Erika Salvi

List of Publications by Year
in descending order

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83 papers	13,436 citations	81900 39 h-index	64796 79 g-index
85 all docs	85 docs citations	85 times ranked	24210 citing authors

#	Article	IF	Citations
1	Dissecting the Polygenic Basis of Primary Hypertension: Identification of Key Pathway-Specific Components. Frontiers in Cardiovascular Medicine, 2022, 9, 814502.	2.4	5
2	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nature Genetics, 2022, 54, 437-449.	21.4	215
3	Association of colorectal cancer with genetic and epigenetic variation in PEAR1â€"A population-based cohort study. PLoS ONE, 2022, 17, e0266481.	2.5	1
4	A multi-step genomic approach prioritized TBKBP1 gene as relevant for multiple sclerosis susceptibility. Journal of Neurology, 2022, 269, 4510-4522.	3.6	2
5	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
6	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
7	Peripheral Ion Channel Gene Screening in Painful- and Painless-Diabetic Neuropathy. International Journal of Molecular Sciences, 2022, 23, 7190.	4.1	9
8	Genome sequencing analysis identifies new loci associated with Lewy body dementia and provides insights into its genetic architecture. Nature Genetics, 2021, 53, 294-303.	21.4	198
9	Ricolinostat induces microtubule acetylation and neurite regeneration in cellular models of diabetic and chemotheraphy-induced neuropathy. Journal of the Neurological Sciences, 2021, 429, 119951.	0.6	0
10	Congenital insensitivity to pain. Pain, 2021, Publish Ahead of Print, .	4.2	6
11	Computational pipeline to probe NaV1.7 gain-of-function variants in neuropathic painful syndromes. Scientific Reports, 2020, 10, 17930.	3.3	3
12	Evaluation of molecular inversion probe versus TruSeqÂ® custom methods for targeted next-generation sequencing. PLoS ONE, 2020, 15, e0238467.	2.5	17
13	Genome-Wide Meta-Analysis Identifies Three Novel Susceptibility Loci and Reveals Ethnic Heterogeneity of Genetic Susceptibility for IgA Nephropathy. Journal of the American Society of Nephrology: JASN, 2020, 31, 2949-2963.	6.1	42
14	Abstract P122: Lanosterol Synthase (LSS) Gene As Predictor Of Kidney Dysfunction In Hypertensive Patients. Hypertension, 2020, 76, .	2.7	0
15	Genomeâ€Wide Metaâ€Analysis of Blood Pressure Response to Î² ₁ â€Blockers: Results From ICAPS (International Consortium of Antihypertensive Pharmacogenomics Studies). Journal of the American Heart Association, 2019, 8, e013115.	3.7	21
16	Diagnostic criteria for small fibre neuropathy in clinical practice and research. Brain, 2019, 142, 3728-3736.	7.6	111
17	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
18	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251

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19	A red orange and lemon byâ€products extract rich in anthocyanins inhibits the progression of diabetic nephropathy. Journal of Cellular Physiology, 2019, 234, 23268-23278.	4.1	23
20	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
21	Shared polygenic risk and causal inferences in amyotrophic lateral sclerosis. Annals of Neurology, 2019, 85, 470-481.	5.3	118
22	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. Nature Genetics, 2019, 51, 245-257.	21.4	536
23	Re: Claudin-14 Gene Polymorphisms and Urine Calcium Excretion. Journal of Urology, 2019, 201, 662-662.	0.4	0
24	The risk of nephrolithiasis is causally related to inactive matrix Gla protein, a marker of vitamin K status: a Mendelian randomization study in a Flemish population. Nephrology Dialysis Transplantation, 2018, 33, 514-522.	0.7	15
25	Claudin-14 Gene Polymorphisms and Urine Calcium Excretion. Clinical Journal of the American Society of Nephrology: CJASN, 2018, 13, 1542-1549.	4.5	14
26	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. Nature Genetics, 2018, 50, 1112-1121.	21.4	1,835
27	A novel SCN9A splicing mutation in a compound heterozygous girl with congenital insensitivity to pain, hyposmia and hypogeusia. Journal of the Peripheral Nervous System, 2018, 23, 202-206.	3.1	25
28	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	12.8	95
29	Pseudoexfoliation syndrome-associated genetic variants affect transcription factor binding and alternative splicing of LOXL1. Nature Communications, 2017, 8, 15466.	12.8	57
30	Nextâ€generation sequencing of a family with a high penetrance of monoclonal gammopathies for the identification of candidate risk alleles. Cancer, 2017, 123, 3701-3708.	4.1	12
31	Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci. Nature Genetics, 2017, 49, 993-1004.	21.4	114
32	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. Journal of the American Society of Nephrology: JASN, 2017, 28, 981-994.	6.1	39
33	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	12.8	64
34	PEAR1 is not a major susceptibility gene for cardiovascular disease in a Flemish population. BMC Medical Genetics, 2017, 18, 45.	2.1	13
35	Genome-Wide and Gene-Based Meta-Analyses Identify Novel Loci Influencing Blood Pressure Response to Hydrochlorothiazide. Hypertension, 2017, 69, 51-59.	2.7	34
36	A novel network analysis approach reveals DNA damage, oxidative stress and calcium/cAMP homeostasis-associated biomarkers in frontotemporal dementia. PLoS ONE, 2017, 12, e0185797.	2.5	21

