Carole Ober

List of Publications by Year
in descending order

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323 papers	30,066 citations	4146 87 h-index	6300 158 g-index
349 all docs	349 docs citations	349 times ranked	32354 citing authors

#	Article	IF	Citations
1	Genomeâ€wide association and multiâ€omics studies identify MGMT as a novel risk gene for Alzheimer's disease among women. Alzheimer's and Dementia, 2023, 19, 896-908.	0.8	19
2	Genomeâ€wide association study identifies TNFSF15 associated with childhood asthma. Allergy: European Journal of Allergy and Clinical Immunology, 2022, 77, 218-229.	5.7	11
3	Genome-wide study of early and severe childhood asthma identifies interaction between CDHR3 and GSDMB. Journal of Allergy and Clinical Immunology, 2022, 150, 622-630.	2.9	8
4	17q12â€q21 variants interact with earlyâ€life exposures to modify asthma risk in Black children. Clinical and Experimental Allergy, 2022, 52, 565-568.	2.9	3
5	Genome-wide association study identifies kallikrein 5 in type 2 inflammation-low asthma. Journal of Allergy and Clinical Immunology, 2022, 150, 972-978.e7.	2.9	5
6	17q12-21 Asthma Risk Genes Interact with Early Life Nasal Microbiota to Increase Risk of Childhood Wheeze. , 2022, , .		0
7	New Insights Relating Gasdermin B to the Onset of Childhood Asthma. American Journal of Respiratory Cell and Molecular Biology, 2022, 67, 430-437.	2.9	6
8	Il-4 Receptor Alpha Chain Q576R Genotype and Aspirin Exacerbated Respiratory Disease. , 2022, , .		0
9	Childhood Asthma Incidence, Early and Persistent Wheeze, and Neighborhood Socioeconomic Factors in the ECHO/CREW Consortium. JAMA Pediatrics, 2022, 176, 759.	6.2	41
10	Fine-mapping studies distinguish genetic risks for childhood- and adult-onset asthma in the HLA region. Genome Medicine, 2022, 14, .	8.2	2
11	DNA methylation signatures in airway cells from adult children of asthmatic mothers reflect subtypes of severe asthma. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	11
12	Longitudinal data reveal strong genetic and weak non-genetic components of ethnicity-dependent blood DNA methylation levels. Epigenetics, 2021, 16, 662-676.	2.7	18
13	Twoâ€stage genomeâ€wide association study of chronic rhinosinusitis and disease subphenotypes highlights mucosal immunity contributing to risk. International Forum of Allergy and Rhinology, 2021, 11, 814-817.	2.8	4
14	A-to-I editing of miR-200b-3p in airway cells is associated with moderate-to-severe asthma. European Respiratory Journal, 2021, 58, 2003862.	6.7	10
15	Sex-specific differences in peripheral blood leukocyte transcriptional response to LPS are enriched for HLA region and X chromosome genes. Scientific Reports, 2021, 11, 1107.	3.3	11
16	Chromosome 17q12-21 Variants Are Associated with Multiple Wheezing Phenotypes in Childhood. American Journal of Respiratory and Critical Care Medicine, 2021, 203, 864-870.	5.6	24
17	Enhanced Neutralizing Antibody Responses to Rhinovirus C and Age-Dependent Patterns of Infection. American Journal of Respiratory and Critical Care Medicine, 2021, 203, 822-830.	5.6	24
18	Pluripotent stem cell-derived endometrial stromal fibroblasts in a cyclic, hormone-responsive, coculture model of human decidua. Cell Reports, 2021, 35, 109138.	6.4	30

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19	Inducible expression quantitative trait locus analysis of the MUC5AC gene in asthma in urban populations of children. Journal of Allergy and Clinical Immunology, 2021, 148, 1505-1514.	2.9	14
20	Extensive pleiotropism and allelic heterogeneity mediate metabolic effects of IRX3 and IRX5. Science, 2021, 372, 1085-1091.	12.6	66
21	Unconjugated bilirubin is associated with protection from early-life wheeze and childhood asthma. Journal of Allergy and Clinical Immunology, 2021, 148, 128-138.	2.9	12
22	A functional genomics pipeline identifies pleiotropy and cross-tissue effects within obesity-associated GWAS loci. Nature Communications, 2021, 12, 5253.	12.8	19
