Ryan D Morin

List of Publications by Citations

138 papers	13,740 citations	51 h-index	117 g-index
149 ext. papers	15,996 ext. citations	8.4 avg, IF	5.49 L-index

#	Paper	IF	Citations
138	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. *Nature Genetics*, **2010**, 42, 181-5	36.3	1273
137	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. *Nature*, **2011**, 476, 298-303	50.4	1180
136	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. *Nature*, **2009**, 461, 809-13	50.4	879
135	Application of massively parallel sequencing to microRNA profiling and discovery in human embryonic stem cells. *Genome Research*, **2008**, 18, 610-21	9.7	879
134	Mutation of FOXL2 in granulosa-cell tumors of the ovary. *New England Journal of Medicine*, **2009**, 360, 2719-29	59.2	551
133	Genetic alterations activating kinase and cytokine receptor signaling in high-risk acute lymphoblastic leukemia. *Cancer Cell*, **2012**, 22, 153-66	24.3	515
132	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, 15582-7	11.5	515
131	Identification of miR-145 and miR-146a as mediators of the 5q- syndrome phenotype. *Nature Medicine*, **2010**, 16, 49-58	50.5	494
130	Somatic mutations at EZH2 Y641 act dominantly through a mechanism of selectively altered PRC2 catalytic activity, to increase H3K27 trimethylation. *Blood*, **2011**, 117, 2451-9	2.2	458
129	The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC). *Genome Research*, **2004**, 14, 2121-7	9.7	404
128	De novo transcriptome assembly with ABySS. *Bioinformatics*, **2009**, 25, 2872-7	7.2	326
127	Profiling the HeLa S3 transcriptome using randomly primed cDNA and massively parallel short-read sequencing. *BioTechniques*, **2008**, 45, 81-94	2.5	322
126	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. *Blood*, **2013**, 122, 1256-65	2.2	289
125	Comparative analysis of the small RNA transcriptomes of Pinus contorta and Oryza sativa. *Genome Research*, **2008**, 18, 571-84	9.7	278
124	Next-generation tag sequencing for cancer gene expression profiling. *Genome Research*, **2009**, 19, 1825-35	9.7	271
123	Whole transcriptome sequencing reveals recurrent NOTCH1 mutations in mantle cell lymphoma. *Blood*, **2012**, 119, 1963-71	2.2	264
122	Alternative expression analysis by RNA sequencing. *Nature Methods*, **2010**, 7, 843-7	21.6	227

121	A Probabilistic Classification Tool for Genetic Subtypes of Diffuse Large B Cell Lymphoma with Therapeutic Implications. *Cancer Cell*, **2020**, 37, 551-568.e14	24.3	194
120	Cell-free DNA (cfDNA): Clinical Significance and Utility in Cancer Shaped By Emerging Technologies. *Molecular Cancer Research*, **2016**, 14, 898-908	6.6	193
119	SNVMix: predicting single nucleotide variants from next-generation sequencing of tumors. *Bioinformatics*, **2010**, 26, 730-6	7.2	174
118	Activating mutations in genes related to TCR signaling in angioimmunoblastic and other follicular helper T-cell-derived lymphomas. *Blood*, **2016**, 128, 1490-502	2.2	170
117	In-depth characterization of the microRNA transcriptome in a leukemia progression model. *Genome Research*, **2008**, 18, 1787-97	9.7	148
116	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. *Genome Biology*, **2010**, 11, R82	18.3	144
115	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	2.2	137
114	JointSNVMix: a probabilistic model for accurate detection of somatic mutations in normal/tumour paired next-generation sequencing data. *Bioinformatics*, **2012**, 28, 907-13	7.2	136
113	Acquired TNFRSF14 mutations in follicular lymphoma are associated with worse prognosis. *Cancer Research*, **2010**, 70, 9166-74	10.1	133
112	Genetic Landscapes of Relapsed and Refractory Diffuse Large B-Cell Lymphomas. *Clinical Cancer Research*, **2016**, 22, 2290-300	12.9	130
111	Molecular and Genetic Characterization of MHC Deficiency Identifies EZH2 as Therapeutic Target for Enhancing Immune Recognition. *Cancer Discovery*, **2019**, 9, 546-563	24.4	123
110	MicroRNA transcriptome in the newborn mouse ovaries determined by massive parallel sequencing. *Molecular Human Reproduction*, **2010**, 16, 463-71	4.4	110
109	Histological Transformation and Progression in Follicular Lymphoma: A Clonal Evolution Study. *PLoS Medicine*, **2016**, 13, e1002197	11.6	110
108	Recurrent targets of aberrant somatic hypermutation in lymphoma. *Oncotarget*, **2012**, 3, 1308-19	3.3	101
107	Analysis of FOXO1 mutations in diffuse large B-cell lymphoma. *Blood*, **2013**, 121, 3666-74	2.2	100
106	The completion of the Mammalian Gene Collection (MGC). *Genome Research*, **2009**, 19, 2324-33	9.7	98
105	Conifers have a unique small RNA silencing signature. *Rna*, **2008**, 14, 1508-15	5.8	91
104	Genetic heterogeneity in primary and relapsed mantle cell lymphomas: Impact of recurrent CARD11 mutations. *Oncotarget*, **2016**, 7, 38180-38190	3.3	91

