Ryan D Morin

List of Publications by Year
in descending order

141 papers	17,340 citations	30070 54 h-index	17592 121 g-index
150 all docs	150 docs citations	150 times ranked	24356 citing authors

#	Article	IF	Citations
1	Molecular profiling in diffuse large Bâ€cell lymphoma: why so many types of subtypes?. British Journal of Haematology, 2022, 196, 814-829.	2.5	51
2	Mutated RAS-associating proteins and ERK activation in relapse/refractory diffuse large B cell lymphoma. Scientific Reports, 2022, 12, 779.	3.3	1
3	Shared and distinct genetic features in human and canine B-cell lymphomas. Blood Advances, 2022, 6, 3404-3409.	5.2	2
4	Combinatorial and Machine Learning Approaches for Improved Somatic Variant Calling From Formalin-Fixed Paraffin-Embedded Genome Sequence Data. Frontiers in Genetics, 2022, 13, 834764.	2.3	1
5	Impact of MYC and BCL2 structural variants in tumors of DLBCL morphology and mechanisms of false-negative MYC IHC. Blood, 2021, 137, 2196-2208.	1.4	18
6	Molecular attributes underlying central nervous system and systemic relapse in diffuse large B-cell lymphoma. Haematologica, 2021, 106, 1466-1471.	3.5	9
7	Mast Cell and Eosinophil Activation Are Associated With COVID-19 and TLR-Mediated Viral Inflammation: Implications for an Anti-Siglec-8 Antibody. Frontiers in Immunology, 2021, 12, 650331.	4.8	72
8	Characterization of DLBCL with a PMBL gene expression signature. Blood, 2021, 138, 136-148.	1.4	19
9	Treating lymphoma is now a bit EZ-er. Blood Advances, 2021, 5, 2256-2263.	5.2	22
10	DNA-based species identification of ancient salmonid remains provides new insight into pre-contact Coast Salish salmon fisheries in Burrard Inlet, British Columbia, Canada. Journal of Archaeological Science: Reports, 2021, 37, 102956.	0.5	3
11	Prognostic significance of FCGR2B expression for the response of DLBCL patients to rituximab or obinutuzumab treatment. Blood Advances, 2021, 5, 2945-2957.	5.2	7
12	Proteotranscriptomic classification and characterization of pancreatic neuroendocrine neoplasms. Cell Reports, 2021, 37, 109817.	6.4	14
13	Frequent mutations of FBXO11 highlight BCL6 as a therapeutic target in Burkitt lymphoma. Blood Advances, 2021, 5, 5239-5257.	5.2	7
14	Evolutionary conservation of systemic and reversible amyloid aggregation. Journal of Cell Science, 2021, 134, .	2.0	6
15	Constrained FL: A Genetically Distinct Subgroup of Follicular Lymphoma with Low Rates of Somatic Hypermutation and a Reduced Propensity for Histologic Transformation. Blood, 2021, 138, 807-807.	1.4	0
16	Shared and Distinct Genetic Features in Human and Canine B-Cell Lymphomas. Blood, 2021, 138, 3509-3509.	1.4	0
17	Complex Structural Variation Associated with Enhancer Hijacking and Loss of Tumor Suppressors in Mantle Cell Lymphoma. Blood, 2021, 138, 675-675.	1.4	0
18	The Genomic Landscape of Plasmablastic Lymphoma (PBL) - an L.L.M.P.P. Project. Blood, 2021, 138, 1326-1326.	1.4	1

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19	Indigenous sex-selective salmon harvesting demonstrates pre-contact marine resource management in Burrard Inlet, British Columbia, Canada. Scientific Reports, 2021, 11, 21160.	3.3	6
20	Evaluating the quantity, quality and size distribution of cell-free DNA by multiplex droplet digital PCR. Scientific Reports, 2020, 10, 12564.	3.3	69
21	PRPS-ST: A Protocol-Agnostic Self-training Method for Gene Expressionâ€“Based Classification of Blood Cancers. Blood Cancer Discovery, 2020, 1, 244-257.	5.0	4
22	DLBCL subclassification: divide and conquer?. Blood, 2020, 135, 1722-1724.	1.4	12
