

Gaurav Pandey

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

3,746
citations

304743

22
h-index

395702

33
g-index

48
all docs

48
docs citations

48
times ranked

8158
citing authors

#	ARTICLE	IF	CITATIONS
1	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	19.0	789
2	Deciphering the transcriptional network of the dendritic cell lineage. <i>Nature Immunology</i> , 2012, 13, 888-899.	14.5	688
3	Endothelial to mesenchymal transition is common in atherosclerotic lesions and is associated with plaque instability. <i>Nature Communications</i> , 2016, 7, 11853.	12.8	406
4	Evaluation of Combined Artificial Intelligence and Radiologist Assessment to Interpret Screening Mammograms. <i>JAMA Network Open</i> , 2020, 3, e200265.	5.9	236
5	Analysis of Transcriptional Variability in a Large Human iPSC Library Reveals Genetic and Non-genetic Determinants of Heterogeneity. <i>Cell Stem Cell</i> , 2017, 20, 518-532.e9.	11.1	230
6	Clinical features of COVID-19 mortality: development and validation of a clinical prediction model. <i>The Lancet Digital Health</i> , 2020, 2, e516-e525.	12.3	218
7	Enhancing data analysis with noise removal. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2006, 18, 304-319.	5.7	163
8	Microbiota regulate the ability of lung dendritic cells to induce IgA class-switch recombination and generate protective gastrointestinal immune responses. <i>Journal of Experimental Medicine</i> , 2016, 213, 53-73.	8.5	94
9	Improving Breast Cancer Survival Analysis through Competition-Based Multidimensional Modeling. <i>PLoS Computational Biology</i> , 2013, 9, e1003047.	3.2	76
10	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. <i>Nature Communications</i> , 2016, 7, 12460.	12.8	73
11	Radiogenomics Consortium Genome-Wide Association Study Meta-Analysis of Late Toxicity After Prostate Cancer Radiotherapy. <i>Journal of the National Cancer Institute</i> , 2020, 112, 179-190.	6.3	71
12	An Integrative Multi-Network and Multi-Classifer Approach to Predict Genetic Interactions. <i>PLoS Computational Biology</i> , 2010, 6, e1000928.	3.2	69
13	Incorporating functional inter-relationships into protein function prediction algorithms. <i>BMC Bioinformatics</i> , 2009, 10, 142.	2.6	68
14	Objective risk stratification of prostate cancer using machine learning and radiomics applied to multiparametric magnetic resonance images. <i>Scientific Reports</i> , 2019, 9, 1570.	3.3	60
15	Breast Imaging in the Era of Big Data: Structured Reporting and Data Mining. <i>American Journal of Roentgenology</i> , 2016, 206, 259-264.	2.2	51
16	A Nasal Brush-based Classifier of Asthma Identified by Machine Learning Analysis of Nasal RNA Sequence Data. <i>Scientific Reports</i> , 2018, 8, 8826.	3.3	51
17	Using machine learning to identify air pollution exposure profiles associated with early cognitive skills among U.S. children. <i>Environmental Pollution</i> , 2017, 230, 730-740.	7.5	44
18	MetaClean: a machine learning-based classifier for reduced false positive peak detection in untargeted LC-MS metabolomics data. <i>Metabolomics</i> , 2020, 16, 117.	3.0	36

#	ARTICLE	IF	CITATIONS
19	Mining Low-Support Discriminative Patterns from Dense and High-Dimensional Data. IEEE Transactions on Knowledge and Data Engineering, 2012, 24, 279-294.	5.7	33
20	Radiation Therapy Outcomes Models in the Era of Radiomics and Radiogenomics: Uncertainties and Validation. International Journal of Radiation Oncology Biology Physics, 2018, 102, 1070-1073.	0.8	31
21	Prediction of Genetic Interactions Using Machine Learning and Network Properties. Frontiers in Bioengineering and Biotechnology, 2015, 3, 172.	4.1	26
22	Predicting protein function and other biomedical characteristics with heterogeneous ensembles. Methods, 2016, 93, 92-102.	3.8	25
23	Predicting submicron air pollution indicators: a machine learning approach. Environmental Sciences: Processes and Impacts, 2013, 15, 996.	3.5	24
24	A Comparative Analysis of Ensemble Classifiers: Case Studies in Genomics. , 2013, , .		23
25	Pharmacological Silencing of MicroRNA-152 Prevents Pressure Overload-Induced Heart Failure. Circulation: Heart Failure, 2020, 13, e006298.	3.9	15
26	Association Rules Network: Definition and Applications. Statistical Analysis and Data Mining, 2009, 1, 260-279.	2.8	14
27	Decoding dendritic cell function through module and network analysis. Journal of Immunological Methods, 2013, 387, 71-80.	1.4	14
28	A crowdsourced analysis to identify ab initio molecular signatures predictive of susceptibility to viral infection. Nature Communications, 2018, 9, 4418.	12.8	14
29	Predicting youth diabetes risk using NHANES data and machine learning. Scientific Reports, 2021, 11, 11212.	3.3	13
30	NeTFactor, a framework for identifying transcriptional regulators of gene expression-based biomarkers. Scientific Reports, 2019, 9, 12970.	3.3	12
31	Large-scale protein function prediction using heterogeneous ensembles. F1000Research, 2018, 7, 1577.	1.6	12
32	Machine learning-driven identification of early-life air toxic combinations associated with childhood asthma outcomes. Journal of Clinical Investigation, 2021, 131, .	8.2	9
33	LEARNING PARSIMONIOUS ENSEMBLES FOR UNBALANCED COMPUTATIONAL GENOMICS PROBLEMS. , 2017, 22, 288-299.		7
34	Association Analysis Techniques for Discovering Functional Modules from Microarray Data. Nature Precedings, 0, , .	0.1	5
35	Assessing computational predictions of the phenotypic effect of cystathionine-beta-synthase variants. Human Mutation, 2019, 40, 1530-1545.	2.5	5
36	Objective risk stratification of prostate cancer using machine learning and radiomics applied to multiparametric magnetic resonance images. , 2020, , .		5

#	ARTICLE	IF	CITATIONS
37	Enhancing the Functional Content of Eukaryotic Protein Interaction Networks. PLoS ONE, 2014, 9, e109130.	2.5	4
38	Association Analysis Techniques for Discovering Functional Modules from Microarray Data. Nature Precedings, 0, , .	0.1	2
39	Systematic Evaluation of Scaling Methods for Gene Expression Data. , 2008, , .		1
40	Association analysis techniques for analyzing complex biological data sets. , 2009, , .		1
41	Computational performance of heterogeneous ensemble frameworks on high-performance computing platforms. , 2020, , .		0