

Cosetta Minelli

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

6,296
citations

159585

30
h-index

233421

45
g-index

53
all docs

53
docs citations

53
times ranked

7058
citing authors

#	ARTICLE	IF	CITATIONS
1	A framework for the investigation of pleiotropy in two-sample summary data Mendelian randomization. <i>Statistics in Medicine</i> , 2017, 36, 1783-1802.	1.6	975
2	Assessing the suitability of summary data for two-sample Mendelian randomization analyses using MR-Egger regression: the role of the I2 statistic. <i>International Journal of Epidemiology</i> , 2016, 45, dyw220.	1.9	787
3	Detecting pleiotropy in Mendelian randomisation studies with summary data and a continuous outcome. <i>Statistics in Medicine</i> , 2015, 34, 2926-2940.	1.6	671
4	Guidelines for performing Mendelian randomization investigations. <i>Wellcome Open Research</i> , 2019, 4, 186.	1.8	661
5	Guidelines for performing Mendelian randomization investigations. <i>Wellcome Open Research</i> , 2019, 4, 186.	1.8	511
6	Improving the visualization, interpretation and analysis of two-sample summary data Mendelian randomization via the Radial plot and Radial regression. <i>International Journal of Epidemiology</i> , 2018, 47, 1264-1278.	1.9	389
7	Improving the accuracy of two-sample summary-data Mendelian randomization: moving beyond the NOME assumption. <i>International Journal of Epidemiology</i> , 2019, 48, 728-742.	1.9	346
8	The choice of a genetic model in the meta-analysis of molecular association studies. <i>International Journal of Epidemiology</i> , 2005, 34, 1319-1328.	1.9	179
9	The use of two-sample methods for Mendelian randomization analyses on single large datasets. <i>International Journal of Epidemiology</i> , 2021, 50, 1651-1659.	1.9	150
10	Reasons for refusal of admission to intensive care and impact on mortality. <i>Intensive Care Medicine</i> , 2010, 36, 1772-1779.	8.2	112
11	How should we use information about HWE in the meta-analyses of genetic association studies?. <i>International Journal of Epidemiology</i> , 2008, 37, 136-146.	1.9	106
12	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. <i>Journal of Clinical Investigation</i> , 2017, 127, 1798-1812.	8.2	106
13	Data harmonization and federated analysis of population-based studies: the BioSHaRE project. <i>Emerging Themes in Epidemiology</i> , 2013, 10, 12.	2.7	105
14	Glutathione-S-transferase genes and asthma phenotypes: a Human Genome Epidemiology (HuGE) systematic review and meta-analysis including unpublished data. <i>International Journal of Epidemiology</i> , 2010, 39, 539-562.	1.9	100
15	Interactive Effects of Antioxidant Genes and Air Pollution on Respiratory Function and Airway Disease: A HuGE Review. <i>American Journal of Epidemiology</i> , 2011, 173, 603-620.	3.4	84
16	Meta-analysis of genetic studies using Mendelian randomization—a multivariate approach. <i>Statistics in Medicine</i> , 2005, 24, 2241-2254.	1.6	74
17	Age at menarche and adult body mass index: a Mendelian randomization study. <i>International Journal of Obesity</i> , 2018, 42, 1574-1581.	3.4	68
18	An Integrated Approach to the Meta-Analysis of Genetic Association Studies using Mendelian Randomization. <i>American Journal of Epidemiology</i> , 2004, 160, 445-452.	3.4	66

