Levi Waldron

List of Publications by Year
in descending order

110 papers	28,155 citations	66234 42 h-index	31759 101 g-index
146 all docs	146 docs citations	146 times ranked	44497 citing authors

#	Article	IF	Citations
1	Severe Acute Respiratory Syndrome Coronavirus 2 Incidence and Risk Factors in a National, Community-Based Prospective Cohort of US Adults. Clinical Infectious Diseases, 2023, 76, e375-e384.	2.9	9
2	Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space. Cell Genomics, 2022, 2, 100085.	3.0	59
3	Cross-cohort gut microbiome associations with immune checkpoint inhibitor response in advanced melanoma. Nature Medicine, 2022, 28, 535-544.	15.2	158
4	High-sensitivity pattern discovery in large, paired multiomic datasets. Bioinformatics, 2022, 38, i378-i385.	1.8	18
5	Refining colorectal cancer classification and clinical stratification through a single-cell atlas. Genome Biology, 2022, 23, 113.	3.8	48
6	GenomicSuperSignature facilitates interpretation of RNA-seq experiments through robust, efficient comparison to public databases. Nature Communications, 2022, 13, .	5.8	6
7	Toward a gold standard for benchmarking gene set enrichment analysis. Briefings in Bioinformatics, 2021, 22, 545-556.	3.2	83
8	Cohort profile: a national, community-based prospective cohort study of SARS-CoV-2 pandemic outcomes in the USAâ€"the CHASING COVID Cohort study. BMJ Open, 2021, 11, e048778.	0.8	32
9	SIMON: Open-Source Knowledge Discovery Platform. Patterns, 2021, 2, 100178.	3.1	15
10	Microbiome connections with host metabolism and habitual diet from 1,098 deeply phenotyped individuals. Nature Medicine, 2021, 27, 321-332.	15.2	477
11	Patterns of SARS-CoV-2 Testing Preferences in a National Cohort in the United States: Latent Class Analysis of a Discrete Choice Experiment. JMIR Public Health and Surveillance, 2021, 7, e32846.	1.2	5
12	Multivariable association discovery in population-scale meta-omics studies. PLoS Computational Biology, 2021, 17, e1009442.	1.5	691
13	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	15.2	170
14	CNVRanger: association analysis of CNVs with gene expression and quantitative phenotypes. Bioinformatics, 2020, 36, 972-973.	1.8	17
15	The impact of different sources of heterogeneity on loss of accuracy from genomic prediction models. Biostatistics, 2020, 21, 253-268.	0.9	15
16	The Impact of Stroma Admixture on Molecular Subtypes and Prognostic Gene Signatures in Serous Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 509-519.	1.1	34
17	Orchestrating single-cell analysis with Bioconductor. Nature Methods, 2020, 17, 137-145.	9.0	488
18	Gut bacterial taxonomic abundances vary with cognition, personality, and mood in the Wisconsin Longitudinal Study. Brain, Behavior, & Immunity - Health, 2020, 9, 100155.	1.3	6

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19	Transparency and reproducibility in artificial intelligence. Nature, 2020, 586, E14-E16.	13.7	233
20	Assessment of statistical methods from single cell, bulk RNA-seq, and metagenomics applied to microbiome data. Genome Biology, 2020, 21, 191.	3.8	67
21	Multiomic Analysis of Subtype Evolution and Heterogeneity in High-Grade Serous Ovarian Carcinoma. Cancer Research, 2020, 80, 4335-4345.	0.4	57
22	Multiomic Integration of Public Oncology Databases in Bioconductor. JCO Clinical Cancer Informatics, 2020, 4, 958-971.	1.0	42
23	â€œStoma or no stomaâ€: First report of intestinal transplantation without stoma. American Journal of Transplantation, 2020, 20, 3550-3557.	2.6	13
24	Global Alliance for Genomics and Health Meets Bioconductor: Toward Reproducible and Agile Cancer Genomics at Cloud Scale. JCO Clinical Cancer Informatics, 2020, 4, 472-479.	1.0	4
25	Reliable Analysis of Clinical Tumor-Only Whole-Exome Sequencing Data. JCO Clinical Cancer Informatics, 2020, 4, 321-335.	1.0	20
26	HGNChelper: identification and correction of invalid gene symbols for human and mouse. F1000Research, 2020, 9, 1493.	0.8	17
27	SARS-CoV-2 Testing Service Preferences of Adults in the United States: Discrete Choice Experiment. JMIR Public Health and Surveillance, 2020, 6, e25546.	1.2	21
28	Waldron et al. Reply to â€œCommentary on the HMP16SData Bioconductor Packageâ€. American Journal of Epidemiology, 2019, 188, 1031-1032.	1.6	0
29	MetaGxData: Clinically Annotated Breast, Ovarian and Pancreatic Cancer Datasets and their Use in Generating a Multi-Cancer Gene Signature. Scientific Reports, 2019, 9, 8770.	1.6	29
30	Sociodemographic variation in the oral microbiome. Annals of Epidemiology, 2019, 35, 73-80.e2.	0.9	37
31	Tobacco exposure associated with oral microbiota oxygen utilization in the New York City Health and Nutrition Examination Study. Annals of Epidemiology, 2019, 34, 18-25.e3.	0.9	27
32	Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation. Nature Medicine, 2019, 25, 667-678.	15.2	602
33	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. Nature Medicine, 2019, 25, 679-689.	15.2	734
34	Evaluation of Oral Cavity DNA Extraction Methods on Bacterial and Fungal Microbiota. Scientific Reports, 2019, 9, 1531.	1.6	31
35	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	15
36	Impact of an HIV Care Coordination Program on Durable Viral Suppression. Journal of Acquired Immune Deficiency Syndromes (1999), 2019, 80, 46-55.	0.9	33

