Mark J Cowley

List of Publications by Year
in descending order

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146 papers	14,794 citations	38742 50 h-index	20358 116 g-index
160 all docs	160 docs citations	160 times ranked	25487 citing authors

#	Article	IF	Citations
1	Whole-genome sequencing facilitates patient-specific quantitative PCR-based minimal residual disease monitoring in acute lymphoblastic leukaemia, neuroblastoma and Ewing sarcoma. British Journal of Cancer, 2022, 126, 482-491.	6.4	7
2	Unscrambling cancer genomes via integrated analysis of structural variation and copy number. Cell Genomics, 2022, 2, 100112.	6.5	34
3	Whole Genome Sequencing, Focused Assays and Functional Studies Increasing Understanding in Cryptic Inherited Retinal Dystrophies. International Journal of Molecular Sciences, 2022, 23, 3905.	4.1	4
4	Decompensation of cardiorespiratory function and emergence of anemia during pregnancy in a case of mitochondrial myopathy, lactic acidosis, and sideroblastic anemia 2 with compound heterozygous <scp>YARS2</scp> pathogenic variants. American Journal of Medical Genetics, Part A, 2022, 188, 2226-2230.	1.2	4
5	In vitro and inâ€‰vivo drug screens of tumor cells identify novel therapies for highâ€risk child cancer. EMBO Molecular Medicine, 2022, 14, e14608.	6.9	12
6	Use of Whole-Genome Sequencing for Mitochondrial Disease Diagnosis. Neurology, 2022, 99, .	1.1	33
7	Measurable residual disease analysis in paediatric acute lymphoblastic leukaemia patients with ABL-class fusions. British Journal of Cancer, 2022, 127, 908-915.	6.4	2
8	Glutamine addiction promotes glucose oxidation in triple-negative breast cancer. Oncogene, 2022, 41, 4066-4078.	5.9	15
9	Targeting DNA Damage Response and Replication Stress in Pancreatic Cancer. Gastroenterology, 2021, 160, 362-377.e13.	1.3	90
10	Fatal Perinatal Mitochondrial Cardiac Failure Caused by Recurrent De Novo Duplications in the ATAD3 Locus. Med, 2021, 2, 49-73.e10.	4.4	33
11	Targeted Therapy of TERT-Rearranged Neuroblastoma with BET Bromodomain Inhibitor and Proteasome Inhibitor Combination Therapy. Clinical Cancer Research, 2021, 27, 1438-1451.	7.0	20
12	Diagnostic Yield of Whole Genome Sequencing After Nondiagnostic Exome Sequencing or Gene Panel in Developmental and Epileptic Encephalopathies. Neurology, 2021, 96, e1770-e1782.	1.1	53
13	ClinSV: clinical grade structural and copy number variant detection from whole genome sequencing data. Genome Medicine, 2021, 13, 32.	8.2	36
14	Efficacy of MEK inhibition in a recurrent malignant peripheral nerve sheath tumor. Npj Precision Oncology, 2021, 5, 9.	5.4	19
15	A G316A Polymorphism in the Ornithine Decarboxylase Gene Promoter Modulates MYCN-Driven Childhood Neuroblastoma. Cancers, 2021, 13, 1807.	3.7	4
16	Application of Genome Sequencing from Blood to Diagnose Mitochondrial Diseases. Genes, 2021, 12, 607.	2.4	8
17	Different types of diseaseâ€causing noncoding variants revealed by genomic and gene expression analyses in families with Xâ€linked intellectual disability. Human Mutation, 2021, 42, 835-847.	2.5	0
18	Genome sequencing in congenital cataracts improves diagnostic yield. Human Mutation, 2021, 42, 1173-1183.	2.5	10

