Cloning and variation of ground state intestinal stem cells. Nature, 2015, 522, 173-178. | 27.8 | 156 |
| 10 | The Opisthorchis viverrini genome provides insights into life in the bile duct. Nature Communications, 2014, 5, 4378. | 12.8 | 144 |
| 11 | Critical Assessment of Metagenome Interpretation: the second round of challenges. Nature Methods, 2022, 19, 429-440. | 19.0 | 133 |
| 12 | Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. Nature Medicine, 2020, 26, 941-951. | 30.7 | 130 |
| 13 | Whole-genome reconstruction and mutational signatures in gastric cancer. Genome Biology, 2012, 13, R115. | 9.6 | 116 |
| 14 | Recurrent Fusion Genes in Gastric Cancer: CLDN18-ARHGAP26 Induces Loss of Epithelial Integrity. Cell Reports, 2015, 12, 272-285. | 6.4 | 112 |
| 15 | 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 |
| 16 | Predicting Cancer Drug Response using a Recommender System. Bioinformatics, 2018, 34, 3907-3914. | 4.1 | 101 |
| 17 | Tissue Microbiome Profiling Identifies an Enrichment of Specific Enteric Bacteria in Opisthorchis viverrini Associated Cholangiocarcinoma. EBioMedicine, 2016, 8, 195-202. | 6.1 | 94 |
| 18 | OPERA-LG: efficient and exact scaffolding of large, repeat-rich eukaryotic genomes with performance guarantees. Genome Biology, 2016, 17, 102. | 8.8 | 77 |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 19 | Phenotype-driven precision oncology as a guide for clinical decisions one patient at a time. Nature Communications, 2017, 8, 435. | 12.8 | 75 |
| 20 | Mutational spectrum of Barrett's stem cells suggests paths to initiation of a precancerous lesion. Nature Communications, 2016, 7, 10380. | 12.8 | 57 |
| 21 | Evolution of orthologous tandemly arrayed gene clusters. BMC Bioinformatics, 2011, 12, S2. | 2.6 | 40 |
| 22 | Duplication and Inversion History of a Tandemly Repeated Genes Family. Journal of Computational Biology, 2007, 14, 462-478. | 1.6 | 26 |
| 23 | FinIS: Improved in silico Finishing Using an Exact Quadratic Programming Formulation. Lecture Notes in Computer Science, 2012, , 314-325. | 1.3 | 20 |
| 24 | 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 |
| 25 | 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 |
| 26 | Inferring Ancestral Gene Orders for a Family of Tandemly Arrayed Genes. Journal of Computational Biology, 2008, 15, 1063-1077. | 1.6 | 15 |
| 27 | Inferring the Evolutionary History of Gene Clusters from Phylogenetic and Gene Order Data. Molecular Biology and Evolution, 2010, 27, 761-772. | 8.9 | 14 |
| 28 | Duration of Carbapenemase-Producing *Enterobacteriaceae* Carriage in Hospital Patients. Emerging Infectious Diseases, 2020, 26, 2182-2185. | 4.3 | 13 |
| 29 | Evaluating the accuracy of Listeria monocytogenes assemblies from quasimetagenomic samples using long and short reads. BMC Genomics, 2021, 22, 389. | 2.8 | 9 |
| 30 | 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 |
| 31 | Evolution of Tandemly Arrayed Genes in Multiple Species. Lecture Notes in Computer Science, 2007, , 96-109. | 1.3 | 1 |