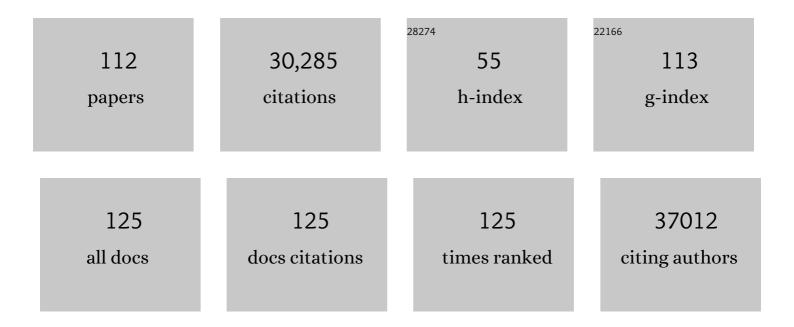
List of Publications by Year in descending order

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IENNIE HIII

#	Article	IF	CITATIONS
1	DXA-Derived vs Standard Anthropometric Measures for Predicting Cardiometabolic Risk in Middle-Aged Australian Men and Women. Journal of Clinical Densitometry, 2022, 25, 299-307.	1.2	6
2	Comprehensive genetic analysis of the human lipidome identifies loci associated with lipid homeostasis with links to coronary artery disease. Nature Communications, 2022, 13, .	12.8	30
3	U-Shaped Relationship of Leukocyte Telomere Length With All-Cause and Cancer-Related Mortality in Older Men. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2021, 76, 164-171.	3.6	6
4	Exposure to household air pollution over 10â€years is related to asthma and lung function decline. European Respiratory Journal, 2021, 57, 2000602.	6.7	18
5	Prevalence and patterns of multimorbidity in Australian baby boomers: the Busselton healthy ageing study. BMC Public Health, 2021, 21, 1539.	2.9	14
6	Airway microbial communities, smoking and asthma in a general population sample. EBioMedicine, 2021, 71, 103538.	6.1	26
7	The prevalence and comorbidities of obstructive sleep apnea in middle-aged men and women: the Busselton Healthy Ageing Study. Journal of Clinical Sleep Medicine, 2021, 17, 2029-2039.	2.6	20
8	The Wittenoom legacy. International Journal of Epidemiology, 2020, 49, 467-476.	1.9	11
9	Early-Life Exposure to Oral Antibiotics andÂLung Function Into Early Adulthood. Chest, 2020, 157, 334-341.	0.8	1
10	High-coverage plasma lipidomics reveals novel sex-specific lipidomic fingerprints of age and BMI: Evidence from two large population cohort studies. PLoS Biology, 2020, 18, e3000870.	5.6	89
11	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. Lancet Respiratory Medicine,the, 2020, 8, 696-708.	10.7	69
12	Phenotype consensus is required to enable largeâ€scale genetic consortium studies of food allergy. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 2383-2387.	5.7	5
13	Early life acetaminophen exposure, glutathione S-transferase genes, and development of adolescent asthma in a high-risk birth cohort. Journal of Allergy and Clinical Immunology, 2020, 146, 1035-1044.e12.	2.9	8
14	Associations of plasma IGF1, IGFBP3 and estradiol with leucocyte telomere length, a marker of biological age, in men. European Journal of Endocrinology, 2020, 182, 23-33.	3.7	10
15	Genome-wide Association Study of Change in Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals. Scientific Reports, 2019, 9, 9439.	3.3	5
16	Why Not Use the Immunoglobulin G N-Glycans as Predictor Variables in Disease Biomarker–Phenotype Association Studies? A Multivariate Analysis. OMICS A Journal of Integrative Biology, 2019, 23, 668-670.	2.0	5
17	PEBBLES study protocol: a randomised controlled trial to prevent atopic dermatitis, food allergy and sensitisation in infants with a family history of allergic disease using a skin barrier improvement strategy. BMJ Open, 2019, 9, e024594.	1.9	45
18	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. Nature Genetics, 2019, 51, 481-493.	21.4	350

