Carole Ober

List of Publications by Year in Descending Order

315 papers	23,745 citations	79 h-index	145 g-index
349 ext. papers	27,677 ext. citations	8.9 avg, IF	6.73 L-index

#	Paper	IF	Citations
315	Asthma-associated genetic variants induce IL33 differential expression through an enhancer-blocking regulatory region. *Nature Communications*, **2021**, 12, 6115	17.4	5
314	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	14.4	2
313	Chromosome 17q12-21 Variants Are Associated with Multiple Wheezing Phenotypes in Childhood. *American Journal of Respiratory and Critical Care Medicine*, **2021**, 203, 864-870	10.2	6
312	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	10.2	3
311	Pluripotent stem cell-derived endometrial stromal fibroblasts in a cyclic, hormone-responsive, coculture model of human decidua. *Cell Reports*, **2021**, 35, 109138	10.6	7
310	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	11.5	1
309	Genome-wide association study identifies TNFSF15 associated with childhood asthma. *Allergy: European Journal of Allergy and Clinical Immunology*, **2021**,	9.3	2
308	Extensive pleiotropism and allelic heterogeneity mediate metabolic effects of and. *Science*, **2021**, 372, 1085-1091	33.3	21
307	Longitudinal data reveal strong genetic and weak non-genetic components of ethnicity-dependent blood DNA methylation levels. *Epigenetics*, **2021**, 16, 662-676	5.7	4
306	Two-stage genome-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	6.3	1
305	A-to-I editing of miR-200b-3p in airway cells is associated with moderate-to-severe asthma. *European Respiratory Journal*, **2021**, 58,	13.6	1
304	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	4.9	2
303	Unconjugated bilirubin is associated with protection from early-life wheeze and childhood asthma. *Journal of Allergy and Clinical Immunology*, **2021**, 148, 128-138	11.5	2
302	A functional genomics pipeline identifies pleiotropy and cross-tissue effects within obesity-associated GWAS loci. *Nature Communications*, **2021**, 12, 5253	17.4	4
301	Multiethnic genome-wide and HLA association study of total serum IgE level. *Journal of Allergy and Clinical Immunology*, **2021**, 148, 1589-1595	11.5	1
300	Establishment of human induced trophoblast stem-like cells from term villous cytotrophoblasts. *Stem Cell Research*, **2021**, 56, 102507	1.6	1
299	Expression quantitative trait locus fine mapping of the 17q12-21 asthma locus in African American children: a genetic association and gene expression study. *Lancet Respiratory Medicine,the*, **2020**, 8, 482-492	35.1	20

298	Epigenome-wide association study of DNA methylation and adult asthma in the Agricultural Lung Health Study. *European Respiratory Journal*, **2020**, 56,	13.6	14
297	Club Cell TRPV4 Serves as a Damage Sensor Driving Lung Allergic Inflammation. *Cell Host and Microbe*, **2020**, 27, 614-628.e6	23.4	18
296	Association of HLA-DRB1*09:01 with tIgE levels among African-ancestry individuals with asthma. *Journal of Allergy and Clinical Immunology*, **2020**, 146, 147-155	11.5	6
295	FUT2-ABO epistasis increases the risk of early childhood asthma and Streptococcus pneumoniae respiratory illnesses. *Nature Communications*, **2020**, 11, 6398	17.4	4
294	Cytokine-induced molecular responses in airway smooth muscle cells inform genome-wide association studies of asthma. *Genome Medicine*, **2020**, 12, 64	14.4	9
293	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	11.5	14
292	Altered transcriptional and chromatin responses to rhinovirus in bronchial epithelial cells from adults with asthma. *Communications Biology*, **2020**, 3, 678	6.7	4
291	Transcriptome and regulatory maps of decidua-derived stromal cells inform gene discovery in preterm birth. *Science Advances*, **2020**, 6,	14.3	9
290	A comparison of humans and baboons suggests germline mutation rates do not track cell divisions. *PLoS Biology*, **2020**, 18, e3000838	9.7	23
289	A comparison of humans and baboons suggests germline mutation rates do not track cell divisions **2020**, 18, e3000838		
288	A comparison of humans and baboons suggests germline mutation rates do not track cell divisions **2020**, 18, e3000838		
287	A comparison of humans and baboons suggests germline mutation rates do not track cell divisions **2020**, 18, e3000838		
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285	A comparison of humans and baboons suggests germline mutation rates do not track cell divisions **2020**, 18, e3000838		
284	A comparison of humans and baboons suggests germline mutation rates do not track cell divisions **2020**, 18, e3000838		
283	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	11.5	17
282	Parent-of-origin effects on quantitative phenotypes in a large Hutterite pedigree. *Communications Biology*, **2019**, 2, 28	6.7	8
281	Lessons Learned From GWAS of Asthma. *Allergy, Asthma and Immunology Research*, **2019**, 11, 170-187	5.3	46

