John D Mcpherson

List of Publications by Year
in descending order

185 papers	66,207 citations	10650 74 h-index	7234 158 g-index
195 all docs	195 docs citations	195 times ranked	79788 citing authors

#	Article	IF	Citations
1	High-Plex Spatial RNA Profiling Reveals Cell Typeâ€'Specific Biomarker Expression during Melanoma Development. Journal of Investigative Dermatology, 2022, 142, 1401-1412.e20.	0.3	10
2	Characteristics of amelanotic <scp>acantholyticâ€like</scp> melanoma resembling squamous cell carcinoma. Journal of Cutaneous Pathology, 2022, 49, 500-503.	0.7	0
3	Whole exome sequencing of a gut-associated lymphoid tissue neoplasm points to precursor or early form of sporadic colon carcinoma. Pathology Research and Practice, 2021, 220, 153406.	1.0	1
4	Effect of Pesticide Exposure on Non-Hodgkin Lymphoma Incidence and Survival in California. Blood, 2021, 138, 5006-5006.	0.6	1
5	Cryptic genomic lesions in adverse-risk acute myeloid leukemia identified by integrated whole genome and transcriptome sequencing. Leukemia, 2020, 34, 306-311.	3.3	14
6	Landscape of somatic single nucleotide variants and indels in colorectal cancer and impact on survival. Nature Communications, 2020, 11, 3644.	5.8	55
7	Novel POFUT1 mutation in patient with flexural and acral hyperpigmented reticulated macules presenting in adolescence. JAAD Case Reports, 2020, 6, 334-336.	0.4	2
8	RAS pathway influences the number of melanocytic nevi in cardiofaciocutaneous and Costello syndromes. Journal of the American Academy of Dermatology, 2020, 82, 1091-1093.	0.6	5
9	Comparative toxicoproteogenomics of mouse and rat liver identifies TCDD-resistance genes. Archives of Toxicology, 2019, 93, 2961-2978.	1.9	3
10	Genome-wide germline correlates of the epigenetic landscape of prostate cancer. Nature Medicine, 2019, 25, 1615-1626.	15.2	45
11	Regional perturbation of gene transcription is associated with intrachromosomal rearrangements and gene fusion transcripts in high grade ovarian cancer. Scientific Reports, 2019, 9, 3590.	1.6	8
12	Activation of hedgehog signaling associates with early disease progression in chronic lymphocytic leukemia. Blood, 2019, 133, 2651-2663.	0.6	15
13	Identification of Distinct Prognostic Groups: Implications for Patient Selection to Targeted Therapies Among Anti-Endocrine Therapyâ€"Resistant Early Breast Cancers. JCO Precision Oncology, 2019, 3, 1-13.	1.5	0
14	Future Promises and Concerns of Ubiquitous Next-Generation Sequencing. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a025783.	2.9	10
15	Next-Generation Sequencing Technologies. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a036798.	2.9	143
16	Improving classification of melanocytic nevi: Association of BRAF V600E expression with distinct histomorphologic features. Journal of the American Academy of Dermatology, 2018, 79, 221-229.	0.6	28
17	Sensitive tumour detection and classification using plasma cell-free DNA methylomes. Nature, 2018, 563, 579-583.	13.7	624
18	Diverse EGFR Exon 20 Insertions and Co-Occurring Molecular Alterations Identified by Comprehensive Genomic Profiling of NSCLC. Journal of Thoracic Oncology, 2018, 13, 1560-1568.	0.5	158

