

# 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

66234

42  
h-index

31759

101  
g-index

146  
all docs

146  
docs citations

146  
times ranked

44497  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Metagenomic biomarker discovery and explanation. <i>Genome Biology</i> , 2011, 12, R60.   | 13.9 | 11,192    |
| 2  | Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015, 12, 115-121.  | 9.0  | 3,070     |
| 3  | Metagenomic microbial community profiling using unique clade-specific marker genes. <i>Nature Methods</i> , 2012, 9, 811-814.   | 9.0  | 1,591     |
| 4  | Stem cell gene expression programs influence clinical outcome in human leukemia. <i>Nature Medicine</i> , 2011, 17, 1086-1093.  | 15.2 | 894       |
| 5  | 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       |
| 6  | 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       |
| 7  | Multivariable association discovery in population-scale meta-omics studies. <i>PLoS Computational Biology</i> , 2021, 17, e1009442.   | 1.5  | 691       |
| 8  | 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       |
| 9  | 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       |
| 10 | 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       |
| 11 | Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , 2020, 17, 137-145.  | 9.0  | 488       |
| 12 | 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       |
| 13 | 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       |
| 14 | Machine Learning Meta-analysis of Large Metagenomic Datasets: Tools and Biological Insights. <i>PLoS Computational Biology</i> , 2016, 12, e1004977.  | 1.5  | 434       |
| 15 | Comprehensive MicroRNA Profiling for Head and Neck Squamous Cell Carcinomas. <i>Clinical Cancer Research</i> , 2010, 16, 1129-1139.   | 3.2  | 353       |
| 16 | Accessible, curated metagenomic data through ExperimentHub. <i>Nature Methods</i> , 2017, 14, 1023-1024.  | 9.0  | 292       |
| 17 | Racial/Ethnic Disparities in Genomic Sequencing. <i>JAMA Oncology</i> , 2016, 2, 1070.  | 3.4  | 250       |
| 18 | MicroRNA-301 Mediates Proliferation and Invasion in Human Breast Cancer. <i>Cancer Research</i> , 2011, 71, 2926-2937.  | 0.4  | 242       |

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 19 | bioBakery: a meta-omic analysis environment. <i>Bioinformatics</i> , 2018, 34, 1235-1237.  | 1.8  | 241       |
| 20 | mRNA transcript quantification in archival samples using multiplexed, color-coded probes. <i>BMC Biotechnology</i> , 2011, 11, 46.   | 1.7  | 234       |
| 21 | Transparency and reproducibility in artificial intelligence. <i>Nature</i> , 2020, 586, E14-E16.   | 13.7 | 233       |
| 22 | Robust global micro-RNA profiling with formalin-fixed paraffin-embedded breast cancer tissues. <i>Laboratory Investigation</i> , 2009, 89, 597-606.  | 1.7  | 221       |
| 23 | 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       |
| 24 | Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.  | 15.2 | 170       |
| 25 | 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       |
| 26 | curatedOvarianData: clinically annotated data for the ovarian cancer transcriptome. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat013.                    | 1.4  | 165       |
| 27 | Cross-cohort gut microbiome associations with immune checkpoint inhibitor response in advanced melanoma. <i>Nature Medicine</i> , 2022, 28, 535-544.   | 15.2 | 158       |
| 28 | Genotype and time of day shape the <i>Populus</i> drought response. <i>Plant Journal</i> , 2009, 60, 703-715.  | 2.8  | 123       |
| 29 | A gene signature in histologically normal surgical margins is predictive of oral carcinoma recurrence. <i>BMC Cancer</i> , 2011, 11, 437.  | 1.1  | 117       |
| 30 | 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       |
| 31 | 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       |
| 32 | Potentially Prognostic miRNAs in HPV-Associated Oropharyngeal Carcinoma. <i>Clinical Cancer Research</i> , 2013, 19, 2154-2162.  | 3.2  | 99        |
| 33 | Consensus on Molecular Subtypes of High-Grade Serous Ovarian Carcinoma. <i>Clinical Cancer Research</i> , 2018, 24, 5037-5047.   | 3.2  | 93        |
| 34 | Microbial community function and biomarker discovery in the human microbiome. <i>Genome Biology</i> , 2011, 12, .  | 13.9 | 89        |
| 35 | Toward a gold standard for benchmarking gene set enrichment analysis. <i>Briefings in Bioinformatics</i> , 2021, 22, 545-556.  | 3.2  | 83        |
| 36 | Software for the Integration of Multiomics Experiments in Bioconductor. <i>Cancer Research</i> , 2017, 77, e39-e42.  | 0.4  | 80        |

