

# Juha Kere

## List of Publications by Year in descending order

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568  
papers

41,664  
citations

2322

98  
h-index

4117

175  
g-index

595  
all docs

595  
docs citations

595  
times ranked

50541  
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome-based identification of novel endotypes in adult atopic dermatitis. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2022, 77, 1486-1498.	5.7	8
2	Characteristics of preeclampsia in donor cell gestations. <i>Pregnancy Hypertension</i> , 2022, 27, 59-61.	1.4	3
3	CRISPR activation enables high-fidelity reprogramming into human pluripotent stem cells. <i>Stem Cell Reports</i> , 2022, 17, 413-426.	4.8	13
4	SkewC: Identifying cells with skewed gene body coverage in single-cell RNA sequencing data. <i>IScience</i> , 2022, 25, 103777.	4.1	4
5	DUX4 is a multifunctional factor priming human embryonic genome activation. <i>IScience</i> , 2022, 25, 104137.	4.1	20
6	Viral infection-related gene upregulation in monocytes in children with signs of cell autoimmunity. <i>Pediatric Diabetes</i> , 2022, 23, 703-713.	2.9	3
7	INFLUENCE OF FLG LOSS-OF-FUNCTION MUTATIONS IN HOST-MICROBE INTERACTIONS DURING ATOPIC SKIN INFLAMMATION. <i>Journal of Dermatological Science</i> , 2022, , .	1.9	0
8	Idiopathic scoliosis: a systematic review and meta-analysis of heritability. <i>EFORT Open Reviews</i> , 2022, 7, 414-421.	4.1	1
9	Transient DUX4 expression in human embryonic stem cells induces blastomere-like expression program that is marked by SLC34A2. <i>Stem Cell Reports</i> , 2022, 17, 1743-1756.	4.8	11
10	Biomarkers of nanomaterials hazard from multi-layer data. <i>Nature Communications</i> , 2022, 13, .	12.8	16
11	Searching for a paternal phenotype for preeclampsia. <i>Acta Obstetrica Et Gynecologica Scandinavica</i> , 2022, 101, 862-870.	2.8	1
12	Genome-wide association study reveals new insights into the heritability and genetic correlates of developmental dyslexia. <i>Molecular Psychiatry</i> , 2021, 26, 3004-3017.	7.9	56
13	Distinct whole-blood transcriptome profile of children with metabolic healthy overweight/obesity compared to metabolic unhealthy overweight/obesity. <i>Pediatric Research</i> , 2021, 89, 1687-1694.	2.3	10
14	Otitis media susceptibility and shifts in the head and neck microbiome due to <i>SPINK5</i> variants. <i>Journal of Medical Genetics</i> , 2021, 58, 442-452.	3.2	14
15	Association of Maternal DNA Methylation and Offspring Birthweight. <i>Reproductive Sciences</i> , 2021, 28, 218-227.	2.5	2
16	Microbial and transcriptional differences elucidate atopic dermatitis heterogeneity across skin sites. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021, 76, 1173-1187.	5.7	16
17	DNA Methylation Levels in Mononuclear Leukocytes from the Mother and Her Child Are Associated with IgE Sensitization to Allergens in Early Life. <i>International Journal of Molecular Sciences</i> , 2021, 22, 801.	4.1	18
18	Nasal upregulation of <i>CST1</i> in dog-sensitised children with severe allergic airway disease. <i>ERJ Open Research</i> , 2021, 7, 00917-2020.	2.6	8