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19	Complex rearrangements and oncogene amplifications revealed by long-read DNA and RNA sequencing of a breast cancer cell line. Genome Research, 2018, 28, 1126-1135.	2.4	142
20	Prediction of acute myeloid leukaemia risk in healthy individuals. Nature, 2018, 559, 400-404.	13.7	617
21	Genomic hallmarks of localized, non-indolent prostate cancer. Nature, 2017, 541, 359-364.	13.7	462
22	Germline BRCA2 mutations drive prostate cancers with distinct evolutionary trajectories. Nature Communications, 2017, 8, 13671.	5.8	182
23	Interrogation of Functional Cell-Surface Markers Identifies CD151 Dependency in High-Grade Serous Ovarian Cancer. Cell Reports, 2017, 18, 2343-2358.	2.9	38
24	Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma. Nature Genetics, 2017, 49, 825-833.	9.4	55
25	Mitochondrial mutations drive prostate cancer aggression. Nature Communications, 2017, 8, 656.	5.8	100
26	Microscopy with ultraviolet surface excitation for rapid slide-free histology. Nature Biomedical Engineering, 2017, 1, 957-966.	11.6	183
27	Tracing the origins of relapse in acute myeloid leukaemia to stem cells. Nature, 2017, 547, 104-108.	13.7	424
28	ISOWN: accurate somatic mutation identification in the absence of normal tissue controls. Genome Medicine, 2017, 9, 59.	3.6	44
29	Molecular heterogeneity of non-small cell lung carcinoma patient-derived xenografts closely reflect their primary tumors. International Journal of Cancer, 2017, 140, 662-673.	2.3	67
30	Association of Distinct Mutational Signatures With Correlates of Increased Immune Activity in Pancreatic Ductal Adenocarcinoma. JAMA Oncology, 2017, 3, 774.	3.4	221
31	Targeted sequencing in a phase III trial of luminal breast cancer: Identification of novel targets.. Journal of Clinical Oncology, 2017, 35, 505-505.	0.8	0
32	Coming of age: ten years of next-generation sequencing technologies. Nature Reviews Genetics, 2016, 17, 333-351.	7.7	3,160
33	A renewed model of pancreatic cancer evolution based on genomic rearrangement patterns. Nature, 2016, 538, 378-382.	13.7	418
34	Fine mapping of chromosome 5p15.33 based on a targeted deep sequencing and high density genotyping identifies novel lung cancer susceptibility loci. Carcinogenesis, 2016, 37, 96-105.	1.3	36
35	Truncating Erythropoietin Receptor Rearrangements in Acute Lymphoblastic Leukemia. Cancer Cell, 2016, 29, 186-200.	7.7	118
36	Candidate DNA repair susceptibility genes identified by exome sequencing in high-risk pancreatic cancer. Cancer Letters, 2016, 370, 302-312.	3.2	47

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37	Distinct routes of lineage development reshape the human blood hierarchy across ontogeny. Science, 2016, 351, aab2116.	6.0	597
38	Abstract 5221: Linking the molecular profile of colorectal tumors to germline genetic and environmental risk factors. , 2016, , .		0
39	Abstract 3124: Prognostic biomarkers for pancreatic cancer. , 2016, , .		0
40	Abstract 118: A comprehensive profile of the genomic architecture of curable prostate cancer. , 2016, , .		0
41	Abstract 850: Comprehensive genome and transcriptome structural analysis of a breast cancer cell line using single molecule sequencing. , 2016, , .		0
42	A cancer cell-line titration series for evaluating somatic classification. BMC Research Notes, 2015, 8, 823.	0.6	10
43	GLI2 inhibition abrogates human leukemia stem cell dormancy. Journal of Translational Medicine, 2015, 13, 98.	1.8	80
44	Spatial genomic heterogeneity within localized, multifocal prostate cancer. Nature Genetics, 2015, 47, 736-745.	9.4	395
45	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	5.8	266
46	Optimization of miRNA-seq data preprocessing. Briefings in Bioinformatics, 2015, 16, 950-963.	3.2	120
47	Abstract 2966: The mutational landscape of localized gleason 6 and 7 prostate cancer. , 2015, , .		0
48	Abstract A1-17: Genomic analysis of metachronous pancreatic ductal adenocarcinoma. , 2015, , .		0
49	Abstract B2-57: Genomic analysis of metachronous pancreatic ductal adenocarcinoma. , 2015, , .		0
50	On the Origins of AML Relapse. Blood, 2015, 126, 223-223.	0.6	0
51	Use of Sequenom Sample ID PlusÂ® SNP Genotyping in Identification of FFPE Tumor Samples. PLoS ONE, 2014, 9, e88163.	1.1	17
52	Massively Parallel Sequencing of Patients with Intellectual Disability, Congenital Anomalies and/or Autism Spectrum Disorders with a Targeted Gene Panel. PLoS ONE, 2014, 9, e93409.	1.1	35
53	WaveCNV: allele-specific copy number alterations in primary tumors and xenograft models from next-generation sequencing. Bioinformatics, 2014, 30, 768-774.	1.8	18
54	Next-generation sequencing identifies rare variants associated with Noonan syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11473-11478.	3.3	158

