Laura L Elo

List of Publications by Year
in descending order

122	5,998	136950	88630
papers	citations	32	70
		h-index	g-index

136	136	136	11621
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A survey of best practices for RNA-seq data analysis. Genome Biology, 2016, 17, 13.	8.8	1,898
2	Comparison of software packages for detecting differential expression in RNA-seq studies. Briefings in Bioinformatics, 2015, 16, 59-70.	6.5	361
3	A systematic evaluation of normalization methods in quantitative label-free proteomics. Briefings in Bioinformatics, 2018, 19, bbw095.	6.5	192
4	Innate Immune Activity Is Detected Prior to Seroconversion in Children With HLA-Conferred Type 1 Diabetes Susceptibility. Diabetes, 2014, 63, 2402-2414.	0.6	158
5	Six-Week Endurance Exercise Alters Gut Metagenome That Is not Reflected in Systemic Metabolism in Over-weight Women. Frontiers in Microbiology, 2018, 9, 2323.	3.5	145
6	Genome-wide Profiling of Interleukin-4 and STAT6 Transcription Factor Regulation of Human Th2 Cell Programming. Immunity, 2010, 32, 852-862.	14.3	139
7	Prediction of overall survival for patients with metastatic castration-resistant prostate cancer: development of a prognostic model through a crowdsourced challenge with open clinical trial data. Lancet Oncology, The, 2017, 18, 132-142.	10.7	124
8	Systematic evaluation of differential splicing tools for RNA-seq studies. Briefings in Bioinformatics, 2020, 21, 2052-2065.	6.5	124
9	ROTS: An R package for reproducibility-optimized statistical testing. PLoS Computational Biology, 2017, 13, e1005562.	3.2	108
10	A practical comparison of methods for detecting transcription factor binding sites in ChIP-seq experiments. BMC Genomics, 2009, 10, 618.	2.8	105
11	Normal stroma suppresses cancer cell proliferation via mechanosensitive regulation of JMJD1a-mediated transcription. Nature Communications, 2016, 7, 12237.	12.8	105
12	Improving missing value estimation in microarray data with gene ontology. Bioinformatics, 2006, 22, 566-572.	4.1	101
13	Systematic construction of gene coexpression networks with applications to human T helper cell differentiation process. Bioinformatics, 2007, 23, 2096-2103.	4.1	94
14	Gut microbiota composition is associated with temperament traits in infants. Brain, Behavior, and Immunity, 2019, 80, 849-858.	4.1	91
15	A comprehensive evaluation of popular proteomics software workflows for label-free proteome quantification and imputation. Briefings in Bioinformatics, 2018, 19, 1344-1355.	6.5	88
16	Comparison of methods to detect differentially expressed genes between single-cell populations. Briefings in Bioinformatics, 2017, 18, bbw057.	6.5	83
17	Th1 Response and Cytotoxicity Genes Are Down-Regulated in Cutaneous T-Cell Lymphoma. Clinical Cancer Research, 2006, 12, 4812-4821.	7.0	74
18	Reproducibility-Optimized Test Statistic for Ranking Genes in Microarray Studies. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 423-431.	3.0	66

