John B Easton

List of Publications by Year
in descending order

144 papers	19,471 citations	27035 58 h-index	14386 132 g-index
157 all docs	157 docs citations	157 times ranked	28309 citing authors

#	Article	IF	Citations
1	EP300 Selectively Controls the Enhancer Landscape of MYCN-Amplified Neuroblastoma. Cancer Discovery, 2022, 12, 730-751.	7.7	64
2	Blood DNA methylation signatures are associated with social determinants of health among survivors of childhood cancer. Epigenetics, 2022, , 1-15.	1.3	5
3	Integrated Genomic Analysis Identifies UBTF Tandem Duplications as a Recurrent Lesion in Pediatric Acute Myeloid Leukemia. Blood Cancer Discovery, 2022, 3, 194-207.	2.6	38
4	A developmentally prometastatic niche to hepatoblastoma in neonatal liver mediated by the Cxcl1/Cxcr2 axis. Hepatology, 2022, 76, 1275-1290.	3.6	6
5	Genome-wide association studies identify novel genetic loci for epigenetic age acceleration among survivors of childhood cancer. Genome Medicine, 2022, 14, 32.	3.6	12
6	Somatic LINE-1 promoter acquisition drives oncogenic FOXR2 activation in pediatric brain tumor. Acta Neuropathologica, 2022, 143, 605-607.	3.9	4
7	Single-cell analysis reveals the Comma-1D cell line as a unique model for mammary gland development and breast cancer. Journal of Cell Science, 2022, 135, .	1.2	2
8	Cell type identification in spatial transcriptomics data can be improved by leveraging cell-type-informative paired tissue images using a Bayesian probabilistic model. Nucleic Acids Research, 2022, 50, e80-e80.	6.5	6
9	Convergent evolution and multi-wave clonal invasion in H3 K27-altered diffuse midline gliomas treated with a PDGFR inhibitor. Acta Neuropathologica Communications, 2022, 10, .	2.4	3
10	A Novel Locus on 6p21.2 for Cancer Treatmentâ€“Induced Cardiac Dysfunction Among Childhood Cancer Survivors. Journal of the National Cancer Institute, 2022, 114, 1109-1116.	3.0	4
11	Impact of T-cell immunity on chemotherapy response in childhood acute lymphoblastic leukemia. Blood, 2022, 140, 1507-1521.	0.6	2
12	Targeting KDM4 for treating PAX3-FOXO1â€“driven alveolar rhabdomyosarcoma. Science Translational Medicine, 2022, 14, .	5.8	16
13	Epigenetic Age Acceleration and Chronic Health Conditions Among Adult Survivors of Childhood Cancer. Journal of the National Cancer Institute, 2021, 113, 597-605.	3.0	37
14	SequencErr: measuring and suppressing sequencer errors in next-generation sequencing data. Genome Biology, 2021, 22, 37.	3.8	15
15	Network-based systems pharmacology reveals heterogeneity in LCK and BCL2 signaling and therapeutic sensitivity of T-cell acute lymphoblastic leukemia. Nature Cancer, 2021, 2, 284-299.	5.7	70
16	Exploration of Coding and Non-coding Variants in Cancer Using GenomePaint. Cancer Cell, 2021, 39, 83-95.e4.	7.7	18
17	The acquisition of molecular drivers in pediatric therapy-related myeloid neoplasms. Nature Communications, 2021, 12, 985.	5.8	31
18	Integrative network analysis reveals USP7 haploinsufficiency inhibits E-protein activity in pediatric T-lineage acute lymphoblastic leukemia (T-ALL). Scientific Reports, 2021, 11, 5154.	1.6	10

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19	The miR-424(322)/503 gene cluster regulates pro- versus anti-inflammatory skin DC subset differentiation by modulating TGF-Î² signaling. Cell Reports, 2021, 35, 109049.	2.9	4
20	Persistent variations of blood DNA methylation associated with treatment exposures and risk for cardiometabolic outcomes in long-term survivors of childhood cancer in the St. Jude Lifetime Cohort. Genome Medicine, 2021, 13, 53.	3.6	16
21	The Association of Mitochondrial Copy Number With Sarcopenia in Adult Survivors of Childhood Cancer. Journal of the National Cancer Institute, 2021, 113, 1570-1580.	3.0	7