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|----|---|-----|-----------|
| 37 | Cross-study validation for the assessment of prediction algorithms. <i>Bioinformatics</i> , 2014, 30, i105-i112.  | 1.8 | 75        |
| 38 | Optimized application of penalized regression methods to diverse genomic data. <i>Bioinformatics</i> , 2011, 27, 3399-3406.   | 1.8 | 73        |
| 39 | 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        |
| 40 | 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        |
| 41 | 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        |
| 42 | Multiomic Analysis of Subtype Evolution and Heterogeneity in High-Grade Serous Ovarian Carcinoma. <i>Cancer Research</i> , 2020, 80, 4335-4345.   | 0.4 | 57        |
| 43 | Refining colorectal cancer classification and clinical stratification through a single-cell atlas. <i>Genome Biology</i> , 2022, 23, 113.   | 3.8 | 48        |
| 44 | 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        |
| 45 | Multiomic Integration of Public Oncology Databases in Bioconductor. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 958-971.  | 1.0 | 42        |
| 46 | 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        |
| 47 | 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        |
| 48 | Sociodemographic variation in the oral microbiome. <i>Annals of Epidemiology</i> , 2019, 35, 73-80.e2.  | 0.9 | 37        |
| 49 | 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        |
| 50 | 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        |
| 51 | 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        |
| 52 | Expression Profiling of Archival Tumors for Long-term Health Studies. <i>Clinical Cancer Research</i> , 2012, 18, 6136-6146.  | 3.2 | 32        |
| 53 | Cohort profile: a national, community-based prospective cohort study of SARS-CoV-2 pandemic outcomes in the USAâ€”the CHASING COVID Cohort study. <i>BMJ Open</i> , 2021, 11, e048778.  | 0.8 | 32        |
| 54 | Two-stage microbial community experimental design. <i>ISME Journal</i> , 2013, 7, 2330-2339.  | 4.4 | 31        |

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|----|---|-----|-----------|
| 55 | Evaluation of Oral Cavity DNA Extraction Methods on Bacterial and Fungal Microbiota. <i>Scientific Reports</i> , 2019, 9, 1531.   | 1.6 | 31        |
| 56 | HMP16SData: Efficient Access to the Human Microbiome Project Through Bioconductor. <i>American Journal of Epidemiology</i> , 2019, 188, 1023-1026.                                    | 1.6 | 30        |
| 57 | Data and Statistical Methods To Analyze the Human Microbiome. <i>MSystems</i> , 2018, 3, .  | 1.7 | 29        |
| 58 | 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        |
| 59 | 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        |
| 60 | Widespread modulation of gene expression by copy number variation in skeletal muscle. <i>Scientific Reports</i> , 2018, 8, 1399.  | 1.6 | 25        |
| 61 | Bayesian nonparametric cross-study validation of prediction methods. <i>Annals of Applied Statistics</i> , 2015, 9, .   | 0.5 | 24        |
| 62 | CellMapper: rapid and accurate inference of gene expression in difficult-to-isolate cell types. <i>Genome Biology</i> , 2016, 17, 201.  | 3.8 | 24        |
| 63 | Prediction of long-term leaching potential of preservative-treated wood by diffusion modeling. <i>Holzforschung</i> , 2005, 59, 581-588.  | 0.9 | 22        |
| 64 | 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        |
| 65 | 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        |
| 66 | Multiparametric Quantitative Ultrasound Imaging in Assessment of Chronic Kidney Disease. <i>Journal of Ultrasound in Medicine</i> , 2017, 36, 2245-2256.                              | 0.8 | 21        |
| 67 | 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        |
| 68 | 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        |
| 69 | Continuity of transcriptomes among colorectal cancer subtypes based on meta-analysis. <i>Genome Biology</i> , 2018, 19, 142.  | 3.8 | 20        |
| 70 | Reliable Analysis of Clinical Tumor-Only Whole-Exome Sequencing Data. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 321-335.  | 1.0 | 20        |
| 71 | 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        |
| 72 | Molecular Subtypes of High-Grade Serous Ovarian Cancer: The Holy Grail?. <i>Journal of the National Cancer Institute</i> , 2014, 106, .   | 3.0 | 18        |

