Simon G Gregory

List of Publications by Year
in descending order

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167 papers	46,502 citations	26567 56 h-index	7136 153 g-index
172 all docs	172 docs citations	172 times ranked	49190 citing authors

#	Article	IF	Citations
1	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	13.7	21,074
2	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	13.7	6,319
3	Identification of the breast cancer susceptibility gene BRCA2. Nature, 1995, 378, 789-792.	13.7	3,230
4	Association of the T-cell regulatory gene CTLA4 with susceptibility to autoimmune disease. Nature, 2003, 423, 506-511.	13.7	1,980
5	Risk Alleles for Multiple Sclerosis Identified by a Genomewide Study. New England Journal of Medicine, 2007, 357, 851-862.	13.9	1,529
6	The DNA sequence of the human X chromosome. Nature, 2005, 434, 325-337.	13.7	985
7	A physical map of the human genome. Nature, 2001, 409, 934-941.	13.7	865
8	A high-resolution HLA and SNP haplotype map for disease association studies in the extended human MHC. Nature Genetics, 2006, 38, 1166-1172.	9.4	686
9	LMNA, encoding lamin A/C, is mutated in partial lipodystrophy. Nature Genetics, 2000, 24, 153-156.	9.4	653
10	Interleukin 7 receptor Î± chain (IL7R) shows allelic and functional association with multiple sclerosis. Nature Genetics, 2007, 39, 1083-1091.	9.4	578
11	Genomic and epigenetic evidence for oxytocin receptor deficiency in autism. BMC Medicine, 2009, 7, 62.	2.3	497
12	A stress response pathway regulates DNA damage through Î²2-adrenoreceptors and Î²-arrestin-1. Nature, 2011, 477, 349-353.	13.7	360
13	Interleukin-2 gene variation impairs regulatory T cell function and causes autoimmunity. Nature Genetics, 2007, 39, 329-337.	9.4	333
14	A physical map of the mouse genome. Nature, 2002, 418, 743-750.	13.7	316
15	A High-Density Screen for Linkage in Multiple Sclerosis. American Journal of Human Genetics, 2005, 77, 454-467.	2.6	268
16	Prospective Multicenter Validation of Androgen Receptor Splice Variant 7 and Hormone Therapy Resistance in High-Risk Castration-Resistant Prostate Cancer: The PROPHECY Study. Journal of Clinical Oncology, 2019, 37, 1120-1129.	0.8	267
17	Mutation of TBCE causes hypoparathyroidismâ€“Âretardationâ€“dysmorphism and autosomal recessive Kennyâ€“Caffey syndrome. Nature Genetics, 2002, 32, 448-452.	9.4	248
18	Mutations in SLC19A2 cause thiamine-responsive megaloblastic anaemia associated with diabetes mellitus and deafness. Nature Genetics, 1999, 22, 300-304.	9.4	245

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19	The DNA sequence and biological annotation of human chromosomeâ€‰1. Nature, 2006, 441, 315-321.	13.7	211
20	Missense Mutations in TCF8 Cause Late-Onset Fuchs Corneal Dystrophy and Interact with FCD4 on Chromosome 9p. American Journal of Human Genetics, 2010, 86, 45-53.	2.6	167
21	Synovial cell cross-talk with cartilage plays a major role in the pathogenesis of osteoarthritis. Scientific Reports, 2020, 10, 10868.	1.6	161
22	A second major histocompatibility complex susceptibility locus for multiple sclerosis. Annals of Neurology, 2007, 61, 228-236.	2.8	156
23	Intranasal Oxytocin in Children and Adolescents with Autism Spectrum Disorder. New England Journal of Medicine, 2021, 385, 1462-1473.	13.9	149
24	Definition and characterization of a region of 1p36.3 consistently deleted in neuroblastoma. Oncogene, 2005, 24, 2684-2694.	2.6	147
25	Novel loci and pathways significantly associated with longevity. Scientific Reports, 2016, 6, 21243.	1.6	145
26	Human distal lung maps and lineage hierarchies reveal a bipotent progenitor. Nature, 2022, 604, 111-119.	13.7	137
27	Association of Autism With Induced or Augmented Childbirth in North Carolina Birth Record (1990-1998) and Education Research (1997-2007) Databases. JAMA Pediatrics, 2013, 167, 959.	3.3	119