22	Accurate genomic variant detection in single cells with primary template-directed amplification. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	69
23	A polygenic score for acute vaso-occlusive pain in pediatric sickle cell disease. Blood Advances, 2021, 5, 2839-2851.	2.5	14
24	Abstract 685: A social epigenomic investigation of racial disparity in pulmonary impairment among aging survivors of childhood cancer. , 2021, , .		0
25	Abstract 237: Inferring spatial organization of tumor microenvironment from single-cell RNA sequencing data using graph embedding. , 2021, , .		0
26	Abstract 904: Epigenome-wide association study of dyslipidemia in survivors of childhood cancer: A report from the St. Jude lifetime cohort. , 2021, , .		0
27	Polygenic Risk Score Improves Risk Stratification and Prediction of Subsequent Thyroid Cancer after Childhood Cancer. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 2096-2104.	1.1	11
28	Integrative Genomic Analysis of Pediatric Myeloid-Related Acute Leukemias Identifies Novel Subtypes and Prognostic Indicators. Blood Cancer Discovery, 2021, 2, 586-599.	2.6	21
29	In a multi-institutional cohort of myeloid sarcomas, NFE2 mutation prevalence is lower than previously reported. Blood Advances, 2021, 5, 5057-5059.	2.5	2
30	The chemotherapeutic CX-5461 primarily targets TOP2B and exhibits selective activity in high-risk neuroblastoma. Nature Communications, 2021, 12, 6468.	5.8	35
31	The landscape of coding RNA editing events in pediatric cancer. BMC Cancer, 2021, 21, 1233.	1.1	7
32	The Impact of T Cell Immunity on Chemotherapy Response in Childhood Acute Lymphoblastic Leukemia. Blood, 2021, 138, 703-703.	0.6	0
33	Integrated Genomic Analysis Identifies UBTF Tandem Duplications As a Subtype-Defining Lesion in Pediatric Acute Myeloid Leukemia. Blood, 2021, 138, LBA-4-LBA-4.	0.6	0
34	Molecular Mechanism of Telomere Length Dynamics and Its Prognostic Value in Pediatric Cancers. Journal of the National Cancer Institute, 2020, 112, 756-764.	3.0	11
35	RNAIndel: discovering somatic coding indels from tumor RNA-Seq data. Bioinformatics, 2020, 36, 1382-1390.	1.8	12
36	Estimated number of adult survivors of childhood cancer in United States with cancerâ€predisposing germline variants. Pediatric Blood and Cancer, 2020, 67, e28047.	0.8	13

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37	Pan-neuroblastoma analysis reveals age- and signature-associated driver alterations. Nature Communications, 2020, 11, 5183.	5.8	87
38	CICERO: a versatile method for detecting complex and diverse driver fusions using cancer RNA sequencing data. Genome Biology, 2020, 21, 126.	3.8	74
39	Pathogenic Germline Mutations in DNA Repair Genes in Combination With Cancer Treatment Exposures and Risk of Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. Journal of Clinical Oncology, 2020, 38, 2728-2740.	0.8	34
40	Discovery of regulatory noncoding variants in individual cancer genomes by using cis-X. Nature Genetics, 2020, 52, 811-818.	9.4	47
41	MYCN amplification and ATRX mutations are incompatible in neuroblastoma. Nature Communications, 2020, 11, 913.	5.8	66
42	Shortened Leukocyte Telomere Length Associates with an Increased Prevalence of Chronic Health Conditions among Survivors of Childhood Cancer: A Report from the St. Jude Lifetime Cohort. Clinical Cancer Research, 2020, 26, 2362-2371.	3.2	34
43	Mutational Landscape and Patterns of Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. Blood Cancer Discovery, 2020, 1, 96-111.	2.6	93
44	A comparison of methods accounting for batch effects in differential expression analysis of UMI count based single cell RNA sequencing. Computational and Structural Biotechnology Journal, 2020, 18, 861-873.	1.9	28
45	Relapse-Fated Latent Diagnosis Subclones in Acute B Lineage Leukemia Are Drug Tolerant and Possess Distinct Metabolic Programs. Cancer Discovery, 2020, 10, 568-587.	7.7	72