103	Phase 2 study of panobinostat with or without rituximab in relapsed diffuse large B-cell lymphoma. *Blood*, **2016**, 128, 185-94	2.2	90
102	Cross-cancer profiling of molecular alterations within the human autophagy interaction network. *Autophagy*, **2015**, 11, 1668-87	10.2	89
101	Genome-wide identification of human microRNAs located in leukemia-associated genomic alterations. *Blood*, **2011**, 117, 595-607	2.2	88
100	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, 4569-82	15.9	88
99	Genetic profiling of and in diffuse large B-cell lymphoma determines cell-of-origin-specific clinical impact. *Blood*, **2017**, 129, 2760-2770	2.2	82
98	Comprehensive analysis of mammalian miRNA* species and their role in myeloid cells. *Blood*, **2011**, 118, 3350-8	2.2	81
97	Immunogenicity of recurrent mutations in MYD88 and EZH2 in non-Hodgkin lymphomas **2015**, 3,		78
96	Personalized oncogenomics **2010**, 11, I5		78
95	Genomic analysis of a rare human tumor. *BMC Bioinformatics*, **2010**, 11,	3.6	78
94	Pediatric-type nodal follicular lymphoma: a biologically distinct lymphoma with frequent MAPK pathway mutations. *Blood*, **2016**, 128, 1093-100	2.2	78
93	Genome-wide discovery of somatic coding and noncoding mutations in pediatric endemic and sporadic Burkitt lymphoma. *Blood*, **2019**, 133, 1313-1324	2.2	75
92	Comprehensive miRNA sequence analysis reveals survival differences in diffuse large B-cell lymphoma patients. *Genome Biology*, **2015**, 16, 18	18.3	71
91	Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. *Nature Communications*, **2018**, 9, 4001	17.4	64
90	A transgenic mouse model demonstrating the oncogenic role of mutations in the polycomb-group gene EZH2 in lymphomagenesis. *Blood*, **2014**, 123, 3914-24	2.2	63
89	Variability in DNA methylation defines novel epigenetic subgroups of DLBCL associated with different clinical outcomes. *Blood*, **2014**, 123, 1699-708	2.2	63
88	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	9.7	59
87	TBL1XR1/TP63: a novel recurrent gene fusion in B-cell non-Hodgkin lymphoma. *Blood*, **2012**, 119, 4949-52	2.2	50
86	Genetic inactivation of TRAF3 in canine and human B-cell lymphoma. *Blood*, **2015**, 125, 999-1005	2.2	48