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19	Childhood acute myeloid leukemia shows a high level of germline predisposition. Blood, 2021, 138, 2293-2298.	1.4	5
20	Genomic diagnostics in polycystic kidney disease: an assessment of real-world use of whole-genome sequencing. European Journal of Human Genetics, 2021, 29, 760-770.	2.8	20
21	Precision Oncology in Surgery. Annals of Surgery, 2020, 272, 366-376.	4.2	48
22	Whole genome, transcriptome and methylome profiling enhances actionable target discovery in high-risk pediatric cancer. Nature Medicine, 2020, 26, 1742-1753.	30.7	185
23	Recurrent SPECC1Lâ€“NTRK fusions in pediatric sarcoma and brain tumors. Journal of Physical Education and Sports Management, 2020, 6, a005710.	1.2	4
24	Mutations in the exocyst component EXOC2 cause severe defects in human brain development. Journal of Experimental Medicine, 2020, 217, .	8.5	17
25	A Novel Orthotopic Patient-Derived Xenograft Model of Radiation-Induced Glioma Following Medulloblastoma. Cancers, 2020, 12, 2937.	3.7	6
26	RLIM Is a Candidate Dosage-Sensitive Gene for Individuals with Varying Duplications of Xq13, Intellectual Disability, and Distinct Facial Features. American Journal of Human Genetics, 2020, 107, 1157-1169.	6.2	6
27	The diagnostic utility of genome sequencing in a pediatric cohort with suspected mitochondrial disease. Genetics in Medicine, 2020, 22, 1254-1261.	2.4	59
28	HNF4A and GATA6 Loss Reveals Therapeutically Actionable Subtypes in Pancreatic Cancer. Cell Reports, 2020, 31, 107625.	6.4	78
29	Molecular patterns in salivary duct carcinoma identify prognostic subgroups. Modern Pathology, 2020, 33, 1896-1909.	5.5	14
30	Proteogenomic analysis of Inhibitor of Differentiation 4 (ID4) in basal-like breast cancer. Breast Cancer Research, 2020, 22, 63.	5.0	8
31	MTOR signaling orchestrates stress-induced mutagenesis, facilitating adaptive evolution in cancer. Science, 2020, 368, 1127-1131.	12.6	83
32	Revealing hidden genetic diagnoses in the ocular anterior segment disorders. Genetics in Medicine, 2020, 22, 1623-1632.	2.4	31
33	Expansion of the phenotypic spectrum of de novo missense variants in kinesin family member 1A () Tj ETQq1 1 0.784314 rgBT /Overlock	2.5	16
34	The Medical Genome Reference Bank contains whole genome and phenotype data of 2570 healthy elderly. Nature Communications, 2020, 11, 435.	12.8	47
35	Infant High-Grade Gliomas Comprise Multiple Subgroups Characterized by Novel Targetable Gene Fusions and Favorable Outcomes. Cancer Discovery, 2020, 10, 942-963.	9.4	157
36	Beyond the panel: preconception screening in consanguineous couples using the TruSight One â€œclinical exomeâ€• Genetics in Medicine, 2019, 21, 608-612.	2.4	20

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37	Seave: a comprehensive web platform for storing and interrogating human genomic variation. Bioinformatics, 2019, 35, 122-125.	4.1	26
38	Genome sequencing as a first-line genetic test in familial dilated cardiomyopathy. Genetics in Medicine, 2019, 21, 650-662.	2.4	52
39	High Degree of Genetic Heterogeneity for Hereditary Cerebellar Ataxias in Australia. Cerebellum, 2019, 18, 137-146.	2.5	21
40	Whole genome sequencing for the genetic diagnosis of heterogenous dystonia phenotypes. Parkinsonism and Related Disorders, 2019, 69, 111-118.	2.2	44
41	Biparental inheritance of mitochondrial DNA in humans is not a common phenomenon. Genetics in Medicine, 2019, 21, 2823-2826.	2.4	44
42	Pathogenic variants in PLOD3 result in a Stickler syndrome-like connective tissue disorder with vascular complications. Journal of Medical Genetics, 2019, 56, 629-638.	3.2	23
43	Increased Diagnostic Yield of Spastic Paraplegia with or Without Cerebellar Ataxia Through Whole-Genome Sequencing. Cerebellum, 2019, 18, 781-790.	2.5	28
44	Next-Generation Sequencing and Emerging Technologies. Seminars in Thrombosis and Hemostasis, 2019, 45, 661-673.	2.7	168
45	Mutational Patterns in Metastatic Cutaneous Squamous Cell Carcinoma. Journal of Investigative Dermatology, 2019, 139, 1449-1458.e1.	0.7	36
46	Genomic stratification and liquid biopsy in a rare adrenocortical carcinoma (ACC) case, with dual lung metastases. Journal of Physical Education and Sports Management, 2019, 5, a003764.	1.2	7
47	De Novo Variants Disrupting the HX Repeat Motif of ATN1 Cause a Recognizable Non-Progressive Neurocognitive Syndrome. American Journal of Human Genetics, 2019, 104, 542-552.	6.2	19
48	Development and validation of a targeted gene sequencing panel for application to disparate cancers. Scientific Reports, 2019, 9, 17052.	3.3	18
49	Clinical Spectrum and Functional Consequences Associated with Bi-Allelic Pathogenic PNPT1 Variants. Journal of Clinical Medicine, 2019, 8, 2020.	2.4	16
50	Denisovan, modern human and mouse TNFAIP3 alleles tune A20 phosphorylation and immunity. Nature Immunology, 2019, 20, 1299-1310.	14.5	53
51	Cryptic intronic NBAS variant reveals the genetic basis of recurrent liver failure in a child. Molecular Genetics and Metabolism, 2019, 126, 77-82.	1.1	11
52	Reanalysis and optimisation of bioinformatic pipelines is critical for mutation detection. Human Mutation, 2019, 40, 374-379.	2.5	7
53	Deep multi-region whole-genome sequencing reveals heterogeneity and gene-by-environment interactions in treatment-naive, metastatic lung cancer. Oncogene, 2019, 38, 1661-1675.	5.9	26
54	Population data improves variant interpretation in autosomal dominant polycystic kidney disease. Genetics in Medicine, 2019, 21, 1425-1434.	2.4	11