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19	Genetic landscape of chronic obstructive pulmonary disease identifies heterogeneous cell-type and phenotype associations. Nature Genetics, 2019, 51, 494-505.	21.4	257
20	Crossâ€sectional associations of sex hormones with leucocyte telomere length, a marker of biological age, in a communityâ€based cohort of older men. Clinical Endocrinology, 2019, 90, 562-569.	2.4	9
21	Interaction of Glutathione S-Transferase M1,ÂT1, and P1 Genes With Early Life Tobacco Smoke Exposure on Lung Function in Adolescents. Chest, 2019, 155, 94-102.	0.8	12
22	Increased central adiposity is associated with pro-inflammatory immunoglobulin G N-glycans. Immunobiology, 2019, 224, 110-115.	1.9	34
23	A 5αâ€reductase (SRD5A2) polymorphism is associated with serum testosterone and sex hormone–binding globulin in men, while aromatase (CYP19A1) polymorphisms are associated with oestradiol and luteinizing hormone reciprocally. Clinical Endocrinology, 2019, 90, 301-311.	2.4	3
24	Earlyâ€life exposure to sibling modifies the relationship between <i>CD14</i> polymorphisms and allergic sensitization. Clinical and Experimental Allergy, 2019, 49, 331-340.	2.9	2
25	Vitamin D and respiratory health in the Busselton Healthy Ageing Study. Respirology, 2018, 23, 576-582.	2.3	15
26	A Canadian genome-wide association study and meta-analysis confirm HLA as a risk factor for peanut allergy independent of asthma. Journal of Allergy and Clinical Immunology, 2018, 141, 1513-1516.	2.9	21
27	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	21.4	426
28	Genome-wide association study and meta-analysis in multiple populations identifies new loci for peanut allergy and establishes C11orf30/EMSY as a genetic risk factor for food allergy. Journal of Allergy and Clinical Immunology, 2018, 141, 991-1001.	2.9	57
29	Pleiotropy of cardiometabolic syndrome with obesity-related anthropometric traits determined using empirically derived kinships from the Busselton Health Study. Human Genetics, 2018, 137, 45-53.	3.8	10
30	Obstructive airway disease in 46–65â€yearâ€old people in Busselton, Western Australia, 1966–2015. Medic Journal of Australia, 2018, 208, 209-213.	al 1.7	1
31	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. Nature Communications, 2018, 9, 4455.	12.8	181
32	Traffic-related air pollution exposure is associated with allergic sensitization, asthma, and poor lung function in middle age. Journal of Allergy and Clinical Immunology, 2017, 139, 122-129.e1.	2.9	117
33	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	7.1	376
34	Risk factors for malignant mesothelioma in people with no known exposure to asbestos. American Journal of Industrial Medicine, 2017, 60, 432-436.	2.1	6
35	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. Nature Genetics, 2017, 49, 416-425.	21.4	257
36	Genetic variants affecting cross-sectional lung function in adults show little or no effect on longitudinal lung function decline. Thorax, 2017, 72, 400-408.	5.6	25

