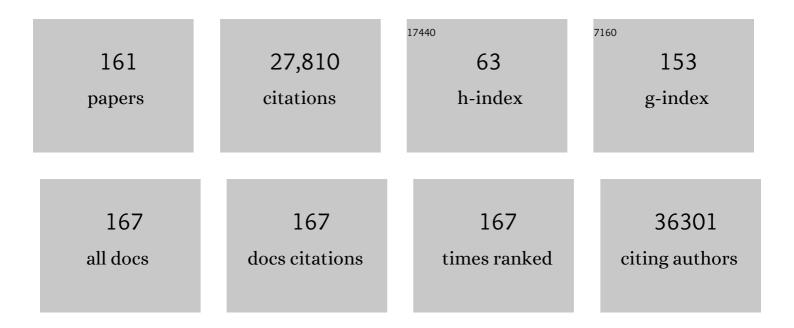
William Cookson

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Merlin—rapid analysis of dense genetic maps using sparse gene flow trees. Nature Genetics, 2002, 30, 97-101.	21.4	3,100
2	Reagent and laboratory contamination can critically impact sequence-based microbiome analyses. BMC Biology, 2014, 12, 87.	3.8	2,677
3	A Large-Scale, Consortium-Based Genomewide Association Study of Asthma. New England Journal of Medicine, 2010, 363, 1211-1221.	27.0	1,762
4	Genetic variants regulating ORMDL3 expression contribute to the risk of childhood asthma. Nature, 2007, 448, 470-473.	27.8	1,446
5	Disordered Microbial Communities in Asthmatic Airways. PLoS ONE, 2010, 5, e8578.	2.5	1,436
6	Exposure to Environmental Microorganisms and Childhood Asthma. New England Journal of Medicine, 2011, 364, 701-709.	27.0	1,339
7	A genome-wide association study of global gene expression. Nature Genetics, 2007, 39, 1202-1207.	21.4	882
8	Mapping complex disease traits with global gene expression. Nature Reviews Genetics, 2009, 10, 184-194.	16.3	790
9	A genome-wide search for quantitative trait loci underlying asthma. Nature, 1996, 383, 247-250.	27.8	750
10	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
11	Genome-wide genetic association of complex traits in heterogeneous stock mice. Nature Genetics, 2006, 38, 879-887.	21.4	508
12	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	21.4	501
13	The Role of Bacteria in the Pathogenesis and Progression of Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2014, 190, 906-913.	5.6	453
14	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	21.4	426
15	The immunogenetics of asthma and eczema: a new focus on the epithelium. Nature Reviews Immunology, 2004, 4, 978-988.	22.7	349
16	Outgrowth of the Bacterial Airway Microbiome after Rhinovirus Exacerbation of Chronic Obstructive Pulmonary Disease. American Journal of Respiratory and Critical Care Medicine, 2013, 188, 1224-1231.	5.6	329
17	Positional cloning of a novel gene influencing asthma from Chromosome 2q14. Nature Genetics, 2003, 35, 258-263.	21.4	326
18	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	27.8	320

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19	Variants of <i>DENND1B</i> Associated with Asthma in Children. New England Journal of Medicine, 2010, 362, 36-44.	27.0	306
20	Positional cloning of a quantitative trait locus on chromosome 13q14 that influences immunoglobulin E levels and asthma. Nature Genetics, 2003, 34, 181-186.	21.4	300
21	Association between a complex insertion/deletion polymorphism in NOD1 (CARD4) and susceptibility to inflammatory bowel disease. Human Molecular Genetics, 2005, 14, 1245-1250.	2.9	299
22	The alliance of genes and environment in asthma and allergy. Nature, 1999, 402, 5-11.	27.8	296
23	Genome-wide Association Analysis Identifies PDE4D as an Asthma-Susceptibility Gene. American Journal of Human Genetics, 2009, 84, 581-593.	6.2	296
24	Atopic Sensitization and the International Variation of Asthma Symptom Prevalence in Children. American Journal of Respiratory and Critical Care Medicine, 2007, 176, 565-574.	5.6	290
25	Genome-Wide Scan on Total Serum IgE Levels Identifies FCER1A as Novel Susceptibility Locus. PLoS Genetics, 2008, 4, e1000166.	3.5	255
26	NOD1 variation, immunoglobulin E and asthma. Human Molecular Genetics, 2005, 14, 935-941.	2.9	245