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37	HMP16SData: Efficient Access to the Human Microbiome Project Through Bioconductor. American Journal of Epidemiology, 2019, 188, 1023-1026.	1.6	30
38	restfulSE: A semantically rich interface for cloud-scale genomics with Bioconductor. F1000Research, 2019, 8, 21.	0.8	0
39	Widespread modulation of gene expression by copy number variation in skeletal muscle. Scientific Reports, 2018, 8, 1399.	1.6	25
40	bioBakery: a metaâ€™omic analysis environment. Bioinformatics, 2018, 34, 1235-1237.	1.8	241
41	Data and Statistical Methods To Analyze the Human Microbiome. MSystems, 2018, 3, .	1.7	29
42	Metaâ€analysis and commentary: Preemptive correction of arteriovenous access stenosis. Hemodialysis International, 2018, 22, 279-280.	0.4	1
43	Short-term effectiveness of HIV care coordination among persons with recent HIV diagnosis or history of poor HIV outcomes. PLoS ONE, 2018, 13, e0204017.	1.1	19
44	Continuity of transcriptomes among colorectal cancer subtypes based on meta-analysis. Genome Biology, 2018, 19, 142.	3.8	20
45	Using Registry Data to Construct a Comparison Group for Programmatic Effectiveness Evaluation. American Journal of Epidemiology, 2018, 187, 1980-1989.	1.6	15
46	Consensus on Molecular Subtypes of High-Grade Serous Ovarian Carcinoma. Clinical Cancer Research, 2018, 24, 5037-5047.	3.2	93
47	Orchestrating a community-developed computational workshop and accompanying training materials. F1000Research, 2018, 7, 1656.	0.8	1
48	Multiparametric Quantitative Ultrasound Imaging in Assessment of Chronic Kidney Disease. Journal of Ultrasound in Medicine, 2017, 36, 2245-2256.	0.8	21
49	Accessible, curated metagenomic data through ExperimentHub. Nature Methods, 2017, 14, 1023-1024.	9.0	292
50	Software for the Integration of Multiomics Experiments in Bioconductor. Cancer Research, 2017, 77, e39-e42.	0.4	80
51	Machine Learning Meta-analysis of Large Metagenomic Datasets: Tools and Biological Insights. PLoS Computational Biology, 2016, 12, e1004977.	1.5	434
52	Racial/Ethnic Disparities in Genomic Sequencing. JAMA Oncology, 2016, 2, 1070.	3.4	250
53	The Doppelgänger Effect: Hidden Duplicates in Databases of Transcriptome Profiles. Journal of the National Cancer Institute, 2016, 108, djw146.	3.0	18
54	Mo1306 Rapid and Accurate Inference of Gene Expression in Difficult-to-Isolate Cell Types. Gastroenterology, 2016, 150, S693.	0.6	0