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19	SATB1 dictates expression of multiple genes including IL-5 involved in human T helper cell differentiation. Blood, 2010, 116, 1443-1453.	1.4	62
20	Transcriptional Repressor HIC1 Contributes to Suppressive Function of Human Induced Regulatory T Cells. Cell Reports, 2018, 22, 2094-2106.	6.4	60
21	Quantitative Proteomics Analysis of the Nuclear Fraction of Human CD4+ Cells in the Early Phases of IL-4-induced Th2 Differentiation. Molecular and Cellular Proteomics, 2010, 9, 1937-1953.	3.8	55
22	Optimization of Statistical Methods Impact on Quantitative Proteomics Data. Journal of Proteome Research, 2015, 14, 4118-4126.	3.7	54
23	Missing value imputation improves clustering and interpretation of gene expression microarray data. BMC Bioinformatics, 2008, 9, 202.	2.6	52
24	Integrating probe-level expression changes across generations of Affymetrix arrays. Nucleic Acids Research, 2005, 33, e193-e193.	14.5	51
25	Early fecal microbiota composition in children who later develop celiac disease and associated autoimmunity. Scandinavian Journal of Gastroenterology, 2018, 53, 403-409.	1.5	49
26	Hydroxysteroid (17Î²) dehydrogenase 13 deficiency triggers hepatic steatosis and inflammation in mice. FASEB Journal, 2018, 32, 3434-3447.	0.5	49
27	Computational strategies for single-cell multi-omics integration. Computational and Structural Biotechnology Journal, 2021, 19, 2588-2596.	4.1	46
28	Decidualization of Human Endometrial Stromal Fibroblasts is a Multiphasic Process Involving Distinct Transcriptional Programs. Reproductive Sciences, 2019, 26, 323-336.	2.5	45
29	ROTS: reproducible RNA-seq biomarker detectorâ€"prognostic markers for clear cell renal cell cancer. Nucleic Acids Research, 2016, 44, e1-e1.	14.5	43
30	Using Peptide-Level Proteomics Data for Detecting Differentially Expressed Proteins. Journal of Proteome Research, 2015, 14, 4564-4570.	3.7	40
31	Brief Isoflurane Anesthesia Produces Prominent Phosphoproteomic Changes in the Adult Mouse Hippocampus. ACS Chemical Neuroscience, 2016, 7, 749-756.	3.5	39
32	Integrative omics approaches provide biological and clinical insights: examples from mitochondrial diseases. Journal of Clinical Investigation, 2020, 130, 20-28.	8.2	39
33	Genetic Variants and Their Interactions in the Prediction of Increased Pre-Clinical Carotid Atherosclerosis: The Cardiovascular Risk in Young Finns Study. PLoS Genetics, 2010, 6, e1001146.	3.5	38
34	Metagenomics analysis of gut microbiota in response to diet intervention and gestational diabetes in overweight and obese women: a randomised, double-blind, placebo-controlled clinical trial. Gut, 2021, 70, gutjnl-2020-321643.	12.1	37
35	Prediction of Adulthood Obesity Using Genetic and Childhood Clinical Risk Factors in the Cardiovascular Risk in Young Finns Study. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	35
36	Enhanced differential expression statistics for data-independent acquisition proteomics. Scientific Reports, 2017, 7, 5869.	3.3	32

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37	Data-Independent Acquisition Mass Spectrometry in Metaproteomics of Gut Microbiotaâ€"Implementation and Computational Analysis. Journal of Proteome Research, 2020, 19, 432-436.	3.7	31
38	Optimized detection of differential expression in global profiling experiments: case studies in clinical transcriptomic and quantitative proteomic datasets. Briefings in Bioinformatics, 2009, 10, 547-555.	6.5	29
39	Early suppression of immune response pathways characterizes children with prediabetes in genome-wide gene expression profiling. Journal of Autoimmunity, 2010, 35, 70-76.	6.5	29
40	Probabilistic Analysis of Probe Reliability in Differential Gene Expression Studies with Short Oligonucleotide Arrays. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 217-225.	3.0	29
41	Chronic nonbacterial prostate inflammation in a rat model is associated with changes of gut microbiota that can be modified with a galactoglucomannanâ€"rich hemicellulose extract in the diet. BJU International, 2019, 123, 899-908.	2.5	29
42	Empirical comparison of structure-based pathway methods. Briefings in Bioinformatics, 2016, 17, 336-345.	6.5	27
43	A fully scalable online pre-processing algorithm for short oligonucleotide microarray atlases. Nucleic Acids Research, 2013, 41, e110-e110.	14.5	26
44	Hypoxia-inducible factor (HIF)-prolyl hydroxylase 3 (PHD3) maintains high HIF2A mRNA levels in clear cell renal cell carcinoma. Journal of Biological Chemistry, 2019, 294, 3760-3771.	3.4	26
45	CIP2A Interacts with TopBP1 and Drives Basal-Like Breast Cancer Tumorigenesis. Cancer Research, 2021, 81, 4319-4331.	0.9	26
46	The L1TD1 Protein Interactome Reveals the Importance of Post-transcriptional Regulation in Human Pluripotency. Stem Cell Reports, 2015, 4, 519-528.	4.8	25
47	Quantitative Proteomics Reveals the Dynamic Protein Landscape during Initiation of Human Th17 Cell Polarization. IScience, 2019, 11, 334-355.	4.1	25
48	HIF prolyl hydroxylase PHD3 regulates translational machinery and glucose metabolism in clear cell renal cell carcinoma. Cancer & Metabolism, 2017, 5, 5.	5.0	24
49	Crowdsourcing digital health measures to predict Parkinsonâ€™s disease severity: the Parkinsonâ€™s Disease Digital Biomarker DREAM Challenge. Npj Digital Medicine, 2021, 4, 53.	10.9	24
50	Probe-level estimation improves the detection of differential splicing in Affymetrix exon array studies. Genome Biology, 2009, 10, R77.	9.6	23
51	Histone deacetylases 1 and 2 restrain CD4+ cytotoxic T lymphocyte differentiation. JCI Insight, 2020, 5, .	5.0	23
52	A carbohydrate-active enzyme (CAZy) profile links successful metabolic specialization of Prevotella to its abundance in gut microbiota. Scientific Reports, 2020, 10, 12411.	3.3	22
53	Compressive stress-mediated p38 activation required for ERÎ±â€‰+â€‰phenotype in breast cancer. Nature Communications, 2021, 12, 6967.	12.8	22
54	Serum Proteomic Profiling to Identify Biomarkers of Premature Carotid Atherosclerosis. Scientific Reports, 2018, 8, 9209.	3.3	20

