## **Cristian Pattaro**

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	27.8	3,249
2	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	21.4	1,982
3	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
4	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. Nature Genetics, 2009, 41, 47-55.	21.4	776
5	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	21.4	710
6	Mendelian Randomization as an Approach to Assess Causality Using Observational Data. Journal of the American Society of Nephrology: JASN, 2016, 27, 3253-3265.	6.1	639
7	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
8	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
9	Common variants at ten loci modulate the QT interval duration in the QTSCD Study. Nature Genetics, 2009, 41, 407-414.	21.4	356
10	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
11	NRXN3 Is a Novel Locus for Waist Circumference: A Genome-Wide Association Study from the CHARGE Consortium. PLoS Genetics, 2009, 5, e1000539.	3.5	230
12	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	21.4	223
13	CUBN Is a Gene Locus for Albuminuria. Journal of the American Society of Nephrology: JASN, 2011, 22, 555-570.	6.1	208
14	Genetic Determinants of Circulating Sphingolipid Concentrations in European Populations. PLoS Genetics, 2009, 5, e1000672.	3.5	184
15	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. PLoS Genetics, 2012, 8, e1002490.	3.5	181
16	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
17	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	2.9	168
18	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	3.5	166

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19	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
20	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.6	131
21	Discovery and prioritization of variants and genes for kidney function in >1.2 million individuals. Nature Communications, 2021, 12, 4350.	12.8	125
22	Most cases of primary salivary mucosa-associated lymphoid tissue lymphoma are associated either with Sjoegren syndrome or hepatitis C virus infection. British Journal of Haematology, 2004, 126, 43-49.	2.5	118
23	Genome-wide association study of kidney function decline in individuals of European descent. Kidney International, 2015, 87, 1017-1029.	5.2	113
24	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	3.3	98
25	Influence of early life exposures on incidence and remission of asthma throughout lifeâ~†. Journal of Allergy and Clinical Immunology, 2004, 113, 845-852.	2.9	93
26	Mapping eGFR loci to the renal transcriptome and phenome in the VA Million Veteran Program. Nature Communications, 2019, 10, 3842.	12.8	90
27	Common variants in the JAZF1 gene associated with height identified by linkage and genome-wide association analysis. Human Molecular Genetics, 2009, 18, 373-380.	2.9	88
28	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
29	Erectile dysfunction in male heroin users, receiving methadone and buprenorphine maintenance treatment. Drug and Alcohol Dependence, 2008, 94, 12-18.	3.2	78
30	Genome-wide linkage analysis of serum creatinine in three isolated European populations. Kidney International, 2009, 76, 297-306.	5.2	71
31	A bidirectional Mendelian randomization study supports causal effects of kidney function onÂbloodÂpressure. Kidney International, 2020, 98, 708-716.	5.2	70
32	A Genome-Wide Association Scan of RR and QT Interval Duration in 3 European Genetically Isolated Populations. Circulation: Cardiovascular Genetics, 2009, 2, 322-328.	5.1	67
33	Identification of a common variant in the TFR2 gene implicated in the physiological regulation of serum iron levels. Human Molecular Genetics, 2011, 20, 1232-1240.	2.9	67
34	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. Human Molecular Genetics, 2012, 21, 5329-5343.	2.9	64
35	The Cooperative Health Research in South Tyrol (CHRIS) study: rationale, objectives, and preliminary results. Journal of Translational Medicine, 2015, 13, 348.	4.4	63
36	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59

