

Joshua M Stuart

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

91 papers	25,156 citations	48 h-index	104 g-index
104 ext. papers	34,700 ext. citations	19.2 avg, IF	5.82 L-index

#	Paper	IF	Citations
91	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013 , 45, 1113-20	36.3	3933
90	The somatic genomic landscape of glioblastoma. <i>Cell</i> , 2013 , 155, 462-77	56.2	2900
89	The Immune Landscape of Cancer. <i>Immunity</i> , 2018 , 48, 812-830.e14	32.3	1754
88	A gene-coexpression network for global discovery of conserved genetic modules. <i>Science</i> , 2003 , 302, 249-55	33.3	1618
87	International network of cancer genome projects. <i>Nature</i> , 2010 , 464, 993-8	50.4	1613
86	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10	56.2	1124
85	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018 , 173, 400-416.e11	56.2	1072
84	Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. <i>Cell</i> , 2014 , 158, 929-944	56.2	935
83	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018 , 173, 291-304.e6	56.2	888
82	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854
81	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018 , 173, 338-354.e15	56.2	560
80	A gene expression map for <i>Caenorhabditis elegans</i> . <i>Science</i> , 2001 , 293, 2087-92	33.3	552
79	Inference of patient-specific pathway activities from multi-dimensional cancer genomics data using PARADIGM. <i>Bioinformatics</i> , 2010 , 26, i237-45	7.2	537
78	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017 , 32, 204-220.e15	24.3	391
77	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018 , 33, 676-689.e3	24.3	377
76	Subtype and pathway specific responses to anticancer compounds in breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 2724-9	11.5	347
75	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018 , 34, 211-224.e6	24.3	327

74	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018 , 6, 271-281.e7	10.6	320
73	Functionally Distinct Subsets of Lineage-Biased Multipotent Progenitors Control Blood Production in Normal and Regenerative Conditions. <i>Cell Stem Cell</i> , 2015 , 17, 35-46	18	301
72	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018 , 33, 690-705.e9	24.3	277
71	Clinical and Genomic Characterization of Treatment-Emergent Small-Cell Neuroendocrine Prostate Cancer: A Multi-institutional Prospective Study. <i>Journal of Clinical Oncology</i> , 2018 , 36, 2492-2503	2.2	271
70	Pathway and network analysis of cancer genomes. <i>Nature Methods</i> , 2015 , 12, 615-621	21.6	235
69	Genomic Hallmarks and Structural Variation in Metastatic Prostate Cancer. <i>Cell</i> , 2018 , 174, 758-769.e9	56.2	234
68	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018 , 33, 721-735.e8	24.3	228
67	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020 , 578, 102-111	50.4	220
66	Combining tumor genome simulation with crowdsourcing to benchmark somatic single-nucleotide-variant detection. <i>Nature Methods</i> , 2015 , 12, 623-30	21.6	201
65	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018 , 23, 3392-3406.e10	10.6	200
64	N-Myc Drives Neuroendocrine Prostate Cancer Initiated from Human Prostate Epithelial Cells. <i>Cancer Cell</i> , 2016 , 29, 536-547	24.3	189
63	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018 , 23, 282-296.e4	10.6	188
62	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10	56.2	166
61	Inferring causal molecular networks: empirical assessment through a community-based effort. <i>Nature Methods</i> , 2016 , 13, 310-8	21.6	158
60	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018 , 23, 194-212.e6	10.6	146
59	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018 , 173, 386-399.e12	56.2	133
58	Phosphoproteome Integration Reveals Patient-Specific Networks in Prostate Cancer. <i>Cell</i> , 2016 , 166, 1041-1054	56.2	132
57	A basal stem cell signature identifies aggressive prostate cancer phenotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E6544-52	11.5	131