280	Evidence for an IL-6-high asthma phenotype in asthmatic patients of African ancestry. *Journal of Allergy and Clinical Immunology*, **2019**, 144, 304-306.e4	11.5	8
279	Characterization of a Unique Form of Arrhythmic Cardiomyopathy Caused by Recessive Mutation in LEMD2. *JACC Basic To Translational Science*, **2019**, 4, 204-221	8.7	14
278	Effects of an FcRIIA polymorphism on leukocyte gene expression and cytokine responses to anti-CD3 and anti-CD28 antibodies. *Genes and Immunity*, **2019**, 20, 462-472	4.4	5
277	Heritability estimation and differential analysis of count data with generalized linear mixed models in genomic sequencing studies. *Bioinformatics*, **2019**, 35, 487-496	7.2	32
276	The Children's Respiratory and Environmental Workgroup (CREW) birth cohort consortium: design, methods, and study population. *Respiratory Research*, **2019**, 20, 115	7.3	12
275	Associations between fungal and bacterial microbiota of airways and asthma endotypes. *Journal of Allergy and Clinical Immunology*, **2019**, 144, 1214-1227.e7	11.5	45
274	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	35.1	111
273	Advances in asthma and allergic disease genetics: Is bigger always better?. *Journal of Allergy and Clinical Immunology*, **2019**, 144, 1495-1506	11.5	34
272	Associations of autozygosity with a broad range of human phenotypes. *Nature Communications*, **2019**, 10, 4957	17.4	40
271	Transcriptional programming and T cell receptor repertoires distinguish human lung and lymph node memory T cells. *Communications Biology*, **2019**, 2, 411	6.7	8
270	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. *Nature Communications*, **2019**, 10, 880	17.4	36
269	Gut Microbiota from Amish but Not Hutterite Children Protect Germ-Free Mice from Experimental Asthma **2019**,		2
268	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. *Nature Genetics*, **2019**, 51, 30-35	36.3	153
267	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	11.5	20
266	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	11.5	17
265	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. *Nature Genetics*, **2018**, 50, 42-53	36.3	246
264	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	11.5	90
263	Determining the genetic basis of anthracycline-cardiotoxicity by molecular response QTL mapping in induced cardiomyocytes. *ELife*, **2018**, 7,	8.9	54