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55	Response to Brodehl et al.. Genetics in Medicine, 2019, 21, 1248-1249.	2.4	0
56	The Cancer Molecular Screening and Therapeutics Program (MoST): Actionable mutation frequencies in a population with rare and less common cancers.. Journal of Clinical Oncology, 2019, 37, 3136-3136.	1.6	1
57	A Mild PUM1 Mutation Is Associated with Adult-Onset Ataxia, whereas Haploinsufficiency Causes Developmental Delay and Seizures. Cell, 2018, 172, 924-936.e11.	28.9	103
58	Reversible Suppression of Lymphoproliferation and Thrombocytopenia with Rapamycin in a Patient with Common Variable Immunodeficiency. Journal of Clinical Immunology, 2018, 38, 159-162.	3.8	3
59	Integrating exome sequencing into a diagnostic pathway for epileptic encephalopathy: Evidence of clinical utility and cost effectiveness. Molecular Genetics & Genomic Medicine, 2018, 6, 186-199.	1.2	83
60	Whole-exome sequencing reanalysis at 12 months boosts diagnosis and is cost-effective when applied early in Mendelian disorders. Genetics in Medicine, 2018, 20, 1564-1574.	2.4	132
61	Tailored first-line and second-line CDK4-targeting treatment combinations in mouse models of pancreatic cancer. Gut, 2018, 67, 2142-2155.	12.1	100
62	Analysis of clinically relevant somatic mutations in high-risk head and neck cutaneous squamous cell carcinoma. Modern Pathology, 2018, 31, 275-287.	5.5	37
63	Integration of genomics, high throughput drug screening, and personalized xenograft models as a novel precision medicine paradigm for high risk pediatric cancer. Cancer Biology and Therapy, 2018, 19, 1078-1087.	3.4	18
64	Oral malignant gastrointestinal neuroectodermal tumour with junctional component mimicking mucosal melanoma. Pathology, 2018, 50, 648-653.	0.6	8
65	Brief Report: Potent clinical and radiological response to larotrectinib in TRK fusion-driven high-grade glioma. British Journal of Cancer, 2018, 119, 693-696.	6.4	90
66	Mitochondrial CoQ deficiency is a common driver of mitochondrial oxidants and insulin resistance. ELife, 2018, 7, .	6.0	91
67	Whole Genome Sequencing Improves Outcomes of Genetic Testing in Patients With Hypertrophic Cardiomyopathy. Journal of the American College of Cardiology, 2018, 72, 419-429.	2.8	138
68	Whole genome sequencing provides better diagnostic yield and future value than whole exome sequencing. Medical Journal of Australia, 2018, 209, 197-199.	1.7	48
69	Expanding the spectrum of PEX16 mutations and novel insights into disease mechanisms. Molecular Genetics and Metabolism Reports, 2018, 16, 46-51.	1.1	21
70	Germline variants in familial pituitary tumour syndrome genes are common in young patients and families with additional endocrine tumours. European Journal of Endocrinology, 2017, 176, 635-644.	3.7	33
71	Whole-genome landscape of pancreatic neuroendocrine tumours. Nature, 2017, 543, 65-71.	27.8	716
72	Unique presentation of cutis laxa with Leighâ€like syndrome due to ECHS1 deficiency. Journal of Inherited Metabolic Disease, 2017, 40, 745-747.	3.6	25

