Eleni Giannoulatou

List of Publications by Year
in descending order

85	10,116	126907	58581
papers	citations	33 h-index	82 g-index

91	91	91	22579
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Whole genome sequencing in transposition of the great arteries and associations with clinically relevant heart, brain and laterality genes. American Heart Journal, 2022, 244, 1-13.	2.7	10
2	Benchmarking the Effectiveness and Accuracy of Multiple Mitochondrial DNA Variant Callers: Practical Implications for Clinical Application. Frontiers in Genetics, 2022, 13, 692257.	2.3	6
3	CHDgene: A Curated Database for Congenital Heart Disease Genes. Circulation Genomic and Precision Medicine, 2022, 15, 101161CIRCGEN121003539.	3.6	4
4	Exploring the Genetic Architecture of Spontaneous Coronary Artery Dissection Using Whole-Genome Sequencing. Circulation Genomic and Precision Medicine, 2022, 15, 101161CIRCGEN121003527.	3.6	14
5	Spontaneous Coronary Artery Dissection and Fibromuscular Dysplasia: Vasculopathies With a Predilection for Women. Heart Lung and Circulation, 2021, 30, 27-35.	0.4	15
6	Heterozygous loss of WBP11 function causes multiple congenital defects in humans and mice. Human Molecular Genetics, 2021, 29, 3662-3678.	2.9	14
7	Genotype-phenotype associations in colorectal adenocarcinomas and their matched metastases. Human Pathology, 2021, 107, 104-116.	2.0	6
8	Transposon clusters as substrates for aberrant splice-site activation. RNA Biology, 2021, 18, 354-367.	3.1	8
9	Genotyping data of routinely processed matched primary/metastatic tumor samples. Data in Brief, 2021, 34, 106646.	1.0	2
10	Maternal iron deficiency perturbs embryonic cardiovascular development in mice. Nature Communications, 2021, 12, 3447.	12.8	17
11	Tumor Genotyping and Homologous Recombination Repair Gene Variants in Patients With Epithelial Ovarian Cancer: Is Pathogenic Enough?. Frontiers in Oncology, 2021, 11, 683057.	2.8	1
12	Functional characterization of a novel PBX1 de novo missense variant identified in a patient with syndromic congenital heart disease. Human Molecular Genetics, 2020, 29, 1068-1082.	2.9	26
13	Is There an Independent Role of TERT and NF1 in High Grade Gliomas?. Translational Oncology, 2020, 13, 346-354.	3.7	11
14	Functional genomics and gene-environment interaction highlight the complexity of congenital heart disease caused by Notch pathway variants. Human Molecular Genetics, 2020, 29, 566-579.	2.9	32
15	Dynamics of Transforming Growth Factor (TGF)-Î² Superfamily Cytokine Induction During HIV-1 Infection Are Distinct From Other Innate Cytokines. Frontiers in Immunology, 2020, 11, 596841.	4.8	15
16	Spontaneous Coronary Artery Dissection. Circulation Genomic and Precision Medicine, 2020, 13, e003030.	3.6	43
17	dv-trio: a family-based variant calling pipeline using DeepVariant. Bioinformatics, 2020, 36, 3549-3551.	4.1	9
18	Tumor Mutational Patterns and Infiltrating Lymphocyte Density in Young and Elderly Patients With Breast Cancer. Cancer Genomics and Proteomics, 2020, 17, 181-193.	2.0	2