262	Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis. *Nature Genetics*, **2018**, 50, 1072-1080	36.3	52
261	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	7.7	22
260	Author response: Determining the genetic basis of anthracycline-cardiotoxicity by molecular response QTL mapping in induced cardiomyocytes **2018**,		4
259	Cadherin-related Family Member 3 Genetics and Rhinovirus C Respiratory Illnesses. *American Journal of Respiratory and Critical Care Medicine*, **2018**, 197, 589-594	10.2	49
258	Positive selection on human gamete-recognition genes. *PeerJ*, **2018**, 6, e4259	3.1	9
257	Genetic-Epigenetic Interactions in Asthma Revealed by a Genome-Wide Gene-Centric Search. *Human Heredity*, **2018**, 83, 130-152	1.1	11
256	Gene Coexpression Networks in Whole Blood Implicate Multiple Interrelated Molecular Pathways in Obesity in People with Asthma. *Obesity*, **2018**, 26, 1938-1948	8	9
255	Parent of origin gene expression in a founder population identifies two new candidate imprinted genes at known imprinted regions. *PLoS ONE*, **2018**, 13, e0203906	3.7	6
254	Association of ORMDL3 with rhinovirus-induced endoplasmic reticulum stress and type I Interferon responses in human leucocytes. *Clinical and Experimental Allergy*, **2017**, 47, 371-382	4.1	23
253	Host genetic variation in mucosal immunity pathways influences the upper airway microbiome. *Microbiome*, **2017**, 5, 16	16.6	43
252	Reducing mitochondrial reads in ATAC-seq using CRISPR/Cas9. *Scientific Reports*, **2017**, 7, 2451	4.9	34
251	Response to correspondence of NDUFS4-related Leigh syndrome in Hutterites. *American Journal of Medical Genetics, Part A*, **2017**, 173, 1452	2.5	
250	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	11.5	7
249	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	11.5	63
248	Pathogenic Variant in , p.Arg183Trp, Causes Juvenile-Onset Dystonia, Hearing Loss, and Developmental Delay without Midline Malformation. *Case Reports in Genetics*, **2017**, 2017, 9184265	0.7	8
247	Rare non-coding variants are associated with plasma lipid traits in a founder population. *Scientific Reports*, **2017**, 7, 16415	4.9	16
246	Immune development and environment: lessons from Amish and Hutterite children. *Current Opinion in Immunology*, **2017**, 48, 51-60	7.8	52
245	Gene Expression Profiling in Blood Provides Reproducible Molecular Insights into Asthma Control. *American Journal of Respiratory and Critical Care Medicine*, **2017**, 195, 179-188	10.2	37

244	A novel NDUFS4 frameshift mutation causes Leigh disease in the Hutterite population. *American Journal of Medical Genetics, Part A*, **2017**, 173, 596-600	2.5	11
243	Genome-Wide Methylation Study Identifies an IL-13-induced Epigenetic Signature in Asthmatic Airways. *American Journal of Respiratory and Critical Care Medicine*, **2016**, 193, 376-85	10.2	70
242	Innate Immunity and Asthma Risk. *New England Journal of Medicine*, **2016**, 375, 1898-1899	59.2	8
241	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. *Nature Communications*, **2016**, 7, 12522	17.4	90
240	Leveraging gene-environment interactions and endotypes for asthma gene discovery. *Journal of Allergy and Clinical Immunology*, **2016**, 137, 667-79	11.5	69
239	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	20.1	9
238	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	6	23
237	Asthma Genetics in the Post-GWAS Era. *Annals of the American Thoracic Society*, **2016**, 13 Suppl 1, S85-90	4.7	52
236	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	4.7	
235	DNA methylation in lung cells is associated with asthma endotypes and genetic risk. *JCI Insight*, **2016**, 1, e90151	9.9	92
234	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	2.3	8
233	Genetic associations with viral respiratory illnesses and asthma control in children. *Clinical and Experimental Allergy*, **2016**, 46, 112-24	4.1	29
232	Integrated analyses of gene expression and genetic association studies in a founder population. *Human Molecular Genetics*, **2016**, 25, 2104-2112	5.6	10
231	Genetic Determinants of the Gut Microbiome in UK Twins. *Cell Host and Microbe*, **2016**, 19, 731-43	23.4	547
230	Innate Immunity and Asthma Risk in Amish and Hutterite Farm Children. *New England Journal of Medicine*, **2016**, 375, 411-421	59.2	537
229	Development of a diagnostic DNA chip to screen for 30 autosomal recessive disorders in the Hutterite population. *Molecular Genetics & Genomic Medicine*, **2016**, 4, 312-21	2.3	2
228	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, 226-34	5.7	24
227	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	30.4	119

