Mohsen Ghanbari

List of Publications by Year
in descending order

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114 papers	6,085 citations	117625 34 h-index	98798 67 g-index
122 all docs	122 docs citations	122 times ranked	9418 citing authors

#	Article	IF	Citations
1	Estimating Global Prevalence of Metabolic Dysfunction-Associated Fatty Liver Disease in Overweight or Obese Adults. Clinical Gastroenterology and Hepatology, 2022, 20, e573-e582.	4.4	84
2	Cardiovascular health, genetic predisposition, and lifetime risk of type 2 diabetes. European Journal of Preventive Cardiology, 2022, 28, 1850-1857.	1.8	10
3	Novel biomarkers of inflammation, kidney function and chronic kidney disease in the general population. Nephrology Dialysis Transplantation, 2022, 37, 1916-1926.	0.7	8
4	Obesity Partially Mediates the Diabetogenic Effect of Lowering LDL Cholesterol. Diabetes Care, 2022, 45, 232-240.	8.6	10
5	Protective association of Klotho rs495392 gene polymorphism against hepatic steatosis in non-alcoholic fatty liver disease patients. Clinical and Molecular Hepatology, 2022, 28, 183-195.	8.9	6
6	Type 2 Diabetes Partitioned Polygenic Scores Associate With Disease Outcomes in 454,193 Individuals Across 13 Cohorts. Diabetes Care, 2022, 45, 674-683.	8.6	29
7	Circulating Metabolome and White Matter Hyperintensities in Women and Men. Circulation, 2022, 145, 1040-1052.	1.6	17
8	Genome-wide analysis of 102,084 migraine cases identifies 123 risk loci and subtype-specific risk alleles. Nature Genetics, 2022, 54, 152-160.	21.4	135
9	Plasma Î²-Amyloid, Total-Tau, and Neurofilament Light Chain Levels and the Risk of Stroke. Neurology, 2022, 98, .	1.1	11
10	Genetic and clinical determinants of abdominal aortic diameter: genome-wide association studies, exome array data and Mendelian randomization study. Human Molecular Genetics, 2022, 31, 3566-3579.	2.9	5
11	Finding Correspondence between Metabolomic Features in Untargeted Liquid Chromatographyâ€“Mass Spectrometry Metabolomics Datasets. Analytical Chemistry, 2022, 94, 5493-5503.	6.5	9
12	Plasma amyloid-Î²40 in relation to subclinical atherosclerosis and cardiovascular disease: A population-based study. Atherosclerosis, 2022, 348, 44-50.	0.8	2
13	Meta-analysis of genome-wide association studies identifies ancestry-specific associations underlying circulating total tau levels. Communications Biology, 2022, 5, 336.	4.4	6
14	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	21.4	700
15	Circulatory MicroRNAs in Plasma and Atrial Fibrillation in the General Population: The Rotterdam Study. Genes, 2022, 13, 11.	2.4	12
16	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases. Nature Communications, 2022, 13, 2408.	12.8	26
17	Associations of Sex Steroids and Sex Hormone-Binding Globulin with Non-Alcoholic Fatty Liver Disease: A Population-Based Study and Meta-Analysis. Genes, 2022, 13, 966.	2.4	7
18	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. Kidney International, 2022, 102, 624-639.	5.2	18