27	Shared genetic and experimental links between obesity-related traits and asthma subtypes in UK Biobank. Journal of Allergy and Clinical Immunology, 2020, 145, 537-549.	2.9	240
28	The genetics of atopic dermatitis. Journal of Allergy and Clinical Immunology, 2006, 118, 24-34.	2.9	220
29	A genome-wide association study on African-ancestry populations for asthma. Journal of Allergy and Clinical Immunology, 2010, 125, 336-346.e4.	2.9	213
30	A genome-wide association study of atopic dermatitis identifies loci with overlapping effects on asthma and psoriasis. Human Molecular Genetics, 2013, 22, 4841-4856.	2.9	202
31	An epigenome-wide association study of total serum immunoglobulin E concentration. Nature, 2015, 520, 670-674.	27.8	193
32	Significance of the microbiome in obstructive lung disease. Thorax, 2012, 67, 456-463.	5.6	190
33	Filaggrin Mutations in Children with Severe Atopic Dermatitis. Journal of Investigative Dermatology, 2007, 127, 1667-1672.	0.7	186
34	Copy number variation leads to considerable diversity for B but not A haplotypes of the human KIR genes encoding NK cell receptors. Genome Research, 2012, 22, 1845-1854.	5.5	173
35	Improved Detection of Bifidobacteria with Optimised 16S rRNA-Gene Based Pyrosequencing. PLoS ONE, 2012, 7, e32543.	2.5	170
36	DNA methylation in childhood asthma: an epigenome-wide meta-analysis. Lancet Respiratory Medicine,the, 2018, 6, 379-388.	10.7	170

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37	Gene Expression in Skin and Lymphoblastoid Cells: Refined Statistical Method Reveals Extensive Overlap in cis-eQTL Signals. American Journal of Human Genetics, 2010, 87, 779-789.	6.2	169
38	Host–Microbial Interactions in Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2017, 195, 1640-1650.	5.6	169
39	Dysbiosis Anticipating Necrotizing Enterocolitis in Very Premature Infants. Clinical Infectious Diseases, 2015, 60, 389-397.	5.8	168
40	Bacterial microbiota of the upper respiratory tract and childhood asthma. Journal of Allergy and Clinical Immunology, 2017, 139, 826-834.e13.	2.9	165
41	Genetic and Environmental Effects on Complex Traits in Mice. Genetics, 2006, 174, 959-984.	2.9	161
42	Airway Microbiota in Severe Asthma and Relationship to Asthma Severity and Phenotypes. PLoS ONE, 2016, 11, e0152724.	2.5	159
43	Changes in the respiratory microbiome during acute exacerbations of idiopathic pulmonary fibrosis. Respiratory Research, 2017, 18, 29.	3.6	156
44	Corticosteroid suppression of antiviral immunity increases bacterial loads and mucus production in COPD exacerbations. Nature Communications, 2018, 9, 2229.	12.8	153
45	Gene-environment interactions in chronic inflammatory disease. Nature Immunology, 2011, 12, 273-277.	14.5	148
46	A cross-platform analysis of 14,177 expression quantitative trait loci derived from lymphoblastoid cell lines. Genome Research, 2013, 23, 716-726.	5.5	135
47	Sequencing the human microbiome in health and disease. Human Molecular Genetics, 2013, 22, R88-R94.	2.9	123
48	Increases in airway responsiveness to histamine precede allergen-induced late asthmatic responses. Journal of Allergy and Clinical Immunology, 1988, 82, 764-770.	2.9	121
49	Validation of a 52-gene risk profile for outcome prediction in patients with idiopathic pulmonary fibrosis: an international, multicentre, cohort study. Lancet Respiratory Medicine,the, 2017, 5, 857-868.	10.7	115
50	Predicting DNA methylation level across human tissues. Nucleic Acids Research, 2014, 42, 3515-3528.	14.5	113