23	Multiethnic genome-wide and HLA association study of total serum IgE level. Journal of Allergy and Clinical Immunology, 2021, 148, 1589-1595.	2.9	15
24	Establishment of human induced trophoblast stem-like cells from term villous cytotrophoblasts. Stem Cell Research, 2021, 56, 102507.	0.7	18
25	Asthma-associated genetic variants induce IL33 differential expression through an enhancer-blocking regulatory region. Nature Communications, 2021, 12, 6115.	12.8	28
26	Multi-omics colocalization with genome-wide association studies reveals a context-specific genetic mechanism at a childhood onset asthma risk locus. Genome Medicine, 2021, 13, 157.	8.2	21
27	Cytokine-induced molecular responses in airway smooth muscle cells inform genome-wide association studies of asthma. Genome Medicine, 2020, 12, 64.	8.2	14
28	Epigenetic landscape links upper airway microbiota in infancy with allergic rhinitis at 6 years of age. Journal of Allergy and Clinical Immunology, 2020, 146, 1358-1366.	2.9	31
29	Altered transcriptional and chromatin responses to rhinovirus in bronchial epithelial cells from adults with asthma. Communications Biology, 2020, 3, 678.	4.4	13
30	Transcriptome and regulatory maps of decidua-derived stromal cells inform gene discovery in preterm birth. Science Advances, 2020, 6, .	10.3	31
31	A comparison of humans and baboons suggests germline mutation rates do not track cell divisions. PLoS Biology, 2020, 18, e3000838.	5.6	64
32	Untargeted Metabolomics Reveals Unconjugated Bilirubin and Linked Pathways in Arachidonic Acid Metabolism and Oxidative Stress Associated with Early Life Recurrent Wheeze. , 2020, , .		0
33	Age Is Differentially Associated with Rhinovirus A and C Species Infections in Children. , 2020, , .		0
34	Expression quantitative trait locus fine mapping of the 17q12â€“21 asthma locus in African American children: a genetic association and gene expression study. Lancet Respiratory Medicine,the, 2020, 8, 482-492.	10.7	47
35	Epigenome-wide association study of DNA methylation and adult asthma in the Agricultural Lung Health Study. European Respiratory Journal, 2020, 56, 2000217.	6.7	40
36	Club Cell TRPV4 Serves as a Damage Sensor Driving Lung Allergic Inflammation. Cell Host and Microbe, 2020, 27, 614-628.e6.	11.0	47

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37	Association of HLA-DRB1âˆ—09:01 with tIgE levels among African-ancestry individuals with asthma. Journal of Allergy and Clinical Immunology, 2020, 146, 147-155.	2.9	14
38	FUT2â€“ABO epistasis increases the risk of early childhood asthma and Streptococcus pneumoniae respiratory illnesses. Nature Communications, 2020, 11, 6398.	12.8	21
39	Effects of an FcÎ³RIIA polymorphism on leukocyte gene expression and cytokine responses to anti-CD3 and anti-CD28 antibodies. Genes and Immunity, 2019, 20, 462-472.	4.1	8
40	Heritability estimation and differential analysis of count data with generalized linear mixed models in genomic sequencing studies. Bioinformatics, 2019, 35, 487-496.	4.1	60
41	The Childrenâ€™s Respiratory and Environmental Workgroup (CREW) birth cohort consortium: design, methods, and study population. Respiratory Research, 2019, 20, 115.	3.6	22
42	Associations between fungal and bacterial microbiota of airways and asthma endotypes. Journal of Allergy and Clinical Immunology, 2019, 144, 1214-1227.e7.	2.9	96
43	Shared and distinct genetic risk factors for childhood-onset and adult-onset asthma: genome-wide and transcriptome-wide studies. Lancet Respiratory Medicine,the, 2019, 7, 509-522.	10.7	238
44	Advances in asthma and allergic disease genetics: Is bigger always better?. Journal of Allergy and Clinical Immunology, 2019, 144, 1495-1506.	2.9	61
45	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
46	Transcriptional programming and T cell receptor repertoires distinguish human lung and lymph node memory T cells. Communications Biology, 2019, 2, 411.	4.4	16
