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	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
2	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. Nature, 2011, 476, 298-303.	27.8	1,428
3	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. Nature, 2009, 461, 809-813.	27.8	984
4	Application of massively parallel sequencing to microRNA profiling and discovery in human embryonic stem cells. Genome Research, 2008, 18, 610-621.	5.5	964
5	Mutation ofFOXL2in Granulosa-Cell Tumors of the Ovary. New England Journal of Medicine, 2009, 360, 2719-2729.	27.0	706
6	Genetic Alterations Activating Kinase and Cytokine Receptor Signaling in High-Risk Acute Lymphoblastic Leukemia. Cancer Cell, 2012, 22, 153-166.	16.8	621
7	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
8	Identification of miR-145 and miR-146a as mediators of the 5qâ€“ syndrome phenotype. Nature Medicine, 2010, 16, 49-58.	30.7	588
9	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
10	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
11	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
12	De novo transcriptome assembly with ABySS. Bioinformatics, 2009, 25, 2872-2877.	4.1	371
13	Profiling the HeLa S3 transcriptome using randomly primed cDNA and massively parallel short-read sequencing. BioTechniques, 2008, 45, 81-94.	1.8	355
14	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. Blood, 2013, 122, 1256-1265.	1.4	349
15	Whole transcriptome sequencing reveals recurrent NOTCH1 mutations in mantle cell lymphoma. Blood, 2012, 119, 1963-1971.	1.4	313
16	Next-generation tag sequencing for cancer gene expression profiling. Genome Research, 2009, 19, 1825-1835.	5.5	306
17	Comparative analysis of the small RNA transcriptomes of Pinus contorta and Oryza sativa. Genome Research, 2008, 18, 571-584.	5.5	305
18	Alternative expression analysis by RNA sequencing. Nature Methods, 2010, 7, 843-847.	19.0	283

#	Article	IF	Citations
19	Cell-free DNA (cfDNA): Clinical Significance and Utility in Cancer Shaped By Emerging Technologies. Molecular Cancer Research, 2016, 14, 898-908.	3.4	279
20	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
21	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
22	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
23	SNVMix: predicting single nucleotide variants from next-generation sequencing of tumors. Bioinformatics, 2010, 26, 730-736.	4.1	192
24	Genetic Landscapes of Relapsed and Refractory Diffuse Large B-Cell Lymphomas. Clinical Cancer Research, 2016, 22, 2290-2300.	7.0	186
25	Histological Transformation and Progression in Follicular Lymphoma: A Clonal Evolution Study. PLoS Medicine, 2016, 13, e1002197.	8.4	185
26	Genome-wide discovery of somatic coding and noncoding mutations in pediatric endemic and sporadic Burkitt lymphoma. Blood, 2019, 133, 1313-1324.	1.4	172
27	In-depth characterization of the microRNA transcriptome in a leukemia progression model. Genome Research, 2008, 18, 1787-1797.	5.5	162
28	Acquired TNFRSF14 Mutations in Follicular Lymphoma Are Associated with Worse Prognosis. Cancer Research, 2010, 70, 9166-9174.	0.9	160
29	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. Genome Biology, 2010, 11, R82.	9.6	159
30	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
31	Analysis of FOXO1 mutations in diffuse large B-cell lymphoma. Blood, 2013, 121, 3666-3674.	1.4	139
32	Genetic heterogeneity in primary and relapsed mantle cell lymphomas: Impact of recurrent CARD11 mutations. Oncotarget, 2016, 7, 38180-38190.	1.8	130
33	Recurrent targets of aberrant somatic hypermutation in lymphoma. Oncotarget, 2012, 3, 1308-1319.	1.8	127
34	Pediatric-type nodal follicular lymphoma: a biologically distinct lymphoma with frequent MAPK pathway mutations. Blood, 2016, 128, 1093-1100.	1.4	126
35	The completion of the Mammalian Gene Collection (MGC). Genome Research, 2009, 19, 2324-2333.	5.5	125
36	MicroRNA transcriptome in the newborn mouse ovaries determined by massive parallel sequencing. Molecular Human Reproduction, 2010, 16, 463-471.	2.8	122

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37	Phase 2 study of panobinostat with or without rituximab in relapsed diffuse large B-cell lymphoma. Blood, 2016, 128, 185-194.	1.4	122
38	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
39	Conifers have a unique small RNA silencing signature. Rna, 2008, 14, 1508-1515.	3.5	108
40	Comprehensive miRNA sequence analysis reveals survival differences in diffuse large B-cell lymphoma patients. Genome Biology, 2015, 16, 18.	8.8	107
41	Cross-cancer profiling of molecular alterations within the human autophagy interaction network. Autophagy, 2015, 11, 1668-1687.	9.1	107
42	Genome-wide identification of human microRNAs located in leukemia-associated genomic alterations. Blood, 2011, 117, 595-607.	1.4	105
43	Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. Nature Communications, 2018, 9, 4001.	12.8	102
44	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
45	Comprehensive analysis of mammalian miRNA* species and their role in myeloid cells. Blood, 2011, 118, 3350-3358.	1.4	90
46	Variability in DNA methylation defines novel epigenetic subgroups of DLBCL associated with different clinical outcomes. Blood, 2014, 123, 1699-1708.	1.4	83
47	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
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	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
50	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
51	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
52	Evaluating the quantity, quality and size distribution of cell-free DNA by multiplex droplet digital PCR. Scientific Reports, 2020, 10, 12564.	3.3	69
53	Genetic inactivation of TRAF3 in canine and human B-cell lymphoma. Blood, 2015, 125, 999-1005.	1.4	67
54	Hypomorphic Temperature-Sensitive Alleles of NSDHL Cause CK Syndrome. American Journal of Human Genetics, 2010, 87, 905-914.	6.2	64