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19	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
20	Biological Aging for Risk Prediction of First-Ever Intracerebral Hemorrhage and Cerebral Infarction in Advanced Age. Journal of Stroke and Cerebrovascular Diseases, 2022, 31, 106568.	1.6	2
21	Genomic analysis of diet composition finds novel loci and associations with health and lifestyle. Molecular Psychiatry, 2021, 26, 2056-2069.	7.9	79
22	Immunity and amyloid beta, total tau and neurofilament light chain: Findings from a communityâ€based cohort study. Alzheimer's and Dementia, 2021, 17, 446-456.	0.8	14
23	Deciphering the role of epigenetic modifications in fatty liver disease: A systematic review. European Journal of Clinical Investigation, 2021, 51, e13479.	3.4	16
24	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
25	miR-142-3p regulates cortical oligodendrocyte gene co-expression networks associated with tauopathy. Human Molecular Genetics, 2021, 30, 103-118.	2.9	5
26	Implications of microRNAs in the Pathogenesis of Atherosclerosis and Prospects for Therapy. Current Drug Targets, 2021, 22, 1738-1749.	2.1	9
27	Common and Rare Variants Genetic Association Analysis of Circulating Neutrophil Extracellular Traps. Frontiers in Immunology, 2021, 12, 615527.	4.8	8
28	Genome-wide transcriptome study using deep RNA sequencing for myocardial infarction and coronary artery calcification. BMC Medical Genomics, 2021, 14, 45.	1.5	5
29	Regulation of <scp>microRNA</scp>â€21 expression by natural products in cancer. Phytotherapy Research, 2021, 35, 3732-3746.	5.8	6
30	Circulatory MicroRNAs as Potential Biomarkers for Stroke Risk. Stroke, 2021, 52, 945-953.	2.0	26
31	Investigating the relationships between unfavourable habitual sleep and metabolomic traits: evidence from multi-cohort multivariable regression and Mendelian randomization analyses. BMC Medicine, 2021, 19, 69.	5.5	14
32	Herpes simplex virus 1 and the risk of dementia: a population-based study. Scientific Reports, 2021, 11, 8691.	3.3	25
33	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. Nature Communications, 2021, 12, 2830.	12.8	35
34	Genetic analysis in European ancestry individuals identifies 517 loci associated with liver enzymes. Nature Communications, 2021, 12, 2579.	12.8	51
35	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. Nature Communications, 2021, 12, 3987.	12.8	18
36	Meta-analysis of epigenome-wide association studies of carotid intima-media thickness. European Journal of Epidemiology, 2021, 36, 1143-1155.	5.7	10

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37	Biological age in healthy elderly predicts aging-related diseases including dementia. Scientific Reports, 2021, 11, 15929.	3.3	35
38	Sugar-Sweetened Beverage Consumption May Modify Associations Between Genetic Variants in the CHREBP (Carbohydrate Responsive Element Binding Protein) Locus and HDL-C (High-Density Lipoprotein) Tj ETQq0 0 0 rgBT /Overlock 1 e003288.	3.6	8
39	Multiethnic Genome-Wide Association Study of Subclinical Atherosclerosis in Individuals With Type 2 Diabetes. Circulation Genomic and Precision Medicine, 2021, 14, e003258.	3.6	4
40	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	3.1	11
41	Epigenetic Age and the Risk of Incident Atrial Fibrillation. Circulation, 2021, 144, 1899-1911.	1.6	35
42	Validating biomarkers and models for epigenetic inference of alcohol consumption from blood. Clinical Epigenetics, 2021, 13, 198.	4.1	7
43	Higher thyrotropin leads to unfavorable lipid profile and somewhat higher cardiovascular disease risk: evidence from multi-cohort Mendelian randomization and metabolomic profiling. BMC Medicine, 2021, 19, 266.	5.5	11
44	Circulatory microRNAs as potential biomarkers for fatty liver disease: the Rotterdam study. Alimentary Pharmacology and Therapeutics, 2021, 53, 432-442.	3.7	9
45	Genetic Determinants of Serum Calcification Propensity and Cardiovascular Outcomes in the General Population. Frontiers in Cardiovascular Medicine, 2021, 8, 809717.	2.4	5
46	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
47	Circulatory microRNAs as potential biomarkers for fatty liver disease: the Rotterdam study. Alimentary Pharmacology and Therapeutics, 2021, 53, 432-442.	3.7	23
48	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. Nature Communications, 2021, 12, 7173.	12.8	8
49	Meta-analyses identify DNA methylation associated with kidney function and damage. Nature Communications, 2021, 12, 7174.	12.8	30
50	Editorial: microRNAs for the diagnosis of fatty liver disease in the populationâ€”are we inching closer towards the target? Authors' reply. Alimentary Pharmacology and Therapeutics, 2021, 53, 559-560.	3.7	0
51	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	12.8	466
52	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388
53	A cross-omics integrative study of metabolic signatures of chronic obstructive pulmonary disease. BMC Pulmonary Medicine, 2020, 20, 193.	2.0	15
54	Sleep, 24-h activity rhythms, and plasma markers of neurodegenerative disease. Scientific Reports, 2020, 10, 20691.	3.3	8

