Joseph T Glessner

List of Publications by Year
in descending order

160 papers	22,654 citations	20815 60 h-index	9102 144 g-index
176 all docs	176 docs citations	176 times ranked	33640 citing authors

#	Article	IF	Citations
1	A genome-wide association meta-analysis identifies new eosinophilic esophagitis loci. Journal of Allergy and Clinical Immunology, 2022, 149, 988-998.	2.9	19
2	Application of deep learning algorithm on whole genome sequencing data uncovers structural variants associated with multiple mental disorders in African American patients. Molecular Psychiatry, 2022, 27, 1469-1478.	7.9	13
3	Identification of Mitochondrial DNA Variants Associated With Risk of Neuroblastoma. Journal of the National Cancer Institute, 2022, 114, 910-913.	6.3	4
4	Circulating LIGHT (TNFSF14) and Interleukin-18 Levels in Sepsis-Induced Multi-Organ Injuries. Biomedicines, 2022, 10, 264.	3.2	7
5	Mendelian randomization study of obesity and type 2 diabetes in hospitalized COVID-19 patients. Metabolism: Clinical and Experimental, 2022, 129, 155156.	3.4	17
6	Improved genetic risk scoring algorithm for type 1 diabetes prediction. Pediatric Diabetes, 2022, 23, 320-323.	2.9	11
7	Genetic analysis for type 1 diabetes genes in juvenile dermatomyositis unveils genetic disease overlap. Rheumatology, 2022, , .	1.9	2
8	Arrhythmia Variant Associations and Reclassifications in the eMERGE-III Sequencing Study. Circulation, 2022, 145, 877-891.	1.6	18
9	Expansion of Schizophrenia Gene Network Knowledge Using Machine Learning Selected Signals From Dorsolateral Prefrontal Cortex and Amygdala RNA-seq Data. Frontiers in Psychiatry, 2022, 13, 797329.	2.6	9
10	Identification of Novel Loci Shared by Juvenile Idiopathic Arthritis Subtypes Through Integrative Genetic Analysis. Arthritis and Rheumatology, 2022, 74, 1420-1429.	5.6	4
11	Copy Number Variant Risk Scores Associated With Cognition, Psychopathology, and Brain Structure in Youths in the Philadelphia Neurodevelopmental Cohort. JAMA Psychiatry, 2022, 79, 699.	11.0	8
12	Burden of rare coding variants reveals genetic heterogeneity between obese and non-obese asthma patients in the African American population. Respiratory Research, 2022, 23, 116.	3.6	1
13	Mutation burden analysis of six common mental disorders in African Americans by whole genome sequencing. Human Molecular Genetics, 2022, 31, 3769-3776.	2.9	4
14	An electronic health record (EHR) phenotype algorithm to identify patients with attention deficit hyperactivity disorders (ADHD) and psychiatric comorbidities. Journal of Neurodevelopmental Disorders, 2022, 14, .	3.1	9
15	Association of DLL1 with type 1 diabetes in patients characterized by low polygenic risk score. Metabolism: Clinical and Experimental, 2021, 114, 154418.	3.4	6
16	Association of novel rare coding variants with juvenile idiopathic arthritis. Annals of the Rheumatic Diseases, 2021, 80, 626-631.	0.9	6
17	Integrative analysis of genome-wide association studies identifies novel loci associated with neuropsychiatric disorders. Translational Psychiatry, 2021, 11, 69.	4.8	39
18	Rare Recurrent Variants in Noncoding Regions Impact Attention-Deficit Hyperactivity Disorder (ADHD) Gene Networks in Children of both African American and European American Ancestry. Genes, 2021, 12, 310.	2.4	10

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19	MONTAGE: a new tool for high-throughput detection of mosaic copy number variation. BMC Genomics, 2021, 22, 133.	2.8	4
20	Machine Learning Reduced Gene/Non-Coding RNA Features That Classify Schizophrenia Patients Accurately and Highlight Insightful Gene Clusters. International Journal of Molecular Sciences, 2021, 22, 3364.	4.1	4
