Simon Heath

List of Publications by Year
in descending order

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165 papers	42,793 citations	7672 79 h-index	8212 153 g-index
177 all docs	177 docs citations	177 times ranked	65664 citing authors

#	Article	IF	Citations
1	Impact of DNA methylation on 3D genome structure. Nature Communications, 2021, 12, 3243.	5.8	61
2	Blood eosinophil count and airway epithelial transcriptome relationships in COPD versus asthma. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 370-380.	2.7	37
3	gemBS: high throughput processing for DNA methylation data from bisulfite sequencing. Bioinformatics, 2019, 35, 737-742.	1.8	39
4	Whole-genome DNA hyper-methylation in iPSC-derived dopaminergic neurons from Parkinsonâ€™s disease patients. Clinical Epigenetics, 2019, 11, 108.	1.8	16
5	Nucleosome Dynamics: a new tool for the dynamic analysis of nucleosome positioning. Nucleic Acids Research, 2019, 47, 9511-9523.	6.5	12
6	Chromatin-Based Classification of Genetically Heterogeneous AMLs into Two Distinct Subtypes with Diverse Stemness Phenotypes. Cell Reports, 2019, 26, 1059-1069.e6.	2.9	33
7	Linking Cell Dynamics With Gene Coexpression Networks to Characterize Key Events in Chronic Virus Infections. Frontiers in Immunology, 2019, 10, 1002.	2.2	7
8	Systems analysis reveals complex biological processes during virus infection fate decisions. Genome Research, 2019, 29, 907-919.	2.4	21
9	PD-1 signaling affects cristae morphology and leads to mitochondrial dysfunction in human CD8+ T lymphocytes. , 2019, 7, 151.		83
10	Selective single molecule sequencing and assembly of a human Y chromosome of African origin. Nature Communications, 2019, 10, 4.	5.8	90
11	Differential expression of long nonâ€coding <scp>RNA</scp>s are related to proliferation and histological diversity in follicular lymphomas. British Journal of Haematology, 2019, 184, 373-383.	1.2	12
12	A FBN1 3â€²UTR mutation variant is associated with endoplasmic reticulum stress in aortic aneurysm in Marfan syndrome. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2019, 1865, 107-114.	1.8	18
13	Epigenetic regulation of gene expression in Chinese Hamster Ovary cells in response to the changing environment of a batch culture. Biotechnology and Bioengineering, 2019, 116, 677-692.	1.7	37
14	Deciphering the mechanism of action of 089, a compound impairing the fungal cell cycle. Scientific Reports, 2018, 8, 5964.	1.6	6
15	Multi-omics profiling reveals a distinctive epigenome signature for high-risk acute promyelocytic leukemia. Oncotarget, 2018, 9, 25647-25660.	0.8	13
16	DNA Methylation Assays Using Bisulphite Sequencing and Next-Generation Sequencing. Comprehensive Analytical Chemistry, 2018, , 107-136.	0.7	0
17	Transcription Factors Drive Tet2-Mediated Enhancer Demethylation to Reprogram Cell Fate. Cell Stem Cell, 2018, 23, 727-741.e9.	5.2	156
18	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. Cell Reports, 2018, 24, 2784-2794.	2.9	104

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19	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. Nature Medicine, 2018, 24, 868-880.	15.2	157
20	Combined HAT/EZH2 modulation leads to cancer-selective cell death. Oncotarget, 2018, 9, 25630-25646.	0.8	5
21	Single-cell transcriptome conservation in cryopreserved cells and tissues. Genome Biology, 2017, 18, 45.	3.8	134
22	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	1.6	89
23	A Comparison of RNA-Seq Results from Paired Formalin-Fixed Paraffin-Embedded and Fresh-Frozen Glioblastoma Tissue Samples. PLoS ONE, 2017, 12, e0170632.	1.1	100
24	Comprehensive genome and epigenome characterization of CHO cells in response to evolutionary pressures and over time. Biotechnology and Bioengineering, 2016, 113, 2241-2253.	1.7	112
25	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. Nature Communications, 2016, 7, 13555.	5.8	142
26	Epigenome characterization of CHO cells in response to evolutionary pressures and over time. New Biotechnology, 2016, 33, S4-S5.	2.4	0
27	From Wetâ€Lab to Variations: Concordance and Speed of Bioinformatics Pipelines for Whole Genome and Whole Exome Sequencing. Human Mutation, 2016, 37, 1263-1271.	1.1	47
28	Integrative epigenome-wide analysis demonstrates that DNA methylation may mediate genetic risk in inflammatory bowel disease. Nature Communications, 2016, 7, 13507.	5.8	191
29	Information recovery from low coverage whole-genome bisulfite sequencing. Nature Communications, 2016, 7, 11306.	5.8	33
30	Decoding the DNA Methylome of Mantle Cell Lymphoma in the Light of the Entire B Cell Lineage. Cancer Cell, 2016, 30, 806-821.	7.7	103
31	Î²-Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance. Cell, 2016, 167, 1354-1368.e14.	13.5	467
32	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
33	Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. Cell Reports, 2016, 17, 2101-2111.	2.9	54
34	766 Comprehensive Epigenome-Wide DNA Methylation Profiling in Inflammatory Bowel Disease. Gastroenterology, 2016, 150, S156-S157.	0.6	1
35	Saturation analysis for whole-genome bisulfite sequencing data. Nature Biotechnology, 2016, 34, 691-693.	9.4	26
36	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	5.8	412