51	Genetics and genomics of asthma and allergic diseases. Immunological Reviews, 2002, 190, 195-206.	6.0	107
52	Batten disease (Spielmeyer-Vogt disease, juvenile onset neuronal ceroid-lipofuscinosis) gene (CLN3) maps to human chromosome 16. Genomics, 1990, 8, 387-390.	2.9	100
53	A protocol for high-throughput phenotyping, suitable for quantitative trait analysis in mice. Mammalian Genome, 2006, 17, 129-146.	2.2	99
54	Longitudinal assessment of sputum microbiome by sequencing of the 16S rRNA gene in non-cystic fibrosis bronchiectasis patients. PLoS ONE, 2017, 12, e0170622.	2.5	99

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55	Genetic and genomic approaches to asthma. Current Opinion in Pulmonary Medicine, 2012, 18, 6-13.	2.6	92
56	A functional IL-6 receptor (IL6R) variant is a risk factor for persistent atopic dermatitis. Journal of Allergy and Clinical Immunology, 2013, 132, 371-377.	2.9	86
57	New opportunities for managing acute and chronic lung infections. Nature Reviews Microbiology, 2018, 16, 111-120.	28.6	80
58	Vitamin D levels and susceptibility to asthma, elevated immunoglobulin E levels, and atopic dermatitis: A Mendelian randomization study. PLoS Medicine, 2017, 14, e1002294.	8.4	78
59	Late-Onset Bloodstream Infection and Perturbed Maturation of the Gastrointestinal Microbiota in Premature Infants. PLoS ONE, 2015, 10, e0132923.	2.5	75
60	Inhaled corticosteroid suppression of cathelicidin drives dysbiosis and bacterial infection in chronic obstructive pulmonary disease. Science Translational Medicine, 2019, 11, .	12.4	75
61	Imputation of KIR Types from SNP Variation Data. American Journal of Human Genetics, 2015, 97, 593-607.	6.2	73
62	Pulmonary ORMDL3 is critical for induction of Alternaria-induced allergic airways disease. Journal of Allergy and Clinical Immunology, 2017, 139, 1496-1507.e3.	2.9	71
63	The origin, global distribution, and functional impact of the human 8p23 inversion polymorphism. Genome Research, 2012, 22, 1144-1153.	5.5	70
64	The <i>ORMDL3</i> Asthma Gene Regulates <i>ICAM1</i> and Has Multiple Effects on Cellular Inflammation. American Journal of Respiratory and Critical Care Medicine, 2019, 199, 478-488.	5.6	67
65	Genetic and Perinatal Risk Factors for Asthma Onset and Severity: A Review and Theoretical Analysis. Epidemiologic Reviews, 2002, 24, 176-189.	3.5	66
66	A Genome-Wide Screen for Asthma-Associated Quantitative Trait Loci in a Mouse Model of Allergic Asthma. Human Molecular Genetics, 1999, 8, 601-605.	2.9	65
67	Competing Functions Encoded in the Allergy-Associated FcïµRlβ Gene. Immunity, 2003, 18, 665-674.	14.3	63
68	Role of airway glucose in bacterial infections in patients with chronic obstructive pulmonary disease. Journal of Allergy and Clinical Immunology, 2018, 142, 815-823.e6.	2.9	63
69	Allergy-Associated Polymorphisms of the FcεRIβ Subunit Do Not Impact Its Two Amplification Functions. Journal of Immunology, 2000, 165, 3917-3922.	0.8	62
70	Effects of different antibiotic classes on airway bacteria in stable COPD using culture and molecular techniques: a randomised controlled trial. Thorax, 2015, 70, 930-938.	5.6	61
71	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. American Journal of Human Genetics, 2013, 93, 236-248.	6.2	60
72	Benign asbestos pleural diseases. Current Opinion in Pulmonary Medicine, 2003, 9, 266-271.	2.6	57

