Mark J Cowley

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6950377/publications.pdf

Version: 2024-02-01

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	Genomic analyses identify molecular subtypes of pancreatic cancer. Nature, 2016, 531, 47-52.	27.8	2,700
2	Whole genomes redefine the mutational landscape of pancreatic cancer. Nature, 2015, 518, 495-501.	27.8	2,132
3	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. Nature, 2012, 491, 399-405.	27.8	1,741
4	Whole-genome landscape of pancreatic neuroendocrine tumours. Nature, 2017, 543, 65-71.	27.8	716
5	PINA v2.0: mining interactome modules. Nucleic Acids Research, 2012, 40, D862-D865.	14.5	321
6	The deubiquitinase USP9X suppresses pancreatic ductal adenocarcinoma. Nature, 2012, 486, 266-270.	27.8	297
7	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
8	Whole genome, transcriptome and methylome profiling enhances actionable target discovery in high-risk pediatric cancer. Nature Medicine, 2020, 26, 1742-1753.	30.7	185
9	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
10	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
11	Mutation allele burden remains unchanged in chronic myelomonocytic leukaemia responding to hypomethylating agents. Nature Communications, 2016, 7, 10767.	12.8	177
12	Hypermutation In Pancreatic Cancer. Gastroenterology, 2017, 152, 68-74.e2.	1.3	174
13	Next-Generation Sequencing and Emerging Technologies. Seminars in Thrombosis and Hemostasis, 2019, 45, 661-673.	2.7	168
14	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
15	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
16	Histomolecular Phenotypes and Outcome in Adenocarcinoma of the Ampulla of Vater. Journal of Clinical Oncology, 2013, 31, 1348-1356.	1.6	142
17	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
18	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

#	Article	IF	Citations
19	Cold adaptation in the marine bacterium, Sphingopyxis alaskensis, assessed using quantitative proteomics. Environmental Microbiology, 2010, 12, 2658-2676.	3.8	130
20	Normalization and Statistical Analysis of Quantitative Proteomics Data Generated by Metabolic Labeling. Molecular and Cellular Proteomics, 2009, 8, 2227-2242.	3.8	111
21	Gene-expression profiling of Gram-positive and Gram-negative sepsis in critically ill patients*. Critical Care Medicine, 2008, 36, 1125-1128.	0.9	110
22	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. Cell Reports, 2016, 14, 907-919.	6.4	107
23	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
24	A SLC39A8 variant causes manganese deficiency, and glycosylation and mitochondrial disorders. Journal of Inherited Metabolic Disease, 2017, 40, 261-269.	3.6	101
25	Tailored first-line and second-line CDK4-targeting treatment combinations in mouse models of pancreatic cancer. Gut, 2018, 67, 2142-2155.	12.1	100
26	Clinical and molecular characterization of HER2 amplified-pancreatic cancer. Genome Medicine, 2013, 5, 78.	8.2	97
27	Neuropilin-2 Promotes Extravasation and Metastasis by Interacting with Endothelial Î±5 Integrin. Cancer Research, 2013, 73, 4579-4590.	0.9	97
28	qpure: A Tool to Estimate Tumor Cellularity from Genome-Wide Single-Nucleotide Polymorphism Profiles. PLoS ONE, 2012, 7, e45835.	2.5	92
29	The influence of genetic variation on gene expression. Genome Research, 2007, 17, 1707-1716.	5.5	91
30	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
31	Mitochondrial CoQ deficiency is a common driver of mitochondrial oxidants and insulin resistance. ELife, 2018, 7, .	6.0	91
32	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
33	Targeting DNA Damage Response and Replication Stress in Pancreatic Cancer. Gastroenterology, 2021, 160, 362-377.e13.	1.3	90
34	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
35	Human Islets Express a Marked Proinflammatory Molecular Signature Prior to Transplantation. Cell Transplantation, 2012, 21, 2063-2078.	2.5	85
36	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