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37	New technologies for DNA analysis â€“ a review of the READNA Project. New Biotechnology, 2016, 33, 311-330.	2.4	10
38	Bronchial epithelial gene expression of NOX isoforms are related to important clinical characteristics in COPD. , 2016, , .		0
39	Differential bronchial epithelial gene expression in COPD versus controls. , 2016, , .		0
40	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. Clinical Lymphoma, Myeloma and Leukemia, 2015, 15, e86-e87.	0.2	3
41	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. Nature Genetics, 2015, 47, 746-756.	9.4	278
42	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	5.8	266
43	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. Genome Research, 2015, 25, 478-487.	2.4	118
44	Epigenetic remodeling in B-cell acute lymphoblastic leukemia occurs in two tracks and employs embryonic stem cell-like signatures. Nucleic Acids Research, 2015, 43, 2590-2602.	6.5	42
45	Common colorectal cancer risk alleles contribute to the multiple colorectal adenoma phenotype, but do not influence colonic polyposis in FAP. European Journal of Human Genetics, 2015, 23, 260-263.	1.4	17
46	DRD2/ANKK1 Polymorphism Modulates the Effect of Ventral Striatal Activation on Working Memory Performance. Neuropsychopharmacology, 2014, 39, 2357-2365.	2.8	31
47	White-matter microstructure and gray-matter volumes in adolescents with subthreshold bipolar symptoms. Molecular Psychiatry, 2014, 19, 462-470.	4.1	37
48	HMTI-0197. Whole blood transcriptome analysis in migraine with aura patients: a case control study. Journal of Headache and Pain, 2014, 15, .	2.5	0
49	Variation in genomic landscape of clear cell renal cell carcinoma across Europe. Nature Communications, 2014, 5, 5135.	5.8	158
50	Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations. American Journal of Human Genetics, 2014, 95, 49-65.	2.6	73
51	A Note on Exact Differences between Beta Distributions in Genomic (Methylation) Studies. PLoS ONE, 2014, 9, e97349.	1.1	27
52	Common and Rare Variant Analysis in Early-Onset Bipolar Disorder Vulnerability. PLoS ONE, 2014, 9, e104326.	1.1	34
53	Characterization of the DNA Methylome during Human B-Cell Differentiation. Blood, 2014, 124, 4346-4346.	0.6	0
54	Two-Track Epigenetic Remodeling and Backtracking to Embryonic Stem Cell Bivalency in B-Cell Acute Lymphoblastic Leukemias. Blood, 2014, 124, 3557-3557.	0.6	0