21	Omnigenic Impact of Copy Number Variants on Cognition and Psychopathology in the Philadelphia Neurodevelopmental Cohort. Biological Psychiatry, 2021, 89, S320.	1.3	0
22	Genetic correlations between COVID-19 and a variety of traits and diseases. Innovation(China), 2021, 2, 100112.	9.1	7
23	Genome-Wide Detection of Copy Number Variations and Their Association With Distinct Phenotypes in the Worldâ€™s Sheep. Frontiers in Genetics, 2021, 12, 670582.	2.3	11
24	Combined application of genetic and polygenic risk scores for type 1 diabetes risk prediction. Diabetes, Obesity and Metabolism, 2021, 23, 2001-2003.	4.4	2
25	Association Between a Common, Benign Genotype and Unnecessary Bone Marrow Biopsies Among African American Patients. JAMA Internal Medicine, 2021, 181, 1100.	5.1	18
26	Deep learning prediction of attention-deficit hyperactivity disorder in African Americans by copy number variation. Experimental Biology and Medicine, 2021, 246, 2317-2323.	2.4	8
27	Neptune: an environment for the delivery of genomic medicine. Genetics in Medicine, 2021, 23, 1838-1846.	2.4	3
28	Genetic architecture of type 1 diabetes with low genetic risk score informed by 41 unreported loci. Communications Biology, 2021, 4, 908.	4.4	9
29	Discovery of Novel Host Molecular Factors Underlying HBV/HCV Infection. Frontiers in Cell and Developmental Biology, 2021, 9, 690882.	3.7	0
30	Insights into non-autoimmune type 1 diabetes with 13 novel loci in low polygenic risk score patients. Scientific Reports, 2021, 11, 16013.	3.3	7
31	DeepCNV: a deep learning approach for authenticating copy number variations. Briefings in Bioinformatics, 2021, 22, .	6.5	15
32	Ciliopathies: Coloring outside of the lines. American Journal of Medical Genetics, Part A, 2021, 185, 687-694.	1.2	7
33	CNV Association of Diverse Clinical Phenotypes from eMERGE reveals novel disease biology underlying cardiovascular disease. International Journal of Cardiology, 2020, 298, 107-113.	1.7	7
34	Biliary-Atresia-Associated Mannosidase-1-Alpha-2 Gene Regulates Biliary and Ciliary Morphogenesis and Laterality. Frontiers in Physiology, 2020, 11, 538701.	2.8	13
35	Non-coding structural variation differentially impacts attention-deficit hyperactivity disorder (ADHD) gene networks in African American vs Caucasian children. Scientific Reports, 2020, 10, 15252.	3.3	5
36	Mitochondrial DNA haplogroups and risk of attention deficit and hyperactivity disorder in European Americans. Translational Psychiatry, 2020, 10, 370.	4.8	11

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37	Mitochondrial DNA Haplogroups and Susceptibility to Neuroblastoma. Journal of the National Cancer Institute, 2020, 112, 1259-1266.	6.3	10
38	Rare copy number variants in over 100,000 European ancestry subjects reveal multiple disease associations. Nature Communications, 2020, 11, 255.	12.8	48
39	Interpretation of Maturity-Onset Diabetes of the Young Genetic Variants Based on American College of Medical Genetics and Genomics Criteria: Machine-Learning Model Development. JMIR Biomedical Engineering, 2020, 5, e20506.	1.2	2
40	Abstract 14663: High Rate of Arrhythmia Diagnoses Following Return of Pathogenic/likely Pathogenic Variants in an Unselected Population. Circulation, 2020, 142, .	1.6	0
41	Association of Rare Recurrent Copy Number Variants With Congenital Heart Defects Based on Next-Generation Sequencing Data From Family Trios. Frontiers in Genetics, 2019, 10, 819.	2.3	15
42	Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. American Journal of Human Genetics, 2019, 105, 588-605.	6.2	99