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37	Effects of androgen deprivation therapy on telomere length. Clinical Endocrinology, 2017, 87, 381-385.	2.4	9
38	The interaction between farming/rural environment and TLR2, TLR4, TLR6 and CD14 genetic polymorphisms in relation to early- and late-onset asthma. Scientific Reports, 2017, 7, 43681.	3.3	27
39	Genetic variants in HLA are a significant risk factor for peanut allergy independent of asthma. Journal of Allergy and Clinical Immunology, 2017, 139, AB88.	2.9	0
40	Traffic-related air pollution exposure over a 5-year period is associated with increased risk of asthma and poor lung function in middle age. European Respiratory Journal, 2017, 50, 1602357.	6.7	80
41	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	2.7	123
42	Gene-based analysis of regulatory variants identifies 4 putative novel asthma risk genes related to nucleotide synthesis and signaling. Journal of Allergy and Clinical Immunology, 2017, 139, 1148-1157.	2.9	72
43	Cytokine levels and associations with symptom severity in male and female children with autism spectrum disorder. Molecular Autism, 2017, 8, 63.	4.9	80
44	Genome-wide physical activity interactions in adiposity ― A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
45	Estimating eligibility for lung cancer screening in an Australian cohort, including the effect of spirometry. Medical Journal of Australia, 2016, 204, 406-406.	1.7	4
46	Do Variants in GSTs Modify the Association between Traffic Air Pollution and Asthma in Adolescence?. International Journal of Molecular Sciences, 2016, 17, 485.	4.1	20
47	Identification of <i>STOML2</i> as a putative novel asthma risk gene associated with <i>IL6R</i> . Allergy: European Journal of Allergy and Clinical Immunology, 2016, 71, 1020-1030.	5.7	7
48	Common genetic variants associated with thyroid function may be risk alleles for Hashimoto's disease and Graves' disease. Clinical Endocrinology, 2016, 84, 278-283.	2.4	4
49	HABP2 germline variants are uncommon in familial nonmedullary thyroid cancer. BMC Medical Genetics, 2016, 17, 60.	2.1	31
50	Epidemiological and Mendelian Randomization Studies of Dihydrotestosterone and Estradiol and Leukocyte Telomere Length in Men. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 1299-1306.	3.6	37
51	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
52	Genome-wide association study of copy number variation with lung function identifies a novel signal of association near BANP for forced vital capacity. BMC Genetics, 2016, 17, 116.	2.7	0
53	Eligibility for lung cancer screening in Australia and the effect on screening eligibility of using spirometry to identify COPD. , 2016, , .		0
54	Vitamin D and respiratory health in the Busselton healthy ageing study. , 2016, , .		1

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55	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
56	Whole-genome sequence-based analysis of thyroid function. Nature Communications, 2015, 6, 5681.	12.8	75
57	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	12.8	108
58	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
59	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
60	Molecular mechanisms underlying variations in lung function: a systems genetics analysis. Lancet Respiratory Medicine,the, 2015, 3, 782-795.	10.7	66
61	Integrative pathway genomics of lung function and airflow obstruction. Human Molecular Genetics, 2015, 24, 6836-6848.	2.9	28
62	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	7.9	235
63	Exposure to siblings in early life modifies the association between <i>CD14</i> polymorphisms and allergic sensitization in adult life. , 2015, , .		0
64	Identification of Novel Genetic Loci Associated with Thyroid Peroxidase Antibodies and Clinical Thyroid Disease. PLoS Genetics, 2014, 10, e1004123.	3.5	150
65	Genome-wide association analysis identifies 11 risk variants associated with the asthma with hay fever phenotype. Journal of Allergy and Clinical Immunology, 2014, 133, 1564-1571.	2.9	195
66	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	12.8	192
67	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	21.4	131
68	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
69	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	21.4	959
70	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. Nature Genetics, 2013, 45, 902-906.	21.4	221
71	A genome-wide association study for malignant mesothelioma risk. Lung Cancer, 2013, 82, 1-8.	2.0	45
72	Rationale, design and methods for a community-based study of clustering and cumulative effects of chronic disease processes and their effects on ageing: the Busselton healthy ageing study. BMC Public Health, 2013, 13, 936.	2.9	45