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55	Whole-Genome DNA Methylation Analysis of Mantle Cell Lymphoma: Biological and Clinical Implications. Blood, 2014, 124, 3563-3563.	0.6	0
56	Genome-wide association study of multiple congenital heart disease phenotypes identifies a susceptibility locus for atrial septal defect at chromosome 4p16. Nature Genetics, 2013, 45, 822-824.	9.4	123
57	Recurrent inactivation of STAG2 in bladder cancer is not associated with aneuploidy. Nature Genetics, 2013, 45, 1464-1469.	9.4	224
58	A genome-wide association study of atopic dermatitis identifies loci with overlapping effects on asthma and psoriasis. Human Molecular Genetics, 2013, 22, 4841-4856.	1.4	202
59	Genome-wide association study identifies loci on 12q24 and 13q32 associated with Tetralogy of Fallot. Human Molecular Genetics, 2013, 22, 1473-1481.	1.4	82
60	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	1.5	419
61	Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. Nature Genetics, 2012, 44, 1236-1242.	9.4	525
62	SNP calling by sequencing pooled samples. BMC Bioinformatics, 2012, 13, 239.	1.2	63
63	Tuning of Natural Killer Cell Reactivity by NKp46 and Helios Calibrates T Cell Responses. Science, 2012, 335, 344-348.	6.0	190
64	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
65	Comparing The Full Genome Sequence Derived Of Blood And Bronchial Brush Cells From COPD Patients. , 2012, , .		0
66	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	9.4	762
67	Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. Nature Genetics, 2012, 44, 47-52.	9.4	893
68	Distinct DNA methylomes of newborns and centenarians. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10522-10527.	3.3	687
69	A trans-ethnic genetic study of rheumatoid arthritis identified FCGR2A as a candidate common risk factor in Japanese and European populations. Modern Rheumatology, 2012, 22, 52-58.	0.9	4
70	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	13.7	2,400
71	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. Nature, 2011, 475, 101-105.	13.7	1,364
72	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	13.7	1,855

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73	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	9.4	501
74	A Genome-Wide Association Study of Upper Aerodigestive Tract Cancers Conducted within the INHANCE Consortium. PLoS Genetics, 2011, 7, e1001333.	1.5	158
75	Myelin Basic Protein as a Novel Genetic Risk Factor in Rheumatoid Arthritisâ€"A Genome-Wide Study Combined with Immunological Analyses. PLoS ONE, 2011, 6, e20457.	1.1	29
76	ProteinSeq: High-Performance Proteomic Analyses by Proximity Ligation and Next Generation Sequencing. PLoS ONE, 2011, 6, e25583.	1.1	80
77	Two families confirm SchÃ¶pf-Schulz-Passarge syndrome as a discrete entity within the WNT10A phenotypic spectrum. Clinical Genetics, 2011, 79, 92-95.	1.0	20
78	Genome-wide association study of renal cell carcinoma identifies two susceptibility loci on 2p21 and 11q13.3. Nature Genetics, 2011, 43, 60-65.	9.4	220
79	Genome-wide Association Study Identifies Genetic Variation in Neurocan as a Susceptibility Factor for Bipolar Disorder. American Journal of Human Genetics, 2011, 88, 372-381.	2.6	257
80	Genome-wide Association Study Identifies Genetic Variation in Neurocan as a Susceptibility Factor for Bipolar Disorder. American Journal of Human Genetics, 2011, 88, 396.	2.6	6
81	Applications of Second Generation Sequencing Technologies in Complex Disorders. Current Topics in Behavioral Neurosciences, 2011, 12, 321-343.	0.8	3
82	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	1.4	168
83	Novel Breast Cancer Susceptibility Locus at 9q31.2: Results of a Genome-Wide Association Study. Journal of the National Cancer Institute, 2011, 103, 425-435.	3.0	225
84	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	9.4	403
85	Implication of the Immune System in Alzheimer's Disease: Evidence from Genome-Wide Pathway Analysis. Journal of Alzheimer's Disease, 2010, 20, 1107-1118.	1.2	152
86	Systematic Analysis of Candidate Genes for Alzheimer's Disease in a French, Genome-Wide Association Study. Journal of Alzheimer's Disease, 2010, 20, 1181-1188.	1.2	63
87	A Follow-Up Study of a Genome-wide Association Scan Identifies a Susceptibility Locus for Venous Thrombosis on Chromosome 6p24.1. American Journal of Human Genetics, 2010, 86, 592-595.	2.6	57
88	A Follow-Up Study of a Genome-wide Association Scan Identifies a Susceptibility Locus for Venous Thrombosis on Chromosome 6p24.1. American Journal of Human Genetics, 2010, 86, 655.	2.6	0
89	A multiâ€stage multiâ€design strategy provides strong evidence that the BAI3 locus is associated with earlyâ€onset venous thromboembolism. Journal of Thrombosis and Haemostasis, 2010, 8, 2671-2679.	1.9	42
90	International network of cancer genome projects. Nature, 2010, 464, 993-998.	13.7	2,114

