

# Levi Waldron

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8485810/publications.pdf>

Version: 2024-02-01

110  
papers

28,155  
citations

76031

42  
h-index

36203

101  
g-index

146  
all docs

146  
docs citations

146  
times ranked

48213  
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. <i>Clinical Infectious Diseases</i> , 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. <i>Cell Genomics</i> , 2022, 2, 100085.	3.0	59
3	Cross-cohort gut microbiome associations with immune checkpoint inhibitor response in advanced melanoma. <i>Nature Medicine</i> , 2022, 28, 535-544.	15.2	158
4	High-sensitivity pattern discovery in large, paired multiomic datasets. <i>Bioinformatics</i> , 2022, 38, i378-i385.	1.8	18
5	Refining colorectal cancer classification and clinical stratification through a single-cell atlas. <i>Genome Biology</i> , 2022, 23, 113.	3.8	48
6	GenomicSuperSignature facilitates interpretation of RNA-seq experiments through robust, efficient comparison to public databases. <i>Nature Communications</i> , 2022, 13, .	5.8	6
7	Toward a gold standard for benchmarking gene set enrichment analysis. <i>Briefings in Bioinformatics</i> , 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 USA—the CHASING COVID Cohort study. <i>BMJ Open</i> , 2021, 11, e048778.	0.8	32
9	SIMON: Open-Source Knowledge Discovery Platform. <i>Patterns</i> , 2021, 2, 100178.	3.1	15
10	Microbiome connections with host metabolism and habitual diet from 1,098 deeply phenotyped individuals. <i>Nature Medicine</i> , 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. <i>JMIR Public Health and Surveillance</i> , 2021, 7, e32846.	1.2	5
12	Multivariable association discovery in population-scale meta-omics studies. <i>PLoS Computational Biology</i> , 2021, 17, e1009442.	1.5	691
13	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	15.2	170
14	CNVranger: association analysis of CNVs with gene expression and quantitative phenotypes. <i>Bioinformatics</i> , 2020, 36, 972-973.	1.8	17
15	The impact of different sources of heterogeneity on loss of accuracy from genomic prediction models. <i>Biostatistics</i> , 2020, 21, 253-268.	0.9	15
16	The Impact of Stroma Admixture on Molecular Subtypes and Prognostic Gene Signatures in Serous Ovarian Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 509-519.	1.1	34
17	Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , 2020, 17, 137-145.	9.0	488
18	Gut bacterial taxonomic abundances vary with cognition, personality, and mood in the Wisconsin Longitudinal Study. <i>Brain, Behavior, &amp; Immunity - Health</i> , 2020, 9, 100155.	1.3	6

#	ARTICLE	IF	CITATIONS
19	Transparency and reproducibility in artificial intelligence. <i>Nature</i> , 2020, 586, E14-E16.	13.7	233
20	Assessment of statistical methods from single cell, bulk RNA-seq, and metagenomics applied to microbiome data. <i>Genome Biology</i> , 2020, 21, 191.	3.8	67
21	Multiomic Analysis of Subtype Evolution and Heterogeneity in High-Grade Serous Ovarian Carcinoma. <i>Cancer Research</i> , 2020, 80, 4335-4345.	0.4	57
22	Multiomic Integration of Public Oncology Databases in Bioconductor. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 958-971.	1.0	42
23	“Stoma or no stoma” First report of intestinal transplantation without stoma. <i>American Journal of Transplantation</i> , 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. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 472-479.	1.0	4
25	Reliable Analysis of Clinical Tumor-Only Whole-Exome Sequencing Data. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 321-335.	1.0	20
26	HGNChelper: identification and correction of invalid gene symbols for human and mouse. <i>F1000Research</i> , 2020, 9, 1493.	0.8	17
27	SARS-CoV-2 Testing Service Preferences of Adults in the United States: Discrete Choice Experiment. <i>JMIR Public Health and Surveillance</i> , 2020, 6, e25546.	1.2	21
28	Waldron et al. Reply to “Commentary on the HMP16SData Bioconductor Package”. <i>American Journal of Epidemiology</i> , 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. <i>Scientific Reports</i> , 2019, 9, 8770.	1.6	29
30	Sociodemographic variation in the oral microbiome. <i>Annals of Epidemiology</i> , 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. <i>Annals of Epidemiology</i> , 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. <i>Nature Medicine</i> , 2019, 25, 667-678.	15.2	602
33	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. <i>Nature Medicine</i> , 2019, 25, 679-689.	15.2	734
34	Evaluation of Oral Cavity DNA Extraction Methods on Bacterial and Fungal Microbiota. <i>Scientific Reports</i> , 2019, 9, 1531.	1.6	31
35	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	15
36	Impact of an HIV Care Coordination Program on Durable Viral Suppression. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2019, 80, 46-55.	0.9	33