23	Genetic and evolutionary patterns of treatment resistance in relapsed B-cell lymphoma. Blood Advances, 2020, 4, 2886-2898.	5.2	59
24	TBL1XR1 Mutations Drive Extranodal Lymphoma by Inducing a Pro-tumorigenic Memory Fate. Cell, 2020, 182, 297-316.e27.	28.9	63
25	IgCaller for reconstructing immunoglobulin gene rearrangements and oncogenic translocations from whole-genome sequencing in lymphoid neoplasms. Nature Communications, 2020, 11, 3390.	12.8	24
26	Integration of Whole-Genome Sequencing With Circulating Tumor DNA Analysis Captures Clonal Evolution and Tumor Heterogeneity in Non-V600 BRAF Mutant Colorectal Cancer. Clinical Colorectal Cancer, 2020, 19, 132-136.e3.	2.3	1
27	TMEM30A loss-of-function mutations drive lymphomagenesis and confer therapeutically exploitable vulnerability in B-cell lymphoma. Nature Medicine, 2020, 26, 577-588.	30.7	46
28	A Probabilistic Classification Tool for Genetic Subtypes of Diffuse Large B Cell Lymphoma with Therapeutic Implications. Cancer Cell, 2020, 37, 551-568.e14.	16.8	589
29	Coding and noncoding drivers of mantle cell lymphoma identified through exome and genome sequencing. Blood, 2020, 136, 572-584.	1.4	44
30	The Copy Number Landscape of Relapsed and Refractory Diffuse Large B-Cell Lymphoma. Blood, 2020, 136, 8-9.	1.4	1
31	Nfkbiz 3â€² UTR Mutations Confer Selective Growth Advantage and Affect Drug Response in Diffuse Large B-Cell Lymphoma. Blood, 2020, 136, 31-31.	1.4	1
32	Collaborative intra-tumor heterogeneity detection. Bioinformatics, 2019, 35, i379-i388.	4.1	10
33	Evaluation of protocols for rRNA depletion-based RNA sequencing of nanogram inputs of mammalian total RNA. PLoS ONE, 2019, 14, e0224578.	2.5	12
34	The double-hit signature identifies double-hit diffuse large B-cell lymphoma with genetic events cryptic to FISH. Blood, 2019, 134, 1528-1532.	1.4	82
35	Molecular and Genetic Characterization of MHC Deficiency Identifies EZH2 as Therapeutic Target for Enhancing Immune Recognition. Cancer Discovery, 2019, 9, 546-563.	9.4	213
36	Integrative genomic analysis of matched primary and metastatic pediatric osteosarcoma. Journal of Pathology, 2019, 249, 319-331.	4.5	36

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37	In vitro analyses of suspected arrhythmogenic thin filament variants as a cause of sudden cardiac death in infants. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 6969-6974.	7.1	16
38	Double-Hit Gene Expression Signature Defines a Distinct Subgroup of Germinal Center B-Cell-Like Diffuse Large B-Cell Lymphoma. Journal of Clinical Oncology, 2019, 37, 190-201.	1.6	257
39	A high-throughput protocol for isolating cell-free circulating tumor DNA from peripheral blood. BioTechniques, 2019, 66, 85-92.	1.8	13
40	Ultrasensitive Detection of Circulating Tumor DNA in Lymphoma via Targeted Hybridization Capture and Deep Sequencing of Barcoded Libraries. Methods in Molecular Biology, 2019, 1956, 383-435.	0.9	9
41	SUBSTRA: Supervised Bayesian Patient Stratification. Bioinformatics, 2019, 35, 3263-3272.	4.1	3
42	A Novel Multiplex Droplet Digital PCR Assay to Identify and Quantify KRAS Mutations in Clinical Specimens. Journal of Molecular Diagnostics, 2019, 21, 214-227.	2.8	32
43	Genome-wide discovery of somatic coding and noncoding mutations in pediatric endemic and sporadic Burkitt lymphoma. Blood, 2019, 133, 1313-1324.	1.4	172
44	Single-agent panobinostat for relapsed/refractory diffuse large B-cell lymphoma: clinical outcome and correlation with genomic data. A phase 2 study of the Fondazione Italiana Linfomi. Leukemia and Lymphoma, 2018, 59, 2904-2910.	1.3	11