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19	A missense variant in IFT122 associated with a canine model of retinitis pigmentosa. <i>Human Genetics</i> , 2021, 140, 1569-1579.	3.8	4
20	Toxicogenomic Profiling of 28 Nanomaterials in Mouse Airways. <i>Advanced Science</i> , 2021, 8, 2004588.	11.2	15
21	Dysfunction of complement receptors CR3 (CD11b/18) and CR4 (CD11c/18) in pre-eclampsia: a genetic and functional study. <i>BJOG: an International Journal of Obstetrics and Gynaecology</i> , 2021, 128, 1282-1291.	2.3	9
22	High-resolution targeted bisulfite sequencing reveals blood cell type-specific DNA methylation patterns in IL13 and ORMDL3. <i>Clinical Epigenetics</i> , 2021, 13, 106.	4.1	0
23	HLA $\alpha$ G expression correlates with histological grade but not with prognosis in colorectal carcinoma. <i>Hla</i> , 2021, 98, 213-217.	0.6	4
24	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	12.8	11
25	The role of CDHR3 in susceptibility to otitis media. <i>Journal of Molecular Medicine</i> , 2021, 99, 1571-1583.	3.9	4
26	Small RNA expression and miRNA modification dynamics in human oocytes and early embryos. <i>Genome Research</i> , 2021, 31, 1474-1485.	5.5	10
27	Dog colour patterns explained by modular promoters of ancient canid origin. <i>Nature Ecology and Evolution</i> , 2021, 5, 1415-1423.	7.8	24
28	Cystatin B-deficiency triggers ectopic histone H3 tail cleavage during neurogenesis. <i>Neurobiology of Disease</i> , 2021, 156, 105418.	4.4	13
29	Motor Function Deficits in the Estrogen Receptor Beta Knockout Mouse: Role on Excitatory Neurotransmission and Myelination in the Motor Cortex. <i>Neuroendocrinology</i> , 2021, 111, 27-44.	2.5	10
30	Embryonic LTR retrotransposons supply promoter modules to somatic tissues. <i>Genome Research</i> , 2021, 31, 1983-1993.	5.5	7
31	Generation of RNA sequencing libraries for transcriptome analysis of globin-rich tissues of the domestic dog. <i>STAR Protocols</i> , 2021, 2, 100995.	1.2	6
32	Acute wheeze-specific gene module shows correlation with vitamin D and asthma medication. <i>European Respiratory Journal</i> , 2020, 55, 1901330.	6.7	9
33	Nagashima-type palmoplantar keratosis in Finland caused by a SERPINB7 founder mutation. <i>Journal of the American Academy of Dermatology</i> , 2020, 83, 643-645.	1.2	14
34	Single-Cell Analysis of Human Ovarian Cortex Identifies Distinct Cell Populations But No Oogonial Stem Cells. <i>Obstetrical and Gynecological Survey</i> , 2020, 75, 354-355.	0.4	1
35	Multiparametric Profiling of Engineered Nanomaterials: Unmasking the Surface Coating Effect. <i>Advanced Science</i> , 2020, 7, 2002221.	11.2	24
36	Fetal HLA-G mediated immune tolerance and interferon response in preeclampsia. <i>EBioMedicine</i> , 2020, 59, 102872.	6.1	25