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91	Genome-Wide Association Study of Major Recurrent Depression in the U.K. Population. American Journal of Psychiatry, 2010, 167, 949-957.	4.0	221
92	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.3	387
93	HLA Has Strongest Association with IgA Nephropathy in Genome-Wide Analysis. Journal of the American Society of Nephrology: JASN, 2010, 21, 1791-1797.	3.0	233
94	Association between a 15q25 gene variant, smoking quantity and tobacco-related cancers among 17 000 individuals. International Journal of Epidemiology, 2010, 39, 563-577.	0.9	125
95	W58 COMMON GENETIC VARIANTS ASSOCIATED WITH LOW Lp(a) KRINGLE-IV COPY NUMBER, HIGH Lp(a) CONCENTRATION, AND INCREASED RISK OF CORONARY HEART DISEASE. Atherosclerosis Supplements, 2010, 11, 13.	1.2	0
96	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	9.4	1,982
97	Interferon Â receptor 2 gene variants are associated with liver fibrosis in patients with chronic hepatitis C infection. Gut, 2010, 59, 1120-1126.	6.1	19
98	A Large-Scale, Consortium-Based Genomewide Association Study of Asthma. New England Journal of Medicine, 2010, 363, 1211-1221.	13.9	1,762
99	The FOXE1 locus is a major genetic determinant for radiation-related thyroid carcinoma in Chernobyl. Human Molecular Genetics, 2010, 19, 2516-2523.	1.4	145
100	Genetic Structure of Europeans: A View from the Northâ€“East. PLoS ONE, 2009, 4, e5472.	1.1	279
101	Common susceptibility alleles are unlikely to contribute as strongly as the FV and ABO loci to VTE risk: results from a GWAS approach. Blood, 2009, 113, 5298-5303.	0.6	283
102	Comprehensive Linkage and Association Analyses Identify Haplotype, Near to the TNFSF15 Gene, Significantly Associated with Spondyloarthritis. PLoS Genetics, 2009, 5, e1000528.	1.5	55
103	Chromosome 9p-linked families with frontotemporal dementia associated with motor neuron disease. Neurology, 2009, 72, 1669-1676.	1.5	90
104	Reduced expression of the Kinesin-Associated Protein 3 (KIFAP3) gene increases survival in sporadic amyotrophic lateral sclerosis. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 9004-9009.	3.3	177
105	A locus for bilateral occipital polymicrogyria maps to chromosome 6q16â€“q22. Neurogenetics, 2009, 10, 35-42.	0.7	10
106	An Association Study of 22 Candidate Genes in Psoriasis Families Reveals Shared Genetic Factors with Other Autoimmune and Skin Disorders. Journal of Investigative Dermatology, 2009, 129, 2637-2645.	0.3	28
107	A common variant on chromosome 11q13 is associated with atopic dermatitis. Nature Genetics, 2009, 41, 596-601.	9.4	297
108	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	9.4	1,104

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109	Genome-wide association study identifies variants at CLU and CR1 associated with Alzheimer's disease. Nature Genetics, 2009, 41, 1094-1099.	9.4	2,155
110	Common variants at five new loci associated with early-onset inflammatory bowel disease. Nature Genetics, 2009, 41, 1335-1340.	9.4	459
111	Mutations of the FHL1 Gene Cause Emery-Dreifuss Muscular Dystrophy. American Journal of Human Genetics, 2009, 85, 338-353.	2.6	208
112	Genetic Variants Associated with Lp(a) Lipoprotein Level and Coronary Disease. New England Journal of Medicine, 2009, 361, 2518-2528.	13.9	1,233
113	Acquired copy number alterations in adult acute myeloid leukemia genomes. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12950-12955.	3.3	231
114	Î±-Synuclein Gene Rearrangements in Dominantly Inherited Parkinsonism. Archives of Neurology, 2009, 66, 102.	4.9	133
115	The Genome Response to Artificial Selection: A Case Study in Dairy Cattle. PLoS ONE, 2009, 4, e6595.	1.1	219
116	Three Genome-wide Association Studies and a Linkage Analysis Identify HERC2 as a Human Iris Color Gene. American Journal of Human Genetics, 2008, 82, 411-423.	2.6	220
117	Three Genome-wide Association Studies and a Linkage Analysis Identify HERC2 as a Human Iris Color Gene. American Journal of Human Genetics, 2008, 82, 801.	2.6	4
118	Investigation of the fine structure of European populations with applications to disease association studies. European Journal of Human Genetics, 2008, 16, 1413-1429.	1.4	147
119	A susceptibility locus for lung cancer maps to nicotinic acetylcholine receptor subunit genes on 15q25. Nature, 2008, 452, 633-637.	13.7	1,169
120	Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease. Nature Genetics, 2008, 40, 955-962.	9.4	2,422
121	Lung cancer susceptibility locus at 5p15.33. Nature Genetics, 2008, 40, 1404-1406.	9.4	514
122	Newly identified loci that influence lipid concentrations and risk of coronary artery disease. Nature Genetics, 2008, 40, 161-169.	9.4	1,488
123	G/T Substitution in Intron 1 of the UNC13B Gene Is Associated With Increased Risk of Nephropathy in Patients With Type 1 Diabetes. Diabetes, 2008, 57, 2843-2850.	0.3	39
124	Genetic factors of susceptibility and of severity in primary biliary cirrhosis. Journal of Hepatology, 2008, 49, 1038-1045.	1.8	115
125	Exploration of associations between phospholipase A2 gene family polymorphisms and AIDS progression using the SNPlexâ„¢ method. Biomedicine and Pharmacotherapy, 2008, 62, 31-40.	2.5	11
126	Systematic Analysis of Glutamatergic Neurotransmission Genes in Alcohol Dependence and Adolescent Risky Drinking Behavior. Archives of General Psychiatry, 2008, 65, 826.	13.8	116