28	Erythromyeloid progenitors give rise to a population of osteoclasts that contribute to bone homeostasis and repair. Nature Cell Biology, 2020, 22, 49-59.	4.6	114
29	Peakwide Mapping on Chromosome 3q13 Identifies the Kalirin Gene as a Novel Candidate Gene for Coronary Artery Disease. American Journal of Human Genetics, 2007, 80, 650-663.	2.6	110
30	Fine Mapping, Gene Content, Comparative Sequencing, and Expression Analyses SupportCtla4andNramp1as Candidates forIdd5.1andIdd5.2in the Nonobese Diabetic Mouse. Journal of Immunology, 2004, 173, 164-173.	0.4	102
31	SNPselector: a web tool for selecting SNPs for genetic association studies. Bioinformatics, 2005, 21, 4181-4186.	1.8	101
32	Genome-wide association study identifies three novel loci in Fuchs endothelial corneal dystrophy. Nature Communications, 2017, 8, 14898.	5.8	101
33	Integrated genomic analyses identify ERRFI1 and TACC3 as glioblastoma-targeted genes. Oncotarget, 2010, 1, 265-277.	0.8	96
34	TMEM231, mutated in orofaciodigital and Meckel syndromes, organizes the ciliary transition zone. Journal of Cell Biology, 2015, 209, 129-142.	2.3	95
35	Fine structure mapping of CIAS1: identification of an ancestral haplotype and a common FCAS mutation, L353P. Human Genetics, 2003, 112, 209-216.	1.8	89
36	Neuropeptide Y Gene Polymorphisms Confer Risk of Early-Onset Atherosclerosis. PLoS Genetics, 2009, 5, e1000318.	1.5	87

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37	Meteorin-like facilitates skeletal muscle repair through a Stat3/IGF-1 mechanism. Nature Metabolism, 2020, 2, 278-289.	5.1	87
38	1p36 is a preferential target of chromosome 1 deletions in astrocytic tumours and homozygously deleted in a subset of glioblastomas. Oncogene, 2008, 27, 2097-2108.	2.6	83
39	Human Epistatic Interaction Controls IL7R Splicing and Increases Multiple Sclerosis Risk. Cell, 2017, 169, 72-84.e13.	13.5	83
40	Early nurture epigenetically tunes the oxytocin receptor. Psychoneuroendocrinology, 2019, 99, 128-136.	1.3	83
41	GATA2 Is Associated with Familial Early-Onset Coronary Artery Disease. PLoS Genetics, 2006, 2, e139.	1.5	82
42	Metabolomic Quantitative Trait Loci (mQTL) Mapping Implicates the Ubiquitin Proteasome System in Cardiovascular Disease Pathogenesis. PLoS Genetics, 2015, 11, e1005553.	1.5	81
43	Genome Mapping by Fluorescentâ€‰Fingerprinting. Genome Research, 1997, 7, 1162-1168.	2.4	72
44	Distinct patterns of 1p and 19q alterations identify subtypes of human gliomas that have different prognosesâ€. Neuro-Oncology, 2010, 12, 664-678.	0.6	71
45	The kinetics of urinary fumonisin <scp>B</scp>₁ excretion in humans consuming maizeâ€based diets. Molecular Nutrition and Food Research, 2012, 56, 1445-1455.	1.5	70
46	An interferon-Î²-resistant and NLRP3 inflammasomeâ€“independent subtype of EAE with neuronal damage. Nature Neuroscience, 2016, 19, 1599-1609.	7.1	70
47	The physical maps for sequencing human chromosomes 1, 6, 9, 10, 13, 20 and X. Nature, 2001, 409, 942-943.	13.7	67
48	Further evidence for a maternal genetic effect and a sexâ€influenced effect contributing to risk for human neural tube defects. Birth Defects Research Part A: Clinical and Molecular Teratology, 2008, 82, 662-669.	1.6	66
49	Comprehensive genetic analysis of the platelet activating factor acetylhydrolase (PLA2G7) gene and cardiovascular disease in caseâ€“control and family datasets. Human Molecular Genetics, 2008, 17, 1318-1328.	1.4	66
50	Alternative splicing in multiple sclerosis and other autoimmune diseases. RNA Biology, 2010, 7, 462-473.	1.5	66
51	Replication of TCF4 through Association and Linkage Studies in Late-Onset Fuchs Endothelial Corneal Dystrophy. PLoS ONE, 2011, 6, e18044.	1.1	66
52	Epigenetic regulation of COL15A1 in smooth muscle cell replicative aging and atherosclerosis. Human Molecular Genetics, 2013, 22, 5107-5120.	1.4	66