43	Microduplications at the 15q11.2 BP1â€“BP2 locus are enriched in patients with anorexia nervosa. Journal of Psychiatric Research, 2019, 113, 34-38.	3.1	7
44	LIMITED CONTRIBUTION OF RARE, NONCODING VARIATION TO AUTISM SPECTRUM DISORDER FROM SEQUENCING OF 2,076 GENOMES IN QUARTET FAMILIES. European Neuropsychopharmacology, 2019, 29, S784-S785.	0.7	1
45	An analytical framework for whole-genome sequence association studies and its implications for autism spectrum disorder. Nature Genetics, 2018, 50, 727-736.	21.4	235
46	Defining the diverse spectrum of inversions, complex structural variation, and chromothripsis in the morbid humanÂgenome. Genome Biology, 2017, 18, 36.	8.8	159
47	Common variants in MMP20 at 11q22.2 predispose to 11q deletion and neuroblastoma risk. Nature Communications, 2017, 8, 569.	12.8	22
48	The genomic landscape of balanced cytogenetic abnormalities associated with human congenital anomalies. Nature Genetics, 2017, 49, 36-45.	21.4	251
49	Copy number variation meta-analysis reveals a novel duplication at 9p24 associated with multiple neurodevelopmental disorders. Genome Medicine, 2017, 9, 106.	8.2	41
50	Mutation in IRF2BP2 is responsible for a familial form of common variable immunodeficiency disorder. Journal of Allergy and Clinical Immunology, 2016, 138, 544-550.e4.	2.9	54
51	An integrative approach to investigate the respective roles of single-nucleotide variants and copy-number variants in Attention-Deficit/Hyperactivity Disorder. Scientific Reports, 2016, 6, 22851.	3.3	18
52	Variants in CXCR4 associate with juvenile idiopathic arthritis susceptibility. BMC Medical Genetics, 2016, 17, 24.	2.1	20
53	Genome-wide investigation of schizophrenia associated plasma Ndel1 enzyme activity. Schizophrenia Research, 2016, 172, 60-67.	2.0	10
54	Psychiatric gene discoveries shape evidence on ADHDâ€™s biology. Molecular Psychiatry, 2016, 21, 1202-1207.	7.9	55

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55	BIOFILTER AS A FUNCTIONAL ANNOTATION PIPELINE FOR COMMON AND RARE COPY NUMBER BURDEN. , 2016, , .		2
56	BIOFILTER AS A FUNCTIONAL ANNOTATION PIPELINE FOR COMMON AND RARE COPY NUMBER BURDEN. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 357-68.	0.7	2
57	Genome-wide association study reveals two loci for serum magnesium concentrations in European-American children. Scientific Reports, 2015, 5, 18792.	3.3	1
58	CNV Analysis Associates AKNAD1 with Type-2 Diabetes in Jordan Subpopulations. Scientific Reports, 2015, 5, 13391.	3.3	18
59	The Role of ARF6 in Biliary Atresia. PLoS ONE, 2015, 10, e0138381.	2.5	66
60	Rare variants at 16p11.2 are associated with common variable immunodeficiency. Journal of Allergy and Clinical Immunology, 2015, 135, 1569-1577.	2.9	22
61	Copy number variation in CEP57L1 predisposes to congenital absence of bilateral ACL and PCL ligaments. Human Genomics, 2015, 9, 31.	2.9	9
62	Mutation in mitochondrial ribosomal protein S7 (MRPS7) causes congenital sensorineural deafness, progressive hepatic and renal failure and lactic acidemia. Human Molecular Genetics, 2015, 24, 2297-2307.	2.9	64
63	Association of CLEC16A with human common variable immunodeficiency disorder and role in murine B cells. Nature Communications, 2015, 6, 6804.	12.8	63
64	Genetic sharing and heritability of paediatric age of onset autoimmune diseases. Nature Communications, 2015, 6, 8442.	12.8	58
65	Meta-analysis of shared genetic architecture across ten pediatric autoimmune diseases. Nature Medicine, 2015, 21, 1018-1027.	30.7	212
66	Copy Number Variations in CTNNA3 and RBFOX1 Associate with Pediatric Food Allergy. Journal of Immunology, 2015, 195, 1599-1607.	0.8	20