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55	Shear Wave Elastography of the Spleen for Monitoring Transjugular Intrahepatic Portosystemic Shunt Function. Journal of Ultrasound in Medicine, 2016, 35, 951-958.	0.8	20
56	CellMapper: rapid and accurate inference of gene expression in difficult-to-isolate cell types. Genome Biology, 2016, 17, 201.	3.8	24
57	Meta-Analysis in Gene Expression Studies. Methods in Molecular Biology, 2016, 1418, 161-176.	0.4	16
58	Public data and open source tools for multi-assay genomic investigation of disease. Briefings in Bioinformatics, 2016, 17, 603-615.	3.2	46
59	Control of Gene Expression by RNA Binding Protein Action on Alternative Translation Initiation Sites. PLoS Computational Biology, 2016, 12, e1005198.	1.5	7
60	Global Transcriptome Differences Between Early-Onset and Late-Onset Colorectal Cancer. American Journal of Gastroenterology, 2015, 110, S604-S605.	0.2	0
61	Creation of a Human Secretome: A Novel Composite Library of Human Secreted Proteins: Validation Using Ovarian Cancer Gene Expression Data and a Virtual Secretome Array. Clinical Cancer Research, 2015, 21, 4960-4969.	3.2	62
62	Orchestrating high-throughput genomic analysis with Bioconductor. Nature Methods, 2015, 12, 115-121.	9.0	3,070
63	Bayesian nonparametric cross-study validation of prediction methods. Annals of Applied Statistics, 2015, 9, .	0.5	24
64	Comparing Platforms for Messenger RNA Expression Profiling of Archival Formalin-Fixed, Paraffin-Embedded Tissues. Journal of Molecular Diagnostics, 2015, 17, 374-381.	1.2	22
65	Associations between host gene expression, the mucosal microbiome, and clinical outcome in the pelvic pouch of patients with inflammatory bowel disease. Genome Biology, 2015, 16, 67.	3.8	166
66	A reproducible approach to high-throughput biological data acquisition and integration. PeerJ, 2015, 3, e791.	0.9	12
67	Molecular Subtypes of High-Grade Serous Ovarian Cancer: The Holy Grail?. Journal of the National Cancer Institute, 2014, 106, .	3.0	18
68	Cross-study validation for the assessment of prediction algorithms. Bioinformatics, 2014, 30, i105-i112.	1.8	75
69	Más-o-menos: a simple sign averaging method for discrimination in genomic data analysis. Bioinformatics, 2014, 30, 3062-3069.	1.8	34
70	Risk Prediction for Late-Stage Ovarian Cancer by Meta-analysis of 1525 Patient Samples. Journal of the National Cancer Institute, 2014, 106, .	3.0	184
71	Relating the metatranscriptome and metagenome of the human gut. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2329-38.	3.3	552
72	Comparative Meta-analysis of Prognostic Gene Signatures for Late-Stage Ovarian Cancer. Journal of the National Cancer Institute, 2014, 106, .	3.0	110

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73	Lineage-specific interface proteins match up the cell cycle and differentiation in embryo stem cells. Stem Cell Research, 2014, 13, 316-328.	0.3	9
74	Meta-analysis of public microarray databases for prognostic and predictive gene signatures of late-stage ovarian cancer.. Journal of Clinical Oncology, 2014, 32, 5531-5531.	0.8	0
75	Abstract 2353: A comparative meta-analysis of prognostic gene signatures for late-stage ovarian cancer. , 2014, , .		0
76	Two-stage microbial community experimental design. ISME Journal, 2013, 7, 2330-2339.	4.4	31
77	MicroRNA Signature Obtained From the Comparison of Aggressive With Indolent Non-Hodgkin Lymphomas: Potential Prognostic Value in Mantle-Cell Lymphoma. Journal of Clinical Oncology, 2013, 31, 2903-2911.	0.8	37
78	A Guide to Enterotypes across the Human Body: Meta-Analysis of Microbial Community Structures in Human Microbiome Datasets. PLoS Computational Biology, 2013, 9, e1002863.	1.5	446
79	Potentially Prognostic miRNAs in HPV-Associated Oropharyngeal Carcinoma. Clinical Cancer Research, 2013, 19, 2154-2162.	3.2	99
80	curatedOvarianData: clinically annotated data for the ovarian cancer transcriptome. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat013.	1.4	165
81	Expression Profiling of Archival Tumors for Long-term Health Studies. Clinical Cancer Research, 2012, 18, 6136-6146.	3.2	32
82	Composition of the adult digestive tract bacterial microbiome based on seven mouth surfaces, tonsils, throat and stool samples. Genome Biology, 2012, 13, R42.	13.9	797
83	Assessment of colorectal cancer molecular features along bowel subsites challenges the conception of distinct dichotomy of proximal versus distal colorectum. Gut, 2012, 61, 847-854.	6.1	518
84	The Murine Caecal MicroRNA Signature Depends on the Presence of the Endogenous Microbiota. International Journal of Biological Sciences, 2012, 8, 171-186.	2.6	102
85	Metagenomic microbial community profiling using unique clade-specific marker genes. Nature Methods, 2012, 9, 811-814.	9.0	1,591
86	Integrative Approaches for Microarray Data Analysis. Methods in Molecular Biology, 2012, 802, 157-182.	0.4	4
87	Abstract 3161: Identification of HPV/p16-associated microRNAs in primary oropharyngeal carcinoma. , 2012, , .		0
88	A 7-Gene Microrna Signature Characteristic of Mantle Cell Lymphoma Reveals Focal Adhesion and Integrin Signalling, Proteasome-Mediated Degradation, and the PI3K Signalling Cascade As Important to MCL Pathogenesis. Blood, 2012, 120, 1586-1586.	0.6	0
89	Stem cell gene expression programs influence clinical outcome in human leukemia. Nature Medicine, 2011, 17, 1086-1093.	15.2	894
90	Metagenomic biomarker discovery and explanation. Genome Biology, 2011, 12, R60.	13.9	11,192