53	Enhancing linkage analysis of complex disorders: an evaluation of high-density genotyping. Human Molecular Genetics, 2004, 13, 1943-1949.	1.4	65
54	Comparison of GC-MS and GCÃ—GC-MS in the Analysis of Human Serum Samples for Biomarker Discovery. Journal of Proteome Research, 2015, 14, 1810-1817.	1.8	64

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55	Human health implications from co-exposure to aflatoxins and fumonisins in maize-based foods in Latin America: Guatemala as a case study. World Mycotoxin Journal, 2015, 8, 143-159.	0.8	63
56	A non-canonical type 2 immune response coordinates tuberculous granuloma formation and epithelialization. Cell, 2021, 184, 1757-1774.e14.	13.5	63
57	Skewing of the population balance of lymphoid and myeloid cells by secreted and intracellular osteopontin. Nature Immunology, 2017, 18, 973-984.	7.0	62
58	A high-resolution integrated physical, cytogenetic, and genetic map of human chromosome 11: distal p13 to proximal p15.1. Genomics, 1995, 25, 447-461.	1.3	58
59	Whole Genomic Copy Number Alterations in Circulating Tumor Cells from Men with Abiraterone or Enzalutamide-Resistant Metastatic Castration-Resistant Prostate Cancer. Clinical Cancer Research, 2017, 23, 1346-1357.	3.2	58
60	Tiling path resolution mapping of constitutional 1p36 deletions by array-CGH: contiguous gene deletion or "deletion with positional effect" syndrome?. Journal of Medical Genetics, 2005, 42, 166-171.	1.5	53
61	Multifactor dimensionality reduction reveals geneâ€“gene interactions associated with multiple sclerosis susceptibility in African Americans. Genes and Immunity, 2006, 7, 310-315.	2.2	52
62	Evidence for fumonisin inhibition of ceramide synthase in humans consuming maizeâ€based foods and living in high exposure communities in Guatemala. Molecular Nutrition and Food Research, 2015, 59, 2209-2224.	1.5	52
63	A candidate gene for congenital bilateral isolated ptosis identified by molecular analysis of a de novo balanced translocation. Human Genetics, 2002, 110, 244-250.	1.8	51
64	Genetic effects in the leukotriene biosynthesis pathway and association with atherosclerosis. Human Genetics, 2009, 125, 217-229.	1.8	51
65	The S1103Y Cardiac Sodium Channel Variant Is Associated With Implantable Cardioverter-Defibrillator Events in Blacks With Heart Failure and Reduced Ejection Fraction. Circulation: Cardiovascular Genetics, 2011, 4, 163-168.	5.1	46
66	Genome-wide Linkage Scan in Fuchs Endothelial Corneal Dystrophy. , 2009, 50, 1093.		44
67	Urinary fumonisin <scp>B</scp>₁ and estimated fumonisin intake in women from highâ€and lowâ€exposure communities in <scp>G</scp>uatemala. Molecular Nutrition and Food Research, 2014, 58, 973-983.	1.5	44
68	Evaluating DNA methylation age on the Illumina MethylationEPIC Bead Chip. PLoS ONE, 2019, 14, e0207834.	1.1	44
69	Single-cell omics analysis reveals functional diversification of hepatocytes during liver regeneration. JCI Insight, 2020, 5, .	2.3	43
70	The human gene for mannan-binding lectin-associated serine protease-2 (MASP-2), the effector component of the lectin route of complement activation, is part of a tightly linked gene cluster on chromosome 1p36.2â€“3. Genes and Immunity, 2001, 2, 119-127.	2.2	42
71	Comprehensive DNA Copy Number Profiling of Meningioma Using a Chromosome 1 Tiling Path Microarray Identifies Novel Candidate Tumor Suppressor Loci. Cancer Research, 2005, 65, 2653-2661.	0.4	42
72	Metabolome-based signature of disease pathology in MS. Multiple Sclerosis and Related Disorders, 2019, 31, 12-21.	0.9	41

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73	Genetic, epigenetic, and environmental factors controlling oxytocin receptor gene expression. Clinical Epigenetics, 2021, 13, 23.	1.8	41
74	Clinical, radiological, and genetic similarities between patients with Chiari Type I and Type 0 malformations. Journal of Neurosurgery: Pediatrics, 2012, 9, 372-378.	0.8	38