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55	Genomic testing in cancer: Patient knowledge, attitudes, and expectations. Cancer, 2014, 120, 3066-3073.	2.0	72
56	Identification of genes expressed by immune cells of the colon that are regulated by colorectal cancerâ€associated variants. International Journal of Cancer, 2014, 134, 2330-2341.	2.3	38
57	Identification of pre-leukaemic haematopoietic stem cells in acute leukaemia. Nature, 2014, 506, 328-333.	13.7	1,241
58	Genomic Support for a Moaâ€“Tinamou Clade and Adaptive Morphological Convergence in Flightless Ratites. Molecular Biology and Evolution, 2014, 31, 1686-1696.	3.5	80
59	Robust global microRNA expression profiling using next-generation sequencing technologies. Laboratory Investigation, 2014, 94, 350-358.	1.7	118
60	A defining decade in DNA sequencing. Nature Methods, 2014, 11, 1003-1005.	9.0	21
61	SeqControl: process control for DNA sequencing. Nature Methods, 2014, 11, 1071-1075.	9.0	10
62	Hotspot activating PRKD1 somatic mutations in polymorphous low-grade adenocarcinomas of the salivary glands. Nature Genetics, 2014, 46, 1166-1169.	9.4	188
63	ShatterProof: operational detection and quantification of chromothripsis. BMC Bioinformatics, 2014, 15, 78.	1.2	49
64	Antioxidant Supplementation Reduces Genomic Aberrations in Human Induced Pluripotent Stem Cells. Stem Cell Reports, 2014, 2, 44-51.	2.3	69
65	A Two-Dimensional Pooling Strategy for Rare Variant Detection on Next-Generation Sequencing Platforms. PLoS ONE, 2014, 9, e93455.	1.1	18
66	Abstract 5185: Redefining the somatic landscape of pancreatic adenocarcinoma. , 2014, , .		0
67	Abstract 09: Contribution of known and novel BRCA-mediated DNA repair pathway genes to pancreatic cancer susceptibility. , 2014, , .		0
68	Exome sequencing identifies nonsegregating nonsense ATM and PALB2 variants in familial pancreatic cancer. Human Genomics, 2013, 7, 11.	1.4	30
69	Variable Clonal Repopulation Dynamics Influence Chemotherapy Response in Colorectal Cancer. Science, 2013, 339, 543-548.	6.0	691
70	Feasibility of real time next generation sequencing of cancer genes linked to drug response: Results from a clinical trial. International Journal of Cancer, 2013, 132, 1547-1555.	2.3	76
71	Clinical genomics information management software linking cancer genome sequence and clinical decisions. Genomics, 2013, 102, 140-147.	1.3	14
72	Abstract A23: Genome-wide discovery of synthetic lethal interactions in PTEN-deficient human mammary epithelial cells. , 2013, , .		1