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19	Prognostic Biomarkers in Early-stage Gastric Adenocarcinoma Treated With Adjuvant Chemoradiotherapy. Cancer Genomics and Proteomics, 2020, 17, 277-290.	2.0	4
20	Multi-omic profiling reveals associations between the gut mucosal microbiome, the metabolome, and host DNA methylation associated gene expression in patients with colorectal cancer. BMC Microbiology, 2020, 20, 83.	3.3	36
21	Pathogenic mutations and overall survival in 3,084 patients with cancer: the Hellenic Cooperative Oncology Group Precision Medicine Initiative. Oncotarget, 2020, 11, 1-14.	1.8	1
22	A gene-centric strategy for identifying disease-causing rare variants in dilated cardiomyopathy. Genetics in Medicine, 2019, 21, 133-143.	2.4	25
23	Host and microbiome multi-omics integration: applications and methodologies. Biophysical Reviews, 2019, 11, 55-65.	3.2	66
24	Big data: the elements of good questions, open data, and powerful software. Biophysical Reviews, 2019, 11, 1-3.	3.2	11
25	Spliceogen: an integrative, scalable tool for the discovery of splice-altering variants. Bioinformatics, 2019, 35, 4405-4407.	4.1	7
26	Opposite Prognostic Impact of Single PTEN-loss andPIK3CAMutations in Early High-risk Breast Cancer. Cancer Genomics and Proteomics, 2019, 16, 195-206.	2.0	13
27	Populationâ€based identityâ€byâ€descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 223-231.	1.7	2
28	VPOT: A Customizable Variant Prioritization Ordering Tool for Annotated Variants. Genomics, Proteomics and Bioinformatics, 2019, 17, 540-545.	6.9	10
29	Comparison of somatic variant detection algorithms using Ion Torrent targeted deep sequencing data. BMC Medical Genomics, 2019, 12, 181.	1.5	9
30	Relapsed and De Novo Metastatic HER2-positive Breast Cancer Treated With Trastuzumab: Tumor Genotypes and Clinical Measures Associated With Patient Outcome. Clinical Breast Cancer, 2019, 19, 113-125.e4.	2.4	8
31	Pathogenic BRCA1 mutations may be necessary but not sufficient for tissue genomic heterogeneity: Deep sequencing data from ovarian cancer patients. Gynecologic Oncology, 2019, 152, 375-386.	1.4	7
32	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. Journal of the American College of Cardiology, 2019, 73, 58-66.	2.8	147
33	Antiviral activity of bone morphogenetic proteins and activins. Nature Microbiology, 2019, 4, 339-351.	13.3	39
34	Identification of clinically actionable variants from genome sequencing of families with congenital heart disease. Genetics in Medicine, 2019, 21, 1111-1120.	2.4	54
35	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. Inflammatory Bowel Diseases, 2018, 24, 136-148.	1.9	11
36	Genetic burden and associations with adverse neurodevelopment in neonates with congenital heart disease. American Heart Journal, 2018, 201, 33-39.	2.7	19

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37	Genetic variation in VAC14 is associated with bacteremia secondary to diverse pathogens in African children. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3601-E3603.	7.1	12
38	A Screening Approach to Identify Clinically Actionable Variants Causing Congenital Heart Disease in Exome Data. Circulation Genomic and Precision Medicine, 2018, 11, e001978.	3.6	65
39	Prevalent somatic BRCA1 mutations shape clinically relevant genomic patterns of nasopharyngeal carcinoma in Southeast Europe. International Journal of Cancer, 2018, 142, 66-80.	5.1	13
40	Survival of Idiopathic Pulmonary Arterial Hypertension Patients in the Modern Era in Australia and New Zealand. Heart Lung and Circulation, 2018, 27, 1368-1375.	0.4	26
41	Selfish mutations dysregulating RAS-MAPK signaling are pervasive in aged human testes. Genome Research, 2018, 28, 1779-1790.	5.5	56
42	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. Medical Oncology, 2018, 35, 101.	2.5	6
43	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	28.9	623
44	Advances in the Genetics of Congenital HeartÂDisease. Journal of the American College of Cardiology, 2017, 69, 859-870.	2.8	115
45	SVPV: a structural variant prediction viewer for paired-end sequencing datasets. Bioinformatics, 2017, 33, 2032-2033.	4.1	9
46	Epidemiology and treatment of pulmonary arterial hypertension. Nature Reviews Cardiology, 2017, 14, 603-614.	13.7	310
47	NAD Deficiency, Congenital Malformations, and Niacin Supplementation. New England Journal of Medicine, 2017, 377, 544-552.	27.0	177
48	Isogenic mice exhibit sexually-dimorphic DNA methylation patterns across multiple tissues. BMC Genomics, 2017, 18, 966.	2.8	26
49	Evaluation of the immunogenicity and impact on the latent HIVâ€1 reservoir of a conserved region vaccine, MVA.HIVconsv, in antiretroviral therapyâ€treated subjects. Journal of the International AIDS Society, 2017, 20, 21171.	3.0	36
50	The miR-200 family is increased in dysplastic lesions in ulcerative colitis patients. PLoS ONE, 2017, 12, e0173664.	2.5	14
51	Whole-genome sequencing of spermatocytic tumors provides insights into the mutational processes operating in the male germline. PLoS ONE, 2017, 12, e0178169.	2.5	36
52	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. Oncotarget, 2016, 7, 32731-32753.	1.8	30
53	Tumor Infiltrating Lymphocytes Affect the Outcome of Patients with Operable Triple-Negative Breast Cancer in Combination with Mutated Amino Acid Classes. PLoS ONE, 2016, 11, e0163138.	2.5	8
54	Familial adenomatous patients with desmoid tumours show increased expression of miR-34a in serum and high levels in tumours. Oncoscience, 2016, 3, 173-185.	2.2	9

