

Francesca Luca

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

3,631
citations

236925

25
h-index

189892

50
g-index

77
all docs

77
docs citations

77
times ranked

6567
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Analyzing and reconciling colocalization and transcriptome-wide association studies from the perspective of inferential reproducibility. <i>American Journal of Human Genetics</i> , 2022, 109, 825-837. | 6.2 | 17 |
| 2 | Probabilistic colocalization of genetic variants from complex and molecular traits: promise and limitations. <i>American Journal of Human Genetics</i> , 2021, 108, 25-35. | 6.2 | 67 |
| 3 | Functional dynamic genetic effects on gene regulation are specific to particular cell types and environmental conditions. <i>ELife</i> , 2021, 10, . | 6.0 | 41 |
| 4 | Psychosocial experiences modulate asthma-associated genes through gene-environment interactions. <i>ELife</i> , 2021, 10, . | 6.0 | 15 |
| 5 | Socioeconomic status, financial stress, and glucocorticoid resistance among youth with asthma: Testing the moderation effects of maternal involvement and warmth. <i>Brain, Behavior, and Immunity</i> , 2021, 96, 92-99. | 4.1 | 6 |
| 6 | A signature of Neanderthal introgression on molecular mechanisms of environmental responses. <i>PLoS Genetics</i> , 2021, 17, e1009493. | 3.5 | 5 |
| 7 | Interspecies variation in hominid gut microbiota controls host gene regulation. <i>Cell Reports</i> , 2021, 37, 110057. | 6.4 | 9 |
| 8 | BAGSE: a Bayesian hierarchical model approach for gene set enrichment analysis. <i>Bioinformatics</i> , 2020, 36, 1689-1695. | 4.1 | 7 |
| 9 | PTWAS: investigating tissue-relevant causal molecular mechanisms of complex traits using probabilistic TWAS analysis. <i>Genome Biology</i> , 2020, 21, 232. | 8.8 | 46 |
| 10 | Derangement of Metabolic and Lysosomal Gene Profiles in Response to Dexamethasone Treatment in Sarcoidosis. <i>Frontiers in Immunology</i> , 2020, 11, 779. | 4.8 | 5 |
| 11 | Does the human placenta express the canonical cell entry mediators for SARS-CoV-2?. <i>ELife</i> , 2020, 9, . | 6.0 | 222 |
| 12 | Differentially expressed gene networks, biomarkers, long noncoding RNAs, and shared responses with cocaine identified in the midbrains of human opioid abusers. <i>Scientific Reports</i> , 2019, 9, 1534. | 3.3 | 33 |
| 13 | Interpreting Coronary Artery Disease Risk Through Gene-Environment Interactions in Gene Regulation. <i>Genetics</i> , 2019, 213, 651-663. | 2.9 | 20 |
| 14 | Gut Microbiota Has a Widespread and Modifiable Effect on Host Gene Regulation. <i>MSystems</i> , 2019, 4, . | 3.8 | 74 |
| 15 | Environmental influences on RNA processing: Biochemical, molecular and genetic regulators of cellular response. <i>Wiley Interdisciplinary Reviews RNA</i> , 2019, 10, e1503. | 6.4 | 31 |
| 16 | Self-Disclosure and Perceived Responsiveness Among Youth With Asthma: Links to Affect and Anti-Inflammatory Gene Expression. <i>Personality and Social Psychology Bulletin</i> , 2019, 45, 1155-1169. | 3.0 | 9 |
| 17 | Single cell transcriptional signatures of the human placenta in term and preterm parturition. <i>ELife</i> , 2019, 8, . | 6.0 | 216 |
| 18 | Socioeconomic status, family negative emotional climate, and anti-inflammatory gene expression among youth with asthma. <i>Psychoneuroendocrinology</i> , 2018, 91, 62-67. | 2.7 | 23 |