56	Discovering causal pathways linking genomic events to transcriptional states using Tied Diffusion Through Interacting Events (TieDIE). <i>Bioinformatics</i> , 2013 , 29, 2757-64	7.2	128
55	A global analysis of genetic interactions in <i>Caenorhabditis elegans</i> . <i>Journal of Biology</i> , 2007 , 6, 8		120
54	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018 , 23, 255-269.e4	10.6	112
53	PARADIGM-SHIFT predicts the function of mutations in multiple cancers using pathway impact analysis. <i>Bioinformatics</i> , 2012 , 28, i640-i646	7.2	74
52	Towards zoomable multidimensional maps of the cell. <i>Nature Biotechnology</i> , 2007 , 25, 547-54	44.5	73
51	Pan-cancer analysis of whole genomes		70
50	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 172-180.e3	10.6	66
49	Pathway-Based Genomics Prediction using Generalized Elastic Net. <i>PLoS Computational Biology</i> , 2016 , 12, e1004790	5	60
48	RADIA: RNA and DNA integrated analysis for somatic mutation detection. <i>PLoS ONE</i> , 2014 , 9, e111516	3.7	59
47	VisANT 3.0: new modules for pathway visualization, editing, prediction and construction. <i>Nucleic Acids Research</i> , 2007 , 35, W625-32	20.1	58
46	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018 , 23, 213-226.e3	26.6	56
45	TumorMap: Exploring the Molecular Similarities of Cancer Samples in an Interactive Portal. <i>Cancer Research</i> , 2017 , 77, e111-e114	10.1	43
44	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020 , 11, 729	17.4	38
43	Global optimization of somatic variant identification in cancer genomes with a global community challenge. <i>Nature Genetics</i> , 2014 , 46, 318-319	36.3	36
42	A community effort to create standards for evaluating tumor subclonal reconstruction. <i>Nature Biotechnology</i> , 2020 , 38, 97-107	44.5	35
41	A factor graph nested effects model to identify networks from genetic perturbations. <i>PLoS Computational Biology</i> , 2009 , 5, e1000274	5	32
40	Toward better benchmarking: challenge-based methods assessment in cancer genomics. <i>Genome Biology</i> , 2014 , 15, 462	18.3	29
39	Combining accurate tumor genome simulation with crowdsourcing to benchmark somatic structural variant detection. <i>Genome Biology</i> , 2018 , 19, 188	18.3	29

38	Transcriptional profiling identifies an androgen receptor activity-low, stemness program associated with enzalutamide resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 12315-12323	11.5	28
37	ONE-CLASS DETECTION OF CELL STATES IN TUMOR SUBTYPES. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2016 , 21, 405-16	1.3	27
36	The NIH BD2K center for big data in translational genomics. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015 , 22, 1143-7	8.6	24
35	The UCSC Interaction Browser: multidimensional data views in pathway context. <i>Nucleic Acids Research</i> , 2013 , 41, W218-24	20.1	20
34	Modeling Human TBX5 Haploinsufficiency Predicts Regulatory Networks for Congenital Heart Disease. <i>Developmental Cell</i> , 2021 , 56, 292-309.e9	10.2	17
33	Computational Identification of Tumor Anatomic Location Associated with Survival in 2 Large Cohorts of Human Primary Glioblastomas. <i>American Journal of Neuroradiology</i> , 2016 , 37, 621-8	4.4	16
32	A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. <i>Cell Systems</i> , 2017 , 5, 485-497.e3	10.6	14
31	Biological process activity transformation of single cell gene expression for cross-species alignment. <i>Nature Communications</i> , 2019 , 10, 4899	17.4	11
30	ONE-CLASS DETECTION OF CELL STATES IN TUMOR SUBTYPES 2016 ,		11
29	Reproducible biomedical benchmarking in the cloud: lessons from crowd-sourced data challenges. <i>Genome Biology</i> , 2019 , 20, 195	18.3	10
28	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020 , 11, 4748	17.4	10
27	Prophetic Granger Causality to infer gene regulatory networks. <i>PLoS ONE</i> , 2017 , 12, e0170340	3.7	9
26	Revealing cancer subtypes with higher-order correlations applied to imaging and omics data. <i>BMC Medical Genomics</i> , 2017 , 10, 20	3.7	7
25	Identifying Aspects of the Post-Transcriptional Program Governing the Proteome of the Green Alga <i>Micromonas pusilla</i> . <i>PLoS ONE</i> , 2016 , 11, e0155839	3.7	6
24	Comparative RNA-Sequencing Analysis Benefits a Pediatric Patient With Relapsed Cancer. <i>JCO Precision Oncology</i> , 2018 , 2,	3.6	6
23	Germline contamination and leakage in whole genome somatic single nucleotide variant detection. <i>BMC Bioinformatics</i> , 2018 , 19, 28	3.6	5
22	A search engine to identify pathway genes from expression data on multiple organisms. <i>BMC Systems Biology</i> , 2007 , 1, 20	3.5	5
21	Clinical and genomic characterization of Low PSA Secretors: a unique subset of metastatic castration resistant prostate cancer. <i>Prostate Cancer and Prostatic Diseases</i> , 2021 , 24, 81-87	6.2	5