47	T-cell phenotypes are associated with serum IgE levels in Amish and Hutterite children. Journal of Allergy and Clinical Immunology, 2019, 144, 1391-1401.e10.	2.9	23
48	Genetic architecture of moderate-to-severe asthma mirrors that of mild asthma. Journal of Allergy and Clinical Immunology, 2019, 144, 1521-1523.	2.9	6
49	Parent-of-origin effects on quantitative phenotypes in a large Hutterite pedigree. Communications Biology, 2019, 2, 28.	4.4	20
50	Lessons Learned From GWAS of Asthma. Allergy, Asthma and Immunology Research, 2019, 11, 170.	2.9	77
51	Evidence for an IL-6â€“high asthma phenotype in asthmatic patients of African ancestry. Journal of Allergy and Clinical Immunology, 2019, 144, 304-306.e4.	2.9	15
52	Genetic Risk Factors for Asthma Age of Onset Implicate Epithelial Barrier Dysfunction and Innate Immune Genes in Earlier Onset Asthma. , 2019, , .		0
53	Reciprocal Fungal and Bacterial Microbiota in Airways of Patients with T2-High Associated Asthma. , 2019, , .		0
54	Characterization of a Unique Form of Arrhythmic Cardiomyopathy Caused by Recessive Mutation in LEMD2. JACC Basic To Translational Science, 2019, 4, 204-221.	4.1	37

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55	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. Nature Communications, 2019, 10, 880.	12.8	71
56	Evidence for an IL-6 High Asthma Phenotype in Asthma Patients of African Ancestry. , 2019, , .		0
57	Primary Airway Smooth Muscle Cells from Subjects with and Without Asthma Reveal Distinct Differences in Contractile, Epigenetic, and Transcriptional Responses to the Asthma-Promoting Cytokines IL-13 + IL-17. , 2019, , .		1
58	Fine Mapping the 17q12-21 Childhood Onset Asthma Locus in Ethnically Diverse Children in the Multi-Center Environment and Child Health Outcomes (ECHO)-Childrenâ€™s Respiratory and Environmental Workgroup (CREW) Consortium. , 2019, , .		0
59	Human Lung CD4 and CD8 Tissue Resident Memory T Cells Have Distinct Transcriptional Programming from Phenotypically Identical Cells in Lung Draining Lymph Node and Activate Asthma-Related Pathways After T Cell Receptor Stimulation. , 2019, , .		0
60	Gut Microbiota from Amish but Not Hutterite Children Protect Germ-Free Mice from Experimental Asthma. , 2019, , .		2
61	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. Nature Genetics, 2019, 51, 30-35.	21.4	276
62	An admixture mapping meta-analysis implicates genetic variation at 18q21 with asthma susceptibility in Latinos. Journal of Allergy and Clinical Immunology, 2019, 143, 957-969.	2.9	33
63	Role of local CpG DNA methylation in mediating the 17q21 asthma susceptibility gasdermin B (GSDMB)/ORMDL sphingolipid biosynthesis regulator 3 (ORMDL3) expression quantitative trait locus. Journal of Allergy and Clinical Immunology, 2018, 141, 2282-2286.e6.	2.9	20
64	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	21.4	426
65	A decade of research on the 17q12-21 asthma locus: Piecing together the puzzle. Journal of Allergy and Clinical Immunology, 2018, 142, 749-764.e3.	2.9	143
66	Cadherin-related Family Member 3 Genetics and Rhinovirus C Respiratory Illnesses. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 589-594.	5.6	80
67	Positive selection on human gamete-recognition genes. PeerJ, 2018, 6, e4259.	2.0	17
68	Genetic-Epigenetic Interactions in Asthma Revealed by a Genome-Wide Gene-Centric Search. Human Heredity, 2018, 83, 130-152.	0.8	18
69	Gene Coexpression Networks in Whole Blood Implicate Multiple Interrelated Molecular Pathways in Obesity in People with Asthma. Obesity, 2018, 26, 1938-1948.	3.0	11
70	Parent of origin gene expression in a founder population identifies two new candidate imprinted genes at known imprinted regions. PLoS ONE, 2018, 13, e0203906.	2.5	9
71	Determining the genetic basis of anthracycline-cardiotoxicity by molecular response QTL mapping in induced cardiomyocytes. ELife, 2018, 7, .	6.0	94