75	Stratified Whole Genome Linkage Analysis of Chiari Type I Malformation Implicates Known Klippel-Feil Syndrome Genes as Putative Disease Candidates. PLoS ONE, 2013, 8, e61521.	1.1	37
76	Complex geneâ€“gene interactions in multiple sclerosis: a multifactorial approach reveals associations with inflammatory genes. Neurogenetics, 2007, 8, 11-20.	0.7	35
77	Outcome and life satisfaction of adults with myelomeningocele. Disability and Health Journal, 2013, 6, 236-243.	1.6	35
78	Cleavage and polyadenylation specificity factor 1 (CPSF1) regulates alternative splicing of interleukin 7 receptor (IL7R) exon 6. Rna, 2013, 19, 103-115.	1.6	35
79	Deletion or Epigenetic Silencing of AJAP1 on 1p36 in Glioblastoma. Molecular Cancer Research, 2012, 10, 208-217.	1.5	34
80	A 6-Mb High-Resolution Physical and Transcription Map Encompassing the Hereditary Prostate Cancer 1 (HPC1) Region. Genomics, 2000, 64, 1-14.	1.3	33
81	SNPs in Multi-Species Conserved Sequences (MCS) as useful markers in association studies: a practical approach. BMC Genomics, 2007, 8, 266.	1.2	33
82	Refined Mapping and YAC Contig Construction of the X-Linked Cleft Palate and Ankyloglossia Locus (CPX) Including the Proximal Xâ€“Y Homology Breakpoint within Xq21.3. Genomics, 1996, 31, 36-43.	1.3	32
83	Aging-related atherosclerosis is exacerbated by arterial expression of tumor necrosis factor receptor-1: evidence from mouse models and human association studies. Human Molecular Genetics, 2010, 19, 2754-2766.	1.4	32
84	Genetic and functional association of FAM5C with myocardial infarction. BMC Medical Genetics, 2008, 9, 33.	2.1	31
85	Genetic Evaluation and Application of Posterior Cranial Fossa Traits as Endophenotypes for Chiari Type I Malformation. Annals of Human Genetics, 2014, 78, 1-12.	0.3	31
86	An Integrated Physical Map of 210 Markers Assigned to the Short Arm of Human Chromosome 11. Genomics, 1994, 21, 538-550.	1.3	30
87	The TFAP2Aâ€“IRF6â€“GRHL3 genetic pathway is conserved in neurulation. Human Molecular Genetics, 2019, 28, 1726-1737.	1.4	30
88	Nonobese Diabetic Congenic Strain Analysis of Autoimmune Diabetes Reveals Genetic Complexity of the Idd18 Locus and Identifies Vav3 as a Candidate Gene. Journal of Immunology, 2010, 184, 5075-5084.	0.4	29
89	Association of mtDNA haplogroup F with healthy longevity in the female Chuang population, China. Experimental Gerontology, 2011, 46, 987-993.	1.2	29
90	Identification of a Structurally Distinct CD101 Molecule Encoded in the 950-kb Idd10 Region of NOD Mice. Diabetes, 2003, 52, 1551-1556.	0.3	27

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91	Association of Roadway Proximity with Fasting Plasma Glucose and Metabolic Risk Factors for Cardiovascular Disease in a Cross-Sectional Study of Cardiac Catheterization Patients. Environmental Health Perspectives, 2015, 123, 1007-1014.	2.8	27
92	Single-cell RNA-seq reveals transcriptomic heterogeneity mediated by hostâ€“pathogen dynamics in lymphoblastoid cell lines. ELife, 2021, 10, .	2.8	26
93	Organization and Evolution of a Gene-Rich Region of the Mouse Genome: A 12.7-Mb Region Deleted in the Del(13)Svea36H Mouse. Genome Research, 2004, 14, 1888-1901.	2.4	25
94	Mapping and characterization of the amplicon near APOA2 in 1q23 in human sarcomas by FISH and array CGH. Molecular Cancer, 2005, 4, 39.	7.9	25
95	Polymorphic variants in tenascin-C (TNC) are associated with atherosclerosis and coronary artery disease. Human Genetics, 2011, 129, 641-654.	1.8	25
96	Whole blood sequencing reveals circulating microRNA associations with high-risk traits in non-ST-segment elevation acute coronary syndrome. Atherosclerosis, 2017, 261, 19-25.	0.4	25
97	Detailed assessment of chromosome 22 aberrations in sporadic pheochromocytoma using array-CGH. International Journal of Cancer, 2006, 118, 1159-1164.	2.3	24