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73	Abstract B129: Clinical implications of inter- and intra- prostatic heterogeneity.. , 2013, , .		0
74	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. Nature, 2012, 491, 399-405.	13.7	1,741
75	Elevated Coding Mutation Rate During the Reprogramming of Human Somatic Cells into Induced Pluripotent Stem Cells. Stem Cells, 2012, 30, 435-440.	1.4	172
76	Cancer Genomics: Technology, Discovery, and Translation. Journal of Clinical Oncology, 2012, 30, 647-660.	0.8	173
77	Abstract 3184: Whole genome sequencing of low-input fresh frozen prostate cancer biopsies. , 2012, , .		0
78	Abstract LB-230: A prospective clinical trial to evaluate DNA sequencing as a diagnostic tool to guide cancer therapy: results from the initial 50 patients. , 2012, , .		0
79	Abstract LB-404: Genomic analysis reveals roles for chromatin modification and axon guidance in pancreatic cancer. , 2012, , .		0
80	Abstract IA3: Genomic analysis reveals roles for chromatin modification and axon guidance in pancreatic cancer.. , 2012, , .		0
81	Abstract A9: The pancreatic ductal adenocarcinoma project at the Ontario Institute for Cancer Research.. , 2012, , .		0
82	Abstract B18: Genomic analysis of pancreatic ductal adenocarcinoma.. , 2012, , .		0
83	Abstract B13: Whole-genome mutation landscape in pancreatic ductal adenocarcinoma.. , 2012, , .		0
84	Abstract A15: Exome sequencing identifies candidate tumor suppressor genes in familial pancreatic cancer.. , 2012, , .		0
85	Abstract B91: Primary tumor xenograft establishment from pancreatic resection specimens.. , 2012, , .		0
86	Exome Sequencing of Ion Channel Genes Reveals Complex Profiles Confounding Personal Risk Assessment in Epilepsy. Cell, 2011, 145, 1036-1048.	13.5	274
87	Unraveling the Genetics of Cancer: Genome Sequencing and Beyond. Annual Review of Genomics and Human Genetics, 2011, 12, 407-430.	2.5	85
88	Abstract B48: Feasibility study of molecular profiling (MP) in patients (Pts) with advanced solid cancers using targeted mutation analysis and targeted exome sequencing.. , 2011, , .		2
89	BCL2 Splice Isoform Switching Promotes Leukemia Stem Cell Survival and Sensitivity to a Novel Pan BCL2 Inhibitor. Blood, 2011, 118, 2735-2735.	0.6	1
90	International network of cancer genome projects. Nature, 2010, 464, 993-998.	13.7	2,114

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91	Evidence that multiple genetic variants of MC4R play a functional role in the regulation of energy expenditure and appetite in Hispanic children. American Journal of Clinical Nutrition, 2010, 91, 191-199.	2.2	65
92	The completion of the Mammalian Gene Collection (MGC). Genome Research, 2009, 19, 2324-2333.	2.4	125
93	The GAAS Metagenomic Tool and Its Estimations of Viral and Microbial Average Genome Size in Four Major Biomes. PLoS Computational Biology, 2009, 5, e1000593.	1.5	177
94	Next-Generation Sequencing: A New Revolution in Molecular Diagnostics?. Clinical Chemistry, 2009, 55, 2088-2092.	1.5	18
95	Single nucleotide polymorphism-mediated translational suppression of endoplasmic reticulum mannosidase I modifies the onset of end-stage liver disease in alpha1-antitrypsin deficiency. Hepatology, 2009, 50, 275-281.	3.6	96
96	Prepublication data sharing. Nature, 2009, 461, 168-170.	13.7	243
97	Next-generation gap. Nature Methods, 2009, 6, S2-S5.	9.0	111
98	Massively parallel bisulphite pyrosequencing reveals the molecular complexity of breast cancer-associated cytosine-methylation patterns obtained from tissue and serum DNA. Genome Research, 2008, 18, 19-29.	2.4	114
99	Demographic Histories and Patterns of Linkage Disequilibrium in Chinese and Indian Rhesus Macaques. Science, 2007, 316, 240-243.	6.0	161
100	MethylScreen: DNA methylation density monitoring using quantitative PCR. BioTechniques, 2007, 43, 683-693.	0.8	50
101	Characterizing the cancer genome in lung adenocarcinoma. Nature, 2007, 450, 893-898.	13.7	1,020
102	Identification of Novel High-Frequency DNA Methylation Changes in Breast Cancer. PLoS ONE, 2007, 2, e1314.	1.1	90
103	Comprehensive DNA methylation profiling in a human cancer genome identifies novel epigenetic targets. Carcinogenesis, 2006, 27, 2409-2423.	1.3	106
104	Spectrum of CHD7 Mutations in 110 Individuals with CHARGE Syndrome and Genotype-Phenotype Correlation. American Journal of Human Genetics, 2006, 78, 303-314.	2.6	352
105	Academic Disqualification and Persistence to Graduation by Financial Aid Category and Academic Ability. The Journal of College Student Retention: Researchory and Practice, 2006, 8, 185-198.	0.9	6
106	Resources for Genetic and Genomic Studies of Xenopus. Methods in Molecular Biology, 2006, 322, 1-16.	0.4	11
107	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. Nature, 2005, 434, 724-731.	13.7	85
108	Lineage-Specific Expansions of Retroviral Insertions within the Genomes of African Great Apes but Not Humans and Orangutans. PLoS Biology, 2005, 3, e110.	2.6	84