85	Hypomorphic temperature-sensitive alleles of NSDHL cause CK syndrome. *American Journal of Human Genetics*, **2010**, 87, 905-14	11	46
84	The double-hit signature identifies double-hit diffuse large B-cell lymphoma with genetic events cryptic to FISH. *Blood*, **2019**, 134, 1528-1532	2.2	40
83	Comprehensive characterization of programmed death ligand structural rearrangements in B-cell non-Hodgkin lymphomas. *Blood*, **2016**, 128, 1206-13	2.2	40
82	High-resolution architecture and partner genes of rearrangements in lymphoma with DLBCL morphology. *Blood Advances*, **2018**, 2, 2755-2765	7.8	38
81	Recurrent genomic rearrangements in primary testicular lymphoma. *Journal of Pathology*, **2015**, 236, 136-41	9.4	36
80	System-level analysis of neuroblastoma tumor-initiating cells implicates AURKB as a novel drug target for neuroblastoma. *Clinical Cancer Research*, **2010**, 16, 4572-82	12.9	36
79	Multiplex Droplet Digital PCR Quantification of Recurrent Somatic Mutations in Diffuse Large B-Cell and Follicular Lymphoma. *Clinical Chemistry*, **2016**, 62, 1238-47	5.5	34
78	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	6	33
77	Genome-wide chemical mapping of O-GlcNAcylated proteins in Drosophila melanogaster. *Nature Chemical Biology*, **2017**, 13, 161-167	11.7	30
76	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	8.4	26
75	Genetic and evolutionary patterns of treatment resistance in relapsed B-cell lymphoma. *Blood Advances*, **2020**, 4, 2886-2898	7.8	24
74	Evaluating the quantity, quality and size distribution of cell-free DNA by multiplex droplet digital PCR. *Scientific Reports*, **2020**, 10, 12564	4.9	24
73	TBL1XR1 Mutations Drive Extranodal Lymphoma by Inducing a Pro-tumorigenic Memory Fate. *Cell*, **2020**, 182, 297-316.e27	56.2	23
72	TMEM30A loss-of-function mutations drive lymphomagenesis and confer therapeutically exploitable vulnerability in B-cell lymphoma. *Nature Medicine*, **2020**, 26, 577-588	50.5	22
71	Mapping the human T cell repertoire to recurrent driver mutations in MYD88 and EZH2 in lymphoma. *OncoImmunology*, **2017**, 6, e1321184	7.2	20
70	Integrative genomic analysis of matched primary and metastatic pediatric osteosarcoma. *Journal of Pathology*, **2019**, 249, 319-331	9.4	19
69	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	5.1	19
68	ALEXA: a microarray design platform for alternative expression analysis. *Nature Methods*, **2008**, 5, 118	21.6	19

67	Coding and noncoding drivers of mantle cell lymphoma identified through exome and genome sequencing. *Blood*, **2020**, 136, 572-584	2.2	19
66	A Novel Multiplex Droplet Digital PCR Assay to Identify and Quantify KRAS Mutations in Clinical Specimens. *Journal of Molecular Diagnostics*, **2019**, 21, 214-227	5.1	19
65	Novel mRNA isoforms and mutations of uridine monophosphate synthetase and 5-fluorouracil resistance in colorectal cancer. *Pharmacogenomics Journal*, **2013**, 13, 148-58	3.5	18
64	Targeted error-suppressed quantification of circulating tumor DNA using semi-degenerate barcoded adapters and biotinylated baits. *Scientific Reports*, **2017**, 7, 10574	4.9	18
63	An RCOR1 loss-associated gene expression signature identifies a prognostically significant DLBCL subgroup. *Blood*, **2015**, 125, 959-66	2.2	18
62	LongSAGE profiling of nine human embryonic stem cell lines. *Genome Biology*, **2007**, 8, R113	18.3	18
61	Toward Personalized Lymphoma Immunotherapy: Identification of Common Driver Mutations Recognized by Patient CD8+ T Cells. *Clinical Cancer Research*, **2016**, 22, 2226-36	12.9	17
60	Newly identified mechanisms in B-cell non-Hodgkin lymphomas uncovered by next-generation sequencing. *Seminars in Hematology*, **2013**, 50, 303-13	4	17
59	Investigating the Genetic Causes of Sudden Unexpected Death in Children Through Targeted Next-Generation Sequencing Analysis. *Circulation: Cardiovascular Genetics*, **2017**, 10,		15
58	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	11.5	13
57	Disruption of the Gut Microbiota With Antibiotics Exacerbates Acute Vascular Rejection. *Transplantation*, **2018**, 102, 1085-1095	1.8	13
56	Preparation and analysis of microRNA libraries using the Illumina massively parallel sequencing technology. *Methods in Molecular Biology*, **2010**, 650, 173-99	1.4	13
55	Characterization of DLBCL with a PMBL gene expression signature. *Blood*, **2021**, 138, 136-148	2.2	9
54	IgCaller for reconstructing immunoglobulin gene rearrangements and oncogenic translocations from whole-genome sequencing in lymphoid neoplasms. *Nature Communications*, **2020**, 11, 3390	17.4	8
53	A high-throughput protocol for isolating cell-free circulating tumor DNA from peripheral blood. *BioTechniques*, **2019**, 66, 85-92	2.5	7
52	Kronos: a workflow assembler for genome analytics and informatics. *GigaScience*, **2017**, 6, 1-10	7.6	7
51	Management and visualization of whole genome shotgun assemblies using SAM. *BioTechniques*, **2005**, 38, 715-6, 718, 720	2.5	7
50	Enhancing knowledge discovery from cancer genomics data with Galaxy. *GigaScience*, **2017**, 6, 1-13	7.6	6