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

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

#	ARTICLE	IF	CITATIONS
73	Lineage-specific interface proteins match up the cell cycle and differentiation in embryo stem cells. <i>Stem Cell Research</i> , 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.. <i>Journal of Clinical Oncology</i> , 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. <i>ISME Journal</i> , 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. <i>Journal of Clinical Oncology</i> , 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. <i>PLoS Computational Biology</i> , 2013, 9, e1002863.	1.5	446
79	Potentially Prognostic miRNAs in HPV-Associated Oropharyngeal Carcinoma. <i>Clinical Cancer Research</i> , 2013, 19, 2154-2162.	3.2	99
80	curatedOvarianData: clinically annotated data for the ovarian cancer transcriptome. Database: the <i>Journal of Biological Databases and Curation</i> , 2013, 2013, bat013.	1.4	165
81	Expression Profiling of Archival Tumors for Long-term Health Studies. <i>Clinical Cancer Research</i> , 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. <i>Genome Biology</i> , 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. <i>Gut</i> , 2012, 61, 847-854.	6.1	518
84	The Murine Caecal MicroRNA Signature Depends on the Presence of the Endogenous Microbiota. <i>International Journal of Biological Sciences</i> , 2012, 8, 171-186.	2.6	102
85	Metagenomic microbial community profiling using unique clade-specific marker genes. <i>Nature Methods</i> , 2012, 9, 811-814.	9.0	1,591
86	Integrative Approaches for Microarray Data Analysis. <i>Methods in Molecular Biology</i> , 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-Genes 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. <i>Blood</i> , 2012, 120, 1586-1586.	0.6	0
89	Stem cell gene expression programs influence clinical outcome in human leukemia. <i>Nature Medicine</i> , 2011, 17, 1086-1093.	15.2	894
90	Metagenomic biomarker discovery and explanation. <i>Genome Biology</i> , 2011, 12, R60.	13.9	11,192

#	ARTICLE	IF	CITATIONS
91	Microbial community function and biomarker discovery in the human microbiome. <i>Genome Biology</i> , 2011, 12, .	13.9	89
92	A gene signature in histologically normal surgical margins is predictive of oral carcinoma recurrence. <i>BMC Cancer</i> , 2011, 11, 437.	1.1	117
93	mRNA transcript quantification in archival samples using multiplexed, color-coded probes. <i>BMC Biotechnology</i> , 2011, 11, 46.	1.7	234
94	Optimized application of penalized regression methods to diverse genomic data. <i>Bioinformatics</i> , 2011, 27, 3399-3406.	1.8	73
95	MicroRNA-301 Mediates Proliferation and Invasion in Human Breast Cancer. <i>Cancer Research</i> , 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. <i>Wood Science and Technology</i> , 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. <i>BMC Biotechnology</i> , 2010, 10, 47.	1.7	39
99	Comprehensive MicroRNA Profiling for Head and Neck Squamous Cell Carcinomas. <i>Clinical Cancer Research</i> , 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. <i>Blood</i> , 2010, 116, 800-800.	0.6	0
101	Genotype and time of day shape the <i>Populus</i> drought response. <i>Plant Journal</i> , 2009, 60, 703-715.	2.8	123
102	Robust global micro-RNA profiling with formalin-fixed paraffin-embedded breast cancer tissues. <i>Laboratory Investigation</i> , 2009, 89, 597-606.	1.7	221
103	Modeling of simultaneous unidirectional leaching and reduction of Cr6+ in unfixed CCA treated wood. <i>Wood Science and Technology</i> , 2008, 42, 299-312.	1.4	3
104	Sustainable urban community development from the grassroots: Challenges and opportunities in a pedestrian street initiative. <i>Local Environment</i> , 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. <i>Holzforschung</i> , 2005, 59, 581-588.	0.9	22
107	Collisional broadening and shifting of Raman lines, and the potential energy surface for H2 <sup>+</sup> Ar. <i>Computational and Theoretical Chemistry</i> , 2002, 591, 245-253.	1.5	8
108	Hydrogen <sup>+</sup> Rare Gas Interactions and Raman Line Shapes. <i>Journal of the Chinese Chemical Society</i> , 2001, 48, 439-448.	0.8	4

#	ARTICLE	IF	CITATIONS
109	Engagement of introductory biostatistics students in a novel hybrid course format. <i>F1000Research</i> , 0, 5, 2624.	0.8	0
110	HGNChelper: identification and correction of invalid gene symbols for human and mouse. <i>F1000Research</i> , 0, 9, 1493.	0.8	11