David E Larson

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1405829/publications.pdf

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40	23,801	159358	276539
papers	citations	30 h-index	41 g-index

49	49	49	39991
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Bam-readcount - rapid generation of basepair-resolution sequence metrics. Journal of Open Source Software, 2022, 7, 3722.	2.0	36
2	Association of structural variation with cardiometabolic traits in Finns. American Journal of Human Genetics, 2021, 108, 583-596.	2.6	22
3	Mitochondrial genome copy number measured by DNA sequencing in human blood is strongly associated with metabolic traits via cell-type composition differences. Human Genomics, 2021, 15, 34.	1.4	7
4	The clonal evolution of metastatic colorectal cancer. Science Advances, 2020, 6, eaay9691.	4.7	41
5	Mapping and characterization of structural variation in 17,795 human genomes. Nature, 2020, 583, 83-89.	13.7	194
6	Exome sequencing of Finnish isolates enhances rare-variant association power. Nature, 2019, 572, 323-328.	13.7	161
7	svtools: population-scale analysis of structural variation. Bioinformatics, 2019, 35, 4782-4787.	1.8	51
8	Functional equivalence of genome sequencing analysis pipelines enables harmonized variant calling across human genetics projects. Nature Communications, 2018, 9, 4038.	5.8	166
9	The prognostic effects of somatic mutations in ER-positive breast cancer. Nature Communications, 2018, 9, 3476.	5.8	89
10	CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. Nature Genetics, 2017, 49, 170-174.	9.4	460
11	Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. Experimental Hematology, 2017, 55, 19-33.	0.2	9
12	Brief Report: The Role of Rare Proteinâ€Coding Variants in Antiâ€“Tumor Necrosis Factor Treatment Response in Rheumatoid Arthritis. Arthritis and Rheumatology, 2017, 69, 735-741.	2.9	8
13	Truncating Prolactin Receptor Mutations Promote Tumor Growth in Murine Estrogen Receptor-Alpha Mammary Carcinomas. Cell Reports, 2016, 17, 249-260.	2.9	21
14	Rare Variation in TET2 Is Associated with Clinically Relevant Prostate Carcinoma in African Americans. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1456-1463.	1.1	22
15	Aromatase inhibition remodels the clonal architecture of estrogen-receptor-positive breast cancers. Nature Communications, 2016, 7, 12498.	5.8	69
16	Comprehensive genomic analysis reveals FLT3 activation and a therapeutic strategy for a patient with relapsed adult B-lymphoblastic leukemia. Experimental Hematology, 2016, 44, 603-613.	0.2	44
17	Optimizing Cancer Genome Sequencing and Analysis. Cell Systems, 2015, 1, 210-223.	2.9	174
18	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	1.5	83

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19	Patterns and functional implications of rare germline variants across 12 cancer types. Nature Communications, 2015, 6, 10086.	5.8	243
20	Identification of Functional Variants for Cleft Lip with or without Cleft Palate in or near PAX7, FGFR2, and NOG by Targeted Sequencing of GWAS Loci. American Journal of Human Genetics, 2015, 96, 397-411.	2.6	150
21	Association Between Mutation Clearance After Induction Therapy and Outcomes in Acute Myeloid Leukemia. JAMA - Journal of the American Medical Association, 2015, 314, 811.	3.8	302
22	TYK2 Protein-Coding Variants Protect against Rheumatoid Arthritis and Autoimmunity, with No Evidence of Major Pleiotropic Effects on Non-Autoimmune Complex Traits. PLoS ONE, 2015, 10, e0122271.	1.1	120
23	Re-sequencing Expands Our Understanding of the Phenotypic Impact of Variants at GWAS Loci. PLoS Genetics, 2014, 10, e1004147.	1.5	50
24	Exome-Based Mapping and Variant Prioritization for Inherited Mendelian Disorders. American Journal of Human Genetics, 2014, 94, 373-384.	2.6	37
25	Using SomaticSniper to Detect Somatic Single Nucleotide Variants. Current Protocols in Bioinformatics, 2014, 45, 15.5.1-8.	25.8	4
26	BreakDancer: Identification of Genomic Structural Variation from Pairedâ€End Read Mapping. Current Protocols in Bioinformatics, 2014, 45, 15.6.1-11.	25.8	135
27	Integrated analysis of germline and somatic variants in ovarian cancer. Nature Communications, 2014, 5, 3156.	5.8	253
28	DGIdb: mining the druggable genome. Nature Methods, 2013, 10, 1209-1210.	9.0	443
29	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	13.9	4,139
30	SomaticSniper: identification of somatic point mutations in whole genome sequencing data. Bioinformatics, 2012, 28, 311-317.	1.8	566
31	Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. Nature, 2012, 481, 506-510.	13.7	1,795
32	VarScan 2: Somatic mutation and copy number alteration discovery in cancer by exome sequencing. Genome Research, 2012, 22, 568-576.	2.4	4,086
33	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. Cell, 2012, 150, 264-278.	13.5	1,365
34	Genome remodelling in a basal-like breast cancer metastasis and xenograft. Nature, 2010, 464, 999-1005.	13.7	1,077
35	BreakDancer: an algorithm for high-resolution mapping of genomic structural variation. Nature Methods, 2009, 6, 677-681.	9.0	1,322
36	Recurring Mutations Found by Sequencing an Acute Myeloid Leukemia Genome. New England Journal of Medicine, 2009, 361, 1058-1066.	13.9	2,009

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37	DNA Sequencing of a Murine Acute Promyelocytic Leukemia (APL) Genome Using Next Generation Technology.. Blood, 2009, 114, 3965-3965.	0.6	0
38	Somatic mutations affect key pathways in lung adenocarcinoma. Nature, 2008, 455, 1069-1075.	13.7	2,694
39	DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. Nature, 2008, 456, 66-72.	13.7	1,275
40	Cellular behavior in the developing Drosophila pupal retina. Mechanisms of Development, 2008, 125, 223-232.	1.7	51