

# Ryan D Morin

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Mutated RAS-associating proteins and ERK activation in relapse/refractory diffuse large B cell lymphoma.. <i>Scientific Reports</i> , <b>2022</b> , 12, 779	4.9	0
137	Combinatorial and Machine Learning Approaches for Improved Somatic Variant Calling From Formalin-Fixed Paraffin-Embedded Genome Sequence Data.. <i>Frontiers in Genetics</i> , <b>2022</b> , 13, 834764	4.5	
136	Constrained FL: A Genetically Distinct Subgroup of Follicular Lymphoma with Low Rates of Somatic Hypermutation and a Reduced Propensity for Histologic Transformation. <i>Blood</i> , <b>2021</b> , 138, 807-807	2.2	
135	Shared and Distinct Genetic Features in Human and Canine B-Cell Lymphomas. <i>Blood</i> , <b>2021</b> , 138, 3509-3509		
134	Complex Structural Variation Associated with Enhancer Hijacking and Loss of Tumor Suppressors in Mantle Cell Lymphoma. <i>Blood</i> , <b>2021</b> , 138, 675-675	2.2	
133	The Genomic Landscape of Plasmablastic Lymphoma (PBL) - an L.L.M.P.P. Project. <i>Blood</i> , <b>2021</b> , 138, 1326-1326	2.2	0
132	Indigenous sex-selective salmon harvesting demonstrates pre-contact marine resource management in Burrard Inlet, British Columbia, Canada. <i>Scientific Reports</i> , <b>2021</b> , 11, 21160	4.9	2
131	Proteotranscriptomic classification and characterization of pancreatic neuroendocrine neoplasms. <i>Cell Reports</i> , <b>2021</b> , 37, 109817	10.6	3
130	Frequent mutations of FBXO11 highlight BCL6 as a therapeutic target in Burkitt lymphoma. <i>Blood Advances</i> , <b>2021</b> , 5, 5239-5257	7.8	1
129	The impact of MYC and BCL2 structural variants in tumors of DLBCL morphology and mechanisms of false-negative MYC IHC. <i>Blood</i> , <b>2021</b> , 137, 2196-2208	2.2	5
128	Characterization of DLBCL with a PMBL gene expression signature. <i>Blood</i> , <b>2021</b> , 138, 136-148	2.2	9
127	Treating lymphoma is now a bit EZ-er. <i>Blood Advances</i> , <b>2021</b> , 5, 2256-2263	7.8	6
126	DNA-based species identification of ancient salmonid remains provides new insight into pre-contact Coast Salish salmon fisheries in Burrard Inlet, British Columbia, Canada. <i>Journal of Archaeological Science: Reports</i> , <b>2021</b> , 37, 102956	0.7	0
125	Molecular attributes underlying central nervous system and systemic relapse in diffuse large B-cell lymphoma. <i>Haematologica</i> , <b>2021</b> , 106, 1466-1471	6.6	4
124	Mast Cell and Eosinophil Activation Are Associated With COVID-19 and TLR-Mediated Viral Inflammation: Implications for an Anti-Siglec-8 Antibody. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 650331	8.4	26
123	Prognostic significance of FCGR2B expression for the response of DLBCL patients to rituximab or obinutuzumab treatment. <i>Blood Advances</i> , <b>2021</b> , 5, 2945-2957	7.8	1
122	Molecular profiling in diffuse large B-cell lymphoma: why so many types of subtypes?. <i>British Journal of Haematology</i> , <b>2021</b> ,	4.5	6

121	PRPS-ST: A protocol-agnostic self-training method for gene expression-based classification of blood cancers. <i>Blood Cancer Discovery</i> , <b>2020</b> , 1, 244-257	7	0
120	DLBCL subclassification: divide and conquer?. <i>Blood</i> , <b>2020</b> , 135, 1722-1724	2.2	5
119	Genetic and evolutionary patterns of treatment resistance in relapsed B-cell lymphoma. <i>Blood Advances</i> , <b>2020</b> , 4, 2886-2898	7.8	24
118	TBL1XR1 Mutations Drive Extranodal Lymphoma by Inducing a Pro-tumorigenic Memory Fate. <i>Cell</i> , <b>2020</b> , 182, 297-316.e27	56.2	23
