

Barbara Elizabeth Engelhardt

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

10,632
citations

201674

27
h-index

233421

45
g-index

66
all docs

66
docs citations

66
times ranked

22289
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic effects on gene expression across human tissues. <i>Nature</i> , 2017, 550, 204-213.	27.8	3,500
2	The GTEx Consortium atlas of genetic regulatory effects across human tissues. <i>Science</i> , 2020, 369, 1318-1330.	12.6	2,385
3	Understanding mechanisms underlying human gene expression variation with RNA sequencing. <i>Nature</i> , 2010, 464, 768-772.	27.8	1,200
4	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , 2020, 181, 236-249.	28.9	334
5	The impact of sex on gene expression across human tissues. <i>Science</i> , 2020, 369, .	12.6	329
6	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. <i>JAMA Psychiatry</i> , 2015, 72, 642.	11.0	289
7	A statin-dependent QTL for GATM expression is associated with statin-induced myopathy. <i>Nature</i> , 2013, 502, 377-380.	27.8	197
8	Computational approaches to fMRI analysis. <i>Nature Neuroscience</i> , 2017, 20, 304-313.	14.8	185
9	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. <i>Behavior Genetics</i> , 2016, 46, 170-182.	2.1	178
10	Predicting genome-wide DNA methylation using methylation marks, genomic position, and DNA regulatory elements. <i>Genome Biology</i> , 2015, 16, 14.	8.8	165
11	Protein Molecular Function Prediction by Bayesian Phylogenomics. <i>PLoS Computational Biology</i> , 2005, 1, e45.	3.2	162
12	Integrative Modeling of eQTLs and Cis-Regulatory Elements Suggests Mechanisms Underlying Cell Type Specificity of eQTLs. <i>PLoS Genetics</i> , 2013, 9, e1003649.	3.5	151
13	Measuring the predictability of life outcomes with a scientific mass collaboration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8398-8403.	7.1	142
14	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. <i>Genome Research</i> , 2017, 27, 1843-1858.	5.5	139
15	Analysis of Population Structure: A Unifying Framework and Novel Methods Based on Sparse Factor Analysis. <i>PLoS Genetics</i> , 2010, 6, e1001117.	3.5	123
16	Clustering gene expression time series data using an infinite Gaussian process mixture model. <i>PLoS Computational Biology</i> , 2018, 14, e1005896.	3.2	123
17	GPCR-specific autoantibody signatures are associated with physiological and pathological immune homeostasis. <i>Nature Communications</i> , 2018, 9, 5224.	12.8	116
18	Glucocorticoid receptor recruits to enhancers and drives activation by motif-directed binding. <i>Genome Research</i> , 2018, 28, 1272-1284.	5.5	102

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19	Genome-Wide Association Study of d-Amphetamine Response in Healthy Volunteers Identifies Putative Associations, Including Cadherin 13 (CDH13). PLoS ONE, 2012, 7, e42646.	2.5	74
20	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	8.8	68
21	netNMF-sc: leveraging gene-gene interactions for imputation and dimensionality reduction in single-cell expression analysis. Genome Research, 2020, 30, 195-204.	5.5	61
22	Detecting differential growth of microbial populations with Gaussian process regression. Genome Research, 2017, 27, 320-333.	5.5	55
23	Genome-scale phylogenetic function annotation of large and diverse protein families. Genome Research, 2011, 21, 1969-1980.	5.5	54
24	Stability selection for regression-based models of transcription factor-DNA binding specificity. Bioinformatics, 2013, 29, i117-i125.	4.1	53
25	Context Specific and Differential Gene Co-expression Networks via Bayesian Biclustering. PLoS Computational Biology, 2016, 12, e1004791.	3.2	46
26	Joint analysis of expression levels and histological images identifies genes associated with tissue morphology. Nature Communications, 2021, 12, 1609.	12.8	45
27	Optimal marker gene selection for cell type discrimination in single cell analyses. Nature Communications, 2021, 12, 1186.	12.8	43
28	Statistical tests for detecting variance effects in quantitative trait studies. Bioinformatics, 2019, 35, 200-210.	4.1	28
29	Sparse multi-output Gaussian processes for online medical time series prediction. BMC Medical Informatics and Decision Making, 2020, 20, 152.	3.0	26
30	Causal network inference from gene transcriptional time-series response to glucocorticoids. PLoS Computational Biology, 2021, 17, e1008223.	3.2	20
31	Genetic variation associated with euphorogenic effects of d-amphetamine is associated with diminished risk for schizophrenia and attention deficit hyperactivity disorder. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5968-5973.	7.1	18
32	Phylogenetic molecular function annotation. Journal of Physics: Conference Series, 2009, 180, 012024.	0.4	12
33	A robust nonlinear low-dimensional manifold for single cell RNA-seq data. BMC Bioinformatics, 2020, 21, 324.	2.6	12
34	ACE inhibition and cardiometabolic risk factors, lung ACE2 and TMPRSS2 gene expression, and plasma ACE2 levels: a Mendelian randomization study. Royal Society Open Science, 2020, 7, 200958.	2.4	12
35	Posterior predictive checks to quantify lack-of-fit in admixture models of latent population structure. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3441-50.	7.1	11
36	Expandable factor analysis. Biometrika, 2017, 104, 649-663.	2.4	10

#	ARTICLE	IF	CITATIONS
37	Bayesian nonparametric discovery of isoforms and individual specific quantification. Nature Communications, 2018, 9, 1681.	12.8	8
38	An Optimal Policy for Patient Laboratory Tests in Intensive Care Units. , 2018, , .		8
39	Molecular function prediction for a family exhibiting evolutionary tendencies toward substrate specificity swapping: Recurrence of tyrosine aminotransferase activity in the Î± subfamily. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1593-1609.	2.6	6
40	Mangravite et al. reply. Nature, 2014, 513, E3-E3.	27.8	4
41	Diving deeper to predict noncoding sequence function. Nature Methods, 2015, 12, 925-926.	19.0	4
42	A self-exciting point process to study multicellular spatial signaling patterns. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	4
43	Nonparametric Bayesian multiarmed bandits for single-cell experiment design. Annals of Applied Statistics, 2020, 14, .	1.1	4
44	Guiding Efficient, Effective, and Patient-Oriented Electrolyte Replacement in Critical Care: An Artificial Intelligence Reinforcement Learning Approach. Journal of Personalized Medicine, 2022, 12, 661.	2.5	2
45	Towards "end-to-end"™ analysis and understanding of biological timecourse data. Biochemical Journal, 2022, 479, 1257-1263.	3.7	2
46	Fast Moment Estimation for Generalized Latent Dirichlet Models. Journal of the American Statistical Association, 2018, 113, 1528-1540.	3.1	1
47	Brain kernel: A new spatial covariance function for fMRI data. NeuroImage, 2021, 245, 118580.	4.2	1
48	Hierarchical Gaussian Processes and Mixtures of Experts to Model COVID-19 Patient Trajectories. , 2021, , .		0