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91	Microbial community function and biomarker discovery in the human microbiome. Genome Biology, 2011, 12, .	13.9	89
92	A gene signature in histologically normal surgical margins is predictive of oral carcinoma recurrence. BMC Cancer, 2011, 11, 437.	1.1	117
93	mRNA transcript quantification in archival samples using multiplexed, color-coded probes. BMC Biotechnology, 2011, 11, 46.	1.7	234
94	Optimized application of penalized regression methods to diverse genomic data. Bioinformatics, 2011, 27, 3399-3406.	1.8	73
95	MicroRNA-301 Mediates Proliferation and Invasion in Human Breast Cancer. Cancer Research, 2011, 71, 2926-2937.	0.4	242
96	Abstract 5073: Proteomic profiling of head and neck squamous cell carcinoma cell lines. , 2011, , .		0
97	Modeling of simultaneous three-dimensional leaching and chemical reaction of CCA components in unfixed wood exposed to water. Wood Science and Technology, 2010, 44, 129-147.	1.4	9
98	Optimization and analysis of a quantitative real-time PCR-based technique to determine microRNA expression in formalin-fixed paraffin-embedded samples. BMC Biotechnology, 2010, 10, 47.	1.7	39
99	Comprehensive MicroRNA Profiling for Head and Neck Squamous Cell Carcinomas. Clinical Cancer Research, 2010, 16, 1129-1139.	3.2	353
100	Comparing MicroRNA Expression In Aggressive and Indolent Non-Hodgkin Lymphomas Identifies a Prognostic Signature for Mantle Cell Lymphoma. Blood, 2010, 116, 800-800.	0.6	0
101	Genotype and time of day shape the <i>Populus</i> drought response. Plant Journal, 2009, 60, 703-715.	2.8	123
102	Robust global micro-RNA profiling with formalin-fixed paraffin-embedded breast cancer tissues. Laboratory Investigation, 2009, 89, 597-606.	1.7	221
103	Modeling of simultaneous unidirectional leaching and reduction of Cr6+ in unfixed CCA treated wood. Wood Science and Technology, 2008, 42, 299-312.	1.4	3
104	Sustainable urban community development from the grassroots: Challenges and opportunities in a pedestrian street initiative. Local Environment, 2008, 13, 129-139.	1.1	22
105	Modeling the Leaching of Inorganic Components of Wood Preservatives in Service. , 2006, , 139-156.		5
106	Prediction of long-term leaching potential of preservative-treated wood by diffusion modeling. Holzforschung, 2005, 59, 581-588.	0.9	22
107	Collisional broadening and shifting of Raman lines, and the potential energy surface for H2â€"Ar. Computational and Theoretical Chemistry, 2002, 591, 245-253.	1.5	8
108	Hydrogenâ€"rare Gas Interactions and Raman Line Shapes. Journal of the Chinese Chemical Society, 2001, 48, 439-448.	0.8	4

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109	Engagement of introductory biostatistics students inÂa novel hybrid course format. F1000Research, 0, 5, 2624.	0.8	0
110	HGNChelper: identification and correction of invalid gene symbols for human and mouse. F1000Research, 0, 9, 1493.	0.8	11