

# Alessia Visconti

## List of Publications by Year in descending order

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Version: 2024-02-01

49  
papers

5,047  
citations

331670

21  
h-index

254184

43  
g-index

65  
all docs

65  
docs citations

65  
times ranked

11760  
citing authors

#	ARTICLE	IF	CITATIONS
1	Yoghurt consumption is associated with changes in the composition of the human gut microbiome and metabolome. <i>BMC Microbiology</i> , 2022, 22, 39.	3.3	31
2	Probable delirium is a presenting symptom of COVID-19 in frail, older adults: a cohort study of 322 hospitalised and 535 community-based older adults. <i>Age and Ageing</i> , 2021, 50, 40-48.	1.6	82
3	Cancer and Risk of COVID-19 Through a General Community Survey. <i>Oncologist</i> , 2021, 26, e182-e185.	3.7	61
4	Looking for Sunshine: Genetic Predisposition to Sun Seeking in 265,000 Individuals of European Ancestry. <i>Journal of Investigative Dermatology</i> , 2021, 141, 779-786.	0.7	5
5	Current smoking and COVID-19 risk: results from a population symptom app in over 2.4 million people. <i>Thorax</i> , 2021, 76, 714-722.	5.6	105
6	Ethnic-specific association of amylase gene copy number with adiposity traits in a large Middle Eastern biobank. <i>Npj Genomic Medicine</i> , 2021, 6, 8.	3.8	8
7	Symptom clusters in COVID-19: A potential clinical prediction tool from the COVID Symptom Study app. <i>Science Advances</i> , 2021, 7, .	10.3	115
8	Immune Trait Shifts in Association With Tobacco Smoking: A Study in Healthy Women. <i>Frontiers in Immunology</i> , 2021, 12, 637974.	4.8	18
9	Diagnostic value of cutaneous manifestation of SARS-CoV-2 infection*. <i>British Journal of Dermatology</i> , 2021, 184, 880-887.	1.5	45
10	144 Probable Delirium is A Presenting Symptom of COVID-19 in Frail, Older Adults: A Study of Hospitalised and Community-Based Cohorts. <i>Age and Ageing</i> , 2021, 50, i12-i42.	1.6	0
11	O- and N-Glycosylation of Serum Immunoglobulin A is Associated with IgA Nephropathy and Glomerular Function. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 2455-2465.	6.1	33
12	Rare variant analysis in eczema identifies exonic variants in DUSP1, NOTCH4 and SLC9A4. <i>Nature Communications</i> , 2021, 12, 6618.	12.8	17
13	Accessible data curation and analytics for international-scale citizen science datasets. <i>Scientific Data</i> , 2021, 8, 297.	5.3	18
14	Body site-specific genetic effects influence naevus count distribution in women. <i>Pigment Cell and Melanoma Research</i> , 2020, 33, 326-333.	3.3	15
15	A reference map of potential determinants for the human serum metabolome. <i>Nature</i> , 2020, 588, 135-140.	27.8	230
16	Real-time tracking of self-reported symptoms to predict potential COVID-19. <i>Nature Medicine</i> , 2020, 26, 1037-1040.	30.7	1,173
17	Genetics plays a role in nevi distribution in women. <i>Melanoma Management</i> , 2020, 7, MMT35.	0.5	2
18	Dysregulated Antibody, Natural Killer Cell and Immune Mediator Profiles in Autoimmune Thyroid Diseases. <i>Cells</i> , 2020, 9, 665.	4.1	18

