## Nicola N Pirastu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4963686/publications.pdf

Version: 2024-02-01

65 papers 10,976 citations

35 h-index 64 g-index

74 all docs

74 docs citations

times ranked

74

23299 citing authors

#	Article	IF	CITATIONS
1	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nature Genetics, 2022, 54, 437-449.	9.4	215
2	Genetic Landscape of the ACE2 Coronavirus Receptor. Circulation, 2022, 145, 1398-1411.	1.6	20
3	Genome-wide Association Study of Liking for Several Types of Physical Activity in the UK Biobank and Two Replication Cohorts. Medicine and Science in Sports and Exercise, 2022, 54, 1252-1260.	0.2	3
4	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits. Nature Communications, 2022, 13, 2743.	5.8	22
5	Using genetic variation to disentangle the complex relationship between food intake and health outcomes. PLoS Genetics, 2022, 18, e1010162.	1.5	12
6	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	2.0	17
7	Genetic analyses identify widespread sex-differential participation bias. Nature Genetics, 2021, 53, 663-671.	9.4	124
8	Mendelian Randomization Identifies the Potential Causal Impact of Dietary Patterns on Circulating Blood Metabolites. Frontiers in Genetics, 2021, 12, 738265.	1.1	5
9	Coffee Consumption and Kidney Function: A Mendelian Randomization Study. American Journal of Kidney Diseases, 2020, 75, 753-761.	2.1	56
10	More Than Smellâ€"COVID-19 Is Associated With Severe Impairment of Smell, Taste, and Chemesthesis. Chemical Senses, 2020, 45, 609-622.	1.1	375
11	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
12	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251
13	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
14	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.	9.4	536
15	A genomeâ€wide association study identifies an association between variants in <scp>EFCAB</scp> 4B gene and periodontal disease in an Italian isolated population. Journal of Periodontal Research, 2018, 53, 992-998.	1.4	15
16	Reply to â€~Misestimation of heritability and prediction accuracy of male-pattern baldness'. Nature Communications, 2018, 9, 2538.	5.8	0
17	Exploring influences on food choice in a large population sample: The Italian Taste project. Food Quality and Preference, 2017, 59, 123-140.	2.3	128
18	<i><scp>LTF</scp></i> and <i><scp>DEFB</scp>1</i> polymorphisms are associated with susceptibility toward chronic periodontitis development. Oral Diseases, 2017, 23, 1001-1008.	1.5	21

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19	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	5.8	118
20	GWAS for male-pattern baldness identifies 71 susceptibility loci explaining 38% of the risk. Nature Communications, 2017, 8, 1584.	5.8	61
21	A Genome-Wide Association Study in isolated populations reveals new genes associated to common food likings. Reviews in Endocrine and Metabolic Disorders, 2016, 17, 209-219.	2.6	22
22	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
23	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
24	<i>KLB</i> is associated with alcohol drinking, and its gene product $\hat{l}^2$ -Klotho is necessary for FGF21 regulation of alcohol preference. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14372-14377.	3.3	208
25	Caries and Innate Immunity: <b><i>DEFB1</i></b> Gene Polymorphisms and Caries Susceptibility in Genetic Isolates from North-Eastern Italy. Caries Research, 2016, 50, 589-594.	0.9	19
26	Non-additive genome-wide association scan reveals a new gene associated with habitual coffee consumption. Scientific Reports, 2016, 6, 31590.	1.6	25
27	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	3.3	110
28	Caffeine metabolism rate influences coffee perception, preferences and intake. Food Quality and Preference, 2016, 53, 97-104.	2.3	20
29	Understanding the role of personality and alexithymia in food preferences and PROP taste perception. Physiology and Behavior, 2016, 157, 72-78.	1.0	37
30	Food Preference Patterns in a UK Twin Cohort. Twin Research and Human Genetics, 2015, 18, 793-805.	0.3	64
31	Uncovering the genetic basis for food preferences: the key to personalized nutrition plans?. Personalized Medicine, 2015, 12, 315-317.	0.8	0
32	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. Obstetrical and Gynecological Survey, 2015, 70, 758-762.	0.2	0
33	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
34	Genome-wide association analysis on five isolated populations identifies variants of the HLA-DOA gene associated with white wine liking. European Journal of Human Genetics, 2015, 23, 1717-1722.	1.4	12
35	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	9.4	357
36	Multicohort analysis of the maternal age effect on recombination. Nature Communications, 2015, 6, 7846.	5.8	29