45	The genomic landscape of two Burkitt lymphoma cases and derived cell lines: comparison between primary and relapse samples. Leukemia and Lymphoma, 2018, 59, 2159-2174.	1.3	6
46	Novel Multiplexing Strategies for Quantification of Rare Alleles Using ddPCR. Methods in Molecular Biology, 2018, 1768, 275-301.	0.9	0
47	Disruption of the Gut Microbiota With Antibiotics Exacerbates Acute Vascular Rejection. Transplantation, 2018, 102, 1085-1095.	1.0	24
48	High-resolution architecture and partner genes of MYC rearrangements in lymphoma with DLBCL morphology. Blood Advances, 2018, 2, 2755-2765.	5.2	74
49	Temporal Dynamics of Genomic Alterations in a BRCA1 Germlineâ€“Mutated Pancreatic Cancer With Low Genomic Instability Burden but Exceptional Response to Fluorouracil, Oxaliplatin, Leucovorin, and Irinotecan. JCO Precision Oncology, 2018, 2, 1-8.	3.0	1
50	Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. Nature Communications, 2018, 9, 4001.	12.8	102
51	Molecular and Genetic Characterization of MHC Deficiency Identifies EZH2 As a Therapeutic Target for Restoring MHC Expression in Diffuse Large B-Cell Lymphoma. Blood, 2018, 132, 1560-1560.	1.4	2
52	The Double-Hit Gene Expression Signature Defines a Clinically and Biologically Distinct Subgroup within GCB-DLBCL. Blood, 2018, 132, 921-921.	1.4	1
53	Obinutuzumab Plus Gemcitabine, Dexamethasone and Cisplatin (O-GDP) As Salvage Chemotherapy Prior to Autologous Stem Cell Transplant in Aggressive B Cell Lymphoma. Blood, 2018, 132, 4610-4610.	1.4	0
54	Recurrent IL4R Somatic Mutations in Diffuse Large B-Cell Lymphoma Lead to an Altered Gene Expression Profile and Changes in Tumor Microenvironment Composition. Blood, 2018, 132, 669-669.	1.4	1

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55	Mapping the human T cell repertoire to recurrent driver mutations in MYD88 and EZH2 in lymphoma. OncoImmunology, 2017, 6, e1321184.	4.6	23
56	Genome-wide chemical mapping of O-GlcNAcylated proteins in Drosophila melanogaster. Nature Chemical Biology, 2017, 13, 161-167.	8.0	33
57	Enhancing knowledge discovery from cancer genomics data with Galaxy. GigaScience, 2017, 6, 1-13.	6.4	6
58	Genetic profiling of MYC and BCL2 in diffuse large B-cell lymphoma determines cell-of-originâ€“specific clinical impact. Blood, 2017, 129, 2760-2770.	1.4	112
59	Targeted error-suppressed quantification of circulating tumor DNA using semi-degenerate barcoded adapters and biotinylated baits. Scientific Reports, 2017, 7, 10574.	3.3	20
60	Investigating the Genetic Causes of Sudden Unexpected Death in Children Through Targeted Next-Generation Sequencing Analysis. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	27
61	Kronos: a workflow assembler for genome analytics and informatics. GigaScience, 2017, 6, 1-10.	6.4	8
62	FOXL2 402C>G Mutation Can Be Identified in the Circulating Tumor DNA of Patients with Adult-Type Granulosa Cell Tumor. Journal of Molecular Diagnostics, 2017, 19, 126-136.	2.8	29
63	Targeted Error-Suppressed Detection of Circulating Paternal DNA to Establish a Diagnosis of Gestational Trophoblastic Neoplasm. JCO Precision Oncology, 2017, 1, 1-6.	3.0	5
64	Genetic heterogeneity in primary and relapsed mantle cell lymphomas: Impact of recurrent CARD11 mutations. Oncotarget, 2016, 7, 38180-38190.	1.8	130
65	Whole-Organism Developmental Expression Profiling Identifies RAB-28 as a Novel Ciliary GTPase Associated with the BBSome and Intraflagellar Transport. PLoS Genetics, 2016, 12, e1006469.	3.5	56