46	Therapy-induced mutations drive the genomic landscape of relapsed acute lymphoblastic leukemia. Blood, 2020, 135, 41-55.	0.6	171
47	Multi-Omic Based Antigen Discovery for the Immunotherapy of Pediatric Acute T Cell Lymphoblastic Leukemia. Blood, 2020, 136, 17-18.	0.6	1
48	Resolving medulloblastoma cellular architecture by single-cell genomics. Nature, 2019, 572, 74-79.	13.7	273
49	Long-read sequencing unveils IGH-DUX4 translocation into the silenced IGH allele in B-cell acute lymphoblastic leukemia. Nature Communications, 2019, 10, 2789.	5.8	14
50	Nucleome Dynamics during Retinal Development. Neuron, 2019, 104, 512-528.e11.	3.8	70
51	Latent cellular analysis robustly reveals subtle diversity in large-scale single-cell RNA-seq data. Nucleic Acids Research, 2019, 47, e143-e143.	6.5	26
52	The Clonal Evolution of Metastatic Osteosarcoma as Shaped by Cisplatin Treatment. Molecular Cancer Research, 2019, 17, 895-906.	1.5	40
53	Acute depletion of CTCF directly affects MYC regulation through loss of enhancerâ€“promoter looping. Nucleic Acids Research, 2019, 47, 6699-6713.	6.5	98
54	Clinical genome sequencing uncovers potentially targetable truncations and fusions of MAP3K8 in spitzoid and other melanomas. Nature Medicine, 2019, 25, 597-602.	15.2	61

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55	Analysis of error profiles in deep next-generation sequencing data. Genome Biology, 2019, 20, 50.	3.8	196
56	H3.3 K27M depletion increases differentiation and extends latency of diffuse intrinsic pontine glioma growth in vivo. Acta Neuropathologica, 2019, 137, 637-655.	3.9	85
57	Forty-five patient-derived xenografts capture the clinical and biological heterogeneity of Wilms tumor. Nature Communications, 2019, 10, 5806.	5.8	27
58	Metabolic heterogeneity underlies reciprocal fates of TH17 cell stemness and plasticity. Nature, 2019, 565, 101-105.	13.7	141
59	Structure and evolution of double minutes in diagnosis and relapse brain tumors. Acta Neuropathologica, 2019, 137, 123-137.	3.9	63
60	Integrative Analysis of Pediatric Acute Leukemia Identifies Immature Subtypes That Span a T Lineage and Myeloid Continuum with Distinct Prognoses. Blood, 2019, 134, 918-918.	0.6	1
61	Polygenic risk of subsequent thyroid cancer after childhood cancer: A report from St. Jude lifetime cohort (SJLIFE) and Childhood Cancer Survivor Study (CCSS).. Journal of Clinical Oncology, 2019, 37, 10060-10060.	0.8	0
62	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. Nature, 2018, 555, 371-376.	13.7	649
63	MYC Drives a Subset of High-Risk Pediatric Neuroblastomas and Is Activated through Mechanisms Including Enhancer Hijacking and Focal Enhancer Amplification. Cancer Discovery, 2018, 8, 320-335.	7.7	172
64	Genetic Risk for Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. Journal of Clinical Oncology, 2018, 36, 2078-2087.	0.8	105
65	Clinical cancer genomic profiling by three-platform sequencing of whole genome, whole exome and transcriptome. Nature Communications, 2018, 9, 3962.	5.8	142
66	Polygenic Determinants for Subsequent Breast Cancer Risk in Survivors of Childhood Cancer: The St Jude Lifetime Cohort Study (SJLIFE). Clinical Cancer Research, 2018, 24, 6230-6235.	3.2	18
67	A Single-Cell Transcriptional Atlas of the Developing Murine Cerebellum. Current Biology, 2018, 28, 2910-2920.e2.	1.8	158
68	Inhibition of SF3B1 by molecules targeting the spliceosome results in massive aberrant exon skipping. Rna, 2018, 24, 1056-1066.	1.6	42
69	High-resolution transcriptional dissection of in vivo Atoh1-mediated hair cell conversion in mature cochleae identifies Isl1 as a co-reprogramming factor. PLoS Genetics, 2018, 14, e1007552.	1.5	68
70	Metabolic signaling directs the reciprocal lineage decisions of Î±Î² and Î³Î´ T cells. Science Immunology, 2018, 3, .	5.6	63