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37	Polymorphisms in sweet taste genes (TAS1R2 and GLUT2), sweet liking, and dental caries prevalence in an adult Italian population. Genes and Nutrition, 2015, 10, 485.	1.2	25
38	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	1.1	64
39	Association Analysis of Bitter Receptor Genes in Five Isolated Populations Identifies a Significant Correlation between TAS2R43 Variants and Coffee Liking. PLoS ONE, 2014, 9, e92065.	1.1	41
40	Identification of Novel Genetic Loci Associated with Thyroid Peroxidase Antibodies and Clinical Thyroid Disease. PLoS Genetics, 2014, 10, e1004123.	1.5	150
41	Salt-inducible kinase 3, SIK3, is a new gene associated with hearing. Human Molecular Genetics, 2014, 23, 6407-6418.	1.4	30
42	A General Approach for Haplotype Phasing across the Full Spectrum of Relatedness. PLoS Genetics, 2014, 10, e1004234.	1.5	553
43	A Population-Based Approach to Study the Impact of PROP Perception on Food Liking in Populations along the Silk Road. PLoS ONE, 2014, 9, e91716.	1.1	34
44	Exome analysis of HIV patients submitted to dendritic cells therapeutic vaccine reveals an association of <i>CNOT1</i> gene with response to the treatment. Journal of the International AIDS Society, 2014, 17, 18938.	1.2	15
45	Genetic landscape of populations along the Silk Road: admixture and migration patterns. BMC Genetics, 2014, 15, 131.	2.7	24
46	Estrogen-related receptor gamma and hearing function: evidence of a role in humans and mice. Neurobiology of Aging, 2013, 34, 2077.e1-2077.e9.	1.5	53
47	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	9.4	675
48	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. PLoS Genetics, 2013, 9, e1003796.	1.5	142
49	Age- And Sex-Related Variations in Platelet Count in Italy: A Proposal of Reference Ranges Based on 40987 Subjects' Data. PLoS ONE, 2013, 8, e54289.	1.1	190
50	Genome Wide Association Analysis of a Founder Population Identified TAF3 as a Gene for MCHC in Humans. PLoS ONE, 2013, 8, e69206.	1.1	9
51	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	1.5	79
52	Genetics of Food Preferences: A First View from Silk Road Populations. Journal of Food Science, 2012, 77, S413-8.	1.5	45
53	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	13.7	320
54	Genome-wide meta-analysis of common variant differences between men and women. Human Molecular Genetics, 2012, 21, 4805-4815.	1.4	33

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55	A strategy analysis for genetic association studies with known inbreeding. BMC Genetics, 2011, 12, 63.	2.7	8
56	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	13.7	401
57	Frequency of hearing loss in a series of rural communities of five developing countries located along the Silk Road. Audiological Medicine, 2011, 9, 135-140.	0.4	15
58	Hearing function and thresholds: a genome-wide association study in European isolated populations identifies new loci and pathways. Journal of Medical Genetics, 2011, 48, 369-374.	1.5	71
59	A novel mutation in the vWFA2 domain of the COCH gene in an Italian DFNA9 family. Audiological Medicine, 2011, 9, 4-7.	0.4	3
60	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	9.4	403
61	Multiple Loci Are Associated with White Blood Cell Phenotypes. PLoS Genetics, 2011, 7, e1002113.	1.5	106
62	High Differentiation among Eight Villages in a Secluded Area of Sardinia Revealed by Genome-Wide High Density SNPs Analysis. PLoS ONE, 2009, 4, e4654.	1.1	30
63	Microsatellites and SNPs linkage analysis in a Sardinian genetic isolate confirms several essential hypertension loci previously identified in different populations. BMC Medical Genetics, 2009, 10, 81.	2.1	8
64	EDA2R Is Associated with Androgenetic Alopecia. Journal of Investigative Dermatology, 2008, 128, 2268-2270.	0.3	79
65	Patterns of Linkage Disequilibrium between SNPs in a Sardinian Population Isolate and the Selection of Markers for Association Studies. Human Heredity, 2008, 65, 9-22.	0.4	14