66	Comprehensive characterization of programmed death ligand structural rearrangements in B-cell non-Hodgkin lymphomas. Blood, 2016, 128, 1206-1213.	1.4	47
67	Pediatric-type nodal follicular lymphoma: a biologically distinct lymphoma with frequent MAPK pathway mutations. Blood, 2016, 128, 1093-1100.	1.4	126
68	Phase 2 study of panobinostat with or without rituximab in relapsed diffuse large B-cell lymphoma. Blood, 2016, 128, 185-194.	1.4	122
69	Activating mutations in genes related to TCR signaling in angioimmunoblastic and other follicular helper T-cellâ€“derived lymphomas. Blood, 2016, 128, 1490-1502.	1.4	255
70	Multiplex Droplet Digital PCR Quantification of Recurrent Somatic Mutations in Diffuse Large B-Cell and Follicular Lymphoma. Clinical Chemistry, 2016, 62, 1238-1247.	3.2	45
71	Cell-free DNA (cfDNA): Clinical Significance and Utility in Cancer Shaped By Emerging Technologies. Molecular Cancer Research, 2016, 14, 898-908.	3.4	279
72	Toward Personalized Lymphoma Immunotherapy: Identification of Common Driver Mutations Recognized by Patient CD8+ T Cells. Clinical Cancer Research, 2016, 22, 2226-2236.	7.0	26

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73	Genetic Landscapes of Relapsed and Refractory Diffuse Large B-Cell Lymphomas. Clinical Cancer Research, 2016, 22, 2290-2300.	7.0	186
74	Burkitt Lymphoma Genome Sequencing Project (BLGSP): Introduction. Blood, 2016, 128, 1760-1760.	1.4	1
75	Histological Transformation and Progression in Follicular Lymphoma: A Clonal Evolution Study. PLoS Medicine, 2016, 13, e1002197.	8.4	185
76	An RCOR1 lossâ€“associated gene expression signature identifies a prognostically significant DLBCL subgroup. Blood, 2015, 125, 959-966.	1.4	24
77	Genetic inactivation of TRAF3 in canine and human B-cell lymphoma. Blood, 2015, 125, 999-1005.	1.4	67
78	Recurrent genomic rearrangements in primary testicular lymphoma. Journal of Pathology, 2015, 236, 136-141.	4.5	47
79	Immunogenicity of recurrent mutations in MYD88 and EZH2 in non-Hodgkin lymphomas. , 2015, 3, .		0
80	Comprehensive miRNA sequence analysis reveals survival differences in diffuse large B-cell lymphoma patients. Genome Biology, 2015, 16, 18.	8.8	107
81	Cross-cancer profiling of molecular alterations within the human autophagy interaction network. Autophagy, 2015, 11, 1668-1687.	9.1	107
82	A Randomized, Phase II Study with Biomarker Analysis of Panobinostat with or without Rituximab in Relapsed Diffuse Large B Cell Lymphoma. Blood, 2015, 126, 2719-2719.	1.4	0
83	Methods for Sample Acquisition and Processing of Serial Blood and Tumor Biopsies for Multicenter Diffuse Large B-cell Lymphoma Clinical Trials. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2688-2693.	2.5	4
84	Cancer Transcriptome Sequencing and Analysis. , 2014, , 31-47.		1
85	A transgenic mouse model demonstrating the oncogenic role of mutations in the polycomb-group gene EZH2 in lymphomagenesis. Blood, 2014, 123, 3914-3924.	1.4	69
86	Variability in DNA methylation defines novel epigenetic subgroups of DLBCL associated with different clinical outcomes. Blood, 2014, 123, 1699-1708.	1.4	83
87	Newly Identified Mechanisms in B-Cell Non-Hodgkin Lymphomas Uncovered by Next-Generation Sequencing. Seminars in Hematology, 2013, 50, 303-313.	3.4	17
88	Novel mRNA isoforms and mutations of uridine monophosphate synthetase and 5-fluorouracil resistance in colorectal cancer. Pharmacogenomics Journal, 2013, 13, 148-158.	2.0	29