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127	Genetic Determination and Linkage Mapping of Plasmodium falciparum Malaria Related Traits in Senegal. PLoS ONE, 2008, 3, e2000.	1.1	49
128	A haplotype of the human CXCR1 gene protective against rapid disease progression in HIV-1+ patients. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3354-3359.	3.3	31
129	A high-resolution linkage map for the Z chromosome in chicken reveals hot spots for recombination. Cytogenetic and Genome Research, 2007, 117, 22-29.	0.6	26
130	Quantitative Trait Loci for Fasting Glucose in Young Europeans Replicate Previous Findings for Type 2 Diabetes in 2q23-24 and Other Locations. Diabetes, 2007, 56, 1742-1745.	0.3	9
131	Novel Crohn Disease Locus Identified by Genome-Wide Association Maps to a Gene Desert on 5p13.1 and Modulates Expression of PTGER4. PLoS Genetics, 2007, 3, e58.	1.5	506
132	ADAM33, a New Candidate for Psoriasis Susceptibility. PLoS ONE, 2007, 2, e906.	1.1	36
133	A QTL influencing F cell production maps to a gene encoding a zinc-finger protein on chromosome 2p15. Nature Genetics, 2007, 39, 1197-1199.	9.4	491
134	A genome-wide association study of global gene expression. Nature Genetics, 2007, 39, 1202-1207.	9.4	882
135	Confirmation of Psoriasis Susceptibility Loci on Chromosome 6p21 and 20p13 in French Families. Journal of Investigative Dermatology, 2007, 127, 1403-1409.	0.3	20
136	Genetic variants regulating ORMDL3 expression contribute to the risk of childhood asthma. Nature, 2007, 448, 470-473.	13.7	1,446
137	Associations of the IL2RÎ±, IL4RÎ±, IL10RÎ±, and IFN Î³ R1 cytokine receptor genes with AIDS progression in a French AIDS cohort. Immunogenetics, 2006, 58, 89-98.	1.2	16
138	Identification of Distinct Quantitative Trait Loci Affecting Length or Weight Variability at Birth in Humans. Journal of Clinical Endocrinology and Metabolism, 2006, 91, 4164-4170.	1.8	14
139	Weight-Adjusted Genome Scan Analysis for Mapping Quantitative Trait Loci for Menarchal Age. Journal of Clinical Endocrinology and Metabolism, 2006, 91, 3534-3537.	1.8	32
140	Analysis of 14 Candidate Genes for Diabetic Nephropathy on Chromosome 3q in European Populations: Strongest Evidence for Association With a Variant in the Promoter Region of the Adiponectin Gene. Diabetes, 2006, 55, 3166-3174.	0.3	74
141	Linkage analysis of quantitative traits for obesity, diabetes, hypertension, and dyslipidemia on the island of Kosrae, Federated States of Micronesia. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 3502-3509.	3.3	65
142	Linkage and mutational analysis of familial thyroid dysgenesis demonstrate genetic heterogeneity implicating novel genes. European Journal of Human Genetics, 2005, 13, 232-239.	1.4	49
143	Single-nucleotide polymorphism versus microsatellite markers in a combined linkage and segregation analysis of a quantitative trait. BMC Genetics, 2005, 6, S32.	2.7	25
144	Exhaustive Genotyping of theCEM15 (APOBEC3G)Gene and Absence of Association with AIDS Progression in a French Cohort. Journal of Infectious Diseases, 2005, 191, 159-163.	1.9	107