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55	Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. Cell Systems, 2020, 11, 186-195.e9.	6.2	19
56	Melanoma-Associated Cancer-Testis Antigen 16 (CT16) Regulates the Expression of Apoptotic and Antiapoptotic Genes and Promotes Cell Survival. PLoS ONE, 2012, 7, e45382.	2.5	18
57	Adrenals Contribute to Growth of Castration-Resistant VCaP Prostate Cancer Xenografts. American Journal of Pathology, 2018, 188, 2890-2901.	3.8	17
58	An unbiased in vitro screen for activating epidermal growth factor receptor mutations. Journal of Biological Chemistry, 2019, 294, 9377-9389.	3.4	17
59	Stable Iterative Variable Selection. Bioinformatics, 2021, 37, 4810-4817.	4.1	17
60	Prediction of complication related death after radical cystectomy for bladder cancer with machine learning methodology. Scandinavian Journal of Urology, 2019, 53, 325-331.	1.0	16
61	Lack of androgen receptor SUMOylation results in male infertility due to epididymal dysfunction. Nature Communications, 2019, 10, 777.	12.8	15
62	Prediction of Adult Dyslipidemia Using Genetic and Childhood Clinical Risk Factors. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	14
63	A crowdsourced analysis to identify ab initio molecular signatures predictive of susceptibility to viral infection. Nature Communications, 2018, 9, 4418.	12.8	14
64	MASTL promotes cell contractility and motility through kinase-independent signaling. Journal of Cell Biology, 2020, 219, .	5.2	14
65	The Transcription Factor MAZR/PATZ1 Regulates the Development of FOXP3+ Regulatory T Cells. Cell Reports, 2019, 29, 4447-4459.e6.	6.4	13
66	Transcriptomic responses to hypoxia in endometrial and decidual stromal cells. Reproduction, 2020, 160, 39-51.	2.6	13
67	Tool evaluation for the detection of variably sized indels from next generation whole genome and targeted sequencing data. PLoS Computational Biology, 2022, 18, e1009269.	3.2	13
68	A DREAM Challenge to Build Prediction Models for Short-Term Discontinuation of Docetaxel in Metastatic Castration-Resistant Prostate Cancer. JCO Clinical Cancer Informatics, 2017, 1, 1-15.	2.1	12
69	Enterovirus-associated changes in blood transcriptomic profiles of children with genetic susceptibility to type 1 diabetes. Diabetologia, 2018, 61, 381-388.	6.3	12
70	CIP2A Constrains Th17 Differentiation by Modulating STAT3 Signaling. IScience, 2020, 23, 100947.	4.1	12
71	A Note on an Exon-Based Strategy to Identify Differentially Expressed Genes in RNA-Seq Experiments. PLoS ONE, 2014, 9, e115964.	2.5	12
72	Mining proteomic data for biomedical research. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2012, 2, 1-13.	6.8	11