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109	Punctuated duplication seeding events during the evolution of human chromosome 2p11. Genome Research, 2005, 15, 914-927.	2.4	32
110	Haplotype Structure of the Mouse Genome. , 2005, , 71-83.		6
111	Large-scale RT-PCR recovery of full-length cDNA clones. BioTechniques, 2004, 36, 690-700.	0.8	11
112	In Silico Genetics: Identification of a Functional Element Regulating H2-EÂ Gene Expression. Science, 2004, 306, 690-695.	6.0	109
113	Fosmid-Based Physical Mapping of the Histoplasma capsulatum Genome. Genome Research, 2004, 14, 1603-1609.	2.4	23
114	Integrated and Sequence-Ordered BAC- and YAC-Based Physical Maps for the Rat Genome. Genome Research, 2004, 14, 766-779.	2.4	44
115	The Status, Quality, and Expansion of the NIH Full-Length cDNA Project: The Mammalian Gene Collection (MGC). Genome Research, 2004, 14, 2121-2127.	2.4	486
116	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	13.7	1,943
117	A physical map of the chicken genome. Nature, 2004, 432, 761-764.	13.7	200
118	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. Nature, 2004, 432, 695-716.	13.7	2,421
119	Levodopa-responsive aromaticL-amino acid decarboxylase deficiency. Annals of Neurology, 2004, 55, 435-438.	2.8	52
120	The DNA sequence and analysis of human chromosome 14. Nature, 2003, 421, 601-607.	13.7	108
121	The male-specific region of the human Y chromosome is a mosaic of discrete sequence classes. Nature, 2003, 423, 825-837.	13.7	1,887
122	The DNA sequence of human chromosome 7. Nature, 2003, 424, 157-164.	13.7	236
123	Software for Automated Analysis of DNA Fingerprinting Gels. Genome Research, 2003, 13, 940-953.	2.4	35
124	A defect in a novel ADAMTS family member is the cause of the belted white-spotting mutation. Development (Cambridge), 2003, 130, 4665-4672.	1.2	80
125	Using a Pericentromeric Interspersed Repeat to Recapitulate the Phylogeny and Expansion of Human Centromeric Segmental Duplications. Molecular Biology and Evolution, 2003, 20, 1463-1479.	3.5	36
126	What is Finished, and Why Does it Matter. Genome Research, 2002, 12, 669-671.	2.4	57

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127	A physical map of the mouse genome. Nature, 2002, 418, 743-750.	13.7	316
128	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	13.7	6,319
129	A physical map of the human genome. Nature, 2001, 409, 934-941.	13.7	865
130	Progress in sequencing the mouse genome. Genesis, 2001, 31, 137-141.	0.8	18
131	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	13.7	21,074
132	A map of human genome sequence variation containing 1.42 million single nucleotide polymorphisms. Nature, 2001, 409, 928-933.	13.7	2,794
133	A physical map of the human Y chromosome. Nature, 2001, 409, 943-945.	13.7	239
134	A high-resolution map of human chromosome 12. Nature, 2001, 409, 945-946.	13.7	29
135	Forum for the genomic onslaught. Nature, 2001, 413, 676-677.	13.7	0
136	The LN54 Radiation Hybrid Map of Zebrafish Expressed Sequences. Genome Research, 2001, 11, 2127-2132.	2.4	65
137	The Syntenic Relationship of the Zebrafish and Human Genomes. Genome Research, 2000, 10, 1351-1358.	2.4	535
138	Molecular refinement of the 1p36 deletion syndrome reveals size diversity and a preponderance of maternally derived deletions. Human Molecular Genetics, 1999, 8, 313-321.	1.4	89
139	Radiation hybrid mapping of the zebrafish genome. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 9745-9750.	3.3	282
140	A map for sequence analysis of the Arabidopsis thaliana genome. Nature Genetics, 1999, 22, 265-270.	9.4	134
141	Promoter analysis of the human centromeric and telomeric survival motor neuron genes (SMNC and) Tj ETQq1 1 0.784314 rgBT /Ove	2.4	77
142	A single nucleotide difference that alters splicing patterns distinguishes the SMA gene SMN1 from the copy gene SMN2. Human Molecular Genetics, 1999, 8, 1177-1183.	1.4	806
143	Screening Largeâ€Insert Libraries by Hybridization. Current Protocols in Human Genetics, 1999, 21, 5.6.1.	3.5	12
144	The CMT2D Locus: Refined Genetic Position and Construction of a Bacterial Clone-Based Physical Map. Genome Research, 1999, 9, 568-574.	2.4	18