71	UMI-count modeling and differential expression analysis for single-cell RNA sequencing. Genome Biology, 2018, 19, 70.	3.8	91
72	Identification of Therapeutic Targets in Rhabdomyosarcoma through Integrated Genomic, Epigenomic, and Proteomic Analyses. Cancer Cell, 2018, 34, 411-426.e19.	7.7	106

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73	Molecular heterogeneity and CXorf67 alterations in posterior fossa group A (PFA) ependymomas. Acta Neuropathologica, 2018, 136, 211-226.	3.9	199
74	Data Access and Interactive Visualization of Whole Genome Sequence of Sickle Cell Patients within the St. Jude Cloud. Blood, 2018, 132, 723-723.	0.6	2
75	Precision Medicine for Sickle Cell Disease through Whole Genome Sequencing. Blood, 2018, 132, 3641-3641.	0.6	3
76	Mutational Landscape and Temporal Evolution during Treatment of Relapsed Acute Lymphoblastic Leukemia. Blood, 2018, 132, 917-917.	0.6	0
77	Pediatric nonâ€“Down syndrome acute megakaryoblastic leukemia is characterized by distinct genomic subsets with varying outcomes. Nature Genetics, 2017, 49, 451-456.	9.4	152
78	Targetable kinase gene fusions in high-risk B-ALL: a study from the Childrenâ€™s Oncology Group. Blood, 2017, 129, 3352-3361.	0.6	236
79	The Dynamic Epigenetic Landscape of the Retina During Development, Reprogramming, and Tumorigenesis. Neuron, 2017, 94, 550-568.e10.	3.8	222
80	Orthotopic patient-derived xenografts of paediatric solid tumours. Nature, 2017, 549, 96-100.	13.7	223
81	The genomic landscape of pediatric myelodysplastic syndromes. Nature Communications, 2017, 8, 1557.	5.8	143
82	The genomic landscape of pediatric and young adult T-lineage acute lymphoblastic leukemia. Nature Genetics, 2017, 49, 1211-1218.	9.4	693
83	Genome-wide segregation of single nucleotide and structural variants into single cancer cells. BMC Genomics, 2017, 18, 906.	1.2	4
84	Exome sequencing analysis of murine medulloblastoma models identifies WDR11 as a potential tumor suppressor in Group 3 tumors. Oncotarget, 2017, 8, 64685-64697.	0.8	10
85	Telomerase Expression by Aberrant Methylation of the TERT Promoter in Melanoma Arising in Giant Congenital Nevi. Journal of Investigative Dermatology, 2016, 136, 339-342.	0.3	36
86	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. Nature Genetics, 2016, 48, 1481-1489.	9.4	231
87	The genomic landscape of core-binding factor acute myeloid leukemias. Nature Genetics, 2016, 48, 1551-1556.	9.4	215
88	Genetic alterations in uncommon low-grade neuroepithelial tumors: BRAF, FGFR1, and MYB mutations occur at high frequency and align with morphology. Acta Neuropathologica, 2016, 131, 833-845.	3.9	288
89	The landscape of fusion transcripts in spitzoid melanoma and biologically indeterminate spitzoid tumors by RNA sequencing. Modern Pathology, 2016, 29, 359-369.	2.9	61
90	Truncating Erythropoietin Receptor Rearrangements in Acute Lymphoblastic Leukemia. Cancer Cell, 2016, 29, 186-200.	7.7	118

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91	Pigment-Synthesizing Melanocytic Neoplasm With Protein Kinase C Alpha (PRKCA) Fusion. JAMA Dermatology, 2016, 152, 318.	2.0	33
92	Association of age at diagnosis and stage of disease with ATRX mutations in neuroblastoma.. Journal of Clinical Oncology, 2016, 34, 10525-10525.	0.8	2
93	Germline Mutations in Predisposition Genes in Pediatric Cancer. New England Journal of Medicine, 2015, 373, 2336-2346.	13.9	949
94	The Genomic Landscape of Childhood and Adolescent Melanoma. Journal of Investigative Dermatology, 2015, 135, 816-823.	0.3	148
95	Genomic landscape of paediatric adrenocortical tumours. Nature Communications, 2015, 6, 6302.	5.8	166
96	Rise and fall of subclones from diagnosis to relapse in pediatric B-acute lymphoblastic leukaemia. Nature Communications, 2015, 6, 6604.	5.8	281