72	Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis. Nature Genetics, 2018, 50, 1072-1080.	21.4	106

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73	Global DNA methylation changes spanning puberty are near predicted estrogen-responsive genes and enriched for genes involved in endocrine and immune processes. Clinical Epigenetics, 2018, 10, 62.	4.1	45
74	Association of ORMDL3 with rhinovirusâ€induced endoplasmic reticulum stress and type I Interferon responses in human leucocytes. Clinical and Experimental Allergy, 2017, 47, 371-382.	2.9	25
75	Host genetic variation in mucosal immunity pathways influences the upper airway microbiome. Microbiome, 2017, 5, 16.	11.1	61
76	Reducing mitochondrial reads in ATAC-seq using CRISPR/Cas9. Scientific Reports, 2017, 7, 2451.	3.3	51
77	Response to correspondence of NDUFS4â€related Leigh syndrome in Hutterites. American Journal of Medical Genetics, Part A, 2017, 173, 1452-1452.	1.2	0
78	Elevated levels of soluble humanleukocyte antigen-G in the airways are a marker for a low-inflammatory endotype of asthma. Journal of Allergy and Clinical Immunology, 2017, 140, 857-860.	2.9	13
79	Epigenome-wide analysis links SMAD3 methylation at birth to asthma in children of asthmatic mothers. Journal of Allergy and Clinical Immunology, 2017, 140, 534-542.	2.9	94
80	Immune development and environment: lessons from Amish and Hutterite children. Current Opinion in Immunology, 2017, 48, 51-60.	5.5	74
81	Gene Expression Profiling in Blood Provides Reproducible Molecular Insights into Asthma Control. American Journal of Respiratory and Critical Care Medicine, 2017, 195, 179-188.	5.6	49
82	A novel NDUFS4 frameshift mutation causes Leigh disease in the Hutterite population. American Journal of Medical Genetics, Part A, 2017, 173, 596-600.	1.2	14
83	Pathogenic Variant in ACTB, p.Arg183Trp, Causes Juvenile-Onset Dystonia, Hearing Loss, and Developmental Delay without Midline Malformation. Case Reports in Genetics, 2017, 2017, 1-4.	0.2	9
84	Rare non-coding variants are associated with plasma lipid traits in a founder population. Scientific Reports, 2017, 7, 16415.	3.3	31
85	DNA methylation in lung cells is associated with asthma endotypes and genetic risk. JCI Insight, 2016, 1, e90151.	5.0	133
86	A LASSO penalized regression approach for genome-wide association analyses using related individuals: application to the Genetic Analysis Workshop 19 simulated data. BMC Proceedings, 2016, 10, 221-226.	1.6	10
87	Genetic associations with viral respiratory illnesses and asthma control inÂchildren. Clinical and Experimental Allergy, 2016, 46, 112-124.	2.9	39
88	Integrated analyses of gene expression and genetic association studies in a founder population. Human Molecular Genetics, 2016, 25, 2104-2112.	2.9	18
89	Genetic Determinants of the Gut Microbiome in UK Twins. Cell Host and Microbe, 2016, 19, 731-743.	11.0	831
90	Innate Immunity and Asthma Risk in Amish and Hutterite Farm Children. New England Journal of Medicine, 2016, 375, 411-421.	27.0	745

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91	Development of a diagnostic <scp>DNA</scp> chip to screen for 30 autosomal recessive disorders in the Hutterite population. Molecular Genetics & Genomic Medicine, 2016, 4, 312-321.	1.2	5
92	Innate Immunity and Asthma Risk. New England Journal of Medicine, 2016, 375, 1897-1899.	27.0	11
93	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. Nature Communications, 2016, 7, 12522.	12.8	136
94	Leveraging gene-environment interactions and endotypes for asthma gene discovery. Journal of Allergy and Clinical Immunology, 2016, 137, 667-679.	2.9	96
95	Ultra-fast local-haplotype variant calling using paired-end DNA-sequencing data reveals somatic mosaicism in tumor and normal blood samples. Nucleic Acids Research, 2016, 44, e25-e25.	14.5	12