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19	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. <i>Nature Genetics</i> , 2020, 52, 494-504.	21.4	138
20	Self-Reported Symptoms of COVID-19, Including Symptoms Most Predictive of SARS-CoV-2 Infection, Are Heritable. <i>Twin Research and Human Genetics</i> , 2020, 23, 316-321.	0.6	57
21	An Aggressive Clinical Presentation of Familial Leiomyomatosis Associated with a Fumarate Hydratase Gene Variant of Uncertain Clinical Significance. <i>Acta Dermato-Venereologica</i> , 2020, 100, adv00211.	1.3	0
22	Interplay between the human gut microbiome and host metabolism. <i>Nature Communications</i> , 2019, 10, 4505.	12.8	450
23	Polygenic risk for neuropsychiatric disease and vulnerability to abnormal deep grey matter development. <i>Scientific Reports</i> , 2019, 9, 1976.	3.3	13
24	Genome-wide association meta-analysis of individuals of European ancestry identifies new loci explaining a substantial fraction of hair color variation and heritability. <i>Nature Genetics</i> , 2018, 50, 652-656.	21.4	86
25	Deep molecular phenotypes link complex disorders and physiological insult to CpG methylation. <i>Human Molecular Genetics</i> , 2018, 27, 1106-1121.	2.9	30
26	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. <i>Nature Communications</i> , 2018, 9, 4774.	12.8	87
27	Whole genome sequencing association studies of lipids levels. <i>Atherosclerosis</i> , 2018, 275, e102.	0.8	0
28	Conducting metagenomic studies in microbiology and clinical research. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 8629-8646.	3.6	26
29	YAMP: a containerized workflow enabling reproducibility in metagenomics research. <i>GigaScience</i> , 2018, 7, .	6.4	22
30	Genome-wide association study in 176,678 Europeans reveals genetic loci for tanning response to sun exposure. <i>Nature Communications</i> , 2018, 9, 1684.	12.8	80
31	IgA1 Glycosylation Is Heritable in Healthy Twins. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 64-68.	6.1	27
32	PopPANTe: population and pedigree association testing for quantitative data. <i>BMC Genomics</i> , 2017, 18, 150.	2.8	6
33	Acne and Telomere Length: A New Spectrum between Senescence and Apoptosis Pathways. <i>Journal of Investigative Dermatology</i> , 2017, 137, 513-515.	0.7	6
34	Genomic expression differences between cutaneous cells from red hair color individuals and black hair color individuals based on bioinformatic analysis. <i>Oncotarget</i> , 2017, 8, 11589-11599.	1.8	5
35	Investigating the effects of copy number variants on reading and language performance. <i>Journal of Neurodevelopmental Disorders</i> , 2016, 8, 17.	3.1	19
36	Epigenetic associations of type 2 diabetes and BMI in an Arab population. <i>Clinical Epigenetics</i> , 2016, 8, 13.	4.1	110

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37	Systems genetics identifies a convergent gene network for cognition and neurodevelopmental disease. <i>Nature Neuroscience</i> , 2016, 19, 223-232.	14.8	131
38	Prediction and interpretation of the lipophilicity of small peptides. <i>Journal of Computer-Aided Molecular Design</i> , 2015, 29, 361-370.	2.9	5
39	Leveraging additional knowledge to support coherent bicluster discovery in gene expression data. <i>Intelligent Data Analysis</i> , 2014, 18, 837-855.	0.9	8
40	The Block Relevance (BR) analysis supports the dominating effect of solutes hydrogen bond acidity on $\log P$ . <i>European Journal of Pharmaceutical Sciences</i> , 2014, 53, 50-54.	4.0	25
41	CDoT: Optimizing MAP Queries on Trees. <i>Lecture Notes in Computer Science</i> , 2013, , 481-492.	1.3	0
42	Wisdom of crowds for robust gene network inference. <i>Nature Methods</i> , 2012, 9, 796-804.	19.0	1,481
43	Improving biomarker discovering for chemosensitivity prediction using an integrated approach. <i>EMBnet Journal</i> , 2012, 18, 24.	0.6	0
44	Tackling the DREAM Challenge for Gene Regulatory Networks Reverse Engineering. <i>Lecture Notes in Computer Science</i> , 2011, , 372-382.	1.3	1
45	Restructuring the Gene Ontology to emphasise regulative pathways and to improve gene similarity queries. <i>International Journal of Computational Biology and Drug Design</i> , 2011, 4, 220.	0.3	1
46	A Modular Database Architecture Enabled to Comparative Sequence Analysis. <i>Lecture Notes in Computer Science</i> , 2011, , 124-147.	1.3	0
47	Gene Ontology Rewritten for Computing Gene Functional Similarity. , 2010, , .		1
48	A new protein motif extraction framework based on constrained co-clustering. , 2009, , .		4
49	Real-time tracking of self-reported symptoms to predict potential COVID-19. , 0, .		1