49	Evaluation of protocols for rRNA depletion-based RNA sequencing of nanogram inputs of mammalian total RNA. *PLoS ONE*, **2019**, 14, e0224578	3.7	6
48	Mutations In MLL2 and MEF2B Genes In Follicular Lymphoma and Diffuse Large B-Cell Lymphoma. *Blood*, **2010**, 116, 473-473	2.2	6
47	Treating lymphoma is now a bit EZ-er. *Blood Advances*, **2021**, 5, 2256-2263	7.8	6
46	Molecular profiling in diffuse large B-cell lymphoma: why so many types of subtypes?. *British Journal of Haematology*, **2021**,	4.5	6
45	DLBCL subclassification: divide and conquer?. *Blood*, **2020**, 135, 1722-1724	2.2	5
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	1.9	5
43	Targeted Error-Suppressed Detection of Circulating Paternal DNA to Establish a Diagnosis of Gestational Trophoblastic Neoplasm.. *JCO Precision Oncology*, **2017**, 1, 1-6	3.6	5
42	The impact of MYC and BCL2 structural variants in tumors of DLBCL morphology and mechanisms of false-negative MYC IHC. *Blood*, **2021**, 137, 2196-2208	2.2	5
41	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	1.4	5
40	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	1.9	4
39	Collaborative intra-tumor heterogeneity detection. *Bioinformatics*, **2019**, 35, i379-i388	7.2	4
38	Molecular attributes underlying central nervous system and systemic relapse in diffuse large B-cell lymphoma. *Haematologica*, **2021**, 106, 1466-1471	6.6	4
37	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		3
36	Proteotranscriptomic classification and characterization of pancreatic neuroendocrine neoplasms. *Cell Reports*, **2021**, 37, 109817	10.6	3
35	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	2.2	2
34	Indigenous sex-selective salmon harvesting demonstrates pre-contact marine resource management in Burrard Inlet, British Columbia, Canada. *Scientific Reports*, **2021**, 11, 21160	4.9	2
33	Kronos: a workflow assembler for genome analytics and informatics		2
32	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	3.8	1