96	Genome-Wide Methylation Study Identifies an IL-13â€“induced Epigenetic Signature in Asthmatic Airways. American Journal of Respiratory and Critical Care Medicine, 2016, 193, 376-385.	5.6	90
97	Expression Quantitative Trait Locus Mapping Studies in Mid-secretory Phase Endometrial Cells Identifies HLA-F and TAP2 as Fecundability-Associated Genes. PLoS Genetics, 2016, 12, e1005858.	3.5	36
98	Asthma Genetics in the Post-GWAS Era. Annals of the American Thoracic Society, 2016, 13, S85-S90.	3.2	93
99	Amish and Hutterite Environmental Farm Products Have Opposite Effects on Experimental Models of Asthma. Annals of the American Thoracic Society, 2016, 13 Suppl 1, S99.	3.2	0
100	Matching Two Independent Cohorts ValidatesDPH1as a Gene Responsible for Autosomal Recessive Intellectual Disability with Short Stature, Craniofacial, and Ectodermal Anomalies. Human Mutation, 2015, 36, 1015-1019.	2.5	32
101	Genome-wide association study and admixture mapping reveal new loci associated with total IgE levels in Latinos. Journal of Allergy and Clinical Immunology, 2015, 135, 1502-1510.	2.9	52
102	PRIMAL: Fast and Accurate Pedigree-based Imputation from Sequence Data in a Founder Population. PLoS Computational Biology, 2015, 11, e1004139.	3.2	36
103	Stress and Bronchodilator Response in Children with Asthma. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 47-56.	5.6	99
104	Evolutionary forward genomics reveals novel insights into the genes and pathways dysregulated in recurrent early pregnancy loss. Human Reproduction, 2015, 30, 519-529.	0.9	28
105	Genome-Wide Association Study Identification of Novel Loci Associated with Airway Responsiveness in Chronic Obstructive Pulmonary Disease. American Journal of Respiratory Cell and Molecular Biology, 2015, 53, 226-234.	2.9	27
106	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
107	Host Genetic Variation Influences Gene Expression Response to Rhinovirus Infection. PLoS Genetics, 2015, 11, e1005111.	3.5	67
108	An siRNA-based functional genomics screen for theÂidentification of regulators of ciliogenesis and ciliopathyÂgenes. Nature Cell Biology, 2015, 17, 1074-1087.	10.3	215

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109	Association of common filaggrin null mutations with atopy but not chronic rhinosinusitis. Annals of Allergy, Asthma and Immunology, 2015, 114, 420-421.	1.0	1
110	Genome-wide association study of recalcitrant atopic dermatitis in Korean children. Journal of Allergy and Clinical Immunology, 2015, 136, 678-684.e4.	2.9	45
111	An Estimate of the Average Number of Recessive Lethal Mutations Carried by Humans. Genetics, 2015, 199, 1243-1254.	2.9	69
112	Targeted Germline Modifications in Rats Using CRISPR/Cas9 and Spermatogonial Stem Cells. Cell Reports, 2015, 10, 1828-1835.	6.4	93
113	Noninvasive Analysis of the Sputum Transcriptome Discriminates Clinical Phenotypes of Asthma. American Journal of Respiratory and Critical Care Medicine, 2015, 191, 1116-1125.	5.6	86
114	A common variant in <scp>RAB</scp>27A gene is associated with fractional exhaled nitric oxide levels in adults. Clinical and Experimental Allergy, 2015, 45, 797-806.	2.9	11
115	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. Nature Genetics, 2015, 47, 1449-1456.	21.4	529
116	Ethnic-specific associations of rare and low-frequency DNA sequence variants with asthma. Nature Communications, 2015, 6, 5965.	12.8	66
117	Future Research Directions in Asthma. An NHLBI Working Group Report. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 1366-1372.	5.6	84
118	Genome-Wide Association Studies of the Human Gut Microbiota. PLoS ONE, 2015, 10, e0140301.	2.5	228
119	Seasonal Variation in Human Gut Microbiome Composition. PLoS ONE, 2014, 9, e90731.	2.5	246
120	Prenatal Tobacco Smoke Exposure Is Associated with Childhood DNA CpG Methylation. PLoS ONE, 2014, 9, e99716.	2.5	105
121	Whole-Genome Sequencing of Individuals from a Founder Population Identifies Candidate Genes for Asthma. PLoS ONE, 2014, 9, e104396.	2.5	42