117	IgCaller for reconstructing immunoglobulin gene rearrangements and oncogenic translocations from whole-genome sequencing in lymphoid neoplasms. <i>Nature Communications</i> , <b>2020</b> , 11, 3390	17.4	8
116	Integration of Whole-Genome Sequencing With Circulating Tumor DNA Analysis Captures Clonal Evolution and Tumor Heterogeneity in Non-V600 BRAF Mutant Colorectal Cancer. <i>Clinical Colorectal Cancer</i> , <b>2020</b> , 19, 132-136.e3	3.8	1
115	TMEM30A loss-of-function mutations drive lymphomagenesis and confer therapeutically exploitable vulnerability in B-cell lymphoma. <i>Nature Medicine</i> , <b>2020</b> , 26, 577-588	50.5	22
114	A Probabilistic Classification Tool for Genetic Subtypes of Diffuse Large B Cell Lymphoma with Therapeutic Implications. <i>Cancer Cell</i> , <b>2020</b> , 37, 551-568.e14	24.3	194
113	The Copy Number Landscape of Relapsed and Refractory Diffuse Large B-Cell Lymphoma. <i>Blood</i> , <b>2020</b> , 136, 8-9	2.2	
112	Nfkbiz 3' UTR Mutations Confer Selective Growth Advantage and Affect Drug Response in Diffuse Large B-Cell Lymphoma. <i>Blood</i> , <b>2020</b> , 136, 31-31	2.2	0
111	Coding and noncoding drivers of mantle cell lymphoma identified through exome and genome sequencing. <i>Blood</i> , <b>2020</b> , 136, 572-584	2.2	19
110	Evaluating the quantity, quality and size distribution of cell-free DNA by multiplex droplet digital PCR. <i>Scientific Reports</i> , <b>2020</b> , 10, 12564	4.9	24
109	The double-hit signature identifies double-hit diffuse large B-cell lymphoma with genetic events cryptic to FISH. <i>Blood</i> , <b>2019</b> , 134, 1528-1532	2.2	40
108	Molecular and Genetic Characterization of MHC Deficiency Identifies EZH2 as Therapeutic Target for Enhancing Immune Recognition. <i>Cancer Discovery</i> , <b>2019</b> , 9, 546-563	24.4	123
107	Integrative genomic analysis of matched primary and metastatic pediatric osteosarcoma. <i>Journal of Pathology</i> , <b>2019</b> , 249, 319-331	9.4	19
106	In vitro analyses of suspected arrhythmogenic thin filament variants as a cause of sudden cardiac death in infants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 6969-6974	11.5	13
105	Double-Hit Gene Expression Signature Defines a Distinct Subgroup of Germinal Center B-Cell-Like Diffuse Large B-Cell Lymphoma. <i>Journal of Clinical Oncology</i> , <b>2019</b> , 37, 190-201	2.2	137
104	A high-throughput protocol for isolating cell-free circulating tumor DNA from peripheral blood. <i>BioTechniques</i> , <b>2019</b> , 66, 85-92	2.5	7

103	Collaborative intra-tumor heterogeneity detection. <i>Bioinformatics</i> , <b>2019</b> , 35, i379-i388	7.2	4
102	Evaluation of protocols for rRNA depletion-based RNA sequencing of nanogram inputs of mammalian total RNA. <i>PLoS ONE</i> , <b>2019</b> , 14, e0224578	3.7	6
101	Ultrasensitive Detection of Circulating Tumor DNA in Lymphoma via Targeted Hybridization Capture and Deep Sequencing of Barcoded Libraries. <i>Methods in Molecular Biology</i> , <b>2019</b> , 1956, 383-435	1.4	5
100	SUBSTRA: Supervised Bayesian Patient Stratification. <i>Bioinformatics</i> , <b>2019</b> , 35, 3263-3272	7.2	1
99	A Novel Multiplex Droplet Digital PCR Assay to Identify and Quantify KRAS Mutations in Clinical Specimens. <i>Journal of Molecular Diagnostics</i> , <b>2019</b> , 21, 214-227	5.1	19
98	Genome-wide discovery of somatic coding and noncoding mutations in pediatric endemic and sporadic Burkitt lymphoma. <i>Blood</i> , <b>2019</b> , 133, 1313-1324	2.2	75
97	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. <i>Leukemia and Lymphoma</i> , <b>2018</b> , 59, 2904-2910	1.9	5