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37	Association Analysis of Noncoding Variants in Neuroligins 3 and 4X Genes with Autism Spectrum Disorder in an Italian Cohort. International Journal of Molecular Sciences, 2016, 17, 1765.	4.1	16
38	Xanthine oxidase gene variants and their association with blood pressure and incident hypertension. Journal of Hypertension, 2016, 34, 2147-2154.	0.5	30
39	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
40	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
41	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
42	Interaction between polyphenols intake and PON1 gene variants on markers of cardiovascular disease: a nutrigenetic observational study. Journal of Translational Medicine, 2016, 14, 186.	4.4	38
43	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
44	Effect of intravenous l-carnitine in Chinese patients with chronic heart failure. European Heart Journal Supplements, 2016, 18, A27-A36.	0.1	9
45	A candidate gene study identifies a haplotype of CD2 as novel susceptibility factor for systemic sclerosis. Clinical and Experimental Rheumatology, 2016, 34 Suppl 100, 43-48.	0.8	1
46	Coronary risk in relation to genetic variation in MEOX2 and TCF15 in a Flemish population. BMC Genetics, 2015, 16, 116.	2.7	12
47	Identification of NF-Î²B and PLCL2 as new susceptibility genes and highlights on a potential role of IRF8 through interferon signature modulation in systemic sclerosis. Arthritis Research and Therapy, 2015, 17, 71.	3.5	41
48	TET2 and CSMD1 genes affect SBP response to hydrochlorothiazide in never-treated essential hypertensives. Journal of Hypertension, 2015, 33, 1301-1309.	0.5	29
49	Copy Number Variations and Cognitive Phenotypes in Unselected Populations. Obstetrical and Gynecological Survey, 2015, 70, 559-560.	0.4	2
50	Copy Number Variations and Cognitive Phenotypes in Unselected Populations. JAMA - Journal of the American Medical Association, 2015, 313, 2044.	7.4	143
51	Pharmacogenomics of Hypertension: A Genomeâ€Wide, Placeboâ€Controlled Crossâ€Over Study, Using Four Classes of Antihypertensive Drugs. Journal of the American Heart Association, 2015, 4, e001521.	3.7	74
52	Cross-Disorder Genome-Wide Analyses Suggest a Complex Genetic Relationship Between Touretteâ€™s Syndrome and OCD. American Journal of Psychiatry, 2015, 172, 82-93.	7.2	117
53	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
54	PEAR1 is not a human hypertension-susceptibility gene. Blood Pressure, 2015, 24, 61-64.	1.5	7