97	The landscape of somatic mutations in infant MLL-rearranged acute lymphoblastic leukemias. Nature Genetics, 2015, 47, 330-337.	9.4	405
98	CONSERTING: integrating copy-number analysis with structural-variation detection. Nature Methods, 2015, 12, 527-530.	9.0	68
99	The Genomic Landscape of Childhood T-Lineage Acute Lymphoblastic Leukemia. Blood, 2015, 126, 691-691.	0.6	4
100	Expression of an Oncogenic ERG isoform Characterizes a Distinct Subtype of B-Progenitor Acute Lymphoblastic Leukemia. Blood, 2015, 126, 693-693.	0.6	1
101	Genomic Landscape of Relapsed Acute Lymphoblastic Leukemia. Blood, 2015, 126, 692-692.	0.6	3
102	Next Generation Sequencing Identifies a Novel Subset of Non-Down Syndrome Acute Megakaryoblastic Leukemia Characterized By Chimeric Transcripts Involving HOX Cluster Genes. Blood, 2015, 126, 171-171.	0.6	0
103	C11ORF95-RELA FUSIONS DRIVE ONCOGENIC NF-KB SIGNALING IN EPENDYMOMA. Neuro-Oncology, 2014, 16, iii16-iii16.	0.6	1
104	The landscape of somatic mutations in epigenetic regulators across 1,000 paediatric cancer genomes. Nature Communications, 2014, 5, 3630.	5.8	342
105	C11orf95â€“RELA fusions drive oncogenic NF-Î²B signalling in ependymoma. Nature, 2014, 506, 451-455.	13.7	559
106	Genomic Landscape of Ewing Sarcoma Defines an Aggressive Subtype with Co-Association of STAG2 and TP53 Mutations. Cancer Discovery, 2014, 4, 1342-1353.	7.7	418
107	Outcomes of Children With BCR-ABL1â€“Like Acute Lymphoblastic Leukemia Treated With Risk-Directed Therapy Based on the Levels of Minimal Residual Disease. Journal of Clinical Oncology, 2014, 32, 3012-3020.	0.8	223
108	Targetable Kinase-Activating Lesions in Ph-like Acute Lymphoblastic Leukemia. New England Journal of Medicine, 2014, 371, 1005-1015.	13.9	1,161

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109	The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. Nature Genetics, 2014, 46, 444-450.	9.4	871
110	Recurrent Somatic Structural Variations Contribute to Tumorigenesis in Pediatric Osteosarcoma. Cell Reports, 2014, 7, 104-112.	2.9	583
111	Incidence of Germline Mutations in Cancer-Predisposition Genes in Children with Hematologic Malignancies: a Report from the Pediatric Cancer Genome Project. Blood, 2014, 124, 127-127.	0.6	9
112	Analysis of TERT promoter mutations in pediatric melanoma.. Journal of Clinical Oncology, 2014, 32, 9023-9023.	0.8	2
113	RB1 gene inactivation by chromothripsis in human retinoblastoma. Oncotarget, 2014, 5, 438-450.	0.8	104
114	Cryptic Truncating Rearrangements of the Erythropoietin Receptor in Ph-like Acute Lymphoblastic Leukemia. Blood, 2014, 124, 128-128.	0.6	0
115	Global chromatin profiling reveals NSD2 mutations in pediatric acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 1386-1391.	9.4	238
116	Targeting Oxidative Stress in Embryonal Rhabdomyosarcoma. Cancer Cell, 2013, 24, 710-724.	7.7	252
117	Whole-genome sequencing identifies genetic alterations in pediatric low-grade gliomas. Nature Genetics, 2013, 45, 602-612.	9.4	704
118	The genomic landscape of hypodiploid acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 242-252.	9.4	588
119	An Inv(16)(p13.3q24.3)-Encoded CBFA2T3-GLIS2 Fusion Protein Defines an Aggressive Subtype of Pediatric Acute Megakaryoblastic Leukemia. Cancer Cell, 2012, 22, 683-697.	7.7	213
120	Assessing telomeric DNA content in pediatric cancers using whole-genome sequencing data. Genome Biology, 2012, 13, R113.	13.9	31
121	The genetic basis of early T-cell precursor acute lymphoblastic leukaemia. Nature, 2012, 481, 157-163.	13.7	1,430
122	A novel retinoblastoma therapy from genomic and epigenetic analyses. Nature, 2012, 481, 329-334.	13.7	442
123	Novel mutations target distinct subgroups of medulloblastoma. Nature, 2012, 488, 43-48.	13.7	742
124	Use of whole genome sequencing to identify novel mutations in distinct subgroups of medulloblastoma.. Journal of Clinical Oncology, 2012, 30, 9518-9518.	0.8	0