96	The genomic landscape of two Burkitt lymphoma cases and derived cell lines: comparison between primary and relapse samples. <i>Leukemia and Lymphoma</i> , <b>2018</b> , 59, 2159-2174	1.9	4
95	Novel Multiplexing Strategies for Quantification of Rare Alleles Using ddPCR. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1768, 275-301	1.4	
94	Disruption of the Gut Microbiota With Antibiotics Exacerbates Acute Vascular Rejection. <i>Transplantation</i> , <b>2018</b> , 102, 1085-1095	1.8	13
93	Molecular and Genetic Characterization of MHC Deficiency Identifies EZH2 As a Therapeutic Target for Restoring MHC Expression in Diffuse Large B-Cell Lymphoma. <i>Blood</i> , <b>2018</b> , 132, 1560-1560	2.2	2
92	The Double-Hit Gene Expression Signature Defines a Clinically and Biologically Distinct Subgroup within GCB-DLBCL. <i>Blood</i> , <b>2018</b> , 132, 921-921	2.2	1
91	Obinutuzumab Plus Gemcitabine, Dexamethasone and Cisplatin (O-GDP) As Salvage Chemotherapy Prior to Autologous Stem Cell Transplant in Aggressive B Cell Lymphoma. <i>Blood</i> , <b>2018</b> , 132, 4610-4610	2.2	
90	Recurrent IL4R Somatic Mutations in Diffuse Large B-Cell Lymphoma Lead to an Altered Gene Expression Profile and Changes in Tumor Microenvironment Composition. <i>Blood</i> , <b>2018</b> , 132, 669-669	2.2	1
89	High-resolution architecture and partner genes of rearrangements in lymphoma with DLBCL morphology. <i>Blood Advances</i> , <b>2018</b> , 2, 2755-2765	7.8	38
88	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. <i>JCO Precision Oncology</i> , <b>2018</b> , 2,	3.6	0
87	Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. <i>Nature Communications</i> , <b>2018</b> , 9, 4001	17.4	64
86	Mapping the human T cell repertoire to recurrent driver mutations in MYD88 and EZH2 in lymphoma. <i>OncImmunity</i> , <b>2017</b> , 6, e1321184	7.2	20

85	Genome-wide chemical mapping of O-GlcNAcylated proteins in <i>Drosophila melanogaster</i> . <i>Nature Chemical Biology</i> , <b>2017</b> , 13, 161-167	11.7	30
84	Enhancing knowledge discovery from cancer genomics data with Galaxy. <i>GigaScience</i> , <b>2017</b> , 6, 1-13	7.6	6
83	Genetic profiling of and in diffuse large B-cell lymphoma determines cell-of-origin-specific clinical impact. <i>Blood</i> , <b>2017</b> , 129, 2760-2770	2.2	82
82	Targeted error-suppressed quantification of circulating tumor DNA using semi-degenerate barcoded adapters and biotinylated baits. <i>Scientific Reports</i> , <b>2017</b> , 7, 10574	4.9	18
81	Investigating the Genetic Causes of Sudden Unexpected Death in Children Through Targeted Next-Generation Sequencing Analysis. <i>Circulation: Cardiovascular Genetics</i> , <b>2017</b> , 10,		15
80	Kronos: a workflow assembler for genome analytics and informatics. <i>GigaScience</i> , <b>2017</b> , 6, 1-10	7.6	7
79	FOXL2 402C>G Mutation Can Be Identified in the Circulating Tumor DNA of Patients with Adult-Type Granulosa Cell Tumor. <i>Journal of Molecular Diagnostics</i> , <b>2017</b> , 19, 126-136	5.1	19
78	Targeted Error-Suppressed Detection of Circulating Paternal DNA to Establish a Diagnosis of Gestational Trophoblastic Neoplasm.. <i>JCO Precision Oncology</i> , <b>2017</b> , 1, 1-6	3.6	5
77	Activating mutations in genes related to TCR signaling in angioimmunoblastic and other follicular helper T-cell-derived lymphomas. <i>Blood</i> , <b>2016</b> , 128, 1490-502	2.2	170
76	Multiplex Droplet Digital PCR Quantification of Recurrent Somatic Mutations in Diffuse Large B-Cell and Follicular Lymphoma. <i>Clinical Chemistry</i> , <b>2016</b> , 62, 1238-47	5.5	34