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37	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	5.5	109
38	PCSK2 expression in neuroendocrine tumors points to a midgut, pulmonary, or pheochromocytoma/paraganglioma origin. <i>Apmis</i> , 2020, 128, 563-572.	2.0	5
39	Epigenetic alterations in skin homing CD4+CLA+ T cells of atopic dermatitis patients. <i>Scientific Reports</i> , 2020, 10, 18020.	3.3	23
40	Multi-omic studies on missense PLG variants in families with otitis media. <i>Scientific Reports</i> , 2020, 10, 15035.	3.3	4
41	Differentiation of ciliated human midbrain-derived LUHMES neurons. <i>Journal of Cell Science</i> , 2020, 133, .	2.0	6
42	Rare variants in dynein heavy chain genes in two individuals with situs inversus and developmental dyslexia: a case report. <i>BMC Medical Genetics</i> , 2020, 21, 87.	2.1	5
43	A putative silencer variant in a spontaneous canine model of retinitis pigmentosa. <i>PLoS Genetics</i> , 2020, 16, e1008659.	3.5	9
44	Epigenome-wide meta-analysis of blood DNA methylation in newborns and children identifies numerous loci related to gestational age. <i>Genome Medicine</i> , 2020, 12, 25.	8.2	81
45	Single-cell analysis of human ovarian cortex identifies distinct cell populations but no oogonial stem cells. <i>Nature Communications</i> , 2020, 11, 1147.	12.8	188
46	Novel Hemizygous IL2RG p.(Pro58Ser) Mutation Impairs IL-2 Receptor Complex Expression on Lymphocytes Causing X-Linked Combined Immunodeficiency. <i>Journal of Clinical Immunology</i> , 2020, 40, 503-514.	3.8	11
47	Congenital chloride diarrhea and Pendred syndrome: case report of siblings with two rare recessive disorders of SLC26 family genes. <i>BMC Medical Genetics</i> , 2020, 21, 79.	2.1	1
48	Dyslexia Candidate Gene and Ciliary Gene Expression Dynamics During Human Neuronal Differentiation. <i>Molecular Neurobiology</i> , 2020, 57, 2944-2958.	4.0	11
49	Phenotypic Variability with SLURP1 Mutations and Diffuse Palmoplantar Keratoderma. <i>Acta Dermato-Venereologica</i> , 2020, 100, adv00060.	1.3	0
50	DNA Methylation Trajectories During Pregnancy. <i>Epigenetics Insights</i> , 2019, 12, 251686571986709.	2.0	26
51	Guide for library design and bias correction for large-scale transcriptome studies using highly multiplexed RNAseq methods. <i>BMC Bioinformatics</i> , 2019, 20, 418.	2.6	9
52	Gain-of-function CEBPE mutation causes noncanonical autoinflammatory inflammasomopathy. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 1364-1376.	2.9	37
53	Dominant TOM1 mutation associated with combined immunodeficiency and autoimmune disease. <i>Npj Genomic Medicine</i> , 2019, 4, 14.	3.8	11
54	Microbe-host interplay in atopic dermatitis and psoriasis. <i>Nature Communications</i> , 2019, 10, 4703.	12.8	217

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55	<i>&lt;i&gt;ABO&lt;/i&gt; Genotype and Blood Type Are Associated with Otitis Media. Genetic Testing and Molecular Biomarkers, 2019, 23, 823-827.</i>	0.7	4
56	Delineating the Healthy Human Skin UV Response and Early Induction of Interferon Pathway in Cutaneous Lupus Erythematosus. Journal of Investigative Dermatology, 2019, 139, 2058-2061.e4.	0.7	16
57	NET-CAGE characterizes the dynamics and topology of human transcribed cis-regulatory elements. Nature Genetics, 2019, 51, 1369-1379.	21.4	72
58	034 Characterization of novel TMEM173 mutation causing a lupus- and SAVI-like phenotype, modified by polymorphisms in TMEM173 and IFIH1. Journal of Investigative Dermatology, 2019, 139, S220.	0.7	0
59	Complement in Human Pre-implantation Embryos: Attack and Defense. Frontiers in Immunology, 2019, 10, 2234.	4.8	11
60	The human long non-coding RNA gene RMRP has pleiotropic effects and regulates cell-cycle progression at G2. Scientific Reports, 2019, 9, 13758.	3.3	22
61	Epigenome-wide meta-analysis of DNA methylation and childhood asthma. Journal of Allergy and Clinical Immunology, 2019, 143, 2062-2074.	2.9	147
62	Pleomorphic Adenoma Gene 1 Is Needed For Timely Zygotic Genome Activation and Early Embryo Development. Scientific Reports, 2019, 9, 8411.	3.3	16
63	Prenatal Particulate Air Pollution and DNA Methylation in Newborns: An Epigenome-Wide Meta-Analysis. Environmental Health Perspectives, 2019, 127, 57012.	6.0	111
64	Pool-seq driven proteogenomic database for Group G Streptococcus. Journal of Proteomics, 2019, 201, 84-92.	2.4	2
65	A preliminary transcriptome analysis suggests a transitory effect of vitamin D on mitochondrial function in obese young Finnish subjects. Endocrine Connections, 2019, 8, 559-570.	1.9	6
66	A2ML1 and otitis media: novel variants, differential expression, and relevant pathways. Human Mutation, 2019, 40, 1156-1171.	2.5	10
67	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. Nature Communications, 2019, 10, 1893.	12.8	140
68	Cationic gold nanoparticles elicit mitochondrial dysfunction: a multi-omics study. Scientific Reports, 2019, 9, 4366.	3.3	54
69	Myoglobinopathy is an adult-onset autosomal dominant myopathy with characteristic sarcoplasmic inclusions. Nature Communications, 2019, 10, 1396.	12.8	11
70	Discovering heritable modes of MEG spectral power. Human Brain Mapping, 2019, 40, 1391-1402.	3.6	17
71	Nocturnal asthma is affected by genetic interactions between <i>&lt;i&gt;RORA&lt;/i&gt;</i> and <i>&lt;i&gt;NPSR1&lt;/i&gt;</i> . Pediatric Pulmonology, 2019, 54, 847-857.	2.0	9
72	Genome-wide association scan identifies new variants associated with a cognitive predictor of dyslexia. Translational Psychiatry, 2019, 9, 77.	4.8	82