98	Identification of Chiari Type I Malformation subtypes using whole genome expression profiles and cranial base morphometrics. BMC Medical Genomics, 2014, 7, 39.	0.7	24
99	A blood spot method for detecting fumonisin-induced changes in putative sphingolipid biomarkers in LM/Bc mice and humans. Food Additives and Contaminants - Part A Chemistry, Analysis, Control, Exposure and Risk Assessment, 2015, 32, 934-949.	1.1	24
100	Polymorphisms of the Tumor Suppressor Gene LSAMP are Associated with Left Main Coronary Artery Disease. Annals of Human Genetics, 2008, 72, 443-453.	0.3	23
101	Genetic Variants in the Bone Morphogenic Protein Gene Family Modify the Association between Residential Exposure to Traffic and Peripheral Arterial Disease. PLoS ONE, 2016, 11, e0152670.	1.1	23
102	ALOX5AP variants are associated with in-stent restenosis after percutaneous coronary intervention. Atherosclerosis, 2008, 201, 148-154.	0.4	22
103	Epigenetic dysregulation of Oxtr in Tet1-deficient mice has implications for neuropsychiatric disorders. JCI Insight, 2018, 3, .	2.3	22
104	Organization of the MASP2 locus and its expression profile in mouse and rat. Mammalian Genome, 2004, 15, 887-900.	1.0	21
105	Fine mapping of a linkage peak with integration of lipid traits identifies novel coronary artery disease genes on chromosome 5. BMC Genetics, 2012, 13, 12.	2.7	21
106	Circulating Tumor Cell Chromosomal Instability and Neuroendocrine Phenotype by Immunomorphology and Poor Outcomes in Men with mCRPC Treated with Abiraterone or Enzalutamide. Clinical Cancer Research, 2021, 27, 4077-4088.	3.2	21
107	Single-Cell RNA Sequencing Reveals Cellular and Transcriptional Changes Associated With M1 Macrophage Polarization in Hidradenitis Suppurativa. Frontiers in Medicine, 2021, 8, 665873.	1.2	21
108	A genome-wide trans-ethnic interaction study links the PIGR-FCAMR locus to coronary atherosclerosis via interactions between genetic variants and residential exposure to traffic. PLoS ONE, 2017, 12, e0173880.	1.1	21

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109	Genomeâ€wide linkage analysis of quantitative biomarker traits of osteoarthritis in a large, multigenerational extended family. Arthritis and Rheumatism, 2010, 62, 781-790.	6.7	20
110	Using circulating tumor cells to inform on prostate cancer biology and clinical utility. Critical Reviews in Clinical Laboratory Sciences, 2015, 52, 191-210.	2.7	20
111	Pregnancy continuation and organizational religious activity following prenatal diagnosis of a lethal fetal defect are associated with improved psychological outcome. Prenatal Diagnosis, 2015, 35, 761-768.	1.1	19
112	Epigenomeâ€Wide Association Study for Allâ€Cause Mortality in a Cardiovascular Cohort Identifies Differential Methylation in Castor Zinc Finger 1 (CASZ1). Journal of the American Heart Association, 2019, 8, e013228.	1.6	19
113	A gene expression signature of confinement in peripheral blood of red wolves (Canis rufus). Molecular Ecology, 2008, 17, 2782-2791.	2.0	18
114	Transcriptome profiling of genes involved in neural tube closure during human embryonic development using long serial analysis of gene expression (longâ€SAGE). Birth Defects Research Part A: Clinical and Molecular Teratology, 2012, 94, 683-692.	1.6	18
115	Discordant and heterogeneous clinically relevant genomic alterations in circulating tumor cells vs plasma DNA from men with metastatic castration resistant prostate cancer. Genes Chromosomes and Cancer, 2020, 59, 225-239.	1.5	18
116	Interactions between Social/ behavioral factors and ADRB2 genotypes may be associated with health at advanced ages in China. BMC Geriatrics, 2013, 13, 91.	1.1	17
117	Whole Exome Sequencing of Cell-Free DNA for Early Lung Cancer: A Pilot Study to Differentiate Benign From Malignant CT-Detected Pulmonary Lesions. Frontiers in Oncology, 2019, 9, 317.	1.3	17