75	Cell-free DNA (cfDNA): Clinical Significance and Utility in Cancer Shaped By Emerging Technologies. <i>Molecular Cancer Research</i> , <b>2016</b> , 14, 898-908	6.6	193
74	Toward Personalized Lymphoma Immunotherapy: Identification of Common Driver Mutations Recognized by Patient CD8+ T Cells. <i>Clinical Cancer Research</i> , <b>2016</b> , 22, 2226-36	12.9	17
73	Genetic Landscapes of Relapsed and Refractory Diffuse Large B-Cell Lymphomas. <i>Clinical Cancer Research</i> , <b>2016</b> , 22, 2290-300	12.9	130
72	Burkitt Lymphoma Genome Sequencing Project (BLGSP): Introduction. <i>Blood</i> , <b>2016</b> , 128, 1760-1760	2.2	1
71	Histological Transformation and Progression in Follicular Lymphoma: A Clonal Evolution Study. <i>PLoS Medicine</i> , <b>2016</b> , 13, e1002197	11.6	110
70	Genetic heterogeneity in primary and relapsed mantle cell lymphomas: Impact of recurrent CARD11 mutations. <i>Oncotarget</i> , <b>2016</b> , 7, 38180-38190	3.3	91
69	Whole-Organism Developmental Expression Profiling Identifies RAB-28 as a Novel Ciliary GTPase Associated with the BBSome and Intraflagellar Transport. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1006469	6	33
68	Comprehensive characterization of programmed death ligand structural rearrangements in B-cell non-Hodgkin lymphomas. <i>Blood</i> , <b>2016</b> , 128, 1206-13	2.2	40

67	Pediatric-type nodal follicular lymphoma: a biologically distinct lymphoma with frequent MAPK pathway mutations. <i>Blood</i> , <b>2016</b> , 128, 1093-100	2.2	78
66	Phase 2 study of panobinostat with or without rituximab in relapsed diffuse large B-cell lymphoma. <i>Blood</i> , <b>2016</b> , 128, 185-94	2.2	90
65	Comprehensive miRNA sequence analysis reveals survival differences in diffuse large B-cell lymphoma patients. <i>Genome Biology</i> , <b>2015</b> , 16, 18	18.3	71
64	Cross-cancer profiling of molecular alterations within the human autophagy interaction network. <i>Autophagy</i> , <b>2015</b> , 11, 1668-87	10.2	89
63	An RCOR1 loss-associated gene expression signature identifies a prognostically significant DLBCL subgroup. <i>Blood</i> , <b>2015</b> , 125, 959-66	2.2	18
62	Genetic inactivation of TRAF3 in canine and human B-cell lymphoma. <i>Blood</i> , <b>2015</b> , 125, 999-1005	2.2	48
61	Recurrent genomic rearrangements in primary testicular lymphoma. <i>Journal of Pathology</i> , <b>2015</b> , 236, 136-41	9.4	36
60	Immunogenicity of recurrent mutations in MYD88 and EZH2 in non-Hodgkin lymphomas <b>2015</b> , 3,		78
59	A Randomized, Phase II Study with Biomarker Analysis of Panobinostat with or without Rituximab in Relapsed Diffuse Large B Cell Lymphoma. <i>Blood</i> , <b>2015</b> , 126, 2719-2719	2.2	
58	Cancer Transcriptome Sequencing and Analysis <b>2014</b> , 31-47		1
57	A transgenic mouse model demonstrating the oncogenic role of mutations in the polycomb-group gene EZH2 in lymphomagenesis. <i>Blood</i> , <b>2014</b> , 123, 3914-24	2.2	63
56	Variability in DNA methylation defines novel epigenetic subgroups of DLBCL associated with different clinical outcomes. <i>Blood</i> , <b>2014</b> , 123, 1699-708	2.2	63
55	Newly identified mechanisms in B-cell non-Hodgkin lymphomas uncovered by next-generation sequencing. <i>Seminars in Hematology</i> , <b>2013</b> , 50, 303-13	4	17
54	Novel mRNA isoforms and mutations of uridine monophosphate synthetase and 5-fluorouracil resistance in colorectal cancer. <i>Pharmacogenomics Journal</i> , <b>2013</b> , 13, 148-58	3.5	18
53	Analysis of FOXO1 mutations in diffuse large B-cell lymphoma. <i>Blood</i> , <b>2013</b> , 121, 3666-74	2.2	100
52	Transcriptomics in the Age of Ultra High-Throughput Sequencing <b>2013</b> , 145-154		
