Murray H Brilliant

List of Publications by Year
in descending order

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Version: 2024-02-01

44 papers	4,091 citations	331670 21 h-index	302126 39 g-index
44 all docs	44 docs citations	44 times ranked	9063 citing authors

#	Article	IF	Citations
1	Development of an Integrated Platform Using Multidisciplinary Realâ€World Data to Facilitate Biomarker Discovery for Medical Products. Clinical and Translational Science, 2020, 13, 98-109.	3.1	2
2	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. BMC Cardiovascular Disorders, 2019, 19, 240.	1.7	22
3	Heritability and genome-wide association study of benign prostatic hyperplasia (BPH) in the eMERGE network. Scientific Reports, 2019, 9, 6077.	3.3	21
4	Preliminary outcomes of preemptive warfarin pharmacogenetic testing at a large rural healthcare center. American Journal of Health-System Pharmacy, 2019, 76, 387-397.	1.0	9
5	Phenotype risk scores identify patients with unrecognized Mendelian disease patterns. Science, 2018, 359, 1233-1239.	12.6	164
6	Pilot screening study of targeted genetic polymorphisms for association with seasonal influenza hospital admission. Journal of Medical Virology, 2018, 90, 436-446.	5.0	10
7	Applying family analyses to electronic health records to facilitate genetic research. Bioinformatics, 2018, 34, 635-642.	4.1	8
8	The Henle Fiber Layer in Albinism: Comparison to Normal and Relationship to Outer Nuclear Layer Thickness and Foveal Cone Density. , 2018, 59, 5336.		26
9	Parentsâ€™ attitudes toward consent and data sharing in biobanks: A multisite experimental survey. AJOB Empirical Bioethics, 2018, 9, 128-142.	1.6	25
10	A study paradigm integrating prospective epidemiologic cohorts and electronic health records to identify disease biomarkers. Nature Communications, 2018, 9, 3522.	12.8	13
11	Testosterone Pathway Genetic Polymorphisms in Relation to Primary Open-Angle Glaucoma: An Analysis in Two Large Datasets. , 2018, 59, 629.		14
12	Public Attitudes toward Consent and Data Sharing in Biobank Research: A Large Multi-site Experimental Survey in the US. American Journal of Human Genetics, 2017, 100, 414-427.	6.2	172
13	Phenome-wide scanning identifies multiple diseases and disease severity phenotypes associated with HLA variants. Science Translational Medicine, 2017, 9, .	12.4	105
14	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	11.4	298
15	Genetic correlations between intraocular pressure, blood pressure and primary open-angle glaucoma: a multi-cohort analysis. European Journal of Human Genetics, 2017, 25, 1261-1267.	2.8	18
16	Is Low FMR1 CGG Repeat Length in Males Correlated with Family History of BRCAâ€Associated Cancers? An Exploratory Analysis of Medical Records. Journal of Genetic Counseling, 2017, 26, 1401-1410.	1.6	7
17	Prototype Development: Context-Driven Dynamic XML Ophthalmologic Data Capture Application. JMIR Medical Informatics, 2017, 5, e27.	2.6	2
18	A Common Variant in MIR182 Is Associated With Primary Open-Angle Glaucoma in the NEIGHBORHOOD Consortium. , 2016, 57, 4528.		42

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19	Phenome-wide association study maps new diseases to the human major histocompatibility complex region. Journal of Medical Genetics, 2016, 53, 681-689.	3.2	29
20	Identifying genetically driven clinical phenotypes using linear mixed models. Nature Communications, 2016, 7, 11433.	12.8	12
21	Conducting a large, multi-site survey about patientsâ€™ views on broad consent: challenges and solutions. BMC Medical Research Methodology, 2016, 16, 162.	3.1	9
22	Mining Retrospective Data for Virtual Prospective Drug Repurposing: L-DOPA and Age-related Macular Degeneration. American Journal of Medicine, 2016, 129, 292-298.	1.5	66
23	A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. Nature Genetics, 2016, 48, 134-143.	21.4	1,167
24	Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle glaucoma. Nature Genetics, 2016, 48, 189-194.	21.4	211
25	Epistatic Gene-Based Interaction Analyses for Glaucoma in eMERGE and NEIGHBOR Consortium. PLoS Genetics, 2016, 12, e1006186.	3.5	38
26	Progress in oral personalized medicine: contribution of â€˜omicsâ€™. Journal of Oral Microbiology, 2015, 7, 28223.	2.7	4
27	A GWAS Study on Liver Function Test Using eMERGE Network Participants. PLoS ONE, 2015, 10, e0138677.	2.5	18
28	Albinism in Africa: a medical and social emergency. International Health, 2015, 7, 223-225.	2.0	28
29	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. Genome Biology, 2015, 16, 133.	8.8	325
30	SeqHBase: a big data toolset for family based sequencing data analysis. Journal of Medical Genetics, 2015, 52, 282-288.	3.2	17
31	Personalized medicine going precise: from genomics to microbiomics. Trends in Molecular Medicine, 2015, 21, 461-462.	6.7	39
32	Penetrance of Hemochromatosis in HFE Genotypes Resulting in p.Cys282Tyr and p.[Cys282Tyr];[His63Asp] in the eMERGE Network. American Journal of Human Genetics, 2015, 97, 512-520.	6.2	47
33	Phenome-wide association studies (PheWASs) for functional variants. European Journal of Human Genetics, 2015, 23, 523-529.	2.8	38
34	Genome-Wide Association Study of Serum Creatinine Levels during Vancomycin Therapy. PLoS ONE, 2015, 10, e0127791.	2.5	19
35	A conceptual model for translating omic data into clinical action. Journal of Pathology Informatics, 2015, 6, 46.	1.7	17
36	Practical considerations in genomic decision support: The eMERGE experience. Journal of Pathology Informatics, 2015, 6, 50.	1.7	42

#	Article	IF	Citations
37	Author Response: Relationship Between Foveal Cone Specialization and Pit Morphology in Albinism. , 2014, 55, 5923.		2
38	Genome wide association study of SNP-, gene-, and pathway-based approaches to identify genes influencing susceptibility to Staphylococcus aureus infections. Frontiers in Genetics, 2014, 5, 125.	2.3	38
39	Genetic-based prediction of disease traits: prediction is very difficult, especially about the futureÃ¢â‚¬Â. Frontiers in Genetics, 2014, 5, 162.	2.3	53
40	Phenome-wide association studies demonstrating pleiotropy of genetic variants within FTO with and without adjustment for body mass index. Frontiers in Genetics, 2014, 5, 250.	2.3	66
41	DNA Copy Number Variants of Known Glaucoma Genes in Relation to Primary Open-Angle Glaucoma. Investigative Ophthalmology and Visual Science, 2014, 55, 8251-8258.	3.3	27
42	Relationship Between Foveal Cone Specialization and Pit Morphology in Albinism. , 2014, 55, 4186.		119
43	Association of CAV1/CAV2 Genomic Variants with Primary Open-Angle Glaucoma Overall and by Gender and Pattern of Visual Field Loss. Ophthalmology, 2014, 121, 508-516.	5.2	91
44	The Electronic Medical Records and Genomics (eMERGE) Network: past, present, and future. Genetics in Medicine, 2013, 15, 761-771.	2.4	611