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73	A multiethnic meta-analysis defined the association of rs12946942 with severe adolescent idiopathic scoliosis. <i>Journal of Human Genetics</i> , 2019, 64, 493-498.	2.3	11
74	Discovery of increased epidermal DNAH10 expression after regeneration of dermis in a randomized with-in person trial – reflections on psoriatic inflammation. <i>Scientific Reports</i> , 2019, 9, 19136.	3.3	3
75	Novel TMEM173 Mutation and the Role of Disease Modifying Alleles. <i>Frontiers in Immunology</i> , 2019, 10, 2770.	4.8	45
76	Impact of obesity on angiogenic and inflammatory markers in the Finnish Genetics of Pre-eclampsia Consortium (FINNPEC) cohort. <i>International Journal of Obesity</i> , 2019, 43, 1070-1081.	3.4	17
77	European families reveal MHC class I and II associations with autoimmune-mediated congenital heart block. <i>Annals of the Rheumatic Diseases</i> , 2018, 77, 1381-1382.	0.9	6
78	DNA methylation in childhood asthma: an epigenome-wide meta-analysis. <i>Lancet Respiratory Medicine</i> , 2018, 6, 379-388.	10.7	170
79	Reduced <i>CDHR3</i> expression in children wheezing with rhinovirus. <i>Pediatric Allergy and Immunology</i> , 2018, 29, 200-206.	2.6	20
80	Characterization of the human RFX transcription factor family by regulatory and target gene analysis. <i>BMC Genomics</i> , 2018, 19, 181.	2.8	73
81	Metabolic and functional changes in transgender individuals following cross-sex hormone treatment: Design and methods of the Gender Dysphoria Treatment in Sweden (GETS) study. <i>Contemporary Clinical Trials Communications</i> , 2018, 10, 148-153.	1.1	27
82	Mlh1 deficiency in normal mouse colon mucosa associates with chromosomally unstable colon cancer. <i>Carcinogenesis</i> , 2018, 39, 788-797.	2.8	18
83	An international meta-analysis confirms the association of BNC2 with adolescent idiopathic scoliosis. <i>Scientific Reports</i> , 2018, 8, 4730.	3.3	20
84	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. <i>International Journal of Epidemiology</i> , 2018, 47, 22-23u.	1.9	105
85	Fetal Microsatellite in the Heme Oxygenase 1 Promoter Is Associated With Severe and Early-Onset Preeclampsia. <i>Hypertension</i> , 2018, 71, 95-102.	2.7	16
86	TAC-seq: targeted DNA and RNA sequencing for precise biomarker molecule counting. <i>Npj Genomic Medicine</i> , 2018, 3, 34.	3.8	26
87	Phylogenetic and mutational analyses of human LEUTX, a homeobox gene implicated in embryogenesis. <i>Scientific Reports</i> , 2018, 8, 17421.	3.3	17
88	A Non-Targeted LC-MS Profiling Reveals Elevated Levels of Carnitine Precursors and Trimethylated Compounds in the Cord Plasma of Pre-Eclamptic Infants. <i>Scientific Reports</i> , 2018, 8, 14616.	3.3	21
89	Single-cell RNA-seq analysis reveals the platinum resistance gene COX7B and the surrogate marker CD63. <i>Cancer Medicine</i> , 2018, 7, 6193-6204.	2.8	29
90	FUT2 Variants Confer Susceptibility to Familial Otitis Media. <i>American Journal of Human Genetics</i> , 2018, 103, 679-690.	6.2	40