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73	L1TD1 - a prognostic marker for colon cancer. BMC Cancer, 2019, 19, 727.	2.6	11
74	Predicting Quantitative Genetic Interactions by Means of Sequential Matrix Approximation. PLoS ONE, 2008, 3, e3284.	2.5	10
75	Resampling Reveals Sample-Level Differential Expression in Clinical Genome-Wide Studies. OMICS A Journal of Integrative Biology, 2009, 13, 381-396.	2.0	10
76	Statistical detection of quantitative protein biomarkers provides insights into signaling networks deregulated in acute myeloid leukemia. Proteomics, 2014, 14, 2443-2453.	2.2	10
77	End-of-life chemotherapy use at a Finnish university hospital: a retrospective cohort study. Acta OncolÃ³gica, 2017, 56, 1272-1276.	1.8	10
78	A systematic comparison of FOSL1, FOSL2 and BATF-mediated transcriptional regulation during early human Th17 differentiation. Nucleic Acids Research, 2022, 50, 4938-4958.	14.5	10
79	Introducing untargeted data-independent acquisition for metaproteomics of complex microbial samples. ISME Communications, 2022, 2, .	4.2	10
80	Antiandrogens Reduce Intratumoral Androgen Concentrations and Induce Androgen Receptor Expression in Castration-Resistant Prostate Cancer Xenografts. American Journal of Pathology, 2018, 188, 216-228.	3.8	9
81	Easy-to-use tool for evaluating the elevated acute kidney injury risk against reduced cardiovascular disease risk during intensive blood pressure control. Journal of Hypertension, 2020, 38, 511-518.	0.5	9
82	Evaluation of tools for identifying large copy number variations from ultra-low-coverage whole-genome sequencing data. BMC Genomics, 2021, 22, 357.	2.8	9
83	Early DNA methylation changes in children developing beta cell autoimmunity at a young age. Diabetologia, 2022, 65, 844-860.	6.3	9
84	Assessing the utilization of radiotherapy near end of life at a Finnish University Hospital: a retrospective cohort study. Acta OncolÃ³gica, 2017, 56, 1265-1271.	1.8	8
85	SimPhospho: a software tool enabling confident phosphosite assignment. Bioinformatics, 2018, 34, 2690-2692.	4.1	8
86	Preoperative Risk Prediction Models for Short-Term Revision and Death After Total Hip Arthroplasty. JBJS Open Access, 2021, 6, e20.00091.	1.5	8
87	Improving Identification of Differentially Expressed Genes by Integrative Analysis of Affymetrix and Illumina Arrays. OMICS A Journal of Integrative Biology, 2006, 10, 369-380.	2.0	7
88	Liver lipid metabolism is altered by increased circulating estrogen to androgen ratio in male mouse. Journal of Proteomics, 2016, 133, 66-75.	2.4	7
89	Analysis of Time-Resolved Gene Expression Measurements across Individuals. PLoS ONE, 2013, 8, e82340.	2.5	7
90	PhosPiR: an automated phosphoproteomic pipeline in R. Briefings in Bioinformatics, 2022, 23, .	6.5	7