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145	Phenotypical Characterisation of the Isolated Norfolk Island Population Focusing on Epidemiological Indicators of Cardiovascular Disease. Human Heredity, 2005, 60, 211-219.	0.4	37
146	Genetic variation at the 22q11PRODH2/DGCR6locus presents an unusual pattern and increases susceptibility to schizophrenia. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 3717-3722.	3.3	301
147	Genetic variation in the 22q11 locus and susceptibility to schizophrenia. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16859-16864.	3.3	183
148	Candidate genes involved in cardiovascular risk factors by a family-based association study on the island of Kosrae, Federated States of Micronesia. American Journal of Medical Genetics Part A, 2002, 110, 234-242.	2.4	38
149	A Transmission/Disequilibrium Test That Allows for Genotyping Errors in the Analysis of Single-Nucleotide Polymorphism Data. American Journal of Human Genetics, 2001, 69, 371-380.	2.6	147
150	A Novel Approach to Search for Identity by Descent in Small Samples of Patients and Controls from the Same Mendelian Breeding Unit: A Pilot Study on Myopia. Human Heredity, 2001, 52, 183-190.	0.4	37
151	Genome Scans for Q1 and Q2 on General Population Replicates Using Loki. Genetic Epidemiology, 2001, 21, S686-S691.	0.6	13
152	Epidemiology and Factor Analysis of Obesity, Type II Diabetes, Hypertension, and Dyslipidemia (Syndrome) Tj ETQq0 0 0 rgBT /Overlock	0.4	71
153	A Cholesterol-Lowering Gene Maps to Chromosome 13q. American Journal of Human Genetics, 2000, 66, 157-166.	2.6	91
154	Heterogeneity for Multiple Disease Loci in Linkage Analysis. Human Heredity, 1999, 49, 229-231.	0.4	25
155	Genetic Background Determines the Extent of Atherosclerosis in ApoE-Deficient Mice. Arteriosclerosis, Thrombosis, and Vascular Biology, 1999, 19, 1960-1968.	1.1	161
156	Distribution of alleles of the methylenetetrahydrofolate reductase (MTHFR) C677T gene polymorphism in familial spina bifida. American Journal of Medical Genetics Part A, 1999, 87, 407-412.	2.4	15
157	Multipoint Oligogenic Analysis of Age-at-Onset Data with Applications to Alzheimer Disease Pedigrees. American Journal of Human Genetics, 1999, 64, 839-851.	2.6	92
158	Searching for alcoholism susceptibility genes using markov chain monte carlo methods. Genetic Epidemiology, 1999, 17, S217-S222.	0.6	3
159	Power loss for multiallelic transmission/disequilibrium test when errors introduced: GAW11 simulated data. Genetic Epidemiology, 1999, 17, S587-S592.	0.6	24
160	Estimation of conditional multilocus gene identity among relatives. Lecture Notes-monograph Series / Institute of Mathematical Statistics, 1999, , 95-113.	1.0	55
161	AN ANALYTIC SOLUTION TO SINGLE NUCLEOTIDE POLYMORPHISM ERROR-DETECTION RATES IN NUCLEAR FAMILIES: IMPLICATIONS FOR STUDY DESIGN. , 1999, , 663-74.		17
162	Generating Consistent Genotypic Configurations for Multi-Allelic Loci and Large Complex Pedigrees. Human Heredity, 1998, 48, 1-11.	0.4	27

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163	Mapping quantitative trait loci for body weight on the X chromosome in mice. II. Analysis of congenic backcrosses. Genetical Research, 1997, 70, 125-133.	0.3	27
164	Markov Chain Monte Carlo Segregation and Linkage Analysis for Oligogenic Models. American Journal of Human Genetics, 1997, 61, 748-760.	2.6	568
165	Managing and Manipulating Genetic Data. , 0, , 17-31.		0