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145	Molecular cytogenetic delineation of the critical deleted region in the 5qâ˜ syndrome. , 1998, 22, 251-256.		70
146	Molecular Cloning and Mapping of Human Semaphorin F from the Cri-du-chat Candidate Interval. Biochemical and Biophysical Research Communications, 1998, 242, 685-691.	1.0	47
147	High Throughput Fingerprint Analysis of Large-Insertâ€‰Clones. Genome Research, 1997, 7, 1072-1084.	2.4	405
148	A Radiation Hybrid Map of Human Chromosome 5 with Integration of Cytogenetic, Genetic, and Transcriptâ€‰Maps. Genome Research, 1997, 7, 897-909.	2.4	11
149	Sequence Readyâ€”or Not?. Genome Research, 1997, 7, 1111-1113.	2.4	11
150	High Resolution Mapping of the Renal Sodium-Phosphate Cotransporter Gene(NPT2) Confirms Its Localization to Human Chromosome 5q35. Pediatric Research, 1997, 41, 632-634.	1.1	9
151	The Generation and Regional Localization of 303 New Chromosome 5 Sequence-Tagged Sites. Genomics, 1996, 32, 91-96.	1.3	11
152	Regional Assignment and Tissue Expression of Twenty-Three Expressed Sequence Tags (ESTs) from Human Chromosome 5. Genomics, 1996, 33, 128-130.	1.3	7
153	Characterization of Î´-Sarcoglycan, a Novel Component of the Oligomeric Sarcoglycan Complex Involved in Limb-Girdle Muscular Dystrophy. Journal of Biological Chemistry, 1996, 271, 32321-32329.	1.6	87
154	Molecular cloning of the microfibrillar protein MFAP3 and assignment of the gene to human chromosome 5q32â€“q33.2. Genomics, 1995, 26, 47-54.	1.3	49
155	Mapping the human corticotropin releasing hormone binding protein gene (CRHBP) to the long arm of chromosome 5 (5q11.2â€“q13.3). Genomics, 1995, 25, 325-327.	1.3	12
156	The Human and Mouse Receptors for Hyaluronan-Mediated Motility, RHAMM, Genes (HMMR) Map to Human Chromosome 5q33.2â€“qter and Mouse Chromosome 11. Genomics, 1995, 30, 115-117.	1.3	22
157	Genes encoding adrenergic receptors are not clustered on the long arm of human chromosome 5. Cytogenetic and Genome Research, 1994, 67, 69-74.	0.6	4
158	Human aldehyde dehydrogenase: chromosomal assignment of the gene for the isozyme that metabolizes ?-aminobutyraldehyde. Human Genetics, 1994, 93, 211-2.	1.8	2
159	Assignment of the Human Î±-Catenin Gene (CTNNA1) to Chromosome 5q21-q22. Genomics, 1994, 19, 188-190.	1.3	43
160	A Multicopy Dinucleotide Marker That Maps Close to the Spinal Muscular Atrophy Gene. Genomics, 1994, 21, 394-402.	1.3	54
161	Physical and Genetic Mapping of a Human Apical Epithelial Na+/H+ Exchanger (NHE3) Isoform to Chromosome 5p15.3. Genomics, 1993, 15, 668-672.	1.3	38
162	Molecular Cloning of the Human Proto-oncogene Wnt-5A and Mapping of the Gene (WNT5A) to Chromosome 3p14-p21. Genomics, 1993, 18, 249-260.	1.3	77

