Barbara Elizabeth Engelhardt

List of Publications by Year
in descending order

48 papers	10,632 citations	230014 27 h-index	263392 45 g-index
66 all docs	66 docs citations	66 times ranked	24888 citing authors

#	Article	IF	Citations
1	Guiding Efficient, Effective, and Patient-Oriented Electrolyte Replacement in Critical Care: An Artificial Intelligence Reinforcement Learning Approach. Journal of Personalized Medicine, 2022, 12, 661.	1.1	2
2	Towards 'end-to-end' analysis and understanding of biological timecourse data. Biochemical Journal, 2022, 479, 1257-1263.	1.7	2
3	Causal network inference from gene transcriptional time-series response to glucocorticoids. PLoS Computational Biology, 2021, 17, e1008223.	1.5	20
4	Optimal marker gene selection for cell type discrimination in single cell analyses. Nature Communications, 2021, 12, 1186.	5.8	43
5	Joint analysis of expression levels and histological images identifies genes associated with tissue morphology. Nature Communications, 2021, 12, 1609.	5.8	45
6	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, .	3.3	4
7	Brain kernel: A new spatial covariance function for fMRI data. NeuroImage, 2021, 245, 118580.	2.1	1
8	Hierarchical Gaussian Processes and Mixtures of Experts to Model COVID-19 Patient Trajectories. , 2021, , .		0
9	A robust nonlinear low-dimensional manifold for single cell RNA-seq data. BMC Bioinformatics, 2020, 21, 324.	1.2	12
10	The GTEx Consortium atlas of genetic regulatory effects across human tissues. Science, 2020, 369, 1318-1330.	6.0	2,385
11	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	6.0	329
12	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	3.8	68
13	Measuring the predictability of life outcomes with a scientific mass collaboration. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 8398-8403.	3.3	142
14	Sparse multi-output Gaussian processes for online medical time series prediction. BMC Medical Informatics and Decision Making, 2020, 20, 152.	1.5	26
15	netNMF-sc: leveraging gene–gene interactions for imputation and dimensionality reduction in single-cell expression analysis. Genome Research, 2020, 30, 195-204.	2.4	61
16	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	13.5	334
17	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.	1.1	12
18	Nonparametric Bayesian multiarmed bandits for single-cell experiment design. Annals of Applied Statistics, 2020, 14, .	0.5	4

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19	Statistical tests for detecting variance effects in quantitative trait studies. Bioinformatics, 2019, 35, 200-210.	1.8	28
20	Bayesian nonparametric discovery of isoforms and individual specific quantification. Nature Communications, 2018, 9, 1681.	5.8	8
21	Fast Moment Estimation for Generalized Latent Dirichlet Models. Journal of the American Statistical Association, 2018, 113, 1528-1540.	1.8	1
22	GPCR-specific autoantibody signatures are associated with physiological and pathological immune homeostasis. Nature Communications, 2018, 9, 5224.	5.8	116
23	Glucocorticoid receptor recruits to enhancers and drives activation by motif-directed binding. Genome Research, 2018, 28, 1272-1284.	2.4	102
24	Clustering gene expression time series data using an infinite Gaussian process mixture model. PLoS Computational Biology, 2018, 14, e1005896.	1.5	123
25	An Optimal Policy for Patient Laboratory Tests in Intensive Care Units. , 2018, , .		8
26	Computational approaches to fMRI analysis. Nature Neuroscience, 2017, 20, 304-313.	7.1	185
27	Genetic effects on gene expression across human tissues. Nature, 2017, 550, 204-213.	13.7	3,500
28	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. Genome Research, 2017, 27, 1843-1858.	2.4	139
29	Detecting differential growth of microbial populations with Gaussian process regression. Genome Research, 2017, 27, 320-333.	2.4	55
30	Expandable factor analysis. Biometrika, 2017, 104, 649-663.	1.3	10
31	Context Specific and Differential Gene Co-expression Networks via Bayesian Biclustering. PLoS Computational Biology, 2016, 12, e1004791.	1.5	46
32	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. Behavior Genetics, 2016, 46, 170-182.	1.4	178
33	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. JAMA Psychiatry, 2015, 72, 642.	6.0	289
34	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.	3.3	11
35	Predicting genome-wide DNA methylation using methylation marks, genomic position, and DNA regulatory elements. Genome Biology, 2015, 16, 14.	3.8	165
36	Diving deeper to predict noncoding sequence function. Nature Methods, 2015, 12, 925-926.	9.0	4

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37	Mangravite et al. reply. Nature, 2014, 513, E3-E3.	13.7	4
38	Genetic variation associated with euphorigenic effects of <i>d</i> -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.	3.3	18
39	A statin-dependent QTL for GATM expression is associated with statin-induced myopathy. Nature, 2013, 502, 377-380.	13.7	197
40	Stability selection for regression-based models of transcription factorâ€"DNA binding specificity. Bioinformatics, 2013, 29, i117-i125.	1.8	53
41	Integrative Modeling of eQTLs and Cis-Regulatory Elements Suggests Mechanisms Underlying Cell Type Specificity of eQTLs. PLoS Genetics, 2013, 9, e1003649.	1.5	151
42	Molecular function prediction for a family exhibiting evolutionary tendencies toward substrate specificity swapping: Recurrence of tyrosine aminotransferase activity in the Iα subfamily. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1593-1609.	1.5	6
43	Genome-Wide Association Study of d-Amphetamine Response in Healthy Volunteers Identifies Putative Associations, Including Cadherin 13 (CDH13). PLoS ONE, 2012, 7, e42646.	1.1	74
44	Genome-scale phylogenetic function annotation of large and diverse protein families. Genome Research, 2011, 21, 1969-1980.	2.4	54
45	Understanding mechanisms underlying human gene expression variation with RNA sequencing. Nature, 2010, 464, 768-772.	13.7	1,200
46	Analysis of Population Structure: A Unifying Framework and Novel Methods Based on Sparse Factor Analysis. PLoS Genetics, 2010, 6, e1001117.	1.5	123
47	Phylogenetic molecular function annotation. Journal of Physics: Conference Series, 2009, 180, 012024.	0.3	12
48	Protein Molecular Function Prediction by Bayesian Phylogenomics. PLoS Computational Biology, 2005, 1, e45.	1.5	162