51	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. <i>Blood</i> , <b>2013</b> , 122, 1256-65	2.2	289
50	Theoretical Investigation of the D83V Mutation within the Myocyte-Specific Enhancer Factor-2 Beta and Its Role in Cancer. <i>Journal of Theoretical Chemistry</i> , <b>2013</b> , 2013, 1-10		3

49	Genetic Alterations In Immune Cell Crosstalk Genes In Diffuse Large B-Cell Lymphoma Predict Survival. <i>Blood</i> , <b>2013</b> , 122, 500-500	2.2	
48	Whole transcriptome sequencing reveals recurrent NOTCH1 mutations in mantle cell lymphoma. <i>Blood</i> , <b>2012</b> , 119, 1963-71	2.2	264
47	TBL1XR1/TP63: a novel recurrent gene fusion in B-cell non-Hodgkin lymphoma. <i>Blood</i> , <b>2012</b> , 119, 4949-522		50
46	Genetic alterations activating kinase and cytokine receptor signaling in high-risk acute lymphoblastic leukemia. <i>Cancer Cell</i> , <b>2012</b> , 22, 153-66	24.3	515
45	Recurrent targets of aberrant somatic hypermutation in lymphoma. <i>Oncotarget</i> , <b>2012</b> , 3, 1308-19	3.3	101
44	JointSNVMix: a probabilistic model for accurate detection of somatic mutations in normal/tumour paired next-generation sequencing data. <i>Bioinformatics</i> , <b>2012</b> , 28, 907-13	7.2	136
43	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. <i>Nature</i> , <b>2011</b> , 476, 298-303	50.4	1180
42	Comprehensive analysis of mammalian miRNA* species and their role in myeloid cells. <i>Blood</i> , <b>2011</b> , 118, 3350-8	2.2	81
41	Genome-wide identification of human microRNAs located in leukemia-associated genomic alterations. <i>Blood</i> , <b>2011</b> , 117, 595-607	2.2	88
40	Somatic mutations at EZH2 Y641 act dominantly through a mechanism of selectively altered PRC2 catalytic activity, to increase H3K27 trimethylation. <i>Blood</i> , <b>2011</b> , 117, 2451-9	2.2	458
39	Novel Chromosomal Rearrangements and Sequence Mutations in High-Risk Ph-Like Acute Lymphoblastic Leukemia. <i>Blood</i> , <b>2011</b> , 118, 67-67	2.2	
38	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. <i>Nature Genetics</i> , <b>2010</b> , 42, 181-5	36.3	1273
37	Identification of miR-145 and miR-146a as mediators of the 5q- syndrome phenotype. <i>Nature Medicine</i> , <b>2010</b> , 16, 49-58	50.5	494
36	Alternative expression analysis by RNA sequencing. <i>Nature Methods</i> , <b>2010</b> , 7, 843-7	21.6	227
35	Acquired TNFRSF14 mutations in follicular lymphoma are associated with worse prognosis. <i>Cancer Research</i> , <b>2010</b> , 70, 9166-74	10.1	133
34	System-level analysis of neuroblastoma tumor-initiating cells implicates AURKB as a novel drug target for neuroblastoma. <i>Clinical Cancer Research</i> , <b>2010</b> , 16, 4572-82	12.9	36
33	SNVMix: predicting single nucleotide variants from next-generation sequencing of tumors. <i>Bioinformatics</i> , <b>2010</b> , 26, 730-6	7.2	174
32	MicroRNA transcriptome in the newborn mouse ovaries determined by massive parallel sequencing. <i>Molecular Human Reproduction</i> , <b>2010</b> , 16, 463-71	4.4	110



31	Preparation and analysis of microRNA libraries using the Illumina massively parallel sequencing technology. <i>Methods in Molecular Biology</i> , <b>2010</b> , 650, 173-99	1.4	13
30	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. <i>Genome Biology</i> , <b>2010</b> , 11, R82	18.3	144
29	Personalized oncogenomics <b>2010</b> , 11, 15		78
28	Hypomorphic temperature-sensitive alleles of NSDHL cause CK syndrome. <i>American Journal of Human Genetics</i> , <b>2010</b> , 87, 905-14	11	46
27	Genomic analysis of a rare human tumor. <i>BMC Bioinformatics</i> , <b>2010</b> , 11,	3.6	78