122	The Effect of Freeze-Thaw Cycles on Gene Expression Levels in Lymphoblastoid Cell Lines. PLoS ONE, 2014, 9, e107166.	2.5	25
123	Genome-wide interaction studies reveal sex-specific asthma risk alleles. Human Molecular Genetics, 2014, 23, 5251-5259.	2.9	70
124	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
125	Variants in DPF3 and DSCAML1 are associated with sperm morphology. Journal of Assisted Reproduction and Genetics, 2014, 31, 131-137.	2.5	8
126	Genome-wide association study of lung function phenotypes in a founder population. Journal of Allergy and Clinical Immunology, 2014, 133, 248-255.e10.	2.9	50

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127	A genome-wide survey of CD4+ lymphocyte regulatory genetic variants identifies novel asthma genes. Journal of Allergy and Clinical Immunology, 2014, 134, 1153-1162.	2.9	46
128	Integrated genome-wide association, coexpression network, and expression single nucleotide polymorphism analysis identifies novel pathway in allergic rhinitis. BMC Medical Genomics, 2014, 7, 48.	1.5	63
129	Disclosure of Genetic Research Results to Members of a Founder Population. Journal of Genetic Counseling, 2014, 23, 984-991.	1.6	5
130	Intellectual disability associated with a homozygous missense mutation in THOC6. Orphanet Journal of Rare Diseases, 2013, 8, 62.	2.7	48
131	Maternal microchimerism protects against the development of asthma. Journal of Allergy and Clinical Immunology, 2013, 132, 39-44.e4.	2.9	22
132	Maternal asthma and microRNA regulation of soluble HLA-G in the airway. Journal of Allergy and Clinical Immunology, 2013, 131, 1496-1503.e4.	2.9	44
133	Recessive TRAPPC11 Mutations Cause a Disease Spectrum of Limb Girdle Muscular Dystrophy and Myopathy with Movement Disorder and Intellectual Disability. American Journal of Human Genetics, 2013, 93, 181-190.	6.2	98
134	A meta-analysis of genome-wide association studies for serum total IgE in diverse study populations. Journal of Allergy and Clinical Immunology, 2013, 131, 1176-1184.	2.9	58
135	Rhinovirus Wheezing Illness and Genetic Risk of Childhood-Onset Asthma. New England Journal of Medicine, 2013, 368, 1398-1407.	27.0	449
136	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
137	Homozygous Founder Mutation in Desmocollin-2 (DSC2) Causes Arrhythmogenic Cardiomyopathy in the Hutterite Population. Circulation: Cardiovascular Genetics, 2013, 6, 327-336.	5.1	47
138	The maternal HLA-G 1597ÂC null mutation is associated with increased risk of pre-eclampsia and reduced HLA-G expression during pregnancy in African-American women. Molecular Human Reproduction, 2013, 19, 144-152.	2.8	38
139	Human Spermatogenic Failure Purges Deleterious Mutation Load from the Autosomes and Both Sex Chromosomes, including the Gene DMRT1. PLoS Genetics, 2013, 9, e1003349.	3.5	118
140	Mutation for Nonsyndromic Mental Retardation in the trans-2-Enoyl-CoA Reductase TER Gene Involved in Fatty Acid Elongation Impairs the Enzyme Activity and Stability, Leading to Change in Sphingolipid Profile. Journal of Biological Chemistry, 2013, 288, 36741-36749.	3.4	29
141	Integration of Mouse and Human Genome-Wide Association Data Identifies KCNIP4 as an Asthma Gene. PLoS ONE, 2013, 8, e56179.	2.5	28
142	The effects of EBV transformation on gene expression levels and methylation profiles. Human Molecular Genetics, 2012, 21, 2142-2142.	2.9	0
143	Increased Protein-Coding Mutations in the Mitochondrial Genome of African American Women With Preeclampsia. Reproductive Sciences, 2012, 19, 1343-1351.	2.5	12
144	The combination of a genome-wide association study of lymphocyte count and analysis of gene expression data reveals novel asthma candidate genes. Human Molecular Genetics, 2012, 21, 2111-2123.	2.9	46

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145	Evaluating the Evidence for Transmission Distortion in Human Pedigrees. Genetics, 2012, 191, 215-232.	2.9	43