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55	Effects of TP53 and PIK3CA mutations in early breast cancer: a matter of co-mutation and tumor-infiltrating lymphocytes. Breast Cancer Research and Treatment, 2016, 158, 307-321.	2.5	16
56	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. American Journal of Human Genetics, 2016, 98, 857-868.	6.2	21
57	A cloud-based framework for applying metamorphic testing to a bioinformatics pipeline. , 2016, , .		4
58	Male-lineage transmission of an acquired metabolic phenotype induced by grand-paternal obesity. Molecular Metabolism, 2016, 5, 699-708.	6.5	154
59	Polymorphism in a lincRNA Associates with a Doubled Risk of Pneumococcal Bacteremia in Kenyan Children. American Journal of Human Genetics, 2016, 98, 1092-1100.	6.2	39
60	Visualizing the origins of selfish de novo mutations in individual seminiferous tubules of human testes. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2454-2459.	7.1	45
61	Binding of transcription factor GabR to DNA requires recognition of DNA shape at a location distinct from its cognate binding site. Nucleic Acids Research, 2016, 44, 1411-1420.	14.5	35
62	Disease evolution and heterogeneity in bilateral breast cancer. American Journal of Cancer Research, 2016, 6, 2611-2630.	1.4	5
63	How to test bioinformatics software?. Biophysical Reviews, 2015, 7, 343-352.	3.2	16
64	Myelodysplastic Syndromes Are Propagated by Rare and Distinct Human Cancer Stem Cells InÂVivo. Cancer Cell, 2015, 27, 603-605.	16.8	0
65	Decoding the complex genetic causes of heart diseases using systems biology. Biophysical Reviews, 2015, 7, 141-159.	3.2	0
66	Rapidly Escalating Hepcidin and Associated Serum Iron Starvation Are Features of the Acute Response to Typhoid Infection in Humans. PLoS Neglected Tropical Diseases, 2015, 9, e0004029.	3.0	38
67	Targeted Next-Generation Sequencing Identifies Pathogenic Variants in Familial Congenital Heart Disease. Journal of the American College of Cardiology, 2014, 64, 2498-2506.	2.8	85
68	An inherited duplication at the gene p21 Protein-Activated Kinase 7 (PAK7) is a risk factor for psychosis. Human Molecular Genetics, 2014, 23, 3316-3326.	2.9	37
69	Myelodysplastic Syndromes Are Propagated by Rare and Distinct Human Cancer Stem Cells InÂVivo. Cancer Cell, 2014, 25, 794-808.	16.8	272
70	Analysis of hundreds of cis-regulatory landscapes at high resolution in a single, high-throughput experiment. Nature Genetics, 2014, 46, 205-212.	21.4	417
71	Distinct patterns of hepcidin and iron regulation during HIV-1, HBV, and HCV infections. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12187-12192.	7.1	79
72	Verification and validation of bioinformatics software without a gold standard: a case study of BWA and Bowtie. BMC Bioinformatics, 2014, 15, S15.	2.6	58

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73	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	21.4	1,395
74	Common variants in the HLA-DRB1â€“HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. Nature Genetics, 2013, 45, 208-213.	21.4	86
75	Early dynamic fate changes in haemogenic endothelium characterized at the single-cell level. Nature Communications, 2013, 4, 2924.	12.8	158
76	Contributions of intrinsic mutation rate and selfish selection to levels of de novo HRAS mutations in the paternal germline. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20152-20157.	7.1	70
77	Cellular interference in craniofrontonasal syndrome: males mosaic for mutations in the X-linked EFNB1 gene are more severely affected than true hemizygotes. Human Molecular Genetics, 2013, 22, 1654-1662.	2.9	66
78	Interferon-induced transmembrane protein-3 genetic variant rs12252-C is associated with severe influenza in Chinese individuals. Nature Communications, 2013, 4, 1418.	12.8	228
79	Pneumococcal genome sequencing tracks a vaccine escape variant formed through a multi-fragment recombination event. Nature Genetics, 2012, 44, 352-355.	21.4	144
80	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. Nature Genetics, 2012, 44, 1341-1348.	21.4	848
81	Genome-Wide Association Study Implicates HLA-C*01:02 as a Risk Factor at the Major Histocompatibility Complex Locus in Schizophrenia. Biological Psychiatry, 2012, 72, 620-628.	1.3	156
82	Smchd1-Dependent and -Independent Pathways Determine Developmental Dynamics of CpG Island Methylation on the Inactive X Chromosome. Developmental Cell, 2012, 23, 265-279.	7.0	160
83	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	27.8	2,400
84	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	27.8	737
85	GenoSNP: a variational Bayes within-sample SNP genotyping algorithm that does not require a reference population. Bioinformatics, 2008, 24, 2209-2214.	4.1	65