# Gaurav Pandey

List of Publications by Year
in descending order

| 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 | Predicting youth diabetes risk using NHANES data and machine learning. Scientific Reports, 2021, 11, 11212. | 3.3 | 13 |
| 2 | Machine learning–driven identification of early-life air toxic combinations associated with childhood asthma outcomes. Journal of Clinical Investigation, 2021, 131, . | 8.2 | 9 |
| 3 | Radiogenomics Consortium Genome-Wide Association Study Meta-Analysis of Late Toxicity After Prostate Cancer Radiotherapy. Journal of the National Cancer Institute, 2020, 112, 179-190. | 6.3 | 71 |
| 4 | Clinical features of COVID-19 mortality: development and validation of a clinical prediction model. The Lancet Digital Health, 2020, 2, e516-e525. | 12.3 | 218 |
| 5 | MetaClean: a machine learning-based classifier for reduced false positive peak detection in untargeted LC–MS metabolomics data. Metabolomics, 2020, 16, 117. | 3.0 | 36 |
| 6 | Pharmacological Silencing of MicroRNA-152 Prevents Pressure Overload–Induced Heart Failure. Circulation: Heart Failure, 2020, 13, e006298. | 3.9 | 15 |
| 7 | Evaluation of Combined Artificial Intelligence and Radiologist Assessment to Interpret Screening Mammograms. JAMA Network Open, 2020, 3, e200265. | 5.9 | 236 |
| 8 | Computational performance of heterogeneous ensemble frameworks on high-performance computing platforms. , 2020, , . | | 0 |
| 9 | Objective risk stratification of prostate cancer using machine learning and radiomics applied to multiparametric magnetic resonance images. , 2020, , . | | 5 |
| 10 | Assessing computational predictions of the phenotypic effect of cystathionine–beta–synthase variants. Human Mutation, 2019, 40, 1530-1545. | 2.5 | 5 |
| 11 | NeTFactor, a framework for identifying transcriptional regulators of gene expression-based biomarkers. Scientific Reports, 2019, 9, 12970. | 3.3 | 12 |
| 12 | Objective risk stratification of prostate cancer using machine learning and radiomics applied to multiparametric magnetic resonance images. Scientific Reports, 2019, 9, 1570. | 3.3 | 60 |
| 13 | 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 |
| 14 | A crowdsourced analysis to identify ab initio molecular signatures predictive of susceptibility to viral infection. Nature Communications, 2018, 9, 4418. | 12.8 | 14 |
| 15 | A Nasal Brush-based Classifier of Asthma Identified by Machine Learning Analysis of Nasal RNA Sequence Data. Scientific Reports, 2018, 8, 8826. | 3.3 | 51 |
| 16 | Large-scale protein function prediction using heterogeneous ensembles. F1000Research, 2018, 7, 1577. | 1.6 | 12 |
| 17 | Analysis of Transcriptional Variability in a Large Human iPSC Library Reveals Genetic and Non-genetic Determinants of Heterogeneity. Cell Stem Cell, 2017, 20, 518-532.e9. | 11.1 | 230 |
| 18 | Using machine learning to identify air pollution exposure profiles associated with early cognitive skills among U.S. children. Environmental Pollution, 2017, 230, 730-740. | 7.5 | 44 |

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|---|---------|-----|-----------|
| 19 | LEARNING PARSIMONIOUS ENSEMBLES FOR UNBALANCED COMPUTATIONAL GENOMICS PROBLEMS. , 2017, 22, 288-299. | | 7 |
| 20 | Endothelial to mesenchymal transition is common in atherosclerotic lesions and is associated with plaque instability. Nature Communications, 2016, 7, 11853. | 12.8 | 406 |
| 21 | Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. Nature Communications, 2016, 7, 12460. | 12.8 | 73 |
| 22 | Microbiota regulate the ability of lung dendritic cells to induce IgA class-switch recombination and generate protective gastrointestinal immune responses. Journal of Experimental Medicine, 2016, 213, 53-73. | 8.5 | 94 |
| 23 | Breast Imaging in the Era of Big Data: Structured Reporting and Data Mining. American Journal of Roentgenology, 2016, 206, 259-264. | 2.2 | 51 |
| 24 | Predicting protein function and other biomedical characteristics with heterogeneous ensembles. Methods, 2016, 93, 92-102. | 3.8 | 25 |
| 25 | Prediction of Genetic Interactions Using Machine Learning and Network Properties. Frontiers in Bioengineering and Biotechnology, 2015, 3, 172. | 4.1 | 26 |
| 26 | Enhancing the Functional Content of Eukaryotic Protein Interaction Networks. PLoS ONE, 2014, 9, e109130. | 2.5 | 4 |
| 27 | A Comparative Analysis of Ensemble Classifiers: Case Studies in Genomics. , 2013, , . | | 23 |
| 28 | Predicting submicron air pollution indicators: a machine learning approach. Environmental Sciences: Processes and Impacts, 2013, 15, 996. | 3.5 | 24 |
| 29 | A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227. | 19.0 | 789 |
| 30 | Decoding dendritic cell function through module and network analysis. Journal of Immunological Methods, 2013, 387, 71-80. | 1.4 | 14 |
| 31 | Improving Breast Cancer Survival Analysis through Competition-Based Multidimensional Modeling. PLoS Computational Biology, 2013, 9, e1003047. | 3.2 | 76 |
| 32 | 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 |
| 33 | Deciphering the transcriptional network of the dendritic cell lineage. Nature Immunology, 2012, 13, 888-899. | 14.5 | 688 |
| 34 | An Integrative Multi-Network and Multi-Classifier Approach to Predict Genetic Interactions. PLoS Computational Biology, 2010, 6, e1000928. | 3.2 | 69 |
| 35 | Incorporating functional inter-relationships into protein function prediction algorithms. BMC Bioinformatics, 2009, 10, 142. | 2.6 | 68 |
| 36 | Association Rules Network: Definition and Applications. Statistical Analysis and Data Mining, 2009, 1, 260-279. | 2.8 | 14 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 37 | Association analysis techniques for analyzing complex biological data sets. , 2009, , . | | 1 |
| 38 | Systematic Evaluation of Scaling Methods for Gene Expression Data. , 2008, , . | | 1 |
| 39 | Enhancing data analysis with noise removal. IEEE Transactions on Knowledge and Data Engineering, 2006, 18, 304-319. | 5.7 | 163 |
| 40 | Association Analysis Techniques for Discovering Functional Modules from Microarray Data. Nature Precedings, 0, , . | 0.1 | 5 |
| 41 | Association Analysis Techniques for Discovering Functional Modules from Microarray Data. Nature Precedings, 0, , . | 0.1 | 2 |