Raha Pazoki

List of Publications by Year
in descending order

36 papers	3,690 citations	279798 23 h-index	302126 39 g-index
42 all docs	42 docs citations	42 times ranked	8960 citing authors

#	Article	IF	Citations
1	Genetic analysis of over half a million people characterises C-reactive protein loci. Nature Communications, 2022, 13, 2198.	12.8	48
2	Molecular Alterations Caused by Alcohol Consumption in the UK Biobank: A Mendelian Randomisation Study. Nutrients, 2022, 14, 2943.	4.1	2
3	Phenome-wide and genome-wide analyses of quality of life in schizophrenia. BJPsych Open, 2021, 7, e13.	0.7	7
4	Genetic analysis in European ancestry individuals identifies 517 loci associated with liver enzymes. Nature Communications, 2021, 12, 2579.	12.8	51
5	Alcohol consumption in the general population is associated with structural changes in multiple organ systems. ELife, 2021, 10, .	6.0	16
6	Age at Natural Menopause and Blood Pressure Traits: Mendelian Randomization Study. Journal of Clinical Medicine, 2021, 10, 4299.	2.4	8
7	Determinants of accelerated metabolomic and epigenetic aging in a UK cohort. Aging Cell, 2020, 19, e13149.	6.7	95
8	Estimated 24-Hour Urinary Sodium Excretion and Incident Cardiovascular Disease and Mortality Among 398 628 Individuals in UK Biobank. Hypertension, 2020, 76, 683-691.	2.7	21
9	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	12.0	75
10	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. BMC Cardiovascular Disorders, 2019, 19, 240.	1.7	22
11	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
12	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
13	Genetic Predisposition to High Blood Pressure and Lifestyle Factors. Circulation, 2018, 137, 653-661.	1.6	169
14	A comprehensive evaluation of the genetic architecture of sudden cardiac arrest. European Heart Journal, 2018, 39, 3961-3969.	2.2	59
15	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
16	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	12.8	484
17	Methods for Polygenic Traits. Methods in Molecular Biology, 2018, 1793, 145-156.	0.9	5
18	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

#	Article	IF	Citations
19	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	21.4	66
20	Whole-Exome Sequencing Identifies Loci Associated with Blood Cell Traits and Reveals a Role for Alternative GFI1B Splice Variants in Human Hematopoiesis. American Journal of Human Genetics, 2016, 99, 481-488.	6.2	45
21	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
22	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. American Journal of Human Genetics, 2016, 99, 22-39.	6.2	50
23	The global impact of non-communicable diseases on households and impoverishment: a systematic review. European Journal of Epidemiology, 2015, 30, 163-188.	5.7	117
24	The global impact of non-communicable diseases on healthcare spending and national income: a systematic review. European Journal of Epidemiology, 2015, 30, 251-277.	5.7	228
25	The global impact of non-communicable diseases on macro-economic productivity: a systematic review. European Journal of Epidemiology, 2015, 30, 357-395.	5.7	103
26	Association of Uric Acid Genetic Risk Score With Blood Pressure. Hypertension, 2014, 64, 1061-1066.	2.7	38
27	SNPs Identified as Modulators of ECG Traits in the General Population Do Not Markedly Affect ECG Traits during Acute Myocardial Infarction nor Ventricular Fibrillation Risk in This Condition. PLoS ONE, 2013, 8, e57216.	2.5	9
28	Complex Inheritance for Susceptibility to Sudden Cardiac Death. Current Pharmaceutical Design, 2013, 19, 6864-6872.	1.9	3
29	Oncogenic human papillomavirus genital infection in southern Iranian women: population-based study versus clinic-based data. Virology Journal, 2012, 9, 194.	3.4	20
30	Identification of a Sudden Cardiac Death Susceptibility Locus at 2q24.2 through Genome-Wide Association in European Ancestry Individuals. PLoS Genetics, 2011, 7, e1002158.	3.5	117
31	Genetic Basis of Ventricular Arrhythmias. Current Cardiovascular Risk Reports, 2010, 4, 454-460.	2.0	3
32	Genome-wide association study identifies a susceptibility locus at 21q21 for ventricular fibrillation in acute myocardial infarction. Nature Genetics, 2010, 42, 688-691.	21.4	170
33	Relationship among insulinlike growth factor I concentrations, bone mineral density, and biochemical markers of bone turnover in postmenopausal women. Menopause, 2008, 15, 934-939.	2.0	14
34	Correlation of Hyperhomocysteinaemia and Chlamydia Pneumoniae IgG Seropositivity with Coronary Artery Disease in a General Population. Heart Lung and Circulation, 2007, 16, 416-422.	0.4	4
35	Effects of a community-based healthy heart program on increasing healthy women's physical activity: a randomized controlled trial guided by Community-based Participatory Research (CBPR). BMC Public Health, 2007, 7, 216.	2.9	77
36	The association of metabolic syndrome and Chlamydia pneumoniae, Helicobacter pylori, cytomegalovirus, and herpes simplex virus type 1: the Persian Gulf Healthy Heart Study. Cardiovascular Diabetology, 2006, 5, 25.	6.8	73