Neil Risch

List of Publications by Year
in descending order

41 papers	4,382 citations	257450 24 h-index	315739 38 g-index
43 all docs	43 docs citations	43 times ranked	9714 citing authors

#	Article	IF	Citations
1	Torsade de pointes: A nested caseâ€“control study in an integrated healthcare delivery system. Annals of Noninvasive Electrocardiology, 2022, 27, e12888.	1.1	2
2	Exome sequencing in bipolar disorder identifies AKAP11 as a risk gene shared with schizophrenia. Nature Genetics, 2022, 54, 541-547.	21.4	65
3	A unified framework identifies new links between plasma lipids and diseases from electronic medical records across large-scale cohorts. Nature Genetics, 2021, 53, 972-981.	21.4	17
4	QT Interval Dynamics and Cardiovascular Outcomes: A Cohort Study in an Integrated Health Care Delivery System. Journal of the American Heart Association, 2021, 10, e018513.	3.7	11
5	The difficulties of broad data sharing in genomic medicine: Empirical evidence from diverse participants in prenatal and pediatric clinical genomics research. Genetics in Medicine, 2021, , .	2.4	5
6	Genetic ancestry does not explain increased atopic dermatitis susceptibility or worse disease control among African American subjects in 2 large US cohorts. Journal of Allergy and Clinical Immunology, 2020, 145, 192-198.e11.	2.9	39
7	A novel truncating variant in ring finger protein 113A (RNF113A) confirms the association of this gene with Xâ€linked trichothiodystrophy. American Journal of Medical Genetics, Part A, 2020, 182, 513-520.	1.2	12
8	Analysis of putative cis-regulatory elements regulating blood pressure variation. Human Molecular Genetics, 2020, 29, 1922-1932.	2.9	7
9	Meta-Analysis of 26 638 Individuals Identifies Two Genetic Loci Associated With Left Ventricular Ejection Fraction. Circulation Genomic and Precision Medicine, 2020, 13, e002804.	3.6	10
10	The impact of adjusting for baseline in pharmacogenomic genome-wide association studies of quantitative change. Npj Genomic Medicine, 2020, 5, 1.	3.8	28
11	Association of Genetic Variants With Primary Open-Angle Glaucoma Among Individuals With African Ancestry. JAMA - Journal of the American Medical Association, 2019, 322, 1682.	7.4	50
12	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
13	A large electronic-health-record-based genome-wide study of serum lipids. Nature Genetics, 2018, 50, 401-413.	21.4	224
14	Characterization of Statin Low-Density Lipoprotein Cholesterol Dose-Response Using Electronic Health Records in a Large Population-Based Cohort. Circulation Genomic and Precision Medicine, 2018, 11, e002043.	3.6	25
15	The Clinical Sequencing Evidence-Generating Research Consortium: Integrating Genomic Sequencing in Diverse and Medically Underserved Populations. American Journal of Human Genetics, 2018, 103, 319-327.	6.2	122
16	Newton E. Morton (1929â€“2018). American Journal of Human Genetics, 2018, 102, 1011-1017.	6.2	0
17	Genome-wide association study of prostate-specific antigen levels identifies novel loci independent of prostate cancer. Nature Communications, 2017, 8, 14248.	12.8	58
18	Pierpont syndrome associated with the p.Tyr446Cys missense mutation in TBL1XR1. European Journal of Medical Genetics, 2017, 60, 504-508.	1.3	15

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19	Genome-wide association analyses using electronic health records identify new loci influencing blood pressure variation. Nature Genetics, 2017, 49, 54-64.	21.4	281
20	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	3.5	88
21	A Large Genome-Wide Association Study of Age-Related Hearing Impairment Using Electronic Health Records. PLoS Genetics, 2016, 12, e1006371.	3.5	78
22	Presidential Address: All in the Family, or â€œGee, Our Old LaSalle Ran Greatâ€•1. American Journal of Human Genetics, 2016, 98, 407-416.	6.2	1
23	The Association of Refractive Error with Glaucoma in a Multiethnic Population. Ophthalmology, 2016, 123, 92-101.	5.2	129
24	Differences in the Genetic Susceptibility to Age-Related Macular Degeneration Clinical Subtypes. , 2015, 56, 4290.		17
25	A Large Multiethnic Genome-Wide Association Study of Prostate Cancer Identifies Novel Risk Variants and Substantial Ethnic Differences. Cancer Discovery, 2015, 5, 878-891.	9.4	111
26	Genotyping Informatics and Quality Control for 100,000 Subjects in the Genetic Epidemiology Research on Adult Health and Aging (GERA) Cohort. Genetics, 2015, 200, 1051-1060.	2.9	177
27	Imputation of the Rare HOXB13 G84E Mutation and Cancer Risk in a Large Population-Based Cohort. PLoS Genetics, 2015, 11, e1004930.	3.5	36
28	Characterizing Race/Ethnicity and Genetic Ancestry for 100,000 Subjects in the Genetic Epidemiology Research on Adult Health and Aging (GERA) Cohort. Genetics, 2015, 200, 1285-1295.	2.9	273
29	Automated Assay of Telomere Length Measurement and Informatics for 100,000 Subjects in the Genetic Epidemiology Research on Adult Health and Aging (GERA) Cohort. Genetics, 2015, 200, 1061-1072.	2.9	132
30	Estimating genotype error rates from high-coverage next-generation sequence data. Genome Research, 2014, 24, 1734-1739.	5.5	121
31	Familial Recurrence of Autism Spectrum Disorder: Evaluating Genetic and Environmental Contributions. American Journal of Psychiatry, 2014, 171, 1206-1213.	7.2	111
32	Multisystem Component Phenotypes of Bipolar Disorder for Genetic Investigations of Extended Pedigrees. JAMA Psychiatry, 2014, 71, 375.	11.0	87
33	Evidence of Reproductive Stoppage in Families With Autism Spectrum Disorder. JAMA Psychiatry, 2014, 71, 943.	11.0	42
34	Genome-wide association and admixture analysis of glaucoma in the Women's Health Initiative. Human Molecular Genetics, 2014, 23, 6634-6643.	2.9	22
35	Next generation genome-wide association tool: Design and coverage of a high-throughput European-optimized SNP array. Genomics, 2011, 98, 79-89.	2.9	186
36	Design and coverage of high throughput genotyping arrays optimized for individuals of East Asian, African American, and Latino race/ethnicity using imputation and a novel hybrid SNP selection algorithm. Genomics, 2011, 98, 422-430.	2.9	156

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37	Study of the genetically complex epilepsies. Epilepsia, 2010, 51, 57-57.	5.1	0
38	Interaction Between the Serotonin Transporter Gene (5-HTTLPR), Stressful Life Events, and Risk of Depression. JAMA - Journal of the American Medical Association, 2009, 301, 2462.	7.4	1,475
39	Ancestry-related assortative mating in Latino populations. Genome Biology, 2009, 10, R132.	9.6	89
40	Twins of Mistaken Zygosity (TOMZ): Evidence for Genetic Contributions to Dietary Patterns and Physiologic Traits. Twin Research and Human Genetics, 2006, 9, 540-549.	0.6	14
41	Response to the Letter â€œGametic and Zygotic Associationsâ€•by Rong-Cai Yang. Genetics, 2003, 165, 451-452.	2.9	1