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19	The Cooperative Health Research in South Tyrol (CHRIS) study: rationale, objectives, and preliminary results. <i>Journal of Translational Medicine</i> , 2015, 13, 348.	4.4	63
20	Mendelian Randomization using Public Data from Genetic Consortia. <i>International Journal of Biostatistics</i> , 2016, 12, .	0.7	59
21	Age at puberty and risk of asthma: A Mendelian randomisation study. <i>PLoS Medicine</i> , 2018, 15, e1002634.	8.4	54
22	Prevalence and Population-Attributable Risk for Chronic Airflow Obstruction in a Large Multinational Study. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2021, 203, 1353-1365.	5.6	52
23	Benefits and harms associated with hormone replacement therapy: clinical decision analysis. <i>BMJ: British Medical Journal</i> , 2004, 328, 371.	2.3	48
24	Bayesian implementation of a genetic model-free approach to the meta-analysis of genetic association studies. <i>Statistics in Medicine</i> , 2005, 24, 3845-3861.	1.6	48
25	Association of Height Growth in Puberty with Lung Function. A Longitudinal Study. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 198, 1539-1548.	5.6	47
26	The association between chronic airflow obstruction and poverty in 12 sites of the multinational BOLD study. <i>European Respiratory Journal</i> , 2017, 49, 1601880.	6.7	46
27	The Quality of Meta-Analyses of Genetic Association Studies: A Review With Recommendations. <i>American Journal of Epidemiology</i> , 2009, 170, 1333-1343.	3.4	41
28	Mendelian randomization incorporating uncertainty about pleiotropy. <i>Statistics in Medicine</i> , 2017, 36, 4627-4645.	1.6	39
29	Age at menarche and lung function: a Mendelian randomization study. <i>European Journal of Epidemiology</i> , 2017, 32, 701-710.	5.7	37
30	Value of Information: A Tool to Improve Research Prioritization and Reduce Waste. <i>PLoS Medicine</i> , 2015, 12, e1001882.	8.4	31
31	Heterozygous <i>Vangl2</i> <i>Looptail</i> mice reveal novel roles for the planar cell polarity pathway in adult lung homeostasis and repair. <i>DMM Disease Models and Mechanisms</i> , 2017, 10, 409-423.	2.4	31
32	Age at menopause and lung function: a Mendelian randomisation study. <i>European Respiratory Journal</i> , 2019, 54, 1802421.	6.7	23
33	Lung Development Genes and Adult Lung Function. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 202, 853-865.	5.6	23
34	Interaction between gas cooking and <i>GSTM1</i> null genotype in bronchial responsiveness: results from the European Community Respiratory Health Survey. <i>Thorax</i> , 2014, 69, 558-564.	5.6	22
35	Ambient heat exposure and COPD hospitalisations in England: a nationwide case-crossover study during 2007–2018. <i>Thorax</i> , 2022, 77, 1098-1104.	5.6	19
36	Choosing between per-genotype, per-allele, and trend approaches for initial detection of gene–disease association. <i>Journal of Applied Statistics</i> , 2009, 36, 633-646.	1.3	17

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37	Association of Forced Vital Capacity with the Developmental Gene NCOR2. PLoS ONE, 2016, 11, e0147388.	2.5	17
38	Assessment of Factors Related to Auto-PEEP. Respiratory Care, 2016, 61, 134-141.	1.6	12
39	Effect of external PEEP in patients under controlled mechanical ventilation with an auto-PEEP of 5ÂcmH2O or higher. Annals of Intensive Care, 2016, 6, 53.	4.6	11
40	The role of antioxidant gene polymorphisms in modifying the health effects of environmental exposures causing oxidative stress: A public health perspective. Free Radical Biology and Medicine, 2011, 51, 925-930.	2.9	8
41	Chronic airflow obstruction and ambient particulate air pollution. Thorax, 2021, 76, 1236-1241.	5.6	7
42	Using reference values to define disease based on the lower limit of normal biased the population attributable fraction, but not the population excess risk: the example of chronic airflow obstruction. Journal of Clinical Epidemiology, 2018, 93, 76-78.	5.0	6
43	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	4
44	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	3
45	Communication of personalised disease risk by general practitioners to motivate smoking cessation in England: A cost-effectiveness and research prioritisation study. Addiction, 2021, , .	3.3	2
46	Response to Letters by Lee et al and Lev et al. Stroke, 2006, 37, 2203-2203.	2.0	0
47	Meta-analysis of genetic association studies: magic tool or dangerous black box?. European Journal of Epidemiology, 2010, 25, 761-763.	5.7	0
48	Effects of the Environment and Its Interplay with Genetics in Lung Function throughout Life. American Journal of Respiratory and Critical Care Medicine, 2020, 201, 1425-1427.	5.6	0
49	BIMAMâ€”a tool for imputing variables missing across datasets using a Bayesian imputation and analysis model. International Journal of Epidemiology, 0, , .	1.9	0