#	Article	IF	Citations
37	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
38	MTOR signaling orchestrates stress-induced mutagenesis, facilitating adaptive evolution in cancer. Science, 2020, 368, 1127-1131.	12.6	83
39	HNF4A and GATA6 Loss Reveals Therapeutically Actionable Subtypes in Pancreatic Cancer. Cell Reports, 2020, 31, 107625.	6.4	78
40	SerpinB2 regulates stromal remodelling and local invasion in pancreatic cancer. Oncogene, 2017, 36, 4288-4298.	5.9	77
41	Maternal obesity and diabetes induces latent metabolic defects and widespread epigenetic changes in isogenic mice. Epigenetics, 2013, 8, 602-611.	2.7	75
42	ELF5 Suppresses Estrogen Sensitivity and Underpins the Acquisition of Antiestrogen Resistance in Luminal Breast Cancer. PLoS Biology, 2012, 10, e1001461.	5.6	74
43	SOX9 regulates ERBB signalling in pancreatic cancer development. Gut, 2015, 64, 1790-1799.	12.1	71
44	Somatic Point Mutation Calling in Low Cellularity Tumors. PLoS ONE, 2013, 8, e74380.	2.5	67
45	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
46	A Sustained Dietary Change Increases Epigenetic Variation in Isogenic Mice. PLoS Genetics, 2011, 7, e1001380.	3.5	65
47	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
48	Sirtuin-1 Regulates Acinar-to-Ductal Metaplasia and Supports Cancer Cell Viability in Pancreatic Cancer. Cancer Research, 2013, 73, 2357-2367.	0.9	59
49	The diagnostic utility of genome sequencing in a pediatric cohort with suspected mitochondrial disease. Genetics in Medicine, 2020, 22, 1254-1261.	2.4	59
50	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
51	Clinical and pathologic features of familial pancreatic cancer. Cancer, 2014, 120, 3669-3675.	4.1	53
52	Denisovan, modern human and mouse TNFAIP3 alleles tune A20 phosphorylation and immunity. Nature Immunology, 2019, 20, 1299-1310.	14.5	53
53	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
54	Genome sequencing as a first-line genetic test in familial dilated cardiomyopathy. Genetics in Medicine, 2019, 21, 650-662.	2.4	52

#	Article	IF	Citations
55	Mitochondrial mutations and metabolic adaptation in pancreatic cancer. Cancer & Metabolism, 2017, 5, 2.	5.0	51
56	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
57	Precision Oncology in Surgery. Annals of Surgery, 2020, 272, 366-376.	4.2	48
58	A Preexistent Hypoxic Gene Signature Predicts Impaired Islet Graft Function and Glucose Homeostasis. Cell Transplantation, 2013, 22, 2147-2159.	2.5	47
59	Asparagine Synthetase Deficiency causes reduced proliferation of cells under conditions of limited asparagine. Molecular Genetics and Metabolism, 2015, 116, 178-186.	1.1	47
60	The Medical Genome Reference Bank contains whole genome and phenotype data of 2570 healthy elderly. Nature Communications, 2020, 11, 435.	12.8	47
61	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
62	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
63	The pseudokinase SgK223 promotes invasion of pancreatic ductal epithelial cells through JAK1/Stat3 signaling. Molecular Cancer, 2015, 14, 139.	19.2	44
64	Whole genome sequencing for the genetic diagnosis of heterogenous dystonia phenotypes. Parkinsonism and Related Disorders, 2019, 69, 111-118.	2.2	44
65	Biparental inheritance of mitochondrial DNA in humans is not a common phenomenon. Genetics in Medicine, 2019, 21, 2823-2826.	2.4	44
66	Impaired B Cell Development in the Absence of KrÃ¼ppel-like Factor 3. Journal of Immunology, 2011, 187, 5032-5042.	0.8	41
67	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
68	An early inflammatory gene profile in visceral adipose tissue in children. Pediatric Obesity, 2011, 6, e360-e363.	3.2	39
69	Cancer-associated noncoding mutations affect RNA G-quadruplex-mediated regulation of gene expression. Scientific Reports, 2017, 7, 708.	3.3	37
70	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
71	Mutational Patterns in Metastatic Cutaneous Squamous Cell Carcinoma. Journal of Investigative Dermatology, 2019, 139, 1449-1458.e1.	0.7	36
72	ClinSV: clinical grade structural and copy number variant detection from whole genome sequencing data. Genome Medicine, 2021, 13, 32.	8.2	36

#	Article	IF	Citations
73	Unscrambling cancer genomes via integrated analysis of structural variation and copy number. Cell Genomics, 2022, 2, 100112.	6.5	34
74	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
75	Fatal Perinatal Mitochondrial Cardiac Failure Caused by Recurrent De Novo Duplications in the ATAD3 Locus. Med, 2021, 2, 49-73.e10.	4.4	33
76	Use of Whole-Genome Sequencing for Mitochondrial Disease Diagnosis. Neurology, 2022, 99, .	1.1	33
77	Defining the genetic basis of early onset hereditary spastic paraplegia using whole genome sequencing. Neurogenetics, 2016, 17, 265-270.	1.4	32
78	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
79	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
80	Understanding pancreatic cancer genomes. Journal of Hepato-Biliary-Pancreatic Sciences, 2013, 20, 549-556.	2.6	31
81	Revealing hidden genetic diagnoses in the ocular anterior segment disorders. Genetics in Medicine, 2020, 22, 1623-1632.	2.4	31
82	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
83	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
84	Normalization procedures and detection of linkage signal in genetical-genomics experiments. Nature Genetics, 2006, 38, 855-856.	21.4	28
85	Increased Diagnostic Yield of Spastic Paraplegia with or Without Cerebellar Ataxia Through Whole-Genome Sequencing. Cerebellum, 2019, 18, 781-790.	2.5	28
86	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
87	Seave: a comprehensive web platform for storing and interrogating human genomic variation. Bioinformatics, 2019, 35, 122-125.	4.1	26
88	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
89	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
90	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

