

# Shona M Kerr

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4376664/publications.pdf>

Version: 2024-02-01

29  
papers

3,234  
citations

430442

18  
h-index

500791

28  
g-index

32  
all docs

32  
docs citations

32  
times ranked

7664  
citing authors

#	ARTICLE	IF	CITATIONS
1	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	9.4	549
2	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. <i>Nature Genetics</i> , 2011, 43, 1082-1090.	9.4	367
3	Cohort Profile: Generation Scotland: Scottish Family Health Study (GS:SFHS). The study, its participants and their potential for genetic research on health and illness. <i>International Journal of Epidemiology</i> , 2013, 42, 689-700.	0.9	353
4	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. <i>Nature Genetics</i> , 2019, 51, 481-493.	9.4	350
5	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. <i>Nature Genetics</i> , 2017, 49, 416-425.	9.4	257
6	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	9.4	251
7	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	13.7	173
8	Molecular genetic contributions to socioeconomic status and intelligence. <i>Intelligence</i> , 2014, 44, 26-32.	1.6	156
9	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. <i>Nature Genetics</i> , 2022, 54, 581-592.	9.4	142
10	Exploration of haplotype research consortium imputation for genome-wide association studies in 20,032 Generation Scotland participants. <i>Genome Medicine</i> , 2017, 9, 23.	3.6	110
11	Flexible and scalable diagnostic filtering of genomic variants using G2P with Ensembl VEP. <i>Nature Communications</i> , 2019, 10, 2373.	5.8	86
12	An RBM homologue maps to the mouse Y chromosome and is expressed in germ cells. <i>Human Molecular Genetics</i> , 1996, 5, 869-874.	1.4	66
13	Tissue-specific subunit of the mouse cytosolic chaperonin-containing TCP-1 1. <i>FEBS Letters</i> , 1997, 402, 53-56.	1.3	53
14	Pedigree and genotyping quality analyses of over 10,000 DNA samples from the Generation Scotland: Scottish Family Health Study. <i>BMC Medical Genetics</i> , 2013, 14, 38.	2.1	51
15	Urinary peptides in heart failure: a link to molecular pathophysiology. <i>European Journal of Heart Failure</i> , 2021, 23, 1875-1887.	2.9	37
16	Novel Urinary Peptidomic Classifier Predicts Incident Heart Failure. <i>Journal of the American Heart Association</i> , 2017, 6, .	1.6	30
17	Analysis of cDNA sequences from mouse testis. <i>Mammalian Genome</i> , 1994, 5, 557-565.	1.0	24
18	The genetic landscape of Scotland and the Isles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19064-19070.	3.3	24

#	ARTICLE	IF	CITATIONS
19	Ott, a mouse X-linked multigene family expressed specifically during meiosis. <i>Human Molecular Genetics</i> , 1996, 5, 1139-1148.	1.4	21
20	Balancing the local and the universal in maintaining ethical access to a genomics biobank. <i>BMC Medical Ethics</i> , 2017, 18, 80.	1.0	20
21	Assessment of dried blood spots for DNA methylation profiling. <i>Wellcome Open Research</i> , 2019, 4, 44.	0.9	20
22	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 2018, 3, 4.	0.9	19
23	An actionable KCNH2 Long QT Syndrome variant detected by sequence and haplotype analysis in a population research cohort. <i>Scientific Reports</i> , 2019, 9, 10964.	1.6	17
24	Increased ultra-rare variant load in an isolated Scottish population impacts exonic and regulatory regions. <i>PLoS Genetics</i> , 2019, 15, e1008480.	1.5	17
25	Electronic health record and genome-wide genetic data in Generation Scotland participants. <i>Wellcome Open Research</i> , 2017, 2, 85.	0.9	14
26	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 0, 3, 4.	0.9	11
27	Sequence and mapping of mouse synaptonemal complex protein genes <i>Sycpl</i> and <i>Sycpl-rs</i> . <i>Mammalian Genome</i> , 1996, 7, 209-211.	1.0	5
28	Generation Scotland: Donor DNA Databank; A control DNA resource. <i>BMC Medical Genetics</i> , 2010, 11, 166.	2.1	2
29	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 0, 3, 4.	0.9	1