Christopher Douville

List of Publications by Year
in descending order

25 papers	4,156 citations	471509 17 h-index	610901 24 g-index
31 all docs	31 docs citations	31 times ranked	8106 citing authors

#	Article	IF	Citations
1	Detection of malignant peripheral nerve sheath tumors in patients with neurofibromatosis using aneuploidy and mutation identification in plasma. ELife, 2022, 11, .	6.0	4
2	Massively Parallel Sequencing of Esophageal Brushings Enables an Aneuploidy-Based Classification of Patients With Barrettâ€™s Esophagus. Gastroenterology, 2021, 160, 2043-2054.e2.	1.3	17
3	Detection of low-frequency DNA variants by targeted sequencing of the Watson and Crick strands. Nature Biotechnology, 2021, 39, 1220-1227.	17.5	40
4	Pembrolizumab for patients with leptomeningeal metastasis from solid tumors: efficacy, safety, and cerebrospinal fluid biomarkers. , 2021, 9, e002473.		33
5	Eliminating accidental deviations to minimize generalization error and maximize replicability: Applications in connectomics and genomics. PLoS Computational Biology, 2021, 17, e1009279.	3.2	28
6	The mutational landscape of spinal chordomas and their sensitive detection using circulating tumor DNA. Neuro-Oncology Advances, 2021, 3, vdaa173.	0.7	6
7	Use of a Polygenic Risk Score Improves Prediction of Myocardial Injury After Non-Cardiac Surgery. Circulation Genomic and Precision Medicine, 2020, 13, e002817.	3.6	9
8	Assessing aneuploidy with repetitive element sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 4858-4863.	7.1	50
9	Feasibility of blood testing combined with PET-CT to screen for cancer and guide intervention. Science, 2020, 369, .	12.6	351
10	BIOM-58. ASSESSMENT OF ANEUPLOIDY BY REPETITIVE ELEMENT SEQUENCING TO DETECT PEDIATRIC AND ADULT BRAIN CANCERS IN PLASMA. Neuro-Oncology, 2020, 22, ii14-ii14.	1.2	0
11	A multimodality test to guide the management of patients with a pancreatic cyst. Science Translational Medicine, 2019, 11, .	12.4	129
12	Detection of aneuploidy in patients with cancer through amplification of long interspersed nucleotide elements (LINEs). Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1871-1876.	7.1	48
13	Detection and localization of surgically resectable cancers with a multi-analyte blood test. Science, 2018, 359, 926-930.	12.6	1,872
14	Evaluation of liquid from the Papanicolaou test and other liquid biopsies for the detection of endometrial and ovarian cancers. Science Translational Medicine, 2018, 10, .	12.4	178
15	Non-invasive detection of urothelial cancer through the analysis of driver gene mutations and aneuploidy. ELife, 2018, 7, .	6.0	118
16	Integration of genetic and metabolic features related to sialic acid metabolism distinguishes human breast cell subtypes. PLoS ONE, 2018, 13, e0195812.	2.5	24
17	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. Human Mutation, 2017, 38, 1266-1276.	2.5	14
18	CRAVAT 4: Cancer-Related Analysis of Variants Toolkit. Cancer Research, 2017, 77, e35-e38.	0.9	51

#	Article	IF	Citations
19	Whole Genome Sequencing Defines the Genetic Heterogeneity of Familial Pancreatic Cancer. Cancer Discovery, 2016, 6, 166-175.	9.4	282
20	Assessing the Pathogenicity of Insertion and Deletion Variants with the Variant Effect Scoring Tool (VESTâ€indel). Human Mutation, 2016, 37, 28-35.	2.5	101
21	A Combination of Molecular Markers and Clinical Features Improve the Classification of Pancreatic Cysts. Gastroenterology, 2015, 149, 1501-1510.	1.3	376
22	Proteins linked to autosomal dominant and autosomal recessive disorders harbor characteristic rare missense mutation distribution patterns. Human Molecular Genetics, 2015, 24, 5995-6002.	2.9	40
23	A Probabilistic Model to Predict Clinical Phenotypic Traits from Genome Sequencing. PLoS Computational Biology, 2014, 10, e1003825.	3.2	10
24	Mutational Signature of Aristolochic Acid Exposure as Revealed by Whole-Exome Sequencing. Science Translational Medicine, 2013, 5, 197ra102.	12.4	220
25	CRAVAT: cancer-related analysis of variants toolkit. Bioinformatics, 2013, 29, 647-648.	4.1	140