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73	Meta-analysis of 20 genome-wide linkage studies evidenced new regions linked to asthma and atopy. European Journal of Human Genetics, 2010, 18, 700-706.	2.8	54
74	An epigenome-wide association study of total serum IgE in Hispanic children. Journal of Allergy and Clinical Immunology, 2017, 140, 571-577.	2.9	53
75	Detection of a recessive major gene for high IgE levels acting independently of specific response to allergens. Genetic Epidemiology, 1995, 12, 93-105.	1.3	52
76	Making Sense of Asthma Genes. New England Journal of Medicine, 2004, 351, 1794-1796.	27.0	50
77	Germline TCR-A restriction of immunoglobulin E responses to allergen. Immunogenetics, 1997, 46, 226-230.	2.4	48
78	Novel childhood asthma genes interact with in utero and early-life tobacco smoke exposure. Journal of Allergy and Clinical Immunology, 2014, 133, 885-888.	2.9	47
79	Addressing unmet needs in understanding asthma mechanisms. European Respiratory Journal, 2017, 49, 1602448.	6.7	47
80	The Genetics and Genomics of Asthma. Annual Review of Genomics and Human Genetics, 2018, 19, 223-246.	6.2	47
81	LD mapping of maternally and non-maternally derived alleles and atopy in FcεRI-β. Human Molecular Genetics, 2003, 12, 2577-2585.	2.9	46
82	PDE11A associations with asthma: Results of a genome-wide association scan. Journal of Allergy and Clinical Immunology, 2010, 126, 871-873.e9.	2.9	45
83	iGWAS: Integrative Genomeâ€Wide Association Studies of Genetic and Genomic Data for Disease Susceptibility Using Mediation Analysis. Genetic Epidemiology, 2015, 39, 347-356.	1.3	45
84	Chromosome 17q21 SNP and severe asthma. Journal of Human Genetics, 2011, 56, 97-98.	2.3	43
85	Opportunities and Challenges in the Genetics of COPD 2010: An International COPD Genetics Conference Report. COPD: Journal of Chronic Obstructive Pulmonary Disease, 2011, 8, 121-135.	1.6	43
86	Grasping nettles: cellular heterogeneity and other confounders in epigenome-wide association studies. Human Molecular Genetics, 2014, 23, R83-R88.	2.9	43
87	The undiagnosed disease burden associated with alpha-1 antitrypsin deficiency genotypes. European Respiratory Journal, 2020, 56, 2001441.	6.7	40
88	A mechanistic target of rapamycin complex 1/2 (mTORC1)/V-Akt murine thymoma viral oncogene homolog 1 (AKT1)/cathepsin H axis controls filaggrin expression and processing in skin, a novel mechanism for skin barrier disruption in patients with atopic dermatitis. Journal of Allergy and Clinical Immunology, 2017, 139, 1228-1241.	2.9	38
89	The natural history of asbestosis in former crocidolite workers of Wittenoom Gorge. The American Review of Respiratory Disease, 1986, 133, 994-8.	2.9	37
90	Impact of Collection and Storage of Lung Tumor Tissue on Whole Genome Expression Profiling. Journal of Molecular Diagnostics, 2012, 14, 140-148.	2.8	36

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91	The fungal airway microbiome in cystic fibrosis and non-cystic fibrosis bronchiectasis. Journal of Cystic Fibrosis, 2021, 20, 295-302.	0.7	36
92	Analgesia and central sideâ€effects: two separate dimensions of morphine response. British Journal of Clinical Pharmacology, 2013, 75, 1340-1350.	2.4	34
93	Fraction of exhaled nitric oxide values in childhood are associated with 17q11.2-q12 and 17q12-q21 variants. Journal of Allergy and Clinical Immunology, 2014, 134, 46-55.	2.9	33