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|----|---|------|-----------|
| 19 | Functional Genomics of Host-Microbiome Interactions in Humans. <i>Trends in Genetics</i> , 2018, 34, 30-40. | 6.7 | 73 |
| 20 | QuASAR-MPRA: accurate allele-specific analysis for massively parallel reporter assays. <i>Bioinformatics</i> , 2018, 34, 787-794. | 4.1 | 28 |
| 21 | A hypermorphic antioxidant response element is associated with increased MS4A6A expression and Alzheimer's disease. <i>Redox Biology</i> , 2018, 14, 686-693. | 9.0 | 21 |
| 22 | High-throughput characterization of genetic effects on DNA-protein binding and gene transcription. <i>Genome Research</i> , 2018, 28, 1701-1708. | 5.5 | 34 |
| 23 | Mothers' Attachment is Linked to Their Children's Anti-Inflammatory Gene Expression via Maternal Warmth. <i>Social Psychological and Personality Science</i> , 2017, 8, 796-805. | 3.9 | 19 |
| 24 | RNA-sequencing Identifies Novel Pathways in Sarcoidosis Monocytes. <i>Scientific Reports</i> , 2017, 7, 2720. | 3.3 | 28 |
| 25 | Environmental perturbations lead to extensive directional shifts in RNA processing. <i>PLoS Genetics</i> , 2017, 13, e1006995. | 3.5 | 25 |
| 26 | Integrating molecular QTL data into genome-wide genetic association analysis: Probabilistic assessment of enrichment and colocalization. <i>PLoS Genetics</i> , 2017, 13, e1006646. | 3.5 | 205 |
| 27 | Which Genetics Variants in DNase-Seq Footprints Are More Likely to Alter Binding?. <i>PLoS Genetics</i> , 2016, 12, e1005875. | 3.5 | 56 |
| 28 | Efficient Integrative Multi-SNP Association Analysis via Deterministic Approximation of Posteriors. <i>American Journal of Human Genetics</i> , 2016, 98, 1114-1129. | 6.2 | 147 |
| 29 | Genetic and Transcriptional Analysis of Human Host Response to Healthy Gut Microbiota. <i>MSystems</i> , 2016, 1, . | 3.8 | 28 |
| 30 | High-throughput allele-specific expression across 250 environmental conditions. <i>Genome Research</i> , 2016, 26, 1627-1638. | 5.5 | 138 |
| 31 | Genetic Ancestry and Natural Selection Drive Population Differences in Immune Responses to Pathogens. <i>Cell</i> , 2016, 167, 657-669.e21. | 28.9 | 419 |
| 32 | A high-throughput RNA-seq approach to profile transcriptional responses. <i>Scientific Reports</i> , 2015, 5, 14976. | 3.3 | 22 |
| 33 | Cross-Population Joint Analysis of eQTLs: Fine Mapping and Functional Annotation. <i>PLoS Genetics</i> , 2015, 11, e1005176. | 3.5 | 93 |
| 34 | Bacterial infection remodels the DNA methylation landscape of human dendritic cells. <i>Genome Research</i> , 2015, 25, 1801-1811. | 5.5 | 195 |
| 35 | QuASAR: quantitative allele-specific analysis of reads. <i>Bioinformatics</i> , 2015, 31, 1235-1242. | 4.1 | 70 |
| 36 | Genetic, Functional and Molecular Features of Glucocorticoid Receptor Binding. <i>PLoS ONE</i> , 2013, 8, e61654. | 2.5 | 23 |

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|----|--|------|-----------|
| 37 | Incomplete Lineage Sorting Is Common in Extant Gibbon Genera. <i>PLoS ONE</i> , 2013, 8, e53682. | 2.5 | 19 |
| 38 | Allelic Imbalance Assays to Quantify Allele-Specific Gene Expression and Transcription Factor Binding. <i>Methods in Molecular Biology</i> , 2013, 1015, 201-211. | 0.9 | 0 |
| 39 | Mapping gene-environment interactions at regulatory polymorphisms: Insights into mechanisms of phenotypic variation. <i>Transcription</i> , 2012, 3, 56-62. | 3.1 | 13 |
| 40 | A reduced representation approach to population genetic analyses and applications to human evolution. <i>Genome Research</i> , 2011, 21, 1087-1098. | 5.5 | 56 |
| 41 | Interactions between Glucocorticoid Treatment and Cis-Regulatory Polymorphisms Contribute to Cellular Response Phenotypes. <i>PLoS Genetics</i> , 2011, 7, e1002162. | 3.5 | 103 |
| 42 | Evolutionary Adaptations to Dietary Changes. <i>Annual Review of Nutrition</i> , 2010, 30, 291-314. | 10.1 | 175 |
| 43 | Adaptive Variation Regulates the Expression of the Human SGK1 Gene in Response to Stress. <i>PLoS Genetics</i> , 2009, 5, e1000489. | 3.5 | 43 |
| 44 | Maternal traces of deep common ancestry and asymmetric gene flow between Pygmy hunter-gatherers and Bantu-speaking farmers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1596-1601. | 7.1 | 157 |
| 45 | The Timing of Selection at the Human FOXP2 Gene. <i>Molecular Biology and Evolution</i> , 2008, 25, 1257-1259. | 8.9 | 132 |
| 46 | Multiple Advantageous Amino Acid Variants in the NAT2 Gene in Human Populations. <i>PLoS ONE</i> , 2008, 3, e3136. | 2.5 | 50 |
| 47 | Y-chromosomal variation in the Czech Republic. <i>American Journal of Physical Anthropology</i> , 2007, 132, 132-139. | 2.1 | 19 |
| 48 | Deciphering the Ancient and Complex Evolutionary History of Human Arylamine N-Acetyltransferase Genes. <i>American Journal of Human Genetics</i> , 2006, 78, 423-436. | 6.2 | 127 |
| 49 | Independent methods for evolutionary genetic dating provide insights into Y-chromosomal STR mutation rates confirming data from direct father-son transmissions. <i>Human Genetics</i> , 2005, 118, 153-165. | 3.8 | 4 |
| 50 | Y chromosomal haplogroup J as a signature of the post-neolithic colonization of Europe. <i>Human Genetics</i> , 2004, 115, 357-371. | 3.8 | 104 |
| 51 | Clinal patterns of human Y chromosomal diversity in continental Italy and Greece are dominated by drift and founder effects. <i>Molecular Phylogenetics and Evolution</i> , 2003, 28, 387-395. | 2.7 | 55 |