

Christopher Douville

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

4,156
citations

471061

17
h-index

610482

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. <i>ELife</i> , 2022, 11, .	2.8	4
2	Massively Parallel Sequencing of Esophageal Brushings Enables an Aneuploidy-Based Classification of Patients With Barrett's Esophagus. <i>Gastroenterology</i> , 2021, 160, 2043-2054.e2.	0.6	17
3	Detection of low-frequency DNA variants by targeted sequencing of the Watson and Crick strands. <i>Nature Biotechnology</i> , 2021, 39, 1220-1227.	9.4	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. <i>PLoS Computational Biology</i> , 2021, 17, e1009279.	1.5	28
6	The mutational landscape of spinal chordomas and their sensitive detection using circulating tumor DNA. <i>Neuro-Oncology Advances</i> , 2021, 3, vdaa173.	0.4	6
7	Use of a Polygenic Risk Score Improves Prediction of Myocardial Injury After Non-Cardiac Surgery. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002817.	1.6	9
8	Assessing aneuploidy with repetitive element sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 4858-4863.	3.3	50
9	Feasibility of blood testing combined with PET-CT to screen for cancer and guide intervention. <i>Science</i> , 2020, 369, .	6.0	351
10	BIOM-58. ASSESSMENT OF ANEUPLOIDY BY REPETITIVE ELEMENT SEQUENCING TO DETECT PEDIATRIC AND ADULT BRAIN CANCERS IN PLASMA. <i>Neuro-Oncology</i> , 2020, 22, ii14-ii14.	0.6	0
11	A multimodality test to guide the management of patients with a pancreatic cyst. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	129
12	Detection of aneuploidy in patients with cancer through amplification of long interspersed nucleotide elements (LINEs). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1871-1876.	3.3	48
13	Detection and localization of surgically resectable cancers with a multi-analyte blood test. <i>Science</i> , 2018, 359, 926-930.	6.0	1,872
14	Evaluation of liquid from the Papanicolaou test and other liquid biopsies for the detection of endometrial and ovarian cancers. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	178
15	Non-invasive detection of urothelial cancer through the analysis of driver gene mutations and aneuploidy. <i>ELife</i> , 2018, 7, .	2.8	118
16	Integration of genetic and metabolic features related to sialic acid metabolism distinguishes human breast cell subtypes. <i>PLoS ONE</i> , 2018, 13, e0195812.	1.1	24
17	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. <i>Human Mutation</i> , 2017, 38, 1266-1276.	1.1	14
18	CRAVAT 4: Cancer-Related Analysis of Variants Toolkit. <i>Cancer Research</i> , 2017, 77, e35-e38.	0.4	51

#	ARTICLE	IF	CITATIONS
19	Whole Genome Sequencing Defines the Genetic Heterogeneity of Familial Pancreatic Cancer. <i>Cancer Discovery</i> , 2016, 6, 166-175.	7.7	282
20	Assessing the Pathogenicity of Insertion and Deletion Variants with the Variant Effect Scoring Tool (VEST). <i>Human Mutation</i> , 2016, 37, 28-35.	1.1	101
21	A Combination of Molecular Markers and Clinical Features Improve the Classification of Pancreatic Cysts. <i>Gastroenterology</i> , 2015, 149, 1501-1510.	0.6	376
22	Proteins linked to autosomal dominant and autosomal recessive disorders harbor characteristic rare missense mutation distribution patterns. <i>Human Molecular Genetics</i> , 2015, 24, 5995-6002.	1.4	40
23	A Probabilistic Model to Predict Clinical Phenotypic Traits from Genome Sequencing. <i>PLoS Computational Biology</i> , 2014, 10, e1003825.	1.5	10
24	Mutational Signature of Aristolochic Acid Exposure as Revealed by Whole-Exome Sequencing. <i>Science Translational Medicine</i> , 2013, 5, 197ra102.	5.8	220
25	CRAVAT: cancer-related analysis of variants toolkit. <i>Bioinformatics</i> , 2013, 29, 647-648.	1.8	140