20	Information-based methods for predicting gene function from systematic gene knock-downs. <i>BMC Bioinformatics</i> , 2008 , 9, 463	3.6	4
19	Pathway and network analysis of more than 2,500 whole cancer genomes		4
18	Copy Number Loss of 17q22 Is Associated with Enzalutamide Resistance and Poor Prognosis in Metastatic Castration-Resistant Prostate Cancer. <i>Clinical Cancer Research</i> , 2020 , 26, 4616-4624	12.9	4
17	Down-regulation of ADRB2 expression is associated with small cell neuroendocrine prostate cancer and adverse clinical outcomes in castration-resistant prostate cancer. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2020 , 38, 931.e9-931.e16	2.8	3
16	Accurate cancer phenotype prediction with AKLIMATE, a stacked kernel learner integrating multimodal genomic data and pathway knowledge. <i>PLoS Computational Biology</i> , 2021 , 17, e1008878	5	3
15	A community challenge to evaluate RNA-seq, fusion detection, and isoform quantification methods for cancer discovery. <i>Cell Systems</i> , 2021 , 12, 827-838.e5	10.6	3
14	VEGA is an interpretable generative model for inferring biological network activity in single-cell transcriptomics. <i>Nature Communications</i> , 2021 , 12, 5684	17.4	3
13	Exploring Integrative Analysis Using the BioMedical Evidence Graph. <i>JCO Clinical Cancer Informatics</i> , 2020 , 4, 147-159	5.2	2
12	The molecular and pathway characterization of patients with metastatic castration resistant prostate cancer (mCRPC) refractory to therapy with abiraterone acetate or enzalutamide: Preliminary results from the SU2C/PCF/AACR West Coast Prostate Cancer Dream Team (WCDT).. <i>Journal of Clinical Oncology</i> , 2014 , 32, 79-79	2.2	2
11	Prioritizing transcriptional factors in gene regulatory networks with PageRank. <i>IScience</i> , 2021 , 24, 102018.1	17.1	2
10	Comprehensive molecular profiling of urothelial bladder cancer at the DNA, RNA, and protein levels: A TCGA project.. <i>Journal of Clinical Oncology</i> , 2014 , 32, 4509-4509	2.2	1
9	Highly Accurate Cancer Phenotype Prediction with AKLIMATE, a Stacked Kernel Learner Integrating Multimodal Genomic Data and Pathway Knowledge		1
8	Towards Inferring Nanopore Sequencing Ionic Currents from Nucleotide Chemical Structures		1
7	Valection: design optimization for validation and verification studies. <i>BMC Bioinformatics</i> , 2018 , 19, 339	3.6	1
6	Dual RNA-Seq analysis of SARS-CoV-2 correlates specific human transcriptional response pathways directly to viral expression.. <i>Scientific Reports</i> , 2022 , 12, 1329	4.9	0
5	Towards inferring nanopore sequencing ionic currents from nucleotide chemical structures. <i>Nature Communications</i> , 2021 , 12, 6545	17.4	0
4	Bioinformatic Approaches and Computational Models for Data Integration and Cross-Species Extrapolation in the Postgenomic Era 2006 , 103-149		
3	Pathway-based signature analysis of RNA-seq data to reveal new targetable avenues for metastatic castration-resistant prostate cancer (mCRPC) patients (pts): Preliminary results from the SU2C/PCF/AACR West Coast Prostate Cancer Dream Team (WCDT).. <i>Journal of Clinical Oncology</i> , 2014 , 32, 11078-11078	2.2	

- 2 Whole genome sequencing to characterize luminal-type breast cancer.. *Journal of Clinical Oncology*, **2012**, 30, 503-503 2.2
- 1 Identification of polo-like kinase 1 (PLK1) in aggressive prostate cancer by paradigm analysis.. *Journal of Clinical Oncology*, **2013**, 31, 5006-5006 2.2