67	Attention-Deficit Hyperactivity Disorder and Pharmacotherapyâ€"Past, Present, and Future: A Review of the Changing Landscape of Drug Therapy. Therapeutic Innovation and Regulatory Science, 2015, 49, 632-642.	1.6	28
68	Genome-wide association study of maternal and inherited effects on left-sided cardiac malformations. Human Molecular Genetics, 2015, 24, 265-273.	2.9	24
69	Genome-Wide Association Study of Maternal and Inherited Loci for Conotruncal Heart Defects. PLoS ONE, 2014, 9, e96057.	2.5	26
70	Copy number variation analysis in the context of electronic medical records and large-scale genomics consortium efforts. Frontiers in Genetics, 2014, 5, 51.	2.3	11
71	Genome-Wide Association Studies of Autism. Current Behavioral Neuroscience Reports, 2014, 1, 234-241.	1.3	21
72	The impact of the metabotropic glutamate receptor and other gene family interaction networks on autism. Nature Communications, 2014, 5, 4074.	12.8	52

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73	Identification of rare DNA sequence variants in high-risk autism families and their prevalence in a large case/control population. Molecular Autism, 2014, 5, 5.	4.9	36
74	Increased Frequency of De Novo Copy Number Variants in Congenital Heart Disease by Integrative Analysis of Single Nucleotide Polymorphism Array and Exome Sequence Data. Circulation Research, 2014, 115, 884-896.	4.5	229
75	Analysis of chromosomal structural variation in patients with congenital leftâ€sided cardiac lesions. Birth Defects Research Part A: Clinical and Molecular Teratology, 2014, 100, 951-964.	1.6	12
76	A Genome-Wide Association Study on Obesity and Obesity-Related Traits. , 2014, , 57-69.		0
77	PECONPI: A novel software for uncovering pathogenic copy number variations in nonâ€syndromic sensorineural hearing loss and other genetically heterogeneous disorders. American Journal of Medical Genetics, Part A, 2013, 161, 2134-2147.	1.2	5
78	Common variation contributes to the genetic architecture of social communication traits. Molecular Autism, 2013, 4, 34.	4.9	34
79	Copy Number Variation on Chromosome 10q26.3 for Obesity Identified by a Genome-Wide Study. Journal of Clinical Endocrinology and Metabolism, 2013, 98, E191-E195.	3.6	19
80	Evidence From Human and Zebrafish That GPC1 Is a Biliary Atresia Susceptibility Gene. Gastroenterology, 2013, 144, 1107-1115.e3.	1.3	125
81	IFR2BP2 Mutations Identified As a Novel Genetic Cause of Familial Common Variable Immunodeficiency Identified Via Support Vector Algorithm and Whole Exome Sequencing. Journal of Allergy and Clinical Immunology, 2013, 131, AB140.	2.9	0
82	A Genomeâ€Wide Association Study of Autism Incorporating Autism Diagnostic Interviewâ€"Revised, Autism Diagnostic Observation Schedule, and Social Responsiveness Scale. Child Development, 2013, 84, 17-33.	3.0	57
83	De novo mutations in histone-modifying genes in congenital heart disease. Nature, 2013, 498, 220-223.	27.8	798
84	Both Rare and De Novo Copy Number Variants Are Prevalent in Agenesis of the Corpus Callosum but Not in Cerebellar Hypoplasia or Polymicrogyria. PLoS Genetics, 2013, 9, e1003823.	3.5	69
85	GWAS of blood cell traits identifies novel associated loci and epistatic interactions in Caucasian and African-American children. Human Molecular Genetics, 2013, 22, 1457-1464.	2.9	82
86	ParseCNV integrative copy number variation association software with quality tracking. Nucleic Acids Research, 2013, 41, e64-e64.	14.5	54
87	A genome wide association study of plasma uric acid levels in obese cases and neverâ€overweight controls. Obesity, 2013, 21, E490-4.	3.0	29