89	Analysis of FOXO1 mutations in diffuse large B-cell lymphoma. Blood, 2013, 121, 3666-3674.	1.4	139
90	Transcriptomics in the Age of Ultra High-Throughput Sequencing. , 2013, , 145-154.		0

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91	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. Blood, 2013, 122, 1256-1265.	1.4	349
92	Theoretical Investigation of the D83V Mutation within the Myocyte-Specific Enhancer Factor-2 Beta and Its Role in Cancer. Journal of Theoretical Chemistry, 2013, 2013, 1-10.	1.5	3
93	Genetic Alterations In Immune Cell Crosstalk Genes In Diffuse Large B-Cell Lymphoma Predict Survival. Blood, 2013, 122, 500-500.	1.4	0
94	JointSNVMix: a probabilistic model for accurate detection of somatic mutations in normal/tumour paired next-generation sequencing data. Bioinformatics, 2012, 28, 907-913.	4.1	159
95	Whole transcriptome sequencing reveals recurrent NOTCH1 mutations in mantle cell lymphoma. Blood, 2012, 119, 1963-1971.	1.4	313
96	TBL1XR1/TP63: a novel recurrent gene fusion in B-cell non-Hodgkin lymphoma. Blood, 2012, 119, 4949-4952.	1.4	60
97	Genetic Alterations Activating Kinase and Cytokine Receptor Signaling in High-Risk Acute Lymphoblastic Leukemia. Cancer Cell, 2012, 22, 153-166.	16.8	621
98	Recurrent targets of aberrant somatic hypermutation in lymphoma. Oncotarget, 2012, 3, 1308-1319.	1.8	127
99	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. Nature, 2011, 476, 298-303.	27.8	1,428
100	Comprehensive analysis of mammalian miRNA* species and their role in myeloid cells. Blood, 2011, 118, 3350-3358.	1.4	90
101	Genome-wide identification of human microRNAs located in leukemia-associated genomic alterations. Blood, 2011, 117, 595-607.	1.4	105
102	Somatic mutations at EZH2 Y641 act dominantly through a mechanism of selectively altered PRC2 catalytic activity, to increase H3K27 trimethylation. Blood, 2011, 117, 2451-2459.	1.4	556
103	Novel Chromosomal Rearrangements and Sequence Mutations in High-Risk Ph-Like Acute Lymphoblastic Leukemia. Blood, 2011, 118, 67-67.	1.4	0
104	Hypomorphic Temperature-Sensitive Alleles of NSDHL Cause CK Syndrome. American Journal of Human Genetics, 2010, 87, 905-914.	6.2	64
105	Genomic analysis of a rare human tumor. BMC Bioinformatics, 2010, 11, .	2.6	0
106	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. Nature Genetics, 2010, 42, 181-185.	21.4	1,504
107	Identification of miR-145 and miR-146a as mediators of the 5qâ€“ syndrome phenotype. Nature Medicine, 2010, 16, 49-58.	30.7	588
108	Alternative expression analysis by RNA sequencing. Nature Methods, 2010, 7, 843-847.	19.0	283

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109	Acquired TNFRSF14 Mutations in Follicular Lymphoma Are Associated with Worse Prognosis. Cancer Research, 2010, 70, 9166-9174.	0.9	160
110	System-Level Analysis of Neuroblastoma Tumorâ€"Initiating Cells Implicates AURKB as a Novel Drug Target for Neuroblastoma. Clinical Cancer Research, 2010, 16, 4572-4582.	7.0	43
111	SNVMix: predicting single nucleotide variants from next-generation sequencing of tumors. Bioinformatics, 2010, 26, 730-736.	4.1	192
112	MicroRNA transcriptome in the newborn mouse ovaries determined by massive parallel sequencing. Molecular Human Reproduction, 2010, 16, 463-471.	2.8	122
113	Preparation and Analysis of MicroRNA Libraries Using the Illumina Massively Parallel Sequencing Technology. Methods in Molecular Biology, 2010, 650, 173-199.	0.9	13
114	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. Genome Biology, 2010, 11, R82.	9.6	159