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73	Mitochondrial mutations and metabolic adaptation in pancreatic cancer. Cancer & Metabolism, 2017, 5, 2.	5.0	51
74	Evaluation of Streck BCT and PAXgene Stabilised Blood Collection Tubes for Cell-Free Circulating DNA Studies in Plasma. Molecular Diagnosis and Therapy, 2017, 21, 563-570.	3.8	58
75	Cancer-associated noncoding mutations affect RNA G-quadruplex-mediated regulation of gene expression. Scientific Reports, 2017, 7, 708.	3.3	37
76	SerpinB2 regulates stromal remodelling and local invasion in pancreatic cancer. Oncogene, 2017, 36, 4288-4298.	5.9	77
77	Gonadal mosaicism of a novel IQSEC2 variant causing female limited intellectual disability and epilepsy. European Journal of Human Genetics, 2017, 25, 763-767.	2.8	14
78	A SLC39A8 variant causes manganese deficiency, and glycosylation and mitochondrial disorders. Journal of Inherited Metabolic Disease, 2017, 40, 261-269.	3.6	101
79	A De Novo Mutation in the Sodium-Activated Potassium Channel KCNT2 Alters Ion Selectivity and Causes Epileptic Encephalopathy. Cell Reports, 2017, 21, 926-933.	6.4	40
80	A Recurrent De Novo Nonsense Variant in ZSWIM6 Results in Severe Intellectual Disability without Frontonasal or Limb Malformations. American Journal of Human Genetics, 2017, 101, 995-1005.	6.2	23
81	Improved Diagnosis and Care for Rare Diseases through Implementation of Precision Public Health Framework. Advances in Experimental Medicine and Biology, 2017, 1031, 55-94.	1.6	20
82	EPG5-Related Vici Syndrome: A Primary Defect of Autophagic Regulation with an Emerging Phenotype Overlapping with Mitochondrial Disorders. JIMD Reports, 2017, 42, 19-29.	1.5	7
83	Hypermutation In Pancreatic Cancer. Gastroenterology, 2017, 152, 68-74.e2.	1.3	174
84	Serum microRNA expression during neoadjuvant chemoradiation for rectal cancer.. Journal of Clinical Oncology, 2017, 35, e15081-e15081.	1.6	3
85	Somatic mutations in salivary duct carcinoma and potential therapeutic targets. Oncotarget, 2017, 8, 75893-75903.	1.8	22
86	The Molecular Screening and Therapeutics (MoST) Program: A precision medicine framework for biomarker-driven signal-seeking clinical studies for rare cancers.. Journal of Clinical Oncology, 2017, 35, TPS2621-TPS2621.	1.6	0
87	Whole-genome sequencing overcomes pseudogene homology to diagnose autosomal dominant polycystic kidney disease. European Journal of Human Genetics, 2016, 24, 1584-1590.	2.8	63
88	Defining the genetic basis of early onset hereditary spastic paraplegia using whole genome sequencing. Neurogenetics, 2016, 17, 265-270.	1.4	32
89	Mutation allele burden remains unchanged in chronic myelomonocytic leukaemia responding to hypomethylating agents. Nature Communications, 2016, 7, 10767.	12.8	177
90	MECR Mutations Cause Childhood-Onset Dystonia and Optic Atrophy, a Mitochondrial Fatty Acid Synthesis Disorder. American Journal of Human Genetics, 2016, 99, 1229-1244.	6.2	91