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55	A genome-wide screening and SNPs-to-genes approach to identify novel genetic risk factors associated with frontotemporal dementia. Neurobiology of Aging, 2015, 36, 2904.e13-2904.e26.	3.1	48
56	The â^'665 C>T polymorphism in the eNOS gene predicts cardiovascular mortality and morbidity in white Europeans. Journal of Human Hypertension, 2015, 29, 167-172.	2.2	10
57	Pharmacogenomics considerations in the control of hypertension. Pharmacogenomics, 2015, 16, 1951-1964.	1.3	10
58	Inactive Matrix Gla Protein Is Causally Related to Adverse Health Outcomes. Hypertension, 2015, 65, 463-470.	2.7	84
59	Genome-wide association study of kidney function decline in individuals of European descent. Kidney International, 2015, 87, 1017-1029.	5.2	113
60	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	3.5	80
61	Genome-wide association study identifies CAMKID variants involved in blood pressure response to losartan: the SOPHIA study. Pharmacogenomics, 2014, 15, 1643-1652.	1.3	27
62	Left ventricular diastolic function associated with common genetic variation in ATP12Ain a general population. BMC Medical Genetics, 2014, 15, 121.	2.1	4
63	Discovery of new risk loci for IgA nephropathy implicates genes involved in immunity against intestinal pathogens. Nature Genetics, 2014, 46, 1187-1196.	21.4	505
64	Dietary Salt Intake, Blood Pressure, and Genes. Current Nutrition Reports, 2013, 2, 134-141.	4.3	2
65	Genetics can contribute to the prognosis of Brugada syndrome: a pilot model for risk stratification. European Journal of Human Genetics, 2013, 21, 911-917.	2.8	58
66	A â€œCandidate-Interactomeâ€•Aggregate Analysis of Genome-Wide Association Data in Multiple Sclerosis. PLoS ONE, 2013, 8, e63300.	2.5	66
67	Target Sequencing, Cell Experiments, and a Population Study Establish Endothelial Nitric Oxide Synthase (eNOS) Gene as Hypertension Susceptibility Gene. Hypertension, 2013, 62, 844-852.	2.7	48
68	Brief Report: A Regulatory Variant in CCR6 Is Associated With Susceptibility to Antitopoisomeraseâ€Positive Systemic Sclerosis. Arthritis and Rheumatism, 2013, 65, 3202-3208.	6.7	26
69	Genomewide Association Study Using a High-Density Single Nucleotide Polymorphism Array and Case-Control Design Identifies a Novel Essential Hypertension Susceptibility Locus in the Promoter Region of Endothelial NO Synthase. Hypertension, 2012, 59, 248-255.	2.7	144
70	Response to Endothelial Nitric Oxide Synthase Polymorphism rs3918226 Associated With Hypertension Does Not Affect Plasma Nitrite Levels in Healthy Subjects. Hypertension, 2012, 59, .	2.7	1
71	Genome-Wide Association Study to Identify Common Variants Associated with Brachial Circumference: A Meta-Analysis of 14 Cohorts. PLoS ONE, 2012, 7, e31369.	2.5	3
72	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	27.8	2,400

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73	Genes Involved in Vasoconstriction and Vasodilation System Affect Salt-Sensitive Hypertension. PLoS ONE, 2011, 6, e19620.	2.5	58
74	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	6.2	159
75	Evidence of the contribution of the X chromosome to systemic sclerosis susceptibility: Association with the functional IRAK1 196Phe/532Ser haplotype. Arthritis and Rheumatism, 2011, 63, 3979-3987.	6.7	56
76	Genome-Wide Scan Identifies TNIP1, PSORS1C1, and RHOB as Novel Risk Loci for Systemic Sclerosis. PLoS Genetics, 2011, 7, e1002091.	3.5	205
77	Population Stratification Analysis in Genome-Wide Association Studies. , 2011, , 177-196.		0
78	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
79	Fine mapping ofAHI1as a schizophrenia susceptibility gene: from association to evolutionary evidence. FASEB Journal, 2010, 24, 3066-3082.	0.5	39
80	Adducin- and Ouabain-Related Gene Variants Predict the Antihypertensive Activity of Rostafuroxin, Part 2: Clinical Studies. Science Translational Medicine, 2010, 2, 59ra87.	12.4	73
81	Hippocampal Atrophy as a Quantitative Trait in a Genome-Wide Association Study Identifying Novel Susceptibility Genes for Alzheimer's Disease. PLoS ONE, 2009, 4, e6501.	2.5	321
82	SNPLims: a data management system for genome wide association studies. BMC Bioinformatics, 2008, 9, S13.	2.6	19
83	Modelling the interaction of steroid receptors with endocrine disrupting chemicals. BMC Bioinformatics, 2005, 6, S10.	2.6	25