88	The missense variation landscape of FTO, MC4R, and TMEM18 in obese children of African Ancestry. Obesity, 2013, 21, 159-163.	3.0	22
89	GWAS meta analysis identifies TSNARE1 as a novel Schizophrenia / Bipolar susceptibility locus. Scientific Reports, 2013, 3, 3075.	3.3	52
90	Copy Number Variations in Alternative Splicing Gene Networks Impact Lifespan. PLoS ONE, 2013, 8, e53846.	2.5	13

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91	Individual common variants exert weak effects on the risk for autism spectrum disorders. Human Molecular Genetics, 2012, 21, 4781-4792.	2.9	334
92	Rare Copy Number Variants in Tourette Syndrome Disrupt Genes in Histaminergic Pathways and Overlap with Autism. Biological Psychiatry, 2012, 71, 392-402.	1.3	167
93	A novel approach of homozygous haplotype sharing identifies candidate genes in autism spectrum disorder. Human Genetics, 2012, 131, 565-579.	3.8	180
94	Phasing of Many Thousands of Genotyped Samples. American Journal of Human Genetics, 2012, 91, 238-251.	6.2	115
95	Genome-wide copy number variation study associates metabotropic glutamate receptor gene networks with attention deficit hyperactivity disorder. Nature Genetics, 2012, 44, 78-84.	21.4	334
96	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. American Journal of Human Genetics, 2012, 90, 410-425.	6.2	239
97	Examination of genetic variants influencing lipid traits in pediatric populations. Journal of Pediatric Genetics, 2012, 1, 85-98.	0.7	4
98	Rare Genomic Deletions and Duplications and their Role in Neurodevelopmental Disorders. Current Topics in Behavioral Neurosciences, 2011, 12, 345-360.	1.7	16
99	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	27.8	2,400
100	Role of BMIâ€Associated Loci Identified in GWAS Metaâ€Analyses in the Context of Common Childhood Obesity in European Americans. Obesity, 2011, 19, 2436-2439.	3.0	88
101	Genome-wide association identifies diverse causes of common variable immunodeficiency. Journal of Allergy and Clinical Immunology, 2011, 127, 1360-1367.e6.	2.9	179
102	A Genome-Wide Association Study on Obesity and Obesity-Related Traits. PLoS ONE, 2011, 6, e18939.	2.5	201
103	Genome-wide Association: From Confounded to Confident. Neuroscientist, 2011, 17, 174-184.	3.5	4
104	BMDâ€Associated Variation at the Osterix Locus Is Correlated With Childhood Obesity in Females. Obesity, 2011, 19, 1311-1314.	3.0	22
105	Phenotype Restricted Genome-Wide Association Study Using a Gene-Centric Approach Identifies Three Low-Risk Neuroblastoma Susceptibility Loci. PLoS Genetics, 2011, 7, e1002026.	3.5	141
106	Integrative genomics identifies LMO1 as a neuroblastoma oncogene. Nature, 2011, 469, 216-220.	27.8	276
107	Microdeletions and Microduplications in Patients with Congenital Heart Disease and Multiple Congenital Anomalies. Congenital Heart Disease, 2011, 6, 592-602.	0.2	82
108	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	6.2	122

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109	The landscape of recombination in African Americans. Nature, 2011, 476, 170-175.	27.8	319
110	A Genome-Wide Meta-Analysis of Six Type 1 Diabetes Cohorts Identifies Multiple Associated Loci. PLoS Genetics, 2011, 7, e1002293.	3.5	297
111	Exome sequencing and unrelated findings in the context of complex disease research: ethical and clinical implications. Discovery Medicine, 2011, 12, 41-55.	0.5	49
112	A large-scale survey of the novel 15q24 microdeletion syndrome in autism spectrum disorders identifies an atypical deletion that narrows the critical region. Molecular Autism, 2010, 1, 5.	4.9	40
113	A Genome-wide Study Reveals Copy Number Variants Exclusive to Childhood Obesity Cases. American Journal of Human Genetics, 2010, 87, 661-666.	6.2	91