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73	Genomeâ€wide association study of body mass index in 23Â000 individuals with and without asthma. Clinical and Experimental Allergy, 2013, 43, 463-474.	2.9	68
74	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	3.5	371
75	Causal and Synthetic Associations of Variants in the SERPINA Gene Cluster with Alpha1-antitrypsin Serum Levels. PLoS Genetics, 2013, 9, e1003585.	3.5	43
76	Risk factors for respiratory symptoms in adults: The <scp>B</scp> usselton <scp>H</scp> ealth <scp>S</scp> tudy. Respirology, 2013, 18, 1256-1260.	2.3	13
77	Genetic Variants Associated with Increased Risk of Malignant Pleural Mesothelioma: A Genome-Wide Association Study. PLoS ONE, 2013, 8, e61253.	2.5	71
78	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	3.5	419
79	Genome-Wide Association Studies Identify <i>CHRNA5/3</i> and <i>HTR4</i> in the Development of Airflow Obstruction. American Journal of Respiratory and Critical Care Medicine, 2012, 186, 622-632.	5.6	164
80	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
81	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	21.4	1,748
82	Impact of Common Variation in Bone-Related Genes on Type 2 Diabetes and Related Traits. Diabetes, 2012, 61, 2176-2186.	0.6	31
83	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	27.8	383
84	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	2.5	197
85	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	21.4	762
86	Genome-wide association study to identify genetic determinants of severe asthma. Thorax, 2012, 67, 762-768.	5.6	169
87	Gastroâ€oesophageal reflux and respiratory symptoms in Busselton adults: the effects of bodyweight and sleep apnoea. Internal Medicine Journal, 2012, 42, 772-779.	0.8	5
88	Identification of IL6R and chromosome 11q13.5 as risk loci for asthma. Lancet, The, 2011, 378, 1006-1014.	13.7	345
89	Patterns Of Airway Disease And The Clinical Diagnosis Of Asthma In The Busselton Population. , 2011, , .		0
90	Comprehensive Evaluation Of Mild-To-Moderate Asthma Genes In Severe Asthma (AUGOSA). , 2011, , .		0

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91	Functional haplotypes in the <i>PTGDR</i> gene fail to associate with asthma in two Australian populations. Respirology, 2011, 16, 359-366.	2.3	9
92	The natural history of nonalcoholic fatty liver disease with advanced fibrosis or cirrhosis: An international collaborative study. Hepatology, 2011, 54, 1208-1216.	7.3	399
93	Effect of Five Genetic Variants Associated with Lung Function on the Risk of Chronic Obstructive Lung Disease, and Their Joint Effects on Lung Function. American Journal of Respiratory and Critical Care Medicine, 2011, 184, 786-795.	5.6	128
94	Patterns of airway disease and the clinical diagnosis of asthma in the Busselton population. European Respiratory Journal, 2011, 38, 1053-1059.	6.7	18
95	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	21.4	367
96	A Comprehensive Evaluation of Potential Lung Function Associated Genes in the SpiroMeta General Population Sample. PLoS ONE, 2011, 6, e19382.	2.5	56
97	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
98	Genome-wide association study identifies five loci associated with lung function. Nature Genetics, 2010, 42, 36-44.	21.4	518
99	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	21.4	836
100	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
101	Changes in the prevalence of asthma in adults since 1966: the Busselton health study. European Respiratory Journal, 2010, 35, 273-278.	6.7	68
102	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
103	A Large-Scale, Consortium-Based Genomewide Association Study of Asthma. New England Journal of Medicine, 2010, 363, 1211-1221.	27.0	1,762
104	The PHF11 gene is not associated with asthma or asthma phenotypes in two independent populations. Thorax, 2009, 64, 620-625.	5.6	8
105	Sequence variants affecting eosinophil numbers associate with asthma and myocardial infarction. Nature Genetics, 2009, 41, 342-347.	21.4	709
106	A genome-wide association scan for asthma in a general Australian population. Human Genetics, 2008, 123, 297-306.	3.8	17
107	AluyMICB dimorphism within the class I region of the major histocompatibility complex is associated with asthma and airflow obstruction in the Busselton population. Clinical and Experimental Allergy, 2006, 36, 728-734.	2.9	7
108	Identification of two new C4 alleles by DNA sequencing and evidence for a historical recombination of serologically defined C4A and C4B alleles. Tissue Antigens, 2004, 63, 263-269.	1.0	3

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109	Comparison of the milk quality of the South African Boer and Australian Rangeland goats. Small Ruminant Research, 2004, 53, 181-184.	1.2	4
110	Alu polymorphism within the MICB gene and association with HLA-B alleles. Immunogenetics, 2002, 53, 975-979.	2.4	23
111	Potential for paralogous mapping to simplify the genetics of diseases and functions associated with MHC haplotypes. , 2000, , 146-157.		0
112	Genomics of the major histocompatibility complex: haplotypes, duplication, retroviruses and disease. Immunological Reviews, 1999, 167, 275-304.	6.0	321