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37	The genetic study of three population microisolates in South Tyrol (MICROS): study design and epidemiological perspectives. BMC Medical Genetics, 2007, 8, 29.	2.1	56
38	Linkage and Genomeâ€wide Association Analysis of Obesityâ€related Phenotypes: Association of Weight With the <i>MGAT1</i> Gene. Obesity, 2010, 18, 803-808.	3.0	54
39	The UMOD Locus: Insights into the Pathogenesis and Prognosis of Kidney Disease. Journal of the American Society of Nephrology: JASN, 2018, 29, 713-726.	6.1	54
40	A meta-analysis of genome-wide data from five European isolates reveals an association of COL22A1, SYT1, and GABRR2with serum creatinine level. BMC Medical Genetics, 2010, 11, 41.	2.1	48
41	Genome-wide association analysis and fine mapping of NT-proBNP level provide novel insight into the role of the MTHFR-CLCN6-NPPA-NPPB gene cluster. Human Molecular Genetics, 2011, 20, 1660-1671.	2.9	47
42	GWAtoolbox: an R package for fast quality control and handling of genome-wide association studies meta-analysis data. Bioinformatics, 2012, 28, 444-445.	4.1	46
43	Genetics in chronic kidney disease: conclusions from a Kidney Disease: Improving Global Outcomes (KDIGO) Controversies Conference. Kidney International, 2022, 101, 1126-1141.	5.2	46
44	Variation in the Uric Acid Transporter Gene SLC2A9 and Its Association with AAO of Parkinson's Disease. Journal of Molecular Neuroscience, 2011, 43, 246-250.	2.3	44
45	Heritability Analysis of Life Span in a Semi-isolated Population Followed Across Four Centuries Reveals the Presence of Pleiotropy Between Life Span and Reproduction. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2011, 66A, 26-37.	3.6	44
46	Methods for Meta-Analyses of Genome-wide Association Studies: Critical Assessment of Empirical Evidence. American Journal of Epidemiology, 2012, 175, 739-749.	3.4	42
47	High dose benzodiazepine dependence: Description of 29 patients treated with flumazenil infusion and stabilised with clonazepam. Psychiatry Research, 2012, 198, 457-462.	3.3	42
48	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
49	Efficient haplotype block recognition of very long and dense genetic sequences. BMC Bioinformatics, 2014, 15, 10.	2.6	41
50	Trans-ethnic Mendelian-randomization study reveals causal relationships between cardiometabolic factors and chronic kidney disease. International Journal of Epidemiology, 2022, 50, 1995-2010.	1.9	39
51	Common Variants in Mendelian Kidney Disease Genes and Their Association with Renal Function. Journal of the American Society of Nephrology: JASN, 2013, 24, 2105-2117.	6.1	33
52	Estimating the Glomerular Filtration Rate in the General Population Using Different Equations: Effects on Classification and Association. Nephron Clinical Practice, 2013, 123, 102-111.	2.3	33
53	Effects of smoking status, history and intensity on heart rate variability in the general population: The CHRIS study. PLoS ONE, 2019, 14, e0215053.	2.5	33
54	Overlap Between Common Genetic Polymorphisms Underpinning Kidney Traits and Cardiovascular Disease Phenotypes: The CKDGen Consortium. American Journal of Kidney Diseases, 2013, 61, 889-898.	1.9	31

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55	Estimates of Genetic and Environmental Contribution to 43 Quantitative Traits Support Sharing of a Homogeneous Environment in an Isolated Population from South Tyrol, Italy. Human Heredity, 2008, 65, 175-182.	0.8	30
56	The CKDGen Consortium: ten years of insights into the genetic basis of kidney function. Kidney International, 2020, 97, 236-242.	5.2	29
57	Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. Journal of the American College of Cardiology, 2019, 73, 3118-3131.	2.8	27
58	Are Requirements to Deposit Data in Research Repositories Compatible With the European Union's General Data Protection Regulation?. Annals of Internal Medicine, 2019, 170, 332.	3.9	27
59	Association between restless legs syndrome and migraine: a populationâ€based study. European Journal of Neurology, 2014, 21, 1205-1210.	3.3	26
60	NFAT5 and SLC4A10 Loci Associate with Plasma Osmolality. Journal of the American Society of Nephrology: JASN, 2017, 28, 2311-2321.	6.1	24
61	Serum iron level and kidney function: a Mendelian randomization study. Nephrology Dialysis Transplantation, 2016, 32, gfw215.	0.7	23
62	Integration of GWAS Summary Statistics and Gene Expression Reveals Target Cell Types Underlying Kidney Function Traits. Journal of the American Society of Nephrology: JASN, 2020, 31, 2326-2340.	6.1	23
63	Haplotype block partitioning as a tool for dimensionality reduction in SNP association studies. BMC Genomics, 2008, 9, 405.	2.8	22
64	Sequential recruitment of study participants may inflate genetic heritability estimates. Human Genetics, 2017, 136, 743-757.	3.8	20
65	Prevalence and risk factors for viral hepatitis in the Kosovarian population: implications for health policy. Journal of Medical Virology, 2008, 80, 833-840.	5.0	18
66	Negative effect of vitamin D on kidney function: a Mendelian randomization study. Nephrology Dialysis Transplantation, 2018, 33, 2139-2145.	0.7	18
67	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
68	Structural Consistency of the Pain Sensitivity Questionnaire in the Cooperative Health Research In South Tyrol (CHRIS) Population-Based Study. Journal of Pain, 2018, 19, 1424-1434.	1.4	15
69	Importance of Different Types of Prior Knowledge in Selecting Genomeâ€Wide Findings for Followâ€Up. Genetic Epidemiology, 2013, 37, 205-213.	1.3	14
70	Classic Kaposi sarcoma in northern Sardinia: A prospective epidemiologic overview (1977-2003) correlated with malaria prevalence (1934). Journal of the American Academy of Dermatology, 2006, 55, 990-995.	1.2	13
71	<scp>SNP</scp> Prioritization Using a <scp>B</scp> ayesian Probability of Association. Genetic Epidemiology, 2013, 37, 214-221.	1.3	13
72	Genome-wide association studies of albuminuria: towards genetic stratification in diabetes?. Journal of Nephrology, 2018, 31, 475-487.	2.0	13