226	Host genetic variation influences gene expression response to rhinovirus infection. *PLoS Genetics*, **2015**, 11, e1005111	6	45
225	An siRNA-based functional genomics screen for the identification of regulators of ciliogenesis and ciliopathy genes. *Nature Cell Biology*, **2015**, 17, 1074-1087	23.4	140
224	Association of common filaggrin null mutations with atopy but not chronic rhinosinusitis. *Annals of Allergy, Asthma and Immunology*, **2015**, 114, 420-421	3.2	1
223	Genome-wide association study of recalcitrant atopic dermatitis in Korean children. *Journal of Allergy and Clinical Immunology*, **2015**, 136, 678-684.e4	11.5	26
222	An estimate of the average number of recessive lethal mutations carried by humans. *Genetics*, **2015** , 199, 1243-54	4	45
221	Targeted Germline Modifications in Rats Using CRISPR/Cas9 and Spermatogonial Stem Cells. *Cell Reports*, **2015**, 10, 1828-35	10.6	78
220	Noninvasive analysis of the sputum transcriptome discriminates clinical phenotypes of asthma. *American Journal of Respiratory and Critical Care Medicine*, **2015**, 191, 1116-25	10.2	62
219	A common variant in RAB27A gene is associated with fractional exhaled nitric oxide levels in adults. *Clinical and Experimental Allergy*, **2015**, 45, 797-806	4.1	9
218	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	36.3	329
217	Ethnic-specific associations of rare and low-frequency DNA sequence variants with asthma. *Nature Communications*, **2015**, 6, 5965	17.4	56
216	Future Research Directions in Asthma. An NHLBI Working Group Report. *American Journal of Respiratory and Critical Care Medicine*, **2015**, 192, 1366-72	10.2	51
215	Matching two independent cohorts validates DPH1 as a gene responsible for autosomal recessive intellectual disability with short stature, craniofacial, and ectodermal anomalies. *Human Mutation*, **2015**, 36, 1015-9	4.7	25
214	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, 1502-10	11.5	40
213	PRIMAL: Fast and accurate pedigree-based imputation from sequence data in a founder population. *PLoS Computational Biology*, **2015**, 11, e1004139	5	27
212	Stress and Bronchodilator Response in Children with Asthma. *American Journal of Respiratory and Critical Care Medicine*, **2015**, 192, 47-56	10.2	71
211	Evolutionary forward genomics reveals novel insights into the genes and pathways dysregulated in recurrent early pregnancy loss. *Human Reproduction*, **2015**, 30, 519-29	5.7	25
210	Genome-Wide Association Studies of the Human Gut Microbiota. *PLoS ONE*, **2015**, 10, e0140301	3.7	153
209	Variants in DPF3 and DSCAML1 are associated with sperm morphology. *Journal of Assisted Reproduction and Genetics*, **2014**, 31, 131-7	3.4	6

208	Genome-wide association study of lung function phenotypes in a founder population. *Journal of Allergy and Clinical Immunology*, **2014**, 133, 248-55.e1-10	11.5	44
207	A genome-wide survey of CD4(+) lymphocyte regulatory genetic variants identifies novel asthma genes. *Journal of Allergy and Clinical Immunology*, **2014**, 134, 1153-62	11.5	40
206	Integrated genome-wide association, coexpression network, and expression single nucleotide polymorphism analysis identifies novel pathway in allergic rhinitis. *BMC Medical Genomics*, **2014**, 7, 48	3.7	45
205	Disclosure of genetic research results to members of a founder population. *Journal of Genetic Counseling*, **2014**, 23, 984-91	2.5	4
204	Seasonal variation in human gut microbiome composition. *PLoS ONE*, **2014**, 9, e90731	3.7	179
203	Prenatal tobacco smoke exposure is associated with childhood DNA CpG methylation. *PLoS ONE*, **2014**, 9, e99716	3.7	94
202	Whole-genome sequencing of individuals from a founder population identifies candidate genes for asthma. *PLoS ONE*, **2014**, 9, e104396	3.7	26
201	The effect of freeze-thaw cycles on gene expression levels in lymphoblastoid cell lines. *PLoS ONE*, **2014**, 9, e107166	3.7	18
200	Genome-wide interaction studies reveal sex-specific asthma risk alleles. *Human Molecular Genetics*, **2014**, 23, 5251-9	5.6	50
199	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	11.5	27
198	Intellectual disability associated with a homozygous missense mutation in THOC6. *Orphanet Journal of Rare Diseases*, **2013**, 8, 62	4.2	34
197	Maternal microchimerism protects against the development of asthma. *Journal of Allergy and Clinical Immunology*, **2013**, 132, 39-44	11.5	18
196	Maternal asthma and microRNA regulation of soluble HLA-G in the airway. *Journal of Allergy and Clinical Immunology*, **2013**, 131, 1496-503	11.5	38
195	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, 181-90	11	76
194	A meta-analysis of genome-wide association studies for serum total IgE in diverse study populations. *Journal of Allergy and Clinical Immunology*, **2013**, 131, 1176-84	11.5	49
193	Rhinovirus wheezing illness and genetic risk of childhood-onset asthma. *New England Journal of Medicine*, **2013**, 368, 1398-407	59.2	336
192	Genome-wide association study of body mass index in 23 000 individuals with and without asthma. *Clinical and Experimental Allergy*, **2013**, 43, 463-74	4.1	54
191	Homozygous founder mutation in desmocollin-2 (DSC2) causes arrhythmogenic cardiomyopathy in the Hutterite population. *Circulation: Cardiovascular Genetics*, **2013**, 6, 327-36		38