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163	Dinucleotide repeat polymorphism proximal to the spinal muscular atrophy region at D5S681. Human Molecular Genetics, 1993, 2, 1753-1753.	1.4	8
164	Linkage mapping detects two secondary microdeletions in cell hybrid HHW1064, used to isolate DNA probes from within 5q11.2â†'q13.3. Cytogenetic and Genome Research, 1993, 64, 46-48.	0.6	0
165	High resolution physical map of the region surrounding the spinal muscular atrophy gene. Human Molecular Genetics, 1993, 2, 1169-1176.	1.4	38
166	A contig of non-chimaeric YACs containing the spinal muscular atrophy gene in 5q13. Human Molecular Genetics, 1993, 2, 1161-1167.	1.4	70
167	Somatic cell mapping of the human cyclophilin B gene (PPIB) to chromosome 15. Cytogenetic and Genome Research, 1992, 60, 219-221.	0.6	7
168	Primary structure, chromosomal localization, and functional expression of a voltage-gated sodium channel from human brain.. Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 8220-8224.	3.3	80
169	Mapping of a human brain voltage-gated calcium channel to human chromosome 12p13-pter. Genomics, 1992, 14, 1092-1094.	1.3	11
170	Human dopa decarboxylase: Localization to human chromosome 7p11 and characterization of hepatic cDNAs. Genomics, 1992, 13, 469-471.	1.3	23
171	Mapping of the versican proteoglycan gene (CSPG2) to the long arm of human chromosome 5 (5q12â€“5q14). Genomics, 1992, 14, 845-851.	1.3	60
172	Localization of the D5 dopamine receptor gene to human chromosome 4p15.1â€“p15.3, centromeric to the Huntington's disease locus. Genomics, 1992, 12, 510-516.	1.3	30
173	Genomic organization, nucleotide sequence, and cellular distribution of a Shaw-related potassium channel gene, Kv3.3, and mapping of Kv3.3 and Kv3.4 to human chromosomes 19 and 1. Genomics, 1992, 12, 190-196.	1.3	42
174	Related subunits of NF-ÎºB map to two distinct loci associated with translocations in leukemia, NFKB1 and NFKB2. Genomics, 1992, 13, 287-292.	1.3	50
175	Chromosomal localization of human glutamate receptor genes. Journal of Neuroscience, 1992, 12, 2555-2562.	1.7	43
176	Identification and characterization of the familial adenomatous polyposis coli gene. Cell, 1991, 66, 589-600.	13.5	2,642
177	Mapping of human chromosome 5 microsatellite DNA polymorphisms. Genomics, 1991, 11, 695-700.	1.3	85
178	Identification of deletion mutations and three new genes at the familial polyposis locus. Cell, 1991, 66, 601-613.	13.5	762
179	Bone morphogenetic protein: Chromosomal localization of human genes for BMP1, BMP2A, and BMP3. Genomics, 1991, 9, 283-289.	1.3	77
180	Role of fructose in glycation and cross-linking of proteins. Biochemistry, 1988, 27, 1901-1907.	1.2	303

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181	Evidence for glycation of horse liver alcohol dehydrogenase in vivo. Biochemical and Biophysical Research Communications, 1988, 152, 711-716.	1.0	10
182	Analysis of glycated amino acids by high-performance liquid chromatography of phenylthiocarbamyl derivatives. Analytical Biochemistry, 1987, 164, 547-553.	1.1	19
183	Synthetic routes to N-(1-deoxy-d-fructos-1-yl)amino acids by way of reductive amination of hexos-2-uloses. Carbohydrate Research, 1987, 167, 123-130.	1.1	30
184	Non-enzymic glycation of proteins: analysis of N-(1-deoxyhexitol-1-yl)amino acids by high-performance liquid chromatography. Carbohydrate Research, 1986, 153, 285-293.	1.1	6
185	Quantitative Chromatographic Estimation of Î±-Amino-Acids. Nature, 1948, 161, 763-763.	13.7	66