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55	Higher Plasma Amyloid-Î² Levels Are Associated with a Higher Risk of Cancer: A Population-Based Prospective Cohort Study. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1993-2001.	2.5	3
56	Smoking-related changes in DNA methylation and gene expression are associated with cardio-metabolic traits. Clinical Epigenetics, 2020, 12, 157.	4.1	31
57	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	28.9	353
58	Objectives, design and main findings until 2020 from the Rotterdam Study. European Journal of Epidemiology, 2020, 35, 483-517.	5.7	314
59	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. PLoS ONE, 2020, 15, e0230815.	2.5	10
60	Multi-Omics Analysis Reveals MicroRNAs Associated With Cardiometabolic Traits. Frontiers in Genetics, 2020, 11, 110.	2.3	17
61	Plasma tau, neurofilament light chain and amyloid-Î² levels and risk of dementia; a population-based cohort study. Brain, 2020, 143, 1220-1232.	7.6	201
62	Unique challenges to control the spread of COVID-19 in the Middle East. Journal of Infection and Public Health, 2020, 13, 1247-1250.	4.1	20
63	Epigenetic Link Between Statin Therapy and Type 2 Diabetes. Diabetes Care, 2020, 43, 875-884.	8.6	43
64	Sexually dimorphic DNA-methylation in cardiometabolic health: A systematic review. Maturitas, 2020, 135, 6-26.	2.4	14
65	Local endothelial DNA repair deficiency causes aging-resembling endothelial-specific dysfunction. Clinical Science, 2020, 134, 727-746.	4.3	25
66	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
67	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
68	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
69	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
70	A metabolic profile of all-cause mortality risk identified in an observational study of 44,168 individuals. Nature Communications, 2019, 10, 3346.	12.8	188
71	A functional variant in the miRâ€142 promoter modulating its expression and conferring risk of Alzheimer disease. Human Mutation, 2019, 40, 2131-2145.	2.5	23
72	FCER2 T2206C variant associated with FENO levels in asthmatic children using inhaled corticosteroids: The PACMAN study. Clinical and Experimental Allergy, 2019, 49, 1429-1436.	2.9	10

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73	The impact of APOE genotype on survival: Results of 38,537 participants from six population-based cohorts (E2-CHARGE). PLoS ONE, 2019, 14, e0219668.	2.5	50
74	Î²2-Adrenergic Receptor (ADRB2) Gene Polymorphisms and Risk of COPD Exacerbations: The Rotterdam Study. Journal of Clinical Medicine, 2019, 8, 1835.	2.4	12
75	Validated inference of smoking habits from blood with a finite DNA methylation marker set. European Journal of Epidemiology, 2019, 34, 1055-1074.	5.7	31
76	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
77	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
78	Epigenetics and Inflammatory Markers: A Systematic Review of the Current Evidence. International Journal of Inflammation, 2019, 2019, 1-14.	1.5	30
79	Quantification of biological age as a determinant of age-related diseases in the Rotterdam Study: a structural equation modeling approach. European Journal of Epidemiology, 2019, 34, 793-799.	5.7	29
80	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
81	Dissecting the association of autophagy-related genes with cardiovascular diseases and intermediate vascular traits: A population-based approach. PLoS ONE, 2019, 14, e0214137.	2.5	12
82	A Peripheral Blood DNA Methylation Signature of Hepatic Fat Reveals a Potential Causal Pathway for Nonalcoholic Fatty Liver Disease. Diabetes, 2019, 68, 1073-1083.	0.6	41
83	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	6.2	106
84	ADRB2 polymorphisms and risk of COPD exacerbations: the Rotterdam Study. , 2019, , .		0
85	A systematic analysis highlights multiple long non-coding RNAs associated with cardiometabolic disorders. Journal of Human Genetics, 2018, 63, 431-446.	2.3	17
86	Life-Course Genome-wide Association Study Meta-analysis of Total Body BMD and Assessment of Age-Specific Effects. American Journal of Human Genetics, 2018, 102, 88-102.	6.2	252
87	Cell Cycle Regulation of Stem Cells by MicroRNAs. Stem Cell Reviews and Reports, 2018, 14, 309-322.	5.6	147
88	An Enrichment Analysis for Cardiometabolic Traits Suggests Non-Random Assignment of Genes to microRNAs. International Journal of Molecular Sciences, 2018, 19, 3666.	4.1	4
89	Whole-Genome Linkage Scan Combined With Exome Sequencing Identifies Novel Candidate Genes for Carotid Intima-Media Thickness. Frontiers in Genetics, 2018, 9, 420.	2.3	3
90	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. Blood, 2018, 132, 1842-1850.	1.4	16