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91	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. Cell Reports, 2016, 14, 907-919.	6.4	107
92	Genomic analyses identify molecular subtypes of pancreatic cancer. Nature, 2016, 531, 47-52.	27.8	2,700
93	JRK is a positive regulator of Î²-catenin transcriptional activity commonly overexpressed in colon, breast and ovarian cancer. Oncogene, 2016, 35, 2834-2841.	5.9	20
94	Abstract 1942: Change in serum microRNA expression during neoadjuvant chemoradiation for rectal cancer. , 2016, , .		1
95	MicroRNA profiling of the pubertal mouse mammary gland identifies miR-184 as a candidate breast tumour suppressor gene. Breast Cancer Research, 2015, 17, 83.	5.0	44
96	Whole genomes redefine the mutational landscape of pancreatic cancer. Nature, 2015, 518, 495-501.	27.8	2,132
97	The pseudokinase SgK223 promotes invasion of pancreatic ductal epithelial cells through JAK1/Stat3 signaling. Molecular Cancer, 2015, 14, 139.	19.2	44
98	Asparagine Synthetase Deficiency causes reduced proliferation of cells under conditions of limited asparagine. Molecular Genetics and Metabolism, 2015, 116, 178-186.	1.1	47
99	SOX9 regulates ERBB signalling in pancreatic cancer development. Gut, 2015, 64, 1790-1799.	12.1	71
100	Clinical and pathologic features of familial pancreatic cancer. Cancer, 2014, 120, 3669-3675.	4.1	53
101	Genomeâ€wide DNA methylation patterns in pancreatic ductal adenocarcinoma reveal epigenetic deregulation of SLITâ€ROBO, ITGA2 and MET signaling. International Journal of Cancer, 2014, 135, 1110-1118.	5.1	192
102	Cell and Molecular Determinants of In Vivo Efficacy of the BH3 Mimetic ABT-263 against Pediatric Acute Lymphoblastic Leukemia Xenografts. Clinical Cancer Research, 2014, 20, 4520-4531.	7.0	67
103	c-Myc and Her2 cooperate to drive a stem-like phenotype with poor prognosis in breast cancer. Oncogene, 2014, 33, 3992-4002.	5.9	88
104	Abstract LB-73: SOX9 regulates EGFR/ERBB signaling in pancreatic cancer. , 2014, , .		0
105	Understanding pancreatic cancer genomes. Journal of Hepato-Biliary-Pancreatic Sciences, 2013, 20, 549-556.	2.6	31
106	Clinical and molecular characterization of HER2 amplified-pancreatic cancer. Genome Medicine, 2013, 5, 78.	8.2	97
107	Histomolecular Phenotypes and Outcome in Adenocarcinoma of the Ampulla of Vater. Journal of Clinical Oncology, 2013, 31, 1348-1356.	1.6	142
108	Neuropilin-2 Promotes Extravasation and Metastasis by Interacting with Endothelial Î±5 Integrin. Cancer Research, 2013, 73, 4579-4590.	0.9	97

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109	BCL-2 Hypermethylation Is a Potential Biomarker of Sensitivity to Antimitotic Chemotherapy in Endocrine-Resistant Breast Cancer. Molecular Cancer Therapeutics, 2013, 12, 1874-1885.	4.1	45
110	Sirtuin-1 Regulates Acinar-to-Ductal Metaplasia and Supports Cancer Cell Viability in Pancreatic Cancer. Cancer Research, 2013, 73, 2357-2367.	0.9	59
111	Extracellular matrix composition significantly influences pancreatic stellate cell gene expression pattern: role of transgelin in PSC function. American Journal of Physiology - Renal Physiology, 2013, 305, G408-G417.	3.4	25
112	Maternal obesity and diabetes induces latent metabolic defects and widespread epigenetic changes in isogenic mice. Epigenetics, 2013, 8, 602-611.	2.7	75
113	Somatic Point Mutation Calling in Low Cellularity Tumors. PLoS ONE, 2013, 8, e74380.	2.5	67
114	A Preexistent Hypoxic Gene Signature Predicts Impaired Islet Graft Function and Glucose Homeostasis. Cell Transplantation, 2013, 22, 2147-2159.	2.5	47
115	PINA v2.0: mining interactome modules. Nucleic Acids Research, 2012, 40, D862-D865.	14.5	321
116	ELF5 Suppresses Estrogen Sensitivity and Underpins the Acquisition of Antiestrogen Resistance in Luminal Breast Cancer. PLoS Biology, 2012, 10, e1001461.	5.6	74
117	The deubiquitinase USP9X suppresses pancreatic ductal adenocarcinoma. Nature, 2012, 486, 266-270.	27.8	297
118	Differential Regulation of the Let-7 Family of MicroRNAs in CD4+ T Cells Alters IL-10 Expression. Journal of Immunology, 2012, 188, 6238-6246.	0.8	152
119	Human Islets Express a Marked Proinflammatory Molecular Signature Prior to Transplantation. Cell Transplantation, 2012, 21, 2063-2078.	2.5	85
120	Expression of Pro- and Antiapoptotic Molecules of the Bcl-2 Family in Human Islets Postisolation. Cell Transplantation, 2012, 21, 49-60.	2.5	22
121	A Pre-Existent Hypoxic Gene Signature Predicts Impaired Islet Graft Function and Glucose Homeostasis. Transplantation, 2012, 94, 710.	1.0	0
122	Inheritance of coronary artery disease in men: an analysis of the role of the Y chromosome. Lancet, The, 2012, 379, 915-922.	13.7	179
123	Influence of atrial fibrillation on microRNA expression profiles in left and right atria from patients with valvular heart disease. Physiological Genomics, 2012, 44, 211-219.	2.3	83
124	RON is not a prognostic marker for resectable pancreatic cancer. BMC Cancer, 2012, 12, 395.	2.6	17
125	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. Nature, 2012, 491, 399-405.	27.8	1,741
126	qpure: A Tool to Estimate Tumor Cellularity from Genome-Wide Single-Nucleotide Polymorphism Profiles. PLoS ONE, 2012, 7, e45835.	2.5	92