118	Circulating Tumor Cell Genomic Evolution and Hormone Therapy Outcomes in Men with Metastatic Castration-Resistant Prostate Cancer. Molecular Cancer Research, 2021, 19, 1040-1050.	1.5	17
119	Epigenetic Profiling Identifies Novel Genes for Ascending Aortic Aneurysm Formation with Bicuspid Aortic Valves. Heart Surgery Forum, 2015, 18, 134.	0.2	17
120	The generation of ordered sets of cosmid DNA clones from human chromosome region 11p. Genomics, 1992, 13, 89-94.	1.3	16
121	Examination of seven candidate regions for multiple sclerosis: strong evidence of linkage to chromosome 1q44. Genes and Immunity, 2006, 7, 73-76.	2.2	16
122	Associations Between Residential Proximity to Traffic and Vascular Disease in a Cardiac Catheterization Cohort. Arteriosclerosis, Thrombosis, and Vascular Biology, 2018, 38, 275-282.	1.1	15
123	Linkage and Association With Type 1 Diabetes on Chromosome 1q42. Diabetes, 2002, 51, 3318-3325.	0.3	15
124	An SSLP markerâ€“anchored BAC framework map of the mouse genome. Nature Genetics, 2001, 29, 133-134.	9.4	14
125	Interaction Between the FOXO1A-209 Genotype and Tea Drinking Is Significantly Associated with Reduced Mortality at Advanced Ages. Rejuvenation Research, 2016, 19, 195-203.	0.9	14
126	Pharmacodynamic study of radium-223 in men with bone metastatic castration resistant prostate cancer. PLoS ONE, 2019, 14, e0216934.	1.1	14

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127	Rationale, design, and methods of the Autism Centers of Excellence (ACE) network Study of Oxytocin in Autism to improve Reciprocal Social Behaviors (SOARS-B). Contemporary Clinical Trials, 2020, 98, 106103.	0.8	14
128	Circulating MicroRNA Profiling in Non-ST Elevated Coronary Artery Syndrome Highlights Genomic Associations with Serial Platelet Reactivity Measurements. Scientific Reports, 2020, 10, 6169.	1.6	14
129	Lifetime marijuana use and epigenetic age acceleration: A 17-year prospective examination. Drug and Alcohol Dependence, 2022, 233, 109363.	1.6	14
130	Comparative Physical and Transcript Maps of âˆ¼1 Mb around loop-tail, a Gene for Severe Neural Tube Defects on Distal Mouse Chromosome 1 and Human Chromosome 1q22â€“q23. Genomics, 2001, 72, 180-192.	1.3	13
131	Missing genetic risk in neural tube defects: Can exome sequencing yield an insight?. Birth Defects Research Part A: Clinical and Molecular Teratology, 2014, 100, 642-646.	1.6	13
132	Human centromere repositioning within euchromatin after partial chromosome deletion. Chromosome Research, 2016, 24, 451-466.	1.0	13
133	Genetic screen of African Americans with Fuchs endothelial corneal dystrophy. Molecular Vision, 2013, 19, 2508-16.	1.1	13
134	Allelic association of sequence variants in the herpes virus entry mediator-B gene (PVRL2) with the severity of multiple sclerosis. Genes and Immunity, 2006, 7, 384-392.	2.2	12
135	Refinement of 2q and 7p loci in a large multiplex NTD family. Birth Defects Research Part A: Clinical and Molecular Teratology, 2008, 82, 441-452.	1.6	12
136	Genome-Wide Linkage Analysis of Cardiovascular Disease Biomarkers in a Large, Multigenerational Family. PLoS ONE, 2013, 8, e71779.	1.1	12
137	Mitochondrial Polymorphism A10398G and Haplogroup I Are Associated With Fuchs' Endothelial Corneal Dystrophy. , 2014, 55, 4577.		12
138	HDMX regulates p53 activity and confers chemoresistance to 3-Bis(2-chloroethyl)-1-nitrosourea. Neuro-Oncology, 2010, 12, 956-966.	0.6	11
139	Geneâ€“smoking interactions in multiple Rho-GTPase pathway genes in an early-onset coronary artery disease cohort. Human Genetics, 2013, 132, 1371-1382.	1.8	10
140	Joint eQTL assessment of whole blood and dura mater tissue from individuals with Chiari type I malformation. BMC Genomics, 2015, 16, 11.	1.2	10