190	The maternal HLA-G 1597Δ 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, 144-52	4.4	28
189	Human spermatogenic failure purges deleterious mutation load from the autosomes and both sex chromosomes, including the gene DMRT1. *PLoS Genetics*, **2013**, 9, e1003349	6	99
188	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, 36741-9	5.4	22
187	Integration of mouse and human genome-wide association data identifies KCNIP4 as an asthma gene. *PLoS ONE*, **2013**, 8, e56179	3.7	25
186	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, 18493-8	11.5	98
185	Variants in DENND1A are associated with polycystic ovary syndrome in women of European ancestry. *Journal of Clinical Endocrinology and Metabolism*, **2012**, 97, E1342-7	5.6	118
184	Estimating the human mutation rate using autozygosity in a founder population. *Nature Genetics*, **2012**, 44, 1277-81	36.3	162
183	HLA-G polymorphisms and soluble HLA-G protein levels in women with recurrent pregnancy loss from Basrah province in Iraq. *Human Immunology*, **2012**, 73, 811-7	2.3	37
182	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	11.5	27
181	Genome-wide association studies of asthma indicate opposite immunopathogenesis direction from autoimmune diseases. *Journal of Allergy and Clinical Immunology*, **2012**, 130, 861-8.e7	11.5	109
180	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, 1294-301	11.5	27
179	A population-based study of autosomal-recessive disease-causing mutations in a founder population. *American Journal of Human Genetics*, **2012**, 91, 608-20	11	41
178	Expression Quantitative Trait Locus (eQTL) Mapping In Diverse Populations And Cell Types Identifies Numerous Asthma-Associated Regulatory Variants **2012**,		2
177	Accurate imputation of rare and common variants in a founder population from a small number of sequenced individuals. *Genetic Epidemiology*, **2012**, 36, 312-9	2.6	18
176	XM: association testing on the X-chromosome in case-control samples with related individuals. *Genetic Epidemiology*, **2012**, 36, 438-50	2.6	21
175	A shared founder mutation underlies restrictive dermopathy in Old Colony (Dutch-German) Mennonite and Hutterite patients in North America. *American Journal of Medical Genetics, Part A*, **2012**, 158A, 1229-32	2.5	9
174	Evolutionary genetics of the human Rh blood group system. *Human Genetics*, **2012**, 131, 1205-16	6.3	12
173	Resequencing candidate genes implicates rare variants in asthma susceptibility. *American Journal of Human Genetics*, **2012**, 90, 273-81	11	55

