

Eleni Giannoulatou

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

83
papers

7,608
citations

30
h-index

87
g-index

91
ext. papers

9,207
ext. citations

10.7
avg, IF

5
L-index

#	Paper	IF	Citations
83	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. <i>Nature</i> , 2011 , 476, 214-9	50.4	1948
82	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. <i>Nature Genetics</i> , 2013 , 45, 1150-9	36.3	1153
81	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. <i>Nature Genetics</i> , 2012 , 44, 1341-8	36.3	681
80	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. <i>Nature</i> , 2010 , 464, 713-20	50.4	639
79	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. <i>Cell</i> , 2018 , 173, 1705-1715.e16	56.2	360
78	Analysis of hundreds of cis-regulatory landscapes at high resolution in a single, high-throughput experiment. <i>Nature Genetics</i> , 2014 , 46, 205-12	36.3	331
77	Myelodysplastic syndromes are propagated by rare and distinct human cancer stem cells in vivo. <i>Cancer Cell</i> , 2014 , 25, 794-808	24.3	216
76	Epidemiology and treatment of pulmonary arterial hypertension. <i>Nature Reviews Cardiology</i> , 2017 , 14, 603-614	14.8	182
75	Interferon-induced transmembrane protein-3 genetic variant rs12252-C is associated with severe influenza in Chinese individuals. <i>Nature Communications</i> , 2013 , 4, 1418	17.4	174
74	Genome-wide association study implicates HLA-C*01:02 as a risk factor at the major histocompatibility complex locus in schizophrenia. <i>Biological Psychiatry</i> , 2012 , 72, 620-8	7.9	130
73	Smchd1-dependent and -independent pathways determine developmental dynamics of CpG island methylation on the inactive X chromosome. <i>Developmental Cell</i> , 2012 , 23, 265-79	10.2	128
72	Early dynamic fate changes in haemogenic endothelium characterized at the single-cell level. <i>Nature Communications</i> , 2013 , 4, 2924	17.4	124
71	NAD Deficiency, Congenital Malformations, and Niacin Supplementation. <i>New England Journal of Medicine</i> , 2017 , 377, 544-552	59.2	114
70	Male-lineage transmission of an acquired metabolic phenotype induced by grand-paternal obesity. <i>Molecular Metabolism</i> , 2016 , 5, 699-708	8.8	104
69	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. <i>Journal of the American College of Cardiology</i> , 2019 , 73, 58-66	15.1	86
68	Pneumococcal genome sequencing tracks a vaccine escape variant formed through a multi-fragment recombination event. <i>Nature Genetics</i> , 2012 , 44, 352-5	36.3	82
67	Advances in the Genetics of Congenital Heart Disease: A Clinician's Guide. <i>Journal of the American College of Cardiology</i> , 2017 , 69, 859-870	15.1	76

66	Common variants in the HLA-DRB1-HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. <i>Nature Genetics</i> , 2013 , 45, 208-13	36.3	76
65	Targeted next-generation sequencing identifies pathogenic variants in familial congenital heart disease. <i>Journal of the American College of Cardiology</i> , 2014 , 64, 2498-506	15.1	60
64	Distinct patterns of hepcidin and iron regulation during HIV-1, HBV, and HCV infections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 12187-92	11.5	56
63	GenoSNP: a variational Bayes within-sample SNP genotyping algorithm that does not require a reference population. <i>Bioinformatics</i> , 2008 , 24, 2209-14	7.2	56
62	Contributions of intrinsic mutation rate and selfish selection to levels of de novo HRAS mutations in the paternal germline. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 20152-7	11.5	51
61	Cellular interference in craniofrontonasal syndrome: males mosaic for mutations in the X-linked EFNB1 gene are more severely affected than true hemizygotes. <i>Human Molecular Genetics</i> , 2013 , 22, 1654-62	5.6	50
60	Host and microbiome multi-omics integration: applications and methodologies. <i>Biophysical Reviews</i> , 2019 , 11, 55-65	3.7	42
59	Verification and validation of bioinformatics software without a gold standard: a case study of BWA and Bowtie. <i>BMC Bioinformatics</i> , 2014 , 15 Suppl 16, S15	3.6	40
58	A Screening Approach to Identify Clinically Actionable Variants Causing Congenital Heart Disease in Exome Data. <i>Circulation Genomic and Precision Medicine</i> , 2018 , 11, e001978	5.2	37
57	Selfish mutations dysregulating RAS-MAPK signaling are pervasive in aged human testes. <i>Genome Research</i> , 2018 , 28, 1779-1790	9.7	36
56	Visualizing the origins of selfish de novo mutations in individual seminiferous tubules of human testes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 2454-9	11.5	34
55	An inherited duplication at the gene p21 Protein-Activated Kinase 7 (PAK7) is a risk factor for psychosis. <i>Human Molecular Genetics</i> , 2014 , 23, 3316-26	5.6	32
54	Polymorphism in a lincRNA Associates with a Doubled Risk of Pneumococcal Bacteremia in Kenyan Children. <i>American Journal of Human Genetics</i> , 2016 , 98, 1092-1100	11	30
53	Binding of transcription factor GabR to DNA requires recognition of DNA shape at a location distinct from its cognate binding site. <i>Nucleic Acids Research</i> , 2016 , 44, 1411-20	20.1	27
52	Evaluation of the immunogenicity and impact on the latent HIV-1 reservoir of a conserved region vaccine, MVA.HIVconsv, in antiretroviral therapy-treated subjects. <i>Journal of the International AIDS Society</i> , 2017 , 20, 21171	5.4	26
51	Rapidly Escalating Hepcidin and Associated Serum Iron Starvation Are Features of the Acute Response to Typhoid Infection in Humans. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0004029	4.8	25
50	TP53 mutations and protein immunopositivity may predict for poor outcome but also for trastuzumab benefit in patients with early breast cancer treated in the adjuvant setting. <i>Oncotarget</i> , 2016 , 7, 32731-53	3.3	25
49	Identification of clinically actionable variants from genome sequencing of families with congenital heart disease. <i>Genetics in Medicine</i> , 2019 , 21, 1111-1120	8.1	25