125	CREST maps somatic structural variation in cancer genomes with base-pair resolution. Nature Methods, 2011, 8, 652-654.	9.0	451
126	Whole Genome Sequence Analysis of 22 MLL Rearranged Infant Acute Lymphoblastic Leukemias Reveals Remarkably Few Somatic Mutations: A Report From the St Jude Childrenâ€˜s Research Hospital - Washington University Pediatric Cancer Genome Project. Blood, 2011, 118, 69-69.	0.6	6

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127	Transcriptome Sequence Analysis of Pediatric Acute Megakaryoblastic Leukemia Identifies An Inv(16)(p13.3;q24.3)-Encoded CBFA2T3-GLIS2 Fusion Protein As a Recurrent Lesion in 39% of Non-Infant Cases: A Report From the St. Jude Children's Research Hospital â€“ Washington University Pediatric Cancer Genome Project. Blood, 2011, 118, 757-757.	0.6	7
128	Discovery of Novel Recurrent Mutations in Childhood Early T-Cell Precursor Acute Lymphoblastic Leukemia by Whole Genome Sequencing - a Report From the St Jude Children's Research Hospital - Washington University Pediatric Cancer Genome Project. Blood, 2011, 118, 68-68.	0.6	0
129	Protection from Rapamycin-Induced Apoptosis by Insulin-Like Growth Factor-I Is Partially Dependent on Protein Kinase C Signaling. Cancer Research, 2010, 70, 2000-2009.	0.4	16
130	mTORC1 Signaling under Hypoxic Conditions Is Controlled by ATM-Dependent Phosphorylation of HIF-1Î±. Molecular Cell, 2010, 40, 509-520.	4.5	244
131	Negative Regulation of ASK1 by p21 Cip1 Involves a Small Domain That Includes Serine 98 That Is Phosphorylated by ASK1 In Vivo. Molecular and Cellular Biology, 2007, 27, 3530-3541.	1.1	46
132	The protein tyrosine phosphatase, Shp2, is required for the complete activation of the RAS/MAPK pathway by brain-derived neurotrophic factor. Journal of Neurochemistry, 2006, 97, 834-845.	2.1	63
133	IRS-1: Auditing the effectiveness of mTOR inhibitors. Cancer Cell, 2006, 9, 153-155.	7.7	70
134	Identification of N10-Substituted Phenoxazines as Potent and Specific Inhibitors of Akt Signaling. Journal of Biological Chemistry, 2005, 280, 31924-31935.	1.6	86
135	Virtual Docking Approaches to Protein Kinase B Inhibition. Journal of Medicinal Chemistry, 2005, 48, 2278-2281.	2.9	50
136	Therapeutic potential of target of rapamycin inhibitors. Expert Opinion on Therapeutic Targets, 2004, 8, 551-564.	1.5	73
137	Inhibition of Mammalian Target of Rapamycin Activates Apoptosis Signal-regulating Kinase 1 Signaling by Suppressing Protein Phosphatase 5 Activity. Journal of Biological Chemistry, 2004, 279, 36490-36496.	1.6	102
138	Sustained Activation of the JNK Cascade and Rapamycin-Induced Apoptosis Are Suppressed by p53/p21Cip1. Molecular Cell, 2003, 11, 1491-1501.	4.5	218
139	Insulin-like growth factor I-mediated protection from rapamycin-induced apoptosis is independent of Ras-Erk1-Erk2 and phosphatidylinositol 3'-kinase-Akt signaling pathways. Cancer Research, 2003, 63, 364-74.	0.4	61
140	Brain-derived Neurotrophic Factor Induces Phosphorylation of Fibroblast Growth Factor Receptor Substrate 2. Journal of Biological Chemistry, 1999, 274, 11321-11327.	1.6	30
141	Abnormalities in the p34cdc2-Related PITSLRE Protein Kinase Gene Complex (CDC2L) on Chromosome Band 1p36 in Melanoma. Cancer Genetics and Cytogenetics, 1999, 108, 91-99.	1.0	56
142	Duplication of a Genomic Region Containing the Cdc2L1-2 and MMP21-22 Genes on Human Chromosome 1p36.3 and their Linkage to D1Z2. Genome Research, 1998, 8, 929-939.	2.4	65
143	Analysis of the 5â€² flanking sequences from the human protein kinase p58 (PITSLREÎ²1)-encoding gene. Gene, 1994, 145, 279-282.	1.0	5
144	?1?4-galactosyltransferase gene expression is regulated during entry into the cell cycle and during the cell cycle. Somatic Cell and Molecular Genetics, 1991, 17, 435-443.	0.7	14