172	Genome-wide association study identifies candidate genes for male fertility traits in humans. *American Journal of Human Genetics*, **2012**, 90, 950-61	11	102
171	The effects of EBV transformation on gene expression levels and methylation profiles. *Human Molecular Genetics*, **2012**, 21, 2142-2142	5.6	78
170	Increased protein-coding mutations in the mitochondrial genome of African American women with preeclampsia. *Reproductive Sciences*, **2012**, 19, 1343-51	3	11
169	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, 2111-23	5.6	38
168	Evaluating the evidence for transmission distortion in human pedigrees. *Genetics*, **2012**, 191, 215-32	4	34
167	Sequence variation in the IL4 gene and resistance to Trypanosoma cruzi infection in Bolivians. *Journal of Allergy and Clinical Immunology*, **2011**, 127, 279-82, 282.e1-3	11.5	17
166	IFNG genotype and sex interact to influence the risk of childhood asthma. *Journal of Allergy and Clinical Immunology*, **2011**, 128, 524-31	11.5	29
165	Rising prevalence of asthma is sex-specific in a US farming population. *Journal of Allergy and Clinical Immunology*, **2011**, 128, 774-9	11.5	20
164	Meta-analysis of genome-wide association studies of asthma in ethnically diverse North American populations. *Nature Genetics*, **2011**, 43, 887-92	36.3	605
163	Asthma Bridge: The Asthma Biorepository For Integrative Genomic Exploration **2011**,		4
162	Loneliness is associated with sleep fragmentation in a communal society. *Sleep*, **2011**, 34, 1519-26	1.1	138
161	Exome sequencing and the genetics of intellectual disability. *Clinical Genetics*, **2011**, 80, 117-26	4	49
160	The genetics of asthma and allergic disease: a 21st century perspective. *Immunological Reviews*, **2011**, 242, 10-30	11.3	417
159	A common spinal muscular atrophy deletion mutation is present on a single founder haplotype in the US Hutterites. *European Journal of Human Genetics*, **2011**, 19, 1045-51	5.3	13
158	Gene-environment interactions in human disease: nuisance or opportunity?. *Trends in Genetics*, **2011**, 27, 107-15	8.5	119
157	TMEM237 is mutated in individuals with a Joubert syndrome related disorder and expands the role of the TMEM family at the ciliary transition zone. *American Journal of Human Genetics*, **2011**, 89, 713-30	11	145
156	Genetic variance components estimation for binary traits using multiple related individuals. *Genetic Epidemiology*, **2011**, 35, 291-302	2.6	5
155	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, 1285-9	5.6	79

154	The effects of EBV transformation on gene expression levels and methylation profiles. *Human Molecular Genetics*, **2011**, 20, 1643-52	5.6	104
153	Drawing the history of the Hutterite population on a genetic landscape: inference from Y-chromosome and mtDNA genotypes. *European Journal of Human Genetics*, **2010**, 18, 463-70	5.3	20
152	Levels of soluble human leukocyte antigen-G are increased in asthmatic airways. *European Respiratory Journal*, **2010**, 35, 925-7	13.6	21
151	The CFTR Met 470 allele is associated with lower birth rates in fertile men from a population isolate. *PLoS Genetics*, **2010**, 6, e1000974	6	18
150	Functional variants of the sphingosine-1-phosphate receptor 1 gene associate with asthma susceptibility. *Journal of Allergy and Clinical Immunology*, **2010**, 126, 241-9, 249.e1-3	11.5	37
149	PRDM9 is a major determinant of meiotic recombination hotspots in humans and mice. *Science*, **2010**, 327, 836-40	33.3	685
148	Sequence variations at the human leukocyte antigen-linked olfactory receptor cluster do not influence female preferences for male odors. *Human Immunology*, **2010**, 71, 100-3	2.3	8
147	Colloquium papers: Heritability of reproductive fitness traits in a human population. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107 Suppl 1, 1772-8	11.5	63
146	Shades of gray: a comparison of linkage disequilibrium between Hutterites and Europeans. *Genetic Epidemiology*, **2010**, 34, 133-9	2.6	8
145	Linkage analysis with dense SNP maps in isolated populations. *Human Heredity*, **2009**, 68, 87-97	1.1	15
144	(Too) great expectations: the challenges in replicating asthma disease genes. *American Journal of Respiratory and Critical Care Medicine*, **2009**, 179, 1078-9	10.2	6
143	Broad-scale recombination patterns underlying proper disjunction in humans. *PLoS Genetics*, **2009**, 5, e1000658	6	77
142	Genome-wide association study of plasma lipoprotein(a) levels identifies multiple genes on chromosome 6q. *Journal of Lipid Research*, **2009**, 50, 798-806	6.3	78
141	Inverted duplications on acentric markers: mechanism of formation. *Human Molecular Genetics*, **2009**, 18, 2241-56	5.6	24
140	A multiple splitting approach to linkage analysis in large pedigrees identifies a linkage to asthma on chromosome 12. *Genetic Epidemiology*, **2009**, 33, 207-16	2.6	10
139	Sequencing the IL4 locus in African Americans implicates rare noncoding variants in asthma susceptibility. *Journal of Allergy and Clinical Immunology*, **2009**, 124, 1204-9.e9	11.5	38
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