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73	Association Between Psoriasis and Coeliac Disease? A Case-control Study. Acta Dermato-Venereologica, 2011, 91, 92-93.	1.3	12
74	Fine-Mapping of Restless Legs Locus 4 (RLS4) Identifies a Haplotype over the SPATS2L and KCTD18 Genes. Journal of Molecular Neuroscience, 2013, 49, 600-605.	2.3	12
75	Combination of mouse models and genomewide association studies highlights novel genes associated with human kidney function. Kidney International, 2016, 90, 764-773.	5.2	11
76	Epistatic Role of the MYH9/APOL1 Region on Familial Hematuria Genes. PLoS ONE, 2013, 8, e57925.	2.5	11
77	Lipidomics, Atrial Conduction, and Body Mass Index. Circulation Genomic and Precision Medicine, 2019, 12, e002384.	3.6	9
78	Occult inflammatory breast cancer: review of clinical, mammographic, US and pathologic signs. Radiologia Medica, 2005, 109, 308-20.	7.7	9
79	Prevalence and determinants of serum antibodies to SARS-CoV-2 in the general population of the Gardena valley. Epidemiology and Infection, 2021, 149, e194.	2.1	8
80	Buprenorphine in Maintenance Treatment: Experience among Italian Physicians in Drug Addiction Centers. American Journal on Addictions, 2010, 19, 222-230.	1.4	7
81	Microbiota, type 2 diabetes and non-alcoholic fatty liver disease: protocol of an observational study. Journal of Translational Medicine, 2019, 17, 408.	4.4	7
82	Heterosexual relationships among heroin users in Italy. Drug and Alcohol Dependence, 2004, 75, 207-213.	3.2	6
83	Linkage and association analysis of hyperthyrotropinaemia in an Alpine population reveal two novel loci on chromosomes 3q28-29 and 6q26-27. Journal of Medical Genetics, 2011, 48, 549-556.	3.2	6
84	Bayesian analysis of censored response data in familyâ€based genetic association studies. Biometrical Journal, 2016, 58, 1039-1053.	1.0	5
85	Genetic and Metabolic Determinants of Atrial Fibrillation in a General Population Sample: The CHRIS Study. Biomolecules, 2021, 11, 1663.	4.0	5
86	FERTILITY PATTERN AND FAMILY STRUCTURE IN THREE ALPINE SETTLEMENTS IN SOUTH TYROL (ITALY): MARRIAGE COHORTS FROM 1750 TO 1949. Journal of Biosocial Science, 2009, 41, 697-701.	1.2	4
87	Prospective epidemiological, molecular, and genetic characterization of a novel coronavirus disease in the Val Venosta/Vinschgau: the CHRIS COVID-19 study protocol. Pathogens and Global Health, 2022, 116, 128-136.	2.3	4
88	A Prospective Nonrandomized Study on Carotid Surgery Performed under General Anesthesia without Intraoperative Cerebral Monitoring. Journal of Stroke and Cerebrovascular Diseases, 2016, 25, 136-143.	1.6	3
89	Comparative assessment of different familial aggregation methods in the context of large and unstructured pedigrees. Bioinformatics, 2019, 35, 69-76.	4.1	3
90	Factors Affecting Long-Term Results of Above-Knee Femoropopliteal Bypass. Vascular and Endovascular Surgery, 2016, 50, 72-79.	0.7	2

#	ARTICLE	IF	CITATIONS
91	SNP-Based Linkage Analysis in Extended Pedigrees: Comparison between Two Alternative Approaches. Human Heredity, 2014, 78, 27-37.	0.8	1
92	Genetics of Blood Pressure Regulation: Possible Paths in the Labyrinth. American Journal of Kidney Diseases, 2019, 74, 421-424.	1.9	1
93	Trans-Ethnic Mendelian Randomization Study Reveals Causal Relationships Between Cardiometabolic Factors and Chronic Kidney Disease. SSRN Electronic Journal, 0, , .	0.4	1
94	ParkScreen: A Low-Cost Rapid Linkage Marker Panel for Parkinson's Disease. Journal of Molecular Neuroscience, 2009, 39, 235-241.	2.3	0
95	Family-based studies to the rescue of genome-wide association studies in renal function. Kidney International, 2013, 83, 196-198.	5.2	0
96	Prognostic Value of ZAP-70 Expression Detected by Immunohistochemistry on Bone Marrow Biopsies in Early Phase Chronic Lymphocytic Leukaemia Blood, 2004, 104, 4800-4800.	1.4	0