94	Whole-Blood Gene Expression in Pulmonary Nontuberculous Mycobacterial Infection. American Journal of Respiratory Cell and Molecular Biology, 2018, 58, 510-518.	2.9	31
95	A new gene for asthma: would you ADAM and Eve it?. Trends in Genetics, 2003, 19, 169-172.	6.7	30
96	Gene-environment interaction in chronic disease: AÂEuropean Science Foundation Forward Look. Journal of Allergy and Clinical Immunology, 2011, 128, S27-S49.	2.9	30
97	A large-scale genome-wide association analysis of lung function in the Chinese population identifies novel loci and highlights shared genetic aetiology with obesity. European Respiratory Journal, 2021, 58, 2100199.	6.7	30
98	Integrating pathway analysis and genetics of gene expression for genome-wide association study of basal cell carcinoma. Human Genetics, 2012, 131, 615-623.	3.8	29
99	Global gene regulation during activation of immunoglobulin class switching in human B cells. Scientific Reports, 2016, 6, 37988.	3.3	28
100	Genetic risks and childhood-onset asthma. Journal of Allergy and Clinical Immunology, 2011, 128, 266-270.	2.9	27
101	COPD is accompanied by co-ordinated transcriptional perturbation in the quadriceps affecting the mitochondria and extracellular matrix. Scientific Reports, 2018, 8, 12165.	3.3	27
102	Comparison of the upper and lower airway microbiota in children with chronic lung diseases. PLoS ONE, 2018, 13, e0201156.	2.5	27
103	Airway mucins promote immunopathology in virus-exacerbated chronic obstructive pulmonary disease. Journal of Clinical Investigation, 2022, 132, .	8.2	27
104	Positive association to IgE levels and a physical map of the 13q14 atopy locus. European Journal of Human Genetics, 2002, 10, 266-270.	2.8	26
105	Dynamic and Physical Clustering of Gene Expression during Epidermal Barrier Formation in Differentiating Keratinocytes. PLoS ONE, 2009, 4, e7651.	2.5	26
106	The impact of persistent bacterial bronchitis on the pulmonary microbiome of children. PLoS ONE, 2017, 12, e0190075.	2.5	26
107	Airway microbial communities, smoking and asthma in a general population sample. EBioMedicine, 2021, 71, 103538.	6.1	26
108	DNA methylation within melatonin receptor 1A (MTNR1A) mediates paternally transmitted genetic variant effect on asthma plus rhinitis. Journal of Allergy and Clinical Immunology, 2016, 138, 748-753.	2.9	25

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109	Identification of a new locus at 16q12 associated with time to asthma onset. Journal of Allergy and Clinical Immunology, 2016, 138, 1071-1080.	2.9	25
110	Utility of Nuclear Grading System in Epithelioid Malignant Pleural Mesothelioma in Biopsy-heavy Setting. American Journal of Surgical Pathology, 2020, 44, 347-356.	3.7	25
111	Genome-wide association studies in the genetics of asthma. Current Allergy and Asthma Reports, 2009, 9, 3-9.	5.3	24
112	Polymorphisms of <i>PHF11</i> and <i>DPP10 </i> Are Associated with Asthma and Related Traits in a Chinese Population. Respiration, 2010, 79, 17-24.	2.6	24
113	A Polymorphism Affecting <scp>MYB</scp> Binding within the Promoter of the <i>PDCD4</i> Gene is Associated with Severe Asthma in Children. Human Mutation, 2013, 34, 1131-1139.	2.5	24
114	Metabolomic, transcriptomic and genetic integrative analysis reveals important roles of adenosine diphosphate in haemostasis and platelet activation in nonâ€smallâ€cell lung cancer. Molecular Oncology, 2019, 13, 2406-2421.	4.6	24
115	Genetics of Complex Airway Disease. Proceedings of the American Thoracic Society, 2011, 8, 149-153.	3.5	20