141	Single-Cell RNA Sequencing Identifies Yes-Associated Protein 1â€“Dependent Hepatic Mesothelial Progenitors in Fibrolamellar Carcinoma. American Journal of Pathology, 2020, 190, 93-107.	1.9	10
142	Follow-up examination of linkage and association to chromosome 1q43 in multiple sclerosis. Genes and Immunity, 2009, 10, 624-630.	2.2	8
143	A general integrative genomic feature transcription factor binding site prediction method applied to analysis of USF1 binding in cardiovascular disease. Human Genomics, 2009, 3, 221.	1.4	7
144	U2AF2 binds IL7R exon 6 ectopically and represses its inclusion. Rna, 2021, 27, 571-583.	1.6	7

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145	Case-Only Survival Analysis Reveals Unique Effects of Genotype, Sex, and Coronary Disease Severity on Survivorship. PLoS ONE, 2016, 11, e0154856.	1.1	6
146	Profiling serum neurofilament light chain and glial fibrillary acidic protein in primary progressive multiple sclerosis. Journal of Neuroimmunology, 2021, 354, 577541.	1.1	6
147	Genetic Association Analyses of Nitric Oxide Synthase Genes and Neural Tube Defects Vary by Phenotype. Birth Defects Research Part B: Developmental and Reproductive Toxicology, 2013, 98, 365-373.	1.4	4
148	Association of autism with induced or augmented childbirth. American Journal of Obstetrics and Gynecology, 2014, 210, 492-493.	0.7	4
149	Associations of osteopontin and NT-proBNP with circulating miRNA levels in acute coronary syndrome. Physiological Genomics, 2019, 51, 506-515.	1.0	4
150	Genetic Variants Associated with Vein Graft Stenosis after Coronary Artery Bypass Grafting. Heart Surgery Forum, 2015, 18, 001.	0.2	4
151	Matroshka and ectopic polymorphisms: Two new classes of DNA sequence variation identified at the Van der Woude syndrome locus on 1q32-q41. Human Mutation, 2001, 18, 422-434.	1.1	2
152	Strategies for Genotype Generation. Current Protocols in Human Genetics, 2005, 47, Unit 1.3.	3.5	2
153	Induction or Augmentation of Labor and Autismâ€"Reply. JAMA Pediatrics, 2014, 168, 191.	3.3	2
154	Characterization of a castrate-resistant prostate cancer xenograft derived from a patient of West African ancestry. Prostate Cancer and Prostatic Diseases, 2022, 25, 513-523.	2.0	2
155	Genetics of the Chiari I and II Malformations. , 2013, , 93-101.		1
156	Sex-dimorphic gene effects on survival outcomes in people with coronary artery disease. American Heart Journal Plus, 2022, 17, 100152.	0.3	1
157	Synteny mapping. , 2005, , .		0
158	Mapping Techniques. , 2005, , 117-133.		0
159	Genomics and Bioinformatics. , 0, , 423-454.		0
160	Genetic predisposition of behavioral response. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1672-1673.	3.3	0
161	Mapping Techniques. Springer Protocols, 2008, , 291-310.	0.1	0
162	The Epigenetics of Autism â€" Running Beyond the Bases. , 2014, , 303-333.		0

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163	Analysis of genomic alterations in matched circulating tumor cell DNA (CTC DNA) and plasma tumor DNA (ctDNA) in men with metastatic castration resistant prostate cancer (mCRPC).. Journal of Clinical Oncology, 2018, 36, 5065-5065.	0.8	0
164	Circulating tumor cell (CTC) genomic signatures of hormone therapy resistance in men with metastatic castration-resistant prostate cancer (mCRPC).. Journal of Clinical Oncology, 2020, 38, 147-147.	0.8	0
165	Association of circulating tumor cell RB1 loss RNA signature with outcomes and immune phenotypes in men with mCRPC.. Journal of Clinical Oncology, 2022, 40, 139-139.	0.8	0
166	Abstract 18660: CVSN Best Abstract Award: Genome-wide Candidates Unique to Females With Coronary Artery Disease Significantly Predict Mortality Risk. Circulation, 2015, 132, .	1.6	0
167	A phase 0/surgical window-of-opportunity study in progress, evaluating evolocumab in patients with high-grade glioma or glioblastoma.. Journal of Clinical Oncology, 2022, 40, TPS2076-TPS2076.	0.8	0