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91	Genome-wide meta-analysis and replication studies in multiple ethnicities identify novel adolescent idiopathic scoliosis susceptibility loci. <i>Human Molecular Genetics</i> , 2018, 27, 3986-3998.	2.9	34
92	Enrichment of rare copy number variation in children with developmental language disorder. <i>Clinical Genetics</i> , 2018, 94, 313-320.	2.0	19
93	Intracellular signalling pathways and cytoskeletal functions converge on the psoriasis candidate gene CCHCR1 expressed at P-bodies and centrosomes. <i>BMC Genomics</i> , 2018, 19, 432.	2.8	17
94	MANF protects human pancreatic beta cells against stress-induced cell death. <i>Diabetologia</i> , 2018, 61, 2202-2214.	6.3	66
95	The Psoriasis Risk Allele <i>HLA-C*06:02</i> Shows Evidence of Association with Chronic or Recurrent Streptococcal Tonsillitis. <i>Infection and Immunity</i> , 2018, 86, .	2.2	17
96	A multi-ethnic meta-analysis confirms the association of rs6570507 with adolescent idiopathic scoliosis. <i>Scientific Reports</i> , 2018, 8, 11575.	3.3	33
97	Human pluripotent reprogramming with CRISPR activators. <i>Nature Communications</i> , 2018, 9, 2643.	12.8	128
98	Human ROBO1 regulates white matter structure in corpus callosum. <i>Brain Structure and Function</i> , 2017, 222, 707-716.	2.3	5
99	Damaging heterozygous mutations in NFKB1 lead to diverse immunologic phenotypes. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 140, 782-796.	2.9	113
100	Ketogenic diet attenuates hepatopathy in mouse model of respiratory chain complex III deficiency caused by a Bcs1l mutation. <i>Scientific Reports</i> , 2017, 7, 957.	3.3	27
101	Estrogen receptor $\beta$ , a regulator of androgen receptor signaling in the mouse ventral prostate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3816-E3822.	7.1	53
102	Optimizing bone morphogenic protein 4-mediated human embryonic stem cell differentiation into trophoblast-like cells using fibroblast growth factor 2 and transforming growth factor- $\beta$ /activin/nodal signalling inhibition. <i>Reproductive BioMedicine Online</i> , 2017, 35, 253-263.	2.4	11
103	Variants in the fetal genome near FLT1 are associated with risk of preeclampsia. <i>Nature Genetics</i> , 2017, 49, 1255-1260.	21.4	205
104	Sequence analysis of pooled bacterial samples enables identification of strain variation in group A streptococcus. <i>Scientific Reports</i> , 2017, 7, 45771.	3.3	3
105	Combined immunodeficiency and hypoglycemia associated with mutations in hypoxia upregulated 1. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 1391-1393.e11.	2.9	14
106	Genome-Wide Interaction Analysis of Air Pollution Exposure and Childhood Asthma with Functional Follow-up. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 195, 1373-1383.	5.6	107
107	A missense mutation in SLC26A3 is associated with human male subfertility and impaired activation of CFTR. <i>Scientific Reports</i> , 2017, 7, 14208.	3.3	20
108	The use of genotyping as a first step in molecular diagnosis of familial hypercholesterolemia. <i>Atherosclerosis</i> , 2017, 263, e62.	0.8	0