115	Personalized oncogenomics. Genome Biology, 2010, 11, I5.	9.6	0
116	BCL6 repression of EP300 in human diffuse large B cell lymphoma cells provides a basis for rational combinatorial therapy. Journal of Clinical Investigation, 2010, 120, 4569-4582.	8.2	101
117	Mutations In MLL2 and MEF2B Genes In Follicular Lymphoma and Diffuse Large B-Cell Lymphoma. Blood, 2010, 116, 473-473.	1.4	6
118	Recurrent DNA Mutations In Non-Hodgkin Lymphomas Reveal Candidate Therapeutic Targets. Blood, 2010, 116, 632-632.	1.4	0
119	Personalized oncogenomics. Genome Biology, 2010, 11, I5.	9.6	0
120	The completion of the Mammalian Gene Collection (MGC). Genome Research, 2009, 19, 2324-2333.	5.5	125
121	De novo transcriptome assembly with ABySS. Bioinformatics, 2009, 25, 2872-2877.	4.1	371
122	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. Nature, 2009, 461, 809-813.	27.8	984
123	Next-generation tag sequencing for cancer gene expression profiling. Genome Research, 2009, 19, 1825-1835.	5.5	306
124	Mutation ofFOXL2in Granulosa-Cell Tumors of the Ovary. New England Journal of Medicine, 2009, 360, 2719-2729.	27.0	706
125	Genome-Wide Identification of Human Micrornas Located in Leukemia-Associated Genomic Alterations.. Blood, 2009, 114, 1287-1287.	1.4	0
126	TNFRSF14 Is Mutated in a Subset of Follicular Lymphoma and Correlated with Inferior Prognosis.. Blood, 2009, 114, 1919-1919.	1.4	1

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127	FAS Mutations in Follicular Lymphoma Are Rare but Associated with Aggressive Clinical Behavior.. Blood, 2009, 114, 3967-3967.	1.4	0
128	ALEXA: a microarray design platform for alternative expression analysis. Nature Methods, 2008, 5, 118-118.	19.0	19
129	In-depth characterization of the microRNA transcriptome in a leukemia progression model. Genome Research, 2008, 18, 1787-1797.	5.5	162
130	Application of massively parallel sequencing to microRNA profiling and discovery in human embryonic stem cells. Genome Research, 2008, 18, 610-621.	5.5	964
131	Profiling the HeLa S3 transcriptome using randomly primed cDNA and massively parallel short-read sequencing. BioTechniques, 2008, 45, 81-94.	1.8	355
132	Comparative analysis of the small RNA transcriptomes of Pinus contorta and Oryza sativa. Genome Research, 2008, 18, 571-584.	5.5	305
133	Conifers have a unique small RNA silencing signature. Rna, 2008, 14, 1508-1515.	3.5	108
134	LongSAGE profiling of nine human embryonic stem cell lines. Genome Biology, 2007, 8, R113.	9.6	21
135	Accurate Detection of the microRNA Transcriptome in a Leukemia Progression Model.. Blood, 2007, 110, 866-866.	1.4	0
136	The complete genome of Rhodococcus sp. RHA1 provides insights into a catabolic powerhouse. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15582-15587.	7.1	586
137	Sequencing and analysis of 10,967 full-length cDNA clones from Xenopus laevis and Xenopus tropicalis reveals post-tetraploidization transcriptome remodeling. Genome Research, 2006, 16, 796-803.	5.5	73
138	Management and visualization of whole genome shotgun assemblies using SAM. BioTechniques, 2005, 38, 715-720.	1.8	7
139	The Status, Quality, and Expansion of the NIH Full-Length cDNA Project: The Mammalian Gene Collection (MGC). Genome Research, 2004, 14, 2121-2127.	5.5	486
140	MASSIVELY PARALLEL MICRORNA PROFILING IN THE HAEMATOLOGIC MALIGNANCIES. , 0, , 71-94.		0
141	BCL10 Mutations Define Distinct Dependencies Guiding Precision Therapy for DLBCL. Cancer Discovery, 0, , OF1-OF20.	9.4	2