116	Longitudinal development of the airway microbiota in infants with cystic fibrosis. Scientific Reports, 2019, 9, 5143.	3.3	19
117	A Pandemic Lesson for Global Lung Diseases: Exacerbations Are Preventable. American Journal of Respiratory and Critical Care Medicine, 2022, 205, 1271-1280.	5.6	19
118	eQTL mapping identifies insertion- and deletion-specific eQTLs in multiple tissues. Nature Communications, 2015, 6, 6821.	12.8	18
119	Metal worker's lung: spatial association with <i>Mycobacterium avium</i> . Thorax, 2018, 73, 151-156.	5.6	18
120	Allergy to <i>Dermatophagoides</i> in a Group of Spanish Gypsies: Genetic Restrictions. International Archives of Allergy and Immunology, 2001, 125, 297-306.	2.1	17
121	A detailed genetic map of the chromosome 7 bronchial hyper-responsiveness locus. European Journal of Human Genetics, 2002, 10, 177-182.	2.8	17
122	Investigation of the Chromosome 17q25 PSORS2 Locus in Atopic Dermatitis. Journal of Investigative Dermatology, 2006, 126, 603-606.	0.7	16
123	A molecular comparison of microbial communities in bronchiectasis and cystic fibrosis. European Respiratory Journal, 2013, 41, 991-993.	6.7	16
124	Y disruption, autosomal hypomethylation and poor male lung cancer survival. Scientific Reports, 2021, 11, 12453.	3.3	15
125	Network-assisted analysis of GWAS data identifies a functionally-relevant gene module for childhood-onset asthma. Scientific Reports, 2017, 7, 938.	3.3	14
126	EGF receptor (EGFR) inhibition promotes a slow-twitch oxidative, over a fast-twitch, muscle phenotype. Scientific Reports, 2019, 9, 9218.	3.3	14

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127	Viral respiratory infections and the oropharyngeal bacterial microbiota in acutely wheezing children. PLoS ONE, 2019, 14, e0223990.	2.5	14
128	Profiling mycobacterial communities in pulmonary nontuberculous mycobacterial disease. PLoS ONE, 2018, 13, e0208018.	2.5	13
129	ENU mutagenesis as a tool for understanding lung development and disease. Biochemical Society Transactions, 2009, 37, 838-842.	3.4	12
130	A Haemophilus sp. dominates the microbiota of sputum from UK adults with non-severe community acquired pneumonia and chronic lung disease. Scientific Reports, 2019, 9, 2388.	3.3	12
131	Integrated genomics point to immune vulnerabilities in pleural mesothelioma. Scientific Reports, 2021, 11, 19138.	3.3	12
132	The genetics of atopy. Journal of Allergy and Clinical Immunology, 1994, 94, 643-644.	2.9	11
133	Manipulation of Dipeptidylpeptidase 10 in mouse and human <i>in vivo</i> and <i>in vitro</i> models indicates a protective role in asthma. DMM Disease Models and Mechanisms, 2018, 11, .	2.4	11
134	A novel role for ciliary function in atopy: ADGRV1 and DNAH5 interactions. Journal of Allergy and Clinical Immunology, 2018, 141, 1659-1667.e11.	2.9	9
135	Genomeâ€wide interaction study of earlyâ€life smoking exposure on timeâ€toâ€asthma onset in childhood. Clinical and Experimental Allergy, 2019, 49, 1342-1351.	2.9	9
136	Presence of pleomorphic features but not growth patterns improves prognostic stratification of epithelioid malignant pleural mesothelioma by 2â€ŧier nuclear grade. Histopathology, 2020, 77, 423-436.	2.9	9
137	Atopy: A Complex Genetic Disease. Annals of Medicine, 1994, 26, 351-353.	3.8	8
138	Bedside to Gene and Back in Idiopathic Pulmonary Fibrosis. New England Journal of Medicine, 2013, 368, 2228-2230.	27.0	8