26	BCL6 repression of EP300 in human diffuse large B cell lymphoma cells provides a basis for rational combinatorial therapy. <i>Journal of Clinical Investigation</i> , <b>2010</b> , 120, 4569-82	15.9	88
25	Mutations In MLL2 and MEF2B Genes In Follicular Lymphoma and Diffuse Large B-Cell Lymphoma. <i>Blood</i> , <b>2010</b> , 116, 473-473	2.2	6
24	Recurrent DNA Mutations In Non-Hodgkin Lymphomas Reveal Candidate Therapeutic Targets. <i>Blood</i> , <b>2010</b> , 116, 632-632	2.2	
23	The completion of the Mammalian Gene Collection (MGC). <i>Genome Research</i> , <b>2009</b> , 19, 2324-33	9.7	98
22	De novo transcriptome assembly with ABySS. <i>Bioinformatics</i> , <b>2009</b> , 25, 2872-7	7.2	326
21	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. <i>Nature</i> , <b>2009</b> , 461, 809-13	50.4	879
20	Next-generation tag sequencing for cancer gene expression profiling. <i>Genome Research</i> , <b>2009</b> , 19, 1825-35	35	271
19	Mutation of FOXL2 in granulosa-cell tumors of the ovary. <i>New England Journal of Medicine</i> , <b>2009</b> , 360, 2719-29	59.2	551
18	Genome-Wide Identification of Human Micrnas Located in Leukemia-Associated Genomic Alterations.. <i>Blood</i> , <b>2009</b> , 114, 1287-1287	2.2	
17	TNFRSF14 Is Mutated in a Subset of Follicular Lymphoma and Correlated with Inferior Prognosis.. <i>Blood</i> , <b>2009</b> , 114, 1919-1919	2.2	1
16	FAS Mutations in Follicular Lymphoma Are Rare but Associated with Aggressive Clinical Behavior.. <i>Blood</i> , <b>2009</b> , 114, 3967-3967	2.2	
15	ALEXA: a microarray design platform for alternative expression analysis. <i>Nature Methods</i> , <b>2008</b> , 5, 118	21.6	19
14	In-depth characterization of the microRNA transcriptome in a leukemia progression model. <i>Genome Research</i> , <b>2008</b> , 18, 1787-97	9.7	148



13	Application of massively parallel sequencing to microRNA profiling and discovery in human embryonic stem cells. <i>Genome Research</i> , <b>2008</b> , 18, 610-21	9.7	879
12	Profiling the HeLa S3 transcriptome using randomly primed cDNA and massively parallel short-read sequencing. <i>BioTechniques</i> , <b>2008</b> , 45, 81-94	2.5	322
11	Comparative analysis of the small RNA transcriptomes of <i>Pinus contorta</i> and <i>Oryza sativa</i> . <i>Genome Research</i> , <b>2008</b> , 18, 571-84	9.7	278
10	Conifers have a unique small RNA silencing signature. <i>Rna</i> , <b>2008</b> , 14, 1508-15	5.8	91
9	LongSAGE profiling of nine human embryonic stem cell lines. <i>Genome Biology</i> , <b>2007</b> , 8, R113	18.3	18
8	Accurate Detection of the microRNA Transcriptome in a Leukemia Progression Model.. <i>Blood</i> , <b>2007</b> , 110, 866-866	2.2	
7	Sequencing and analysis of 10,967 full-length cDNA clones from <i>Xenopus laevis</i> and <i>Xenopus tropicalis</i> reveals post-tetraploidization transcriptome remodeling. <i>Genome Research</i> , <b>2006</b> , 16, 796-803	9.7	59
6	The complete genome of <i>Rhodococcus</i> sp. RHA1 provides insights into a catabolic powerhouse. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 15582-7	11.5	515
5	Management and visualization of whole genome shotgun assemblies using SAM. <i>BioTechniques</i> , <b>2005</b> , 38, 715-6, 718, 720	2.5	7
4	The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC). <i>Genome Research</i> , <b>2004</b> , 14, 2121-7	9.7	404
3	Genome-wide discovery of somatic coding and regulatory variants in Diffuse Large B-cell Lymphoma		1
2	Kronos: a workflow assembler for genome analytics and informatics		2
1	Coding and non-coding drivers of mantle cell lymphoma identified through exome and genome sequencing		1