31	Cancer Transcriptome Sequencing and Analysis **2014**, 31-47		1
30	The Double-Hit Gene Expression Signature Defines a Clinically and Biologically Distinct Subgroup within GCB-DLBCL. *Blood*, **2018**, 132, 921-921	2.2	1
29	Burkitt Lymphoma Genome Sequencing Project (BLGSP): Introduction. *Blood*, **2016**, 128, 1760-1760	2.2	1
28	Frequent mutations of FBXO11 highlight BCL6 as a therapeutic target in Burkitt lymphoma. *Blood Advances*, **2021**, 5, 5239-5257	7.8	1
27	Genome-wide discovery of somatic coding and regulatory variants in Diffuse Large B-cell Lymphoma		1
26	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	2.2	1
25	Coding and non-coding drivers of mantle cell lymphoma identified through exome and genome sequencing		1
24	TNFRSF14 Is Mutated in a Subset of Follicular Lymphoma and Correlated with Inferior Prognosis.. *Blood*, **2009**, 114, 1919-1919	2.2	1
23	SUBSTRA: Supervised Bayesian Patient Stratification. *Bioinformatics*, **2019**, 35, 3263-3272	7.2	1
22	Prognostic significance of FCGR2B expression for the response of DLBCL patients to rituximab or obinutuzumab treatment. *Blood Advances*, **2021**, 5, 2945-2957	7.8	1
21	PRPS-ST: A protocol-agnostic self-training method for gene expression-based classification of blood cancers. *Blood Cancer Discovery*, **2020**, 1, 244-257	7	0
20	Nfkbiz 3? UTR Mutations Confer Selective Growth Advantage and Affect Drug Response in Diffuse Large B-Cell Lymphoma. *Blood*, **2020**, 136, 31-31	2.2	0
19	Mutated RAS-associating proteins and ERK activation in relapse/refractory diffuse large B cell lymphoma.. *Scientific Reports*, **2022**, 12, 779	4.9	0
18	The Genomic Landscape of Plasmablastic Lymphoma (PBL) - an L.L.M.P.P. Project. *Blood*, **2021**, 138, 1326-1326	2.2	0
17	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	0.7	0
16	Temporal Dynamics of Genomic Alterations in a Germline-Mutated Pancreatic Cancer With Low Genomic Instability Burden but Exceptional Response to Fluorouracil, Oxaliplatin, Leucovorin, and Irinotecan. *JCO Precision Oncology*, **2018**, 2,	3.6	0
15	Novel Multiplexing Strategies for Quantification of Rare Alleles Using ddPCR. *Methods in Molecular Biology*, **2018**, 1768, 275-301	1.4	
14	Transcriptomics in the Age of Ultra High-Throughput Sequencing **2013**, 145-154		

List of Publications

13	The Copy Number Landscape of Relapsed and Refractory Diffuse Large B-Cell Lymphoma. *Blood*, **2020**, 136, 8-9	2.2
12	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	2.2
11	Shared and Distinct Genetic Features in Human and Canine B-Cell Lymphomas. *Blood*, **2021**, 138, 3509-3509	2.2
10	Complex Structural Variation Associated with Enhancer Hijacking and Loss of Tumor Suppressors in Mantle Cell Lymphoma. *Blood*, **2021**, 138, 675-675	2.2
9	Accurate Detection of the microRNA Transcriptome in a Leukemia Progression Model.. *Blood*, **2007**, 110, 866-866	2.2
8	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	2.2
7	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	2.2
6	Genome-Wide Identification of Human Microrna Located in Leukemia-Associated Genomic Alterations.. *Blood*, **2009**, 114, 1287-1287	2.2
5	FAS Mutations in Follicular Lymphoma Are Rare but Associated with Aggressive Clinical Behavior.. *Blood*, **2009**, 114, 3967-3967	2.2
4	Recurrent DNA Mutations In Non-Hodgkin Lymphomas Reveal Candidate Therapeutic Targets. *Blood*, **2010**, 116, 632-632	2.2
3	Novel Chromosomal Rearrangements and Sequence Mutations in High-Risk Ph-Like Acute Lymphoblastic Leukemia. *Blood*, **2011**, 118, 67-67	2.2
2	Genetic Alterations In Immune Cell Crosstalk Genes In Diffuse Large B-Cell Lymphoma Predict Survival. *Blood*, **2013**, 122, 500-500	2.2
1	Combinatorial and Machine Learning Approaches for Improved Somatic Variant Calling From Formalin-Fixed Paraffin-Embedded Genome Sequence Data.. *Frontiers in Genetics*, **2022**, 13, 834764	4.5