48	Whole-genome sequencing of spermatocytic tumors provides insights into the mutational processes operating in the male germline. <i>PLoS ONE</i> , 2017 , 12, e0178169	3.7	24
47	Isogenic mice exhibit sexually-dimorphic DNA methylation patterns across multiple tissues. <i>BMC Genomics</i> , 2017 , 18, 966	4.5	21
46	A gene-centric strategy for identifying disease-causing rare variants in dilated cardiomyopathy. <i>Genetics in Medicine</i> , 2019 , 21, 133-143	8.1	20
45	Antiviral activity of bone morphogenetic proteins and activins. <i>Nature Microbiology</i> , 2019 , 4, 339-351	26.6	19
44	Survival of Idiopathic Pulmonary Arterial Hypertension Patients in the Modern Era in Australia and New Zealand. <i>Heart Lung and Circulation</i> , 2018 , 27, 1368-1375	1.8	17
43	Functional genomics and gene-environment interaction highlight the complexity of congenital heart disease caused by Notch pathway variants. <i>Human Molecular Genetics</i> , 2020 , 29, 566-579	5.6	16
42	Genetic burden and associations with adverse neurodevelopment in neonates with congenital heart disease. <i>American Heart Journal</i> , 2018 , 201, 33-39	4.9	15
41	Spontaneous Coronary Artery Dissection: Insights on Rare Genetic Variation From Genome Sequencing. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e003030	5.2	14
40	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. <i>American Journal of Human Genetics</i> , 2016 , 98, 857-868	11	14
39	Functional characterization of a novel PBX1 de novo missense variant identified in a patient with syndromic congenital heart disease. <i>Human Molecular Genetics</i> , 2020 , 29, 1068-1082	5.6	13
38	How to test bioinformatics software?. <i>Biophysical Reviews</i> , 2015 , 7, 343-352	3.7	12
37	Effects of TP53 and PIK3CA mutations in early breast cancer: a matter of co-mutation and tumor-infiltrating lymphocytes. <i>Breast Cancer Research and Treatment</i> , 2016 , 158, 307-21	4.4	12
36	Prevalent somatic BRCA1 mutations shape clinically relevant genomic patterns of nasopharyngeal carcinoma in Southeast Europe. <i>International Journal of Cancer</i> , 2018 , 142, 66-80	7.5	11
35	Multi-omic profiling reveals associations between the gut mucosal microbiome, the metabolome, and host DNA methylation associated gene expression in patients with colorectal cancer. <i>BMC Microbiology</i> , 2020 , 20, 83	4.5	11
34	The miR-200 family is increased in dysplastic lesions in ulcerative colitis patients. <i>PLoS ONE</i> , 2017 , 12, e0173664	3.7	10
33	Separation of Dual Oxidase 2 and Lactoperoxidase Expression in Intestinal Crypts and Species Differences May Limit Hydrogen Peroxide Scavenging During Mucosal Healing in Mice and Humans. <i>Inflammatory Bowel Diseases</i> , 2017 , 24, 136-148	4.5	9
32	Genetic variation in is associated with bacteremia secondary to diverse pathogens in African children. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E3601-E3603	11.5	8
31	Tumor Infiltrating Lymphocytes Affect the Outcome of Patients with Operable Triple-Negative Breast Cancer in Combination with Mutated Amino Acid Classes. <i>PLoS ONE</i> , 2016 , 11, e0163138	3.7	8