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109	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , 2017, 4, 170112.	5.3	195
110	Acute doses of caffeine shift nervous system cell expression profiles toward promotion of neuronal projection growth. <i>Scientific Reports</i> , 2017, 7, 11458.	3.3	14
111	Identification of NCAN as a candidate gene for developmental dyslexia. <i>Scientific Reports</i> , 2017, 7, 9294.	3.3	15
112	Hypomethylation of HOXA4 promoter is common in Silver-Russell syndrome and growth restriction and associates with stature in healthy children. <i>Scientific Reports</i> , 2017, 7, 15693.	3.3	12
113	Protective Low-Frequency Variants for Preeclampsia in the Fms Related Tyrosine Kinase 1 Gene in the Finnish Population. <i>Hypertension</i> , 2017, 70, 365-371.	2.7	37
114	Comprehensive mapping of the effects of azacitidine on DNA methylation, repressive/permmissive histone marks and gene expression in primary cells from patients with MDS and MDS-related disease. <i>Oncotarget</i> , 2017, 8, 28812-28825.	1.8	42
115	The emerging landscape of dynamic DNA methylation in early childhood. <i>BMC Genomics</i> , 2017, 18, 25.	2.8	49
116	Analysis of Complement C3 Gene Reveals Susceptibility to Severe Preeclampsia. <i>Frontiers in Immunology</i> , 2017, 8, 589.	4.8	50
117	Unexpectedly High Prevalence of Common Variable Immunodeficiency in Finland. <i>Frontiers in Immunology</i> , 2017, 8, 1190.	4.8	49
118	Neuropeptide S (NPS) variants modify the signaling and risk effects of NPS Receptor 1 (NPSR1) variants in asthma. <i>PLoS ONE</i> , 2017, 12, e0176568.	2.5	12
119	Exposure to Traffic-Related Air Pollution and Serum Inflammatory Cytokines in Children. <i>Environmental Health Perspectives</i> , 2017, 125, 067007.	6.0	71
120	Epigenome-Wide Meta-Analysis of Methylation in Children Related to Prenatal NO <sub>2</sub> Air Pollution Exposure. <i>Environmental Health Perspectives</i> , 2017, 125, 104-110.	6.0	176
121	CELSR2 is a candidate susceptibility gene in idiopathic scoliosis. <i>PLoS ONE</i> , 2017, 12, e0189591.	2.5	17
122	Molecular Characterization of Three Canine Models of Human Rare Bone Diseases: Caffey, van den Ende-Gupta, and Raine Syndromes. <i>PLoS Genetics</i> , 2016, 12, e1006037.	3.5	32
123	Evidence for genetic regulation of the human parieto-occipital 10â€”Hz rhythmic activity. <i>European Journal of Neuroscience</i> , 2016, 44, 1963-1971.	2.6	20
124	NOD-like receptor signaling and inflammasome-related pathways are highlighted in psoriatic epidermis. <i>Scientific Reports</i> , 2016, 6, 22745.	3.3	63
125	The human PRD-like homeobox gene <i>LEUTX</i> has a central role in embryo genome activation. <i>Development (Cambridge)</i> , 2016, 143, 3459-3469.	2.5	42
126	High-specificity bioinformatics framework for epigenomic profiling of discordant twins reveals specific and shared markers for ACPA and ACPA-positive rheumatoid arthritis. <i>Genome Medicine</i> , 2016, 8, 124.	8.2	27



