

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	Genetic Ancestry and Natural Selection Drive Population Differences in Immune Responses to Pathogens. <i>Cell</i> , 2016, 167, 657-669.e21.	28.9	419
2	Does the human placenta express the canonical cell entry mediators for SARS-CoV-2?. <i>ELife</i> , 2020, 9, .	6.0	222
3	Single cell transcriptional signatures of the human placenta in term and preterm parturition. <i>ELife</i> , 2019, 8, .	6.0	216
4	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
5	Bacterial infection remodels the DNA methylation landscape of human dendritic cells. <i>Genome Research</i> , 2015, 25, 1801-1811.	5.5	195
6	Evolutionary Adaptations to Dietary Changes. <i>Annual Review of Nutrition</i> , 2010, 30, 291-314.	10.1	175
7	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
8	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
9	High-throughput allele-specific expression across 250 environmental conditions. <i>Genome Research</i> , 2016, 26, 1627-1638.	5.5	138
10	The Timing of Selection at the Human FOXP2 Gene. <i>Molecular Biology and Evolution</i> , 2008, 25, 1257-1259.	8.9	132
11	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
12	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
13	Interactions between Glucocorticoid Treatment and Cis-Regulatory Polymorphisms Contribute to Cellular Response Phenotypes. <i>PLoS Genetics</i> , 2011, 7, e1002162.	3.5	103
14	Cross-Population Joint Analysis of eQTLs: Fine Mapping and Functional Annotation. <i>PLoS Genetics</i> , 2015, 11, e1005176.	3.5	93
15	Gut Microbiota Has a Widespread and Modifiable Effect on Host Gene Regulation. <i>MSystems</i> , 2019, 4, .	3.8	74
16	Functional Genomics of Host-Microbiome Interactions in Humans. <i>Trends in Genetics</i> , 2018, 34, 30-40.	6.7	73
17	QuASAR: quantitative allele-specific analysis of reads. <i>Bioinformatics</i> , 2015, 31, 1235-1242.	4.1	70
18	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

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19	A reduced representation approach to population genetic analyses and applications to human evolution. <i>Genome Research</i> , 2011, 21, 1087-1098.	5.5	56
20	Which Genetics Variants in DNase-Seq Footprints Are More Likely to Alter Binding?. <i>PLoS Genetics</i> , 2016, 12, e1005875.	3.5	56
21	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
22	Multiple Advantageous Amino Acid Variants in the NAT2 Gene in Human Populations. <i>PLoS ONE</i> , 2008, 3, e3136.	2.5	50
23	PTWAS: investigating tissue-relevant causal molecular mechanisms of complex traits using probabilistic TWAS analysis. <i>Genome Biology</i> , 2020, 21, 232.	8.8	46
24	Adaptive Variation Regulates the Expression of the Human SGK1 Gene in Response to Stress. <i>PLoS Genetics</i> , 2009, 5, e1000489.	3.5	43
25	Functional dynamic genetic effects on gene regulation are specific to particular cell types and environmental conditions. <i>ELife</i> , 2021, 10, .	6.0	41
26	High-throughput characterization of genetic effects on DNA-protein binding and gene transcription. <i>Genome Research</i> , 2018, 28, 1701-1708.	5.5	34
27	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
28	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
29	Genetic and Transcriptional Analysis of Human Host Response to Healthy Gut Microbiota. <i>MSystems</i> , 2016, 1, .	3.8	28
30	RNA-sequencing Identifies Novel Pathways in Sarcoidosis Monocytes. <i>Scientific Reports</i> , 2017, 7, 2720.	3.3	28
31	QuASAR-MPRA: accurate allele-specific analysis for massively parallel reporter assays. <i>Bioinformatics</i> , 2018, 34, 787-794.	4.1	28
32	Environmental perturbations lead to extensive directional shifts in RNA processing. <i>PLoS Genetics</i> , 2017, 13, e1006995.	3.5	25
33	Genetic, Functional and Molecular Features of Glucocorticoid Receptor Binding. <i>PLoS ONE</i> , 2013, 8, e61654.	2.5	23
34	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
35	A high-throughput RNA-seq approach to profile transcriptional responses. <i>Scientific Reports</i> , 2015, 5, 14976.	3.3	22
36	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

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37	Interpreting Coronary Artery Disease Risk Through Gene-Environment Interactions in Gene Regulation. <i>Genetics</i> , 2019, 213, 651-663.	2.9	20
38	Y-chromosomal variation in the Czech Republic. <i>American Journal of Physical Anthropology</i> , 2007, 132, 132-139.	2.1	19
39	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
40	Incomplete Lineage Sorting Is Common in Extant Gibbon Genera. <i>PLoS ONE</i> , 2013, 8, e53682.	2.5	19
41	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
42	Psychosocial experiences modulate asthma-associated genes through gene-environment interactions. <i>ELife</i> , 2021, 10, .	6.0	15
43	Mapping gene-environment interactions at regulatory polymorphisms: Insights into mechanisms of phenotypic variation. <i>Transcription</i> , 2012, 3, 56-62.	3.1	13
44	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
45	Interspecies variation in hominid gut microbiota controls host gene regulation. <i>Cell Reports</i> , 2021, 37, 110057.	6.4	9
46	BAGSE: a Bayesian hierarchical model approach for gene set enrichment analysis. <i>Bioinformatics</i> , 2020, 36, 1689-1695.	4.1	7
47	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
48	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
49	A signature of Neanderthal introgression on molecular mechanisms of environmental responses. <i>PLoS Genetics</i> , 2021, 17, e1009493.	3.5	5
50	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
51	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