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|----|---|-----|-----------|
| 73 | The Doppelg nger Effect: Hidden Duplicates in Databases of Transcriptome Profiles. Journal of the National Cancer Institute, 2016, 108, djw146.   | 3.0 | 18        |
| 74 | High-sensitivity pattern discovery in large, paired multiomic datasets. Bioinformatics, 2022, 38, i378-i385.  | 1.8 | 18        |
| 75 | CNVranger: association analysis of CNVs with gene expression and quantitative phenotypes. Bioinformatics, 2020, 36, 972-973.  | 1.8 | 17        |
| 76 | HGNChelper: identification and correction of invalid gene symbols for human and mouse. F1000Research, 2020, 9, 1493.  | 0.8 | 17        |
| 77 | Meta-Analysis in Gene Expression Studies. Methods in Molecular Biology, 2016, 1418, 161-176.  | 0.4 | 16        |
| 78 | Using Registry Data to Construct a Comparison Group for Programmatic Effectiveness Evaluation. American Journal of Epidemiology, 2018, 187, 1980-1989.  | 1.6 | 15        |
| 79 | 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        |
| 80 | The impact of different sources of heterogeneity on loss of accuracy from genomic prediction models. Biostatistics, 2020, 21, 253-268.  | 0.9 | 15        |
| 81 | SIMON: Open-Source Knowledge Discovery Platform. Patterns, 2021, 2, 100178.   | 3.1 | 15        |
| 82 |   Stoma or no stoma   First report of intestinal transplantation without stoma. American Journal of Transplantation, 2020, 20, 3550-3557.   | 2.6 | 13        |
| 83 | A reproducible approach to high-throughput biological data acquisition and integration. PeerJ, 2015, 3, e791.   | 0.9 | 12        |
| 84 | HGNChelper: identification and correction of invalid gene symbols for human and mouse. F1000Research, 0, 9, 1493.   | 0.8 | 11        |
| 85 | 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         |
| 86 | 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         |
| 87 | 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         |
| 88 | Collisional broadening and shifting of Raman lines, and the potential energy surface for H2  Ar. Computational and Theoretical Chemistry, 2002, 591, 245-253.                                 | 1.5 | 8         |
| 89 | Control of Gene Expression by RNA Binding Protein Action on Alternative Translation Initiation Sites. PLoS Computational Biology, 2016, 12, e1005198.   | 1.5 | 7         |
| 90 | 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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|-----|---|-----|-----------|
| 91  | GenomicSuperSignature facilitates interpretation of RNA-seq experiments through robust, efficient comparison to public databases. Nature Communications, 2022, 13, .  | 5.8 | 6         |
| 92  | Modeling the Leaching of Inorganic Components of Wood Preservatives in Service. , 2006, , 139-156.  |     | 5         |
| 93  | 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         |
| 94  | Hydrogenâ€rare Gas Interactions and Raman Line Shapes. Journal of the Chinese Chemical Society, 2001, 48, 439-448.  | 0.8 | 4         |
| 95  | 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         |
| 96  | Integrative Approaches for Microarray Data Analysis. Methods in Molecular Biology, 2012, 802, 157-182.  | 0.4 | 4         |
| 97  | 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         |
| 98  | Metaâ€analysis and commentary: Preemptive correction of arteriovenous access stenosis. Hemodialysis International, 2018, 22, 279-280.   | 0.4 | 1         |
| 99  | Orchestrating a community-developed computational workshop and accompanying training materials. F1000Research, 2018, 7, 1656.   | 0.8 | 1         |
| 100 | Global Transcriptome Differences Between Early-Onset and Late-Onset Colorectal Cancer. American Journal of Gastroenterology, 2015, 110, S604-S605.  | 0.2 | 0         |
| 101 | Mo1306 Rapid and Accurate Inference of Gene Expression in Difficult-to-Isolate Cell Types. Gastroenterology, 2016, 150, S693.   | 0.6 | 0         |
| 102 | Waldron et al. Reply to â€Commentary on the HMP16SData Bioconductor Packageâ€ American Journal of Epidemiology, 2019, 188, 1031-1032.   | 1.6 | 0         |
| 103 | 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         |
| 104 | Abstract 5073: Proteomic profiling of head and neck squamous cell carcinoma cell lines. , 2011, , .   |     | 0         |
| 105 | Abstract 3161: Identification of HPV/p16-associated microRNAs in primary oropharyngeal carcinoma. , 2012, , .   |     | 0         |
| 106 | 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. Blood, 2012, 120, 1586-1586. | 0.6 | 0         |
| 107 | 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         |
| 108 | Abstract 2353: A comparative meta-analysis of prognostic gene signatures for late-stage ovarian cancer. , 2014, , .   |     | 0         |

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|-----|--|-----|-----------|
| 109 | Engagement of introductory biostatistics students in a novel hybrid course format. F1000Research, 0, 5, 2624.    | 0.8 | 0         |
| 110 | restfulSE: A semantically rich interface for cloud-scale genomics with Bioconductor. F1000Research, 2019, 8, 21. | 0.8 | 0         |