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127	Proteomic comparison of colorectal tumours and non-neoplastic mucosa from paired patient samples using iTRAQ mass spectrometry. Molecular BioSystems, 2011, 7, 2997.	2.9	31
128	An early inflammatory gene profile in visceral adipose tissue in children. Pediatric Obesity, 2011, 6, e360-e363.	3.2	39
129	Evaluation of the NOD/SCID xenograft model for glucocorticoid-regulated gene expression in childhood B-cell precursor acute lymphoblastic leukemia. BMC Genomics, 2011, 12, 565.	2.8	27
130	Identification of Novel GH-Regulated Pathway of Lipid Metabolism in Adipose Tissue: A Gene Expression Study in Hypopituitary Men. Journal of Clinical Endocrinology and Metabolism, 2011, 96, E1188-E1196.	3.6	31
131	Impaired B Cell Development in the Absence of KrÃ¼ppel-like Factor 3. Journal of Immunology, 2011, 187, 5032-5042.	0.8	41
132	A Sustained Dietary Change Increases Epigenetic Variation in Isogenic Mice. PLoS Genetics, 2011, 7, e1001380.	3.5	65
133	Clonal expansions of cytotoxic T cells exist in the blood of patients with WaldenstrÃ¶m macroglobulinemia but exhibit anergic properties and are eliminated by nucleoside analogue therapy. Blood, 2010, 115, 3580-3588.	1.4	30
134	Consolidation of the cancer genome into domains of repressive chromatin by long-range epigenetic silencing (LRES) reduces transcriptional plasticity. Nature Cell Biology, 2010, 12, 235-246.	10.3	178
135	Cold adaptation in the marine bacterium, Sphingopyxis alaskensis, assessed using quantitative proteomics. Environmental Microbiology, 2010, 12, 2658-2676.	3.8	130
136	The Antiproliferative Effects of Progestins in T47D Breast Cancer Cells Are Tempered by Progestin Induction of the ETS Transcription Factor Elf5. Molecular Endocrinology, 2010, 24, 1380-1392.	3.7	16
137	Normalization and Statistical Analysis of Quantitative Proteomics Data Generated by Metabolic Labeling. Molecular and Cellular Proteomics, 2009, 8, 2227-2242.	3.8	111
138	Detection of Growth Hormone Doping by Gene Expression Profiling of Peripheral Blood. Journal of Clinical Endocrinology and Metabolism, 2009, 94, 4703-4709.	3.6	29
139	Intra- and inter-individual genetic differences in gene expression. Mammalian Genome, 2009, 20, 281-295.	2.2	21
140	Clonal Expansions of Cytotoxic T Cells in the Blood of Patients with Waldenstrom's Macroglobulinaemia Are Anergic and Disappear After Nucleoside Analogue Therapy.. Blood, 2009, 114, 1820-1820.	1.4	3
141	Gene-expression profiling of Gram-positive and Gram-negative sepsis in critically ill patients*. Critical Care Medicine, 2008, 36, 1125-1128.	0.9	110
142	Intra- and inter-individual genetic differences in gene expression. Nature Precedings, 2008, , .	0.1	2
143	The influence of genetic variation on gene expression. Genome Research, 2007, 17, 1707-1716.	5.5	91
144	Hierarchical Bayes variable selection and microarray experiments. Journal of Multivariate Analysis, 2007, 98, 852-872.	1.0	4

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145	Normalization procedures and detection of linkage signal in genetical-genomics experiments. Nature Genetics, 2006, 38, 855-856.	21.4	28
146	Genetic dissection of gene regulation in multiple mouse tissues. Mammalian Genome, 2006, 17, 490-495.	2.2	13