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91	Epigenetics of Diabetes inÂHumans. , 2018, , 457-488.		1
92	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
93	Epigenetic Link between Statin Use and Diabetes. Diabetes, 2018, 67, .	0.6	2
94	Novel inflammatory markers for incident pre-diabetes and type 2 diabetes: the Rotterdam Study. European Journal of Epidemiology, 2017, 32, 217-226.	5.7	48
95	Genetic variants in microRNAs and their binding sites within gene 3â€²UTRs associate with susceptibility to age-related macular degeneration. Human Mutation, 2017, 38, 827-838.	2.5	30
96	Epigenome-Wide Association Study Identifies Methylation Sites Associated With Liver Enzymes and Hepatic Steatosis. Gastroenterology, 2017, 153, 1096-1106.e2.	1.3	52
97	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. American Journal of Human Genetics, 2017, 100, 51-63.	6.2	45
98	Bivariate genome-wide association meta-analysis of pediatric musculoskeletal traits reveals pleiotropic effects at the SREBF1/TOM1L2 locus. Nature Communications, 2017, 8, 121.	12.8	82
99	Association of SRD5A2 gene mutations with risk of hypospadias in the Iranian population. Journal of Endocrinological Investigation, 2017, 40, 391-396.	3.3	11
100	A Genome-Wide Scan for MicroRNA-Related Genetic Variants Associated With Primary Open-Angle Glaucoma. , 2017, 58, 5368.		25
101	Genetic Polymorphism of miR-196a-2 is Associated with Bone Mineral Density (BMD). International Journal of Molecular Sciences, 2017, 18, 2529.	4.1	14
102	Genetic Variants in MicroRNAs and Their Binding Sites Are Associated with the Risk of Parkinson Disease. Human Mutation, 2016, 37, 292-300.	2.5	52
103	Genome-wide identification of microRNA-related variants associated with risk of Alzheimerâ€™s disease. Scientific Reports, 2016, 6, 28387.	3.3	43
104	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	2.9	73
105	LSC Abstract â€“ Association of single nucleotide polymorphisms located in miRNA binding sites with lung function. , 2016, , .		0
106	LSC Abstract â€“ Association of single nucleotide polymorphisms located in miRNA binding sites with lung function. , 2016, , .		0
107	Phosphodiesterase 1 regulation is a key mechanism in vascular aging. Clinical Science, 2015, 129, 1061-1075.	4.3	53
108	The association of common polymorphisms in miR-196a2 with waist to hip ratio and miR-1908 with serum lipid and glucose. Obesity, 2015, 23, 495-503.	3.0	30

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109	Genetic Variations in MicroRNA-Binding Sites Affect MicroRNA-Mediated Regulation of Several Genes Associated With Cardio-metabolic Phenotypes. Circulation: Cardiovascular Genetics, 2015, 8, 473-486.	5.1	57
110	A Genetic Variant in the Seed Region of miR-4513 Shows Pleiotropic Effects on Lipid and Glucose Homeostasis, Blood Pressure, and Coronary Artery Disease. Human Mutation, 2014, 35, 1524-1531.	2.5	45
111	Association of IL-10 Gene Polymorphisms and Human T Lymphotropic Virus Type I-Associated Myelopathy/tropical Spastic Paraparesis in North-East of Iran (Mashhad). Iranian Journal of Basic Medical Sciences, 2013, 16, 258-63.	1.0	6
112	Human T-Lymphotropic Virus Type 1 Prevalence in Northeastern Iran, Sabzevar: An Epidemiologic-Based Study and Phylogenetic Analysis. AIDS Research and Human Retroviruses, 2012, 28, 1095-1101.	1.1	65
113	Association between vitamin D receptor gene polymorphisms and type 1 diabetes mellitus in Iranian population. Molecular Biology Reports, 2012, 39, 831-837.	2.3	47
114	Afghanistan's Ethnic Groups Share a Y-Chromosomal Heritage Structured by Historical Events. PLoS ONE, 2012, 7, e34288.	2.5	46