114	Genome wide association (GWA) predictors of anti-TNFÎ± therapeutic responsiveness in pediatric inflammatory bowel disease. Inflammatory Bowel Diseases, 2010, 16, 1357-1366.	1.9	124
115	Analysis of GWAS top hits in ADHD suggests association to two polymorphisms located in genes expressed in the cerebellum. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 1127-1133.	1.7	27
116	The role of height-associated loci identified in genome wide association studies in the determination of pediatric stature. BMC Medical Genetics, 2010, 11, 96.	2.1	54
117	Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372.	27.8	1,803
118	Duplication of the SLIT3 Locus on 5q35.1 Predisposes to Major Depressive Disorder. PLoS ONE, 2010, 5, e15463.	2.5	63
119	A genome-wide scan for common alleles affecting risk for autism. Human Molecular Genetics, 2010, 19, 4072-4082.	2.9	538
120	Comparative genetic analysis of inflammatory bowel disease and type 1 diabetes implicates multiple loci with opposite effects. Human Molecular Genetics, 2010, 19, 2059-2067.	2.9	157
121	Large Copy-Number Variations Are Enriched in Cases With Moderate to Extreme Obesity. Diabetes, 2010, 59, 2690-2694.	0.6	60
122	Strong synaptic transmission impact by copy number variations in schizophrenia. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10584-10589.	7.1	212
123	Examination of All Type 2 Diabetes GWAS Loci Reveals HHEX-IDE as a Locus Influencing Pediatric BMI. Diabetes, 2010, 59, 751-755.	0.6	56
124	Common Variants in HSPB7 and FRMD4B Associated With Advanced Heart Failure. Circulation: Cardiovascular Genetics, 2010, 3, 147-154.	5.1	119
125	Association Between a High-Risk Autism Locus on 5p14 and Social Communication Spectrum Phenotypes in the General Population. American Journal of Psychiatry, 2010, 167, 1364-1372.	7.2	57
126	Common variants at 5q22 associate with pediatric eosinophilic esophagitis. Nature Genetics, 2010, 42, 289-291.	21.4	397

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127	Variants ofDENND1BAssociated with Asthma in Children. New England Journal of Medicine, 2010, 362, 36-44.	27.0	306
128	Genomic copy number determination in cancer cells from single nucleotide polymorphism microarrays based on quantitative genotyping corrected for aneuploidy. Genome Research, 2009, 19, 276-283.	5.5	69
129	Examination of Type 2 Diabetes Loci Implicates CDKAL1 as a Birth Weight Gene. Diabetes, 2009, 58, 2414-2418.	0.6	61
130	Follow-Up Analysis of Genome-Wide Association Data Identifies Novel Loci for Type 1 Diabetes. Diabetes, 2009, 58, 290-295.	0.6	136
131	High-resolution mapping and analysis of copy number variations in the human genome: A data resource for clinical and research applications. Genome Research, 2009, 19, 1682-1690.	5.5	313
132	Genome-Wide Analyses of Exonic Copy Number Variants in a Family-Based Study Point to Novel Autism Susceptibility Genes. PLoS Genetics, 2009, 5, e1000536.	3.5	374
133	From Disease Association to Risk Assessment: An Optimistic View from Genome-Wide Association Studies on Type 1 Diabetes. PLoS Genetics, 2009, 5, e1000678.	3.5	186
134	A Genome-Wide Association Study Identifies a Locus for Nonsyndromic Cleft Lip with or without Cleft Palate on 8q24. Journal of Pediatrics, 2009, 155, 909-913.	1.8	252
135	SNP array mapping of chromosome 20p deletions: Genotypes, phenotypes, and copy number variation. Human Mutation, 2009, 30, 371-378.	2.5	61
136	Autism genome-wide copy number variation reveals ubiquitin and neuronal genes. Nature, 2009, 459, 569-573.	27.8	1,270
137	Common genetic variants on 5p14.1 associate with autism spectrum disorders. Nature, 2009, 459, 528-533.	27.8	912