30	Familial adenomatous patients with desmoid tumours show increased expression of miR-34a in serum and high levels in tumours. <i>Oncoscience</i> , 2016 , 3, 173-85	0.8	8
29	SVPV: a structural variant prediction viewer for paired-end sequencing datasets. <i>Bioinformatics</i> , 2017 , 33, 2032-2033	7.2	7
28	Opposite Prognostic Impact of Single PTEN-loss and Mutations in Early High-risk Breast Cancer. <i>Cancer Genomics and Proteomics</i> , 2019 , 16, 195-206	3.3	7
27	Is There an Independent Role of TERT and NF1 in High Grade Gliomas?. <i>Translational Oncology</i> , 2020 , 13, 346-354	4.9	7
26	Pathogenic BRCA1 mutations may be necessary but not sufficient for tissue genomic heterogeneity: Deep sequencing data from ovarian cancer patients. <i>Gynecologic Oncology</i> , 2019 , 152, 375-386	4.9	6
25	Phase II study of panitumumab combined with capecitabine and oxaliplatin as first-line treatment in metastatic colorectal cancer patients: clinical results including extended tumor genotyping. <i>Medical Oncology</i> , 2018 , 35, 101	3.7	6
24	Maternal iron deficiency perturbs embryonic cardiovascular development in mice. <i>Nature Communications</i> , 2021 , 12, 3447	17.4	5
23	Relapsed and De Novo Metastatic HER2-positive Breast Cancer Treated With Trastuzumab: Tumor Genotypes and Clinical Measures Associated With Patient Outcome. <i>Clinical Breast Cancer</i> , 2019 , 19, 113-125.e4	3	5
22	dv-trio: a family-based variant calling pipeline using DeepVariant. <i>Bioinformatics</i> , 2020 , 36, 3549-3551	7.2	4
21	Disease evolution and heterogeneity in bilateral breast cancer. <i>American Journal of Cancer Research</i> , 2016 , 6, 2611-2630	4.4	4
20	Transposon clusters as substrates for aberrant splice-site activation. <i>RNA Biology</i> , 2021 , 18, 354-367	4.8	4
19	Spliceogen: an integrative, scalable tool for the discovery of splice-altering variants. <i>Bioinformatics</i> , 2019 , 35, 4405-4407	7.2	3
18	A cloud-based framework for applying metamorphic testing to a bioinformatics pipeline 2016 ,		3
17	Dynamics of Transforming Growth Factor (TGF)- β Superfamily Cytokine Induction During HIV-1 Infection Are Distinct From Other Innate Cytokines. <i>Frontiers in Immunology</i> , 2020 , 11, 596841	8.4	3
16	Comparison of somatic variant detection algorithms using Ion Torrent targeted deep sequencing data. <i>BMC Medical Genomics</i> , 2019 , 12, 181	3.7	3
15	Heterozygous loss of WBP11 function causes multiple congenital defects in humans and mice. <i>Human Molecular Genetics</i> , 2020 , 29, 3662-3678	5.6	3
14	Population-based identity-by-descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019 , 180, 223-231	3.5	2
13	Tumor Mutational Patterns and Infiltrating Lymphocyte Density in Young and Elderly Patients With Breast Cancer. <i>Cancer Genomics and Proteomics</i> , 2020 , 17, 181-193	3.3	2

12	VPOT: A Customizable Variant Prioritization Ordering Tool for Annotated Variants. <i>Genomics, Proteomics and Bioinformatics</i> , 2019 , 17, 540-545	6.5	2
11	Genotype-phenotype associations in colorectal adenocarcinomas and their matched metastases. <i>Human Pathology</i> , 2021 , 107, 104-116	3.7	2
10	Prognostic Biomarkers in Early-stage Gastric Adenocarcinoma Treated With Adjuvant Chemoradiotherapy. <i>Cancer Genomics and Proteomics</i> , 2020 , 17, 277-290	3.3	1
9	Whole genome sequencing in transposition of the great arteries and associations with clinically relevant heart, brain and laterality genes. <i>American Heart Journal</i> , 2021 , 244, 1-13	4.9	1
8	Spontaneous Coronary Artery Dissection and Fibromuscular Dysplasia: Vasculopathies With a Predilection for Women. <i>Heart Lung and Circulation</i> , 2021 , 30, 27-35	1.8	1
7	Genotyping data of routinely processed matched primary/metastatic tumor samples. <i>Data in Brief</i> , 2021 , 34, 106646	1.2	1
6	Benchmarking the Effectiveness and Accuracy of Multiple Mitochondrial DNA Variant Callers: Practical Implications for Clinical Application.. <i>Frontiers in Genetics</i> , 2022 , 13, 692257	4.5	1
5	Exploring the Genetic Architecture of Spontaneous Coronary Artery Dissection Using Whole-Genome Sequencing.. <i>Circulation Genomic and Precision Medicine</i> , 2022 , 101161CIRCGEN121003527	5.2	1
4	Pathogenic mutations and overall survival in 3,084 patients with cancer: the Hellenic Cooperative Oncology Group Precision Medicine Initiative. <i>Oncotarget</i> , 2020 , 11, 1-14	3.3	0
3	Decoding the complex genetic causes of heart diseases using systems biology. <i>Biophysical Reviews</i> , 2015 , 7, 141-159	3.7	
2	Tumor Genotyping and Homologous Recombination Repair Gene Variants in Patients With Epithelial Ovarian Cancer: Is Pathogenic Enough?. <i>Frontiers in Oncology</i> , 2021 , 11, 683057	5.3	
1	Congenital Heart Disease Gene: a Curated Database for Congenital Heart Disease Genes.. <i>Circulation Genomic and Precision Medicine</i> , 2022 , 101161CIRCGEN121003539	5.2	