139	Functional analysis of a novel ENU-induced PHD finger 11 (Phf11) mouse mutant. Mammalian Genome, 2014, 25, 573-582.	2.2	7
140	Reply to "Atopy in Australia― Nature Genetics, 1995, 10, 260-260.	21.4	5
141	Genetic variation in the beta subunit of the high affinity IgE receptor and atopy and asthma. Clinical and Experimental Allergy, 2006, 36, 855-857.	2.9	5
142	Outside In: Sequencing the Lung Microbiome. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 403-404.	5.6	5
143	Bacterial Signatures of Paediatric Respiratory Disease: An Individual Participant Data Meta-Analysis. Frontiers in Microbiology, 2021, 12, 711134.	3.5	5
144	Atopy, respiratory function and HLA-DR in Aboriginal Australians. Human Molecular Genetics, 2003, 12, 625-30.	2.9	5

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145	Evidence of immunometabolic dysregulation and airway dysbiosis in athletes susceptible to respiratory illness. EBioMedicine, 2022, 79, 104024.	6.1	5
146	ORMDL3 regulates poly I:C induced inflammatory responses in airway epithelial cells. BMC Pulmonary Medicine, 2021, 21, 167.	2.0	3
147	Comparison of the airway microbiota in children with chronic suppurative lung disease. BMJ Open Respiratory Research, 2021, 8, e001106.	3.0	3
148	Asthma and Chitinases. New England Journal of Medicine, 2008, 358, 1725-1726.	27.0	2
149	MA23.10 Low Number of Mutations and Frequent Co-Deletions of CDKN2A and IFN Type I Characterize Malignant Pleural Mesothelioma. Journal of Thoracic Oncology, 2019, 14, S345.	1.1	2
150	Estimating cell-type-specific DNA methylation effects in heterogeneous cellular populations. Epigenomics, 2021, 13, 87-97.	2.1	2
151	Naked DNA: New shots for allergy?. Nature Medicine, 1996, 2, 515-516.	30.7	1
152	Haplotypes and Asthma. American Journal of Respiratory and Critical Care Medicine, 2005, 171, 1066-1067.	5.6	1
153	In the Wrong Place at the Wrong Time: Microbial Misplacement and Acute Respiratory Distress Syndrome. American Journal of Respiratory and Critical Care Medicine, 2020, 201, 506-507.	5.6	1
154	P200 Preliminary Evaluation Of The Fungal Airway Microbiome In Adult Cystic Fibrosis By Next-generation Sequencing, Culture And Staining Techniques. Thorax, 2014, 69, A164-A164.	5.6	0
155	MA 06.13 Direct Metabolomic Profiling of Lung Cancers. Journal of Thoracic Oncology, 2017, 12, S1824.	1.1	0
156	P2.06-41 Differentiating Sarcomatoid Mesothelioma from Pleomorphic Carcinoma and Chest Wall Sarcoma Using GATA-3/MUC4/BAP1 IHC. Journal of Thoracic Oncology, 2018, 13, S758-S759.	1.1	0
157	MA21.03 Heterogeneity in MET Copy Number and Intratumoural Subsets in Pleomorphic Lung Carcinoma: Implications for MET Directed Therapy in NSCLC. Journal of Thoracic Oncology, 2018, 13, S430.	1.1	0
158	P2.03-10 Comprehensive Molecular Profiling and Comparison of Common and Rarer Subtypes of Lung Cancer. Journal of Thoracic Oncology, 2019, 14, S686.	1.1	0
159	MA23.11 Analysis of Immune Phenotype Composition in Malignant Pleural Mesothelioma (MPM) Using Bulk RNA Sequencing. Journal of Thoracic Oncology, 2019, 14, S345-S346.	1.1	0
160	P1.04-63 Correlation of Mutations in TP53, CDKN2A and PIK3CA with VISTA Expression in Pleomorphic Lung Carcinoma. Journal of Thoracic Oncology, 2019, 14, S465-S466.	1.1	0
161	P1.06-08 WDPM-Like but Not Cribriform as Secondary Growth Patterns Modify Survival in Epithelioid Malignant Pleural Mesothelioma. Journal of Thoracic Oncology, 2019, 14, S480-S481.	1.1	0