138	Copy number variation at 1q21.1 associated with neuroblastoma. Nature, 2009, 459, 987-991.	27.8	329
139	Common variations in BARD1 influence susceptibility to high-risk neuroblastoma. Nature Genetics, 2009, 41, 718-723.	21.4	266
140	Common variants at five new loci associated with early-onset inflammatory bowel disease. Nature Genetics, 2009, 41, 1335-1340.	21.4	459
141	The Role of Obesityâ€associated Loci Identified in Genomeâ€wide Association Studies in the Determination of Pediatric BMI. Obesity, 2009, 17, 2254-2257.	3.0	159
142	Diverse Genome-wide Association Studies Associate the IL12/IL23 Pathway with Crohn Disease. American Journal of Human Genetics, 2009, 84, 399-405.	6.2	246
143	17q12-21 variants interact with smoke exposure as a risk factor for pediatric asthma but are equally associated with early-onset versus late-onset asthma in North Americans of European ancestry. Journal of Allergy and Clinical Immunology, 2009, 124, 605-607.	2.9	68
144	Common variants in polygenic schizophrenia. Genome Biology, 2009, 10, 236.	9.6	35

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145	Investigation of the Locus Near MC4R With Childhood Obesity in Americans of European and African Ancestry. Obesity, 2009, 17, 1461-1465.	3.0	66
146	Association of the TRAF1â€“C5 locus on chromosome 9 with juvenile idiopathic arthritis. Arthritis and Rheumatism, 2008, 58, 2206-2207.	6.7	52
147	Loci on 20q13 and 21q22 are associated with pediatric-onset inflammatory bowel disease. Nature Genetics, 2008, 40, 1211-1215.	21.4	310
148	Concept, Design and Implementation of a Cardiovascular Gene-Centric 50 K SNP Array for Large-Scale Genomic Association Studies. PLoS ONE, 2008, 3, e3583.	2.5	339
149	ORMDL3 variants associated with asthma susceptibility in North Americans of European ancestry. Journal of Allergy and Clinical Immunology, 2008, 122, 1225-1227.	2.9	89
150	A Novel Susceptibility Locus for Type 1 Diabetes on Chr12q13 Identified by a Genome-Wide Association Study. Diabetes, 2008, 57, 1143-1146.	0.6	137
151	Adjustment of genomic waves in signal intensities from whole-genome SNP genotyping platforms. Nucleic Acids Research, 2008, 36, e126-e126.	14.5	297
152	Chromosome 6p22 Locus Associated with Clinically Aggressive Neuroblastoma. New England Journal of Medicine, 2008, 358, 2585-2593.	27.0	271
153	Modeling genetic inheritance of copy number variations. Nucleic Acids Research, 2008, 36, e138-e138.	14.5	77
154	Association Analysis of the FTO Gene with Obesity in Children of Caucasian and African Ancestry Reveals a Common Tagging SNP. PLoS ONE, 2008, 3, e1746.	2.5	176
155	Association of the BANK1 R61H variant with systemic lupus erythematosus in Americans of European and African ancestry. The Application of Clinical Genetics, 2008, Volume 2, 1-5.	3.0	8
156	Association of HMGA2 Gene Variation with Height in Specific Pediatric Age Categories. Genomics Insights, 2008, 1, GEI.S944.	3.0	1
157	Association of the T300A non-synonymous variant of the ATG16L1 gene with susceptibility to paediatric Crohn's disease. Gut, 2007, 56, 1171-1173.	12.1	60
158	PennCNV: An integrated hidden Markov model designed for high-resolution copy number variation detection in whole-genome SNP genotyping data. Genome Research, 2007, 17, 1665-1674.	5.5	1,586
159	Association of Variants of the Interleukin-23 Receptor Gene With Susceptibility to Pediatric Crohnâ€™s Disease. Clinical Gastroenterology and Hepatology, 2007, 5, 972-976.	4.4	56
160	A genome-wide association study identifies KIAA0350 as a type 1 diabetes gene. Nature, 2007, 448, 591-594.	27.8	497