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91	Optimized detection of transcription factor-binding sites in ChIP-seq experiments. Nucleic Acids Research, 2012, 40, e1-e1.	14.5	6
92	Protein interactome of the Cancerous Inhibitor of protein phosphatase 2A (CIP2A) in Th17 cells. Current Research in Immunology, 2020, 1, 10-22.	2.8	6
93	Likelihood contrasts: a machine learning algorithm for binary classification of longitudinal data. Scientific Reports, 2020, 10, 1016.	3.3	6
94	Phosphonormalizer: an R package for normalization of MS-based label-free phosphoproteomics. Bioinformatics, 2018, 34, 693-694.	4.1	5
95	How Reliable are Trial-based Prognostic Models in Real-world Patients with Metastatic Castration-resistant Prostate Cancer?. European Urology, 2017, 71, 838-840.	1.9	4
96	PASI: A novel pathway method to identify delicate group effects. PLoS ONE, 2018, 13, e0199991.	2.5	4
97	A Data Analysis Protocol for Quantitative Data-Independent Acquisition Proteomics. Methods in Molecular Biology, 2019, 1871, 455-465.	0.9	4
98	Posterior approach, fracture diagnosis, and American Society of Anesthesiology class III–IV are associated with increased risk of revision for dislocation after total hip arthroplasty: An analysis of 33,337 operations from the Finnish Arthroplasty Register. Scandinavian Journal of Surgery, 2020, 110, 145749692093061.	2.6	4
99	Improved risk prediction of chemotherapy†induced neutropenia—model development and validation with real†world data. Cancer Medicine, 2021, , .	2.8	4
100	Weight Loss Trajectories in Healthy Weight Coaching: Cohort Study. JMIR Formative Research, 2022, 6, e26374.	1.4	4
101	Histone H3K4me3 breadth in hypoxia reveals endometrial core functions and stress adaptation linked to endometriosis. IScience, 2022, 25, 104235.	4.1	4
102	High intratumoral dihydrotestosterone is associated with antiandrogen resistance in VCaP prostate cancer xenografts in castrated mice. IScience, 2022, 25, 104287.	4.1	4
103	Umbilical cord blood DNA methylation in children who later develop type 1 diabetes. Diabetologia, 2022, 65, 1534-1540.	6.3	4
104	Statistical Analysis of Protein Microarray Data: A Case Study in Type 1 Diabetes Research. Journal of Proteomics and Bioinformatics, 2015, 08, .	0.4	3
105	Longitudinal modeling of ultrasensitive and traditional prostate-specific antigen and prediction of biochemical recurrence after radical prostatectomy. Scientific Reports, 2016, 6, 36161.	3.3	3
106	Predicting Skeletal Muscle and Whole-Body Insulin Sensitivity Using NMR-Metabolomic Profiling. Journal of the Endocrine Society, 2020, 4, bvaa026.	0.2	3
107	OUP accepted manuscript. Briefings in Bioinformatics, 2021, , .	6.5	3
108	Computational deconvolution to estimate cell type-specific gene expression from bulk data. NAR Genomics and Bioinformatics, 2021, 3, lqaa110.	3.2	3

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109	Persistent coxsackievirus B1 infection triggers extensive changes in the transcriptome of human pancreatic ductal cells. IScience, 2022, 25, 103653.	4.1	3
110	Statistical and machine learning methods to study human CD4+ T cell proteome profiles. Immunology Letters, 2022, 245, 8-17.	2.5	3
111	Optimizing Detection of Transcription Factor-Binding Sites in ChIP-seq Experiments. Methods in Molecular Biology, 2013, 1038, 181-191.	0.9	2
112	Accurate Detection of Differential Expression and Splicing Using Low-Level Features. Methods in Molecular Biology, 2017, 1507, 141-151.	0.9	2
113	Exon-level estimates improve the detection of differentially expressed genes in RNA-seq studies. RNA Biology, 2021, 18, 1739-1746.	3.1	2
114	Differential ATAC-seq and ChIP-seq peak detection using ROTS. NAR Genomics and Bioinformatics, 2021, 3, lqab059.	3.2	2
115	An Unbiased Functional Genetics Screen Identifies Rare Activating ERBB4 Mutations. Cancer Research Communications, 2022, 2, 10-27.	1.7	2
116	An Infancy-Onset 20-Year Dietary Counselling Intervention and Gut Microbiota Composition in Adulthood. Nutrients, 2022, 14, 2667.	4.1	2
117	Predicting Gene Expression from Combined Expression and Promoter Profile Similarity with Application to Missing Value Imputation. , 2007, , 97-104.		1
118	Reproducibility-optimized detection of differential DNA methylation. Epigenomics, 2020, 12, 747-755.	2.1	1
119	Type 1 Diabetes in Children With Genetic Risk May Be Predicted Very Early With a Blood miRNA. Diabetes Care, 2022, , .	8.6	1
120	Reply to Tuomas Mirtti and Tero Aittokallio's Letter to the Editor re: Fatemeh Seyednasrollah, Mehrad Mahmoudian, Liisa Rautakorpi, et al. How Reliable are Trial-based Prognostic Models in Real-world Patients with Metastatic Castration-resistant Prostate Cancer? Eur Urol. 2017;71:838â€"40. Clinical Utility of Trial-estimated Prognostic Models. European Urology, 2017, 72, e70-e71.	1.9	0
121	Inference of Gene Coexpression Networks by Integrative Analysis across Microarray Experiments. Journal of Integrative Bioinformatics, 2006, 3, 137-147.	1.5	0
122	Pancreas Whole Tissue Transcriptomics Highlights the Role of the Exocrine Pancreas in Patients With Recently Diagnosed Type 1 Diabetes. Frontiers in Endocrinology, 2022, 13, 861985.	3.5	0