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55	TBL1XR1 Mutations Drive Extranodal Lymphoma by Inducing a Pro-tumorigenic Memory Fate. Cell, 2020, 182, 297-316.e27.	28.9	63
56	TBL1XR1/TP63: a novel recurrent gene fusion in B-cell non-Hodgkin lymphoma. Blood, 2012, 119, 4949-4952.	1.4	60
57	Genetic and evolutionary patterns of treatment resistance in relapsed B-cell lymphoma. Blood Advances, 2020, 4, 2886-2898.	5.2	59
58	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
59	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
60	Recurrent genomic rearrangements in primary testicular lymphoma. Journal of Pathology, 2015, 236, 136-141.	4.5	47
61	Comprehensive characterization of programmed death ligand structural rearrangements in B-cell non-Hodgkin lymphomas. Blood, 2016, 128, 1206-1213.	1.4	47
62	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
63	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
64	Coding and noncoding drivers of mantle cell lymphoma identified through exome and genome sequencing. Blood, 2020, 136, 572-584.	1.4	44
65	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
66	Integrative genomic analysis of matched primary and metastatic pediatric osteosarcoma. Journal of Pathology, 2019, 249, 319-331.	4.5	36
67	Genome-wide chemical mapping of O-GlcNAcylated proteins in Drosophila melanogaster. Nature Chemical Biology, 2017, 13, 161-167.	8.0	33
68	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
69	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
70	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
71	Investigating the Genetic Causes of Sudden Unexpected Death in Children Through Targeted Next-Generation Sequencing Analysis. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	27
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	An RCOR1 lossâ€“associated gene expression signature identifies a prognostically significant DLBCL subgroup. Blood, 2015, 125, 959-966.	1.4	24
74	Disruption of the Gut Microbiota With Antibiotics Exacerbates Acute Vascular Rejection. Transplantation, 2018, 102, 1085-1095.	1.0	24
75	IgCaller for reconstructing immunoglobulin gene rearrangements and oncogenic translocations from whole-genome sequencing in lymphoid neoplasms. Nature Communications, 2020, 11, 3390.	12.8	24
76	Mapping the human T cell repertoire to recurrent driver mutations in MYD88 and EZH2 in lymphoma. OncoImmunology, 2017, 6, e1321184.	4.6	23
77	Treating lymphoma is now a bit EZ-er. Blood Advances, 2021, 5, 2256-2263.	5.2	22
78	LongSAGE profiling of nine human embryonic stem cell lines. Genome Biology, 2007, 8, R113.	9.6	21
79	Targeted error-suppressed quantification of circulating tumor DNA using semi-degenerate barcoded adapters and biotinylated baits. Scientific Reports, 2017, 7, 10574.	3.3	20
80	ALEXA: a microarray design platform for alternative expression analysis. Nature Methods, 2008, 5, 118-118.	19.0	19
81	Characterization of DLBCL with a PMBL gene expression signature. Blood, 2021, 138, 136-148.	1.4	19
82	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
83	Newly Identified Mechanisms in B-Cell Non-Hodgkin Lymphomas Uncovered by Next-Generation Sequencing. Seminars in Hematology, 2013, 50, 303-313.	3.4	17
84	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
85	Proteotranscriptomic classification and characterization of pancreatic neuroendocrine neoplasms. Cell Reports, 2021, 37, 109817.	6.4	14
86	Preparation and Analysis of MicroRNA Libraries Using the Illumina Massively Parallel Sequencing Technology. Methods in Molecular Biology, 2010, 650, 173-199.	0.9	13
87	A high-throughput protocol for isolating cell-free circulating tumor DNA from peripheral blood. BioTechniques, 2019, 66, 85-92.	1.8	13
88	Evaluation of protocols for rRNA depletion-based RNA sequencing of nanogram inputs of mammalian total RNA. PLoS ONE, 2019, 14, e0224578.	2.5	12
89	DLBCL subclassification: divide and conquer?. Blood, 2020, 135, 1722-1724.	1.4	12
90	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