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127	Cohort profile: the Finnish Genetics of Pre-eclampsia Consortium (FINNPEC). <i>BMJ Open</i> , 2016, 6, e013148.	1.9	32
128	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. <i>American Journal of Human Genetics</i> , 2016, 98, 680-696.	6.2	717
129	The pruritus- and TH2-associated cytokine IL-31 promotes growth of sensory nerves. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 138, 500-508.e24.	2.9	201
130	Preeclampsia does not share common risk alleles in 9p21 with coronary artery disease and type 2 diabetes. <i>Annals of Medicine</i> , 2016, 48, 330-336.	3.8	2
131	The Hydroxysteroid (17 $\beta$ ) Dehydrogenase Family Gene HSD17B12 Is Involved in the Prostaglandin Synthesis Pathway, the Ovarian Function, and Regulation of Fertility. <i>Endocrinology</i> , 2016, 157, 3719-3730.	2.8	43
132	An RGS2 3'UTR polymorphism is associated with preeclampsia in overweight women. <i>BMC Genetics</i> , 2016, 17, 121.	2.7	13
133	The diagnosis of pre-eclampsia using two revised classifications in the Finnish Pre-eclampsia Consortium (FINNPEC) cohort. <i>BMC Pregnancy and Childbirth</i> , 2016, 16, 221.	2.4	32
134	Ciliary dyslexia candidate genes <i>DYX1C1</i> and <i>DCDC2</i> are regulated by Regulatory Factor X (RFX) transcription factors through X-box promoter motifs. <i>FASEB Journal</i> , 2016, 30, 3578-3587.	0.5	28
135	Whole-Exome Sequencing Suggests <i>LAMB3</i> as a Susceptibility Gene for Morbid Obesity. <i>Diabetes</i> , 2016, 65, 2980-2989.	0.6	16
136	Characterization and target genes of nine human PRD-like homeobox domain genes expressed exclusively in early embryos. <i>Scientific Reports</i> , 2016, 6, 28995.	3.3	33
137	Globin mRNA reduction for whole-blood transcriptome sequencing. <i>Scientific Reports</i> , 2016, 6, 31584.	3.3	42
138	Exome sequencing in pooled DNA samples to identify maternal pre-eclampsia risk variants. <i>Scientific Reports</i> , 2016, 6, 29085.	3.3	19
139	Investigation of rare and low-frequency variants using high-throughput sequencing with pooled DNA samples. <i>Scientific Reports</i> , 2016, 6, 33256.	3.3	13
140	Genome-wide association analysis reveals variants on chromosome 19 that contribute to childhood risk of chronic otitis media with effusion. <i>Scientific Reports</i> , 2016, 6, 33240.	3.3	21
141	Targeted high-throughput sequencing of candidate genes for chronic obstructive pulmonary disease. <i>BMC Pulmonary Medicine</i> , 2016, 16, 146.	2.0	12
142	Genomic sequencing of a dyslexia susceptibility haplotype encompassing <i>ROBO1</i> . <i>Journal of Neurodevelopmental Disorders</i> , 2016, 8, 4.	3.1	8
143	Single-cell transcriptome analysis of endometrial tissue. <i>Human Reproduction</i> , 2016, 31, 844-853.	0.9	95
144	Increased YKL-40 and Chitotriosidase in Asthma and Chronic Obstructive Pulmonary Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 193, 131-142.	5.6	107

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145	The Salivary Scavenger and Agglutinin (SALSA) in Healthy and Complicated Pregnancy. PLoS ONE, 2016, 11, e0147867.	2.5	14
146	Gene-Expression Profiling Suggests Impaired Signaling via the Interferon Pathway in Cstb <sup>-/-</sup> Microglia. PLoS ONE, 2016, 11, e0158195.	2.5	9
147	Identification of Novel Transcribed Regions in Zebrafish ( <i>Danio rerio</i> ) Using RNA-Sequencing. PLoS ONE, 2016, 11, e0160197.	2.5	3
148	meQTL analysis of asthma GWAS loci and DNA methylation. , 2016, , .		0
149	Differentially methylated genes related to gestational age are also expressed during fetal lung development. , 2016, , .		0
150	Aberrant splicing of genes involved in haemoglobin synthesis and impaired terminal erythroid maturation in <i>SF3B1</i> mutated refractory anaemia with ring sideroblasts. British Journal of Haematology, 2015, 171, 478-490.	2.5	37
151	Gene expression profiling of pre-eclamptic placentae by RNA sequencing. Scientific Reports, 2015, 5, 14107.	3.3	89
152	Autoimmunity, hypogammaglobulinemia, lymphoproliferation, and mycobacterial disease in patients with activating mutations in STAT3. Blood, 2015, 125, 639-648.	1.4	229
153	High-throughput mutational screening adds clinically important information in myelodysplastic syndromes and secondary or therapy-related acute myeloid leukemia. Haematologica, 2015, 100, e223-e225.	3.5	12
154	Genome-wide association study identifies new susceptibility loci for cutaneous lupus erythematosus. Experimental Dermatology, 2015, 24, 510-515.	2.9	66
155	Discovery of Molecular Markers to Discriminate Corneal Endothelial Cells in the Human Body. PLoS ONE, 2015, 10, e0117581.	2.5	28
156	The Constrained Maximal Expression Level Owing to Haploidy Shapes Gene Content on the Mammalian X Chromosome. PLoS Biology, 2015, 13, e1002315.	5.6	32
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