#	Article	IF	Citations
91	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
92	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
93	Expression of Pro- and Antiapoptotic Molecules of the Bcl-2 Family in Human Islets Postisolation. Cell Transplantation, 2012, 21, 49-60.	2.5	22
94	Somatic mutations in salivary duct carcinoma and potential therapeutic targets. Oncotarget, 2017, 8, 75893-75903.	1.8	22
95	Intra- and inter-individual genetic differences in gene expression. Mammalian Genome, 2009, 20, 281-295.	2.2	21
96	Expanding the spectrum of PEX16 mutations and novel insights into disease mechanisms. Molecular Genetics and Metabolism Reports, 2018, 16, 46-51.	1.1	21
97	High Degree of Genetic Heterogeneity for Hereditary Cerebellar Ataxias in Australia. Cerebellum, 2019, 18, 137-146.	2.5	21
98	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
99	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
100	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
101	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
102	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
103	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
104	Efficacy of MEK inhibition in a recurrent malignant peripheral nerve sheath tumor. Npj Precision Oncology, 2021, 5, 9.	5.4	19
105	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
106	Development and validation of a targeted gene sequencing panel for application to disparate cancers. Scientific Reports, 2019, 9, 17052.	3.3	18
107	RON is not a prognostic marker for resectable pancreatic cancer. BMC Cancer, 2012, 12, 395.	2.6	17
108	Mutations in the exocyst component EXOC2 cause severe defects in human brain development. Journal of Experimental Medicine, 2020, 217, .	8.5	17

#	Article	IF	Citations
109	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
110	Clinical Spectrum and Functional Consequences Associated with Bi-Allelic Pathogenic PNPT1 Variants. Journal of Clinical Medicine, 2019, 8, 2020.	2.4	16
111	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
112	Glutamine addiction promotes glucose oxidation in triple-negative breast cancer. Oncogene, 2022, 41, 4066-4078.	5.9	15
113	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
114	Molecular patterns in salivary duct carcinoma identify prognostic subgroups. Modern Pathology, 2020, 33, 1896-1909.	5.5	14
115	Genetic dissection of gene regulation in multiple mouse tissues. Mammalian Genome, 2006, 17, 490-495.	2.2	13
116	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
117	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
118	Population data improves variant interpretation in autosomal dominant polycystic kidney disease. Genetics in Medicine, 2019, 21, 1425-1434.	2.4	11
119	Genome sequencing in congenital cataracts improves diagnostic yield. Human Mutation, 2021, 42, 1173-1183.	2.5	10
120	Oral malignant gastrointestinal neuroectodermal tumour with junctional component mimicking mucosal melanoma. Pathology, 2018, 50, 648-653.	0.6	8
121	Proteogenomic analysis of Inhibitor of Differentiation 4 (ID4) in basal-like breast cancer. Breast Cancer Research, 2020, 22, 63.	5.0	8
122	Application of Genome Sequencing from Blood to Diagnose Mitochondrial Diseases. Genes, 2021, 12, 607.	2.4	8
123	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
124	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
125	Reanalysis and optimisation of bioinformatic pipelines is critical for mutation detection. Human Mutation, 2019, 40, 374-379.	2.5	7
126	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

#	Article	IF	Citations
127	A Novel Orthotopic Patient-Derived Xenograft Model of Radiation-Induced Glioma Following Medulloblastoma. Cancers, 2020, 12, 2937.	3.7	6
128	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
129	Childhood acute myeloid leukemia shows a high level of germline predisposition. Blood, 2021, 138, 2293-2298.	1.4	5
130	Hierarchical Bayes variable selection and microarray experiments. Journal of Multivariate Analysis, 2007, 98, 852-872.	1.0	4
131	Recurrent SPECC1Lâ€“NTRK fusions in pediatric sarcoma and brain tumors. Journal of Physical Education and Sports Management, 2020, 6, a005710.	1.2	4
132	A G316A Polymorphism in the Ornithine Decarboxylase Gene Promoter Modulates MYCN-Driven Childhood Neuroblastoma. Cancers, 2021, 13, 1807.	3.7	4
133	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
134	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
135	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
136	Serum microRNA expression during neoadjuvant chemoradiation for rectal cancer.. Journal of Clinical Oncology, 2017, 35, e15081-e15081.	1.6	3
137	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
138	Intra- and inter-individual genetic differences in gene expression. Nature Precedings, 2008, , .	0.1	2
139	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
140	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
141	Abstract 1942: Change in serum microRNA expression during neoadjuvant chemoradiation for rectal cancer. , 2016, , .		1
142	A Pre-Existent Hypoxic Gene Signature Predicts Impaired Islet Graft Function and Glucose Homeostasis. Transplantation, 2012, 94, 710.	1.0	0
143	Response to Brodehl et al.. Genetics in Medicine, 2019, 21, 1248-1249.	2.4	0
144	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

#	Article	IF	Citations
145	Abstract LB-73: SOX9 regulates EGFR/ERBB signaling in pancreatic cancer. , 2014, , .		0
146	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