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91	Collaborative intra-tumor heterogeneity detection. Bioinformatics, 2019, 35, i379-i388.	4.1	10
92	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
93	Molecular attributes underlying central nervous system and systemic relapse in diffuse large B-cell lymphoma. Haematologica, 2021, 106, 1466-1471.	3.5	9
94	Kronos: a workflow assembler for genome analytics and informatics. GigaScience, 2017, 6, 1-10.	6.4	8
95	Management and visualization of whole genome shotgun assemblies using SAM. BioTechniques, 2005, 38, 715-720.	1.8	7
96	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
97	Frequent mutations of FBXO11 highlight BCL6 as a therapeutic target in Burkitt lymphoma. Blood Advances, 2021, 5, 5239-5257.	5.2	7
98	Enhancing knowledge discovery from cancer genomics data with Galaxy. GigaScience, 2017, 6, 1-13.	6.4	6
99	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
100	Mutations In MLL2 and MEF2B Genes In Follicular Lymphoma and Diffuse Large B-Cell Lymphoma. Blood, 2010, 116, 473-473.	1.4	6
101	Evolutionary conservation of systemic and reversible amyloid aggregation. Journal of Cell Science, 2021, 134, .	2.0	6
102	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
103	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
104	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
105	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
106	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
107	SUBSTRA: Supervised Bayesian Patient Stratification. Bioinformatics, 2019, 35, 3263-3272.	4.1	3
108	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

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109	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
110	Shared and distinct genetic features in human and canine B-cell lymphomas. Blood Advances, 2022, 6, 3404-3409.	5.2	2
111	BCL10 Mutations Define Distinct Dependencies Guiding Precision Therapy for DLBCL. Cancer Discovery, 0, , OF1-OF20.	9.4	2
112	Cancer Transcriptome Sequencing and Analysis. , 2014, , 31-47.		1
113	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
114	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
115	The Double-Hit Gene Expression Signature Defines a Clinically and Biologically Distinct Subgroup within GCB-DLBCL. Blood, 2018, 132, 921-921.	1.4	1
116	Burkitt Lymphoma Genome Sequencing Project (BLGSP): Introduction. Blood, 2016, 128, 1760-1760.	1.4	1
117	TNFRSF14 Is Mutated in a Subset of Follicular Lymphoma and Correlated with Inferior Prognosis.. Blood, 2009, 114, 1919-1919.	1.4	1
118	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
119	The Genomic Landscape of Plasmablastic Lymphoma (PBL) - an L.L.M.P.P. Project. Blood, 2021, 138, 1326-1326.	1.4	1
120	The Copy Number Landscape of Relapsed and Refractory Diffuse Large B-Cell Lymphoma. Blood, 2020, 136, 8-9.	1.4	1
121	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
122	Mutated RAS-associating proteins and ERK activation in relapse/refractory diffuse large B cell lymphoma. Scientific Reports, 2022, 12, 779.	3.3	1
123	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
124	Genomic analysis of a rare human tumor. BMC Bioinformatics, 2010, 11, .	2.6	0
125	Personalized oncogenomics. Genome Biology, 2010, 11, I5.	9.6	0
126	Transcriptomics in the Age of Ultra High-Throughput Sequencing. , 2013, , 145-154.		0

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127	Immunogenicity of recurrent mutations in MYD88 and EZH2 in non-Hodgkin lymphomas. , 2015, 3, .		0
128	Novel Multiplexing Strategies for Quantification of Rare Alleles Using ddPCR. Methods in Molecular Biology, 2018, 1768, 275-301.	0.9	0
129	Accurate Detection of the microRNA Transcriptome in a Leukemia Progression Model.. Blood, 2007, 110, 866-866.	1.4	0
130	Genome-Wide Identification of Human Micrornas Located in Leukemia-Associated Genomic Alterations.. Blood, 2009, 114, 1287-1287.	1.4	0
131	FAS Mutations in Follicular Lymphoma Are Rare but Associated with Aggressive Clinical Behavior.. Blood, 2009, 114, 3967-3967.	1.4	0
132	Recurrent DNA Mutations In Non-Hodgkin Lymphomas Reveal Candidate Therapeutic Targets. Blood, 2010, 116, 632-632.	1.4	0
133	Novel Chromosomal Rearrangements and Sequence Mutations in High-Risk Ph-Like Acute Lymphoblastic Leukemia. Blood, 2011, 118, 67-67.	1.4	0
134	Genetic Alterations In Immune Cell Crosstalk Genes In Diffuse Large B-Cell Lymphoma Predict Survival. Blood, 2013, 122, 500-500.	1.4	0
135	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
136	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
137	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
138	Shared and Distinct Genetic Features in Human and Canine B-Cell Lymphomas. Blood, 2021, 138, 3509-3509.	1.4	0
139	Complex Structural Variation Associated with Enhancer Hijacking and Loss of Tumor Suppressors in Mantle Cell Lymphoma. Blood, 2021, 138, 675-675.	1.4	0
140	MASSIVELY PARALLEL MICRORNA PROFILING IN THE HAEMATOLOGIC MALIGNANCIES. , 0, , 71-94.		0
141	Personalized oncogenomics. Genome Biology, 2010, 11, I5.	9.6	0