146	The ABO blood group is a trans-species polymorphism in primates. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 18493-18498.	7.1	127
147	Variants inDENND1AAre Associated with Polycystic Ovary Syndrome in Women of European Ancestry. Journal of Clinical Endocrinology and Metabolism, 2012, 97, E1342-E1347.	3.6	142
148	Estimating the human mutation rate using autozygosity in a founder population. Nature Genetics, 2012, 44, 1277-1281.	21.4	202
149	HLA-G polymorphisms and soluble HLA-G protein levels in women with recurrent pregnancy loss from Basrah province in Iraq. Human Immunology, 2012, 73, 811-817.	2.4	42
150	Genome-wide ancestry association testing identifies a common European variant on 6q14.1 as a risk factor for asthma in African American subjects. Journal of Allergy and Clinical Immunology, 2012, 130, 622-629.e9.	2.9	31
151	Genome-wide association studies of asthma indicate opposite immunopathogenesis direction from autoimmune diseases. Journal of Allergy and Clinical Immunology, 2012, 130, 861-868.e7.	2.9	130
152	Further replication studies of the EVE Consortium meta-analysis identifies 2 asthma risk loci in European Americans. Journal of Allergy and Clinical Immunology, 2012, 130, 1294-1301.	2.9	30
153	A Population-Based Study of Autosomal-Recessive Disease-Causing Mutations in a Founder Population. American Journal of Human Genetics, 2012, 91, 608-620.	6.2	50
154	Expression Quantitative Trait Locus (eQTL) Mapping In Diverse Populations And Cell Types Identifies Numerous Asthma-Associated Regulatory Variants. , 2012, , .		2
155	Accurate Imputation of Rare and Common Variants in a Founder Population From a Small Number of Sequenced Individuals. Genetic Epidemiology, 2012, 36, 312-319.	1.3	19
156	XM: Association Testing on the Xâ€Chromosome in Caseâ€Control Samples With Related Individuals. Genetic Epidemiology, 2012, 36, 438-450.	1.3	27
157	A shared founder mutation underlies restrictive dermopathy in Old Colony (Dutchâ€German) Mennonite and Hutterite patients in North America. American Journal of Medical Genetics, Part A, 2012, 158A, 1229-1232.	1.2	14
158	Evolutionary genetics of the human Rh blood group system. Human Genetics, 2012, 131, 1205-1216.	3.8	16
159	Resequencing Candidate Genes Implicates Rare Variants in Asthma Susceptibility. American Journal of Human Genetics, 2012, 90, 273-281.	6.2	65
160	Genome-wide Association Study Identifies Candidate Genes for Male Fertility Traits in Humans. American Journal of Human Genetics, 2012, 90, 950-961.	6.2	117
161	Exome sequencing reveals a novel mutation for autosomal recessive non-syndromic mental retardation in the TECR gene on chromosome 19p13. Human Molecular Genetics, 2011, 20, 1285-1289.	2.9	94
162	Sequence variation in the IL4 gene and resistance to Trypanosoma cruzi infection in Bolivians. Journal of Allergy and Clinical Immunology, 2011, 127, 279-282.e3.	2.9	21

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163	IFNG genotype and sex interact to influence the risk of childhood asthma. Journal of Allergy and Clinical Immunology, 2011, 128, 524-531.	2.9	38
164	Rising prevalence of asthma is sex-specific in a US farming population. Journal of Allergy and Clinical Immunology, 2011, 128, 774-779.	2.9	26
165	Meta-analysis of genome-wide association studies of asthma in ethnically diverse North American populations. Nature Genetics, 2011, 43, 887-892.	21.4	736
166	Asthma Bridge: The Asthma Biorepository For Integrative Genomic Exploration. , 2011, , .		4
167	Loneliness Is Associated with Sleep Fragmentation in a Communal Society. Sleep, 2011, 34, 1519-1526.	1.1	179
168	Exome sequencing and the genetics of intellectual disability. Clinical Genetics, 2011, 80, 117-126.	2.0	59
169	The genetics of asthma and allergic disease: a 21st century perspective. Immunological Reviews, 2011, 242, 10-30.	6.0	537
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