Satoru Miyano

List of Publications by Citations

332 papers	12,305 citations	54 h-index	105 g-index
368 ext. papers	15,721 ext. citations	6.6 avg, IF	5.6 L-index

#	Paper	IF	Citations
332	Frequent pathway mutations of splicing machinery in myelodysplasia. *Nature*, **2011**, 478, 64-9	50.4	1415
331	Integrated molecular analysis of clear-cell renal cell carcinoma. *Nature Genetics*, **2013**, 45, 860-7	36.3	723
330	Mutational landscape and clonal architecture in grade II and III gliomas. *Nature Genetics*, **2015**, 47, 458-68	36.3	543
329	Integrated molecular analysis of adult T cell leukemia/lymphoma. *Nature Genetics*, **2015**, 47, 1304-15	36.3	469
328	Whole-genome mutational landscape and characterization of noncoding and structural mutations in liver cancer. *Nature Genetics*, **2016**, 48, 500-9	36.3	423
327	Somatic RHOA mutation in angioimmunoblastic T cell lymphoma. *Nature Genetics*, **2014**, 46, 171-5	36.3	411
326	Aberrant PD-L1 expression through 3SUTR disruption in multiple cancers. *Nature*, **2016**, 534, 402-6	50.4	403
325	Age-related remodelling of oesophageal epithelia by mutated cancer drivers. *Nature*, **2019**, 565, 312-317	50.4	270
324	Dynamics of clonal evolution in myelodysplastic syndromes. *Nature Genetics*, **2017**, 49, 204-212	36.3	228
323	Inherited and Somatic Defects in DDX41 in Myeloid Neoplasms. *Cancer Cell*, **2015**, 27, 658-70	24.3	228
322	Genomic Landscape of Esophageal Squamous Cell Carcinoma in´a Japanese Population. *Gastroenterology*, **2016**, 150, 1171-1182	13.3	195
321	Identification of genetic networks from a small number of gene expression patterns under the Boolean network model. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **1999**, 17-28	1.3	188
320	Genetic abnormalities in myelodysplasia and secondary acute myeloid leukemia: impact on outcome of stem cell transplantation. *Blood*, **2017**, 129, 2347-2358	2.2	184
319	Exome sequencing identifies secondary mutations of SETBP1 and JAK3 in juvenile myelomonocytic leukemia. *Nature Genetics*, **2013**, 45, 937-41	36.3	175
318	Acquired initiating mutations in early hematopoietic cells of CLL patients. *Cancer Discovery*, **2014**, 4, 1088-101	24.4	172
317	ACTN1 mutations cause congenital macrothrombocytopenia. *American Journal of Human Genetics*, **2013**, 92, 431-8	11	154
316	Genomic characterization of biliary tract cancers identifies driver genes and predisposing mutations. *Journal of Hepatology*, **2018**, 68, 959-969	13.4	149

315	Recurrent somatic mutations underlie corticotropin-independent Cushing's syndrome. *Science*, **2014**, 344, 917-20	33.3	142
314	Aberrant splicing of U12-type introns is the hallmark of ZRSR2 mutant myelodysplastic syndrome. *Nature Communications*, **2015**, 6, 6042	17.4	139
313	Whole-genome mutational landscape of liver cancers displaying biliary phenotype reveals hepatitis impact and molecular diversity. *Nature Communications*, **2015**, 6, 6120	17.4	139
312	Profiling of somatic mutations in acute myeloid leukemia with FLT3-ITD at diagnosis and relapse. *Blood*, **2015**, 126, 2491-501	2.2	134
311	An empirical Bayesian framework for somatic mutation detection from cancer genome sequencing data. *Nucleic Acids Research*, **2013**, 41, e89	20.1	129
310	Prognostic relevance of genetic alterations in diffuse lower-grade gliomas. *Neuro-Oncology*, **2018**, 20, 66-77	1	128
309	Global implementation of genomic medicine: We are not alone. *Science Translational Medicine*, **2015** , 7, 290ps13	17.5	112
308	Integrated genetic and epigenetic analysis defines novel molecular subgroups in rhabdomyosarcoma. *Nature Communications*, **2015**, 6, 7557	17.4	110
307	Algorithms for identifying Boolean networks and related biological networks based on matrix multiplication and fingerprint function. *Journal of Computational Biology*, **2000**, 7, 331-43	1.7	109
306	Integrated Multiregional Analysis Proposing a New Model of Colorectal Cancer Evolution. *PLoS Genetics*, **2016**, 12, e1005778	6	102
305	Circulating exosomal microRNA-203 is associated with metastasis possibly via inducing tumor-associated macrophages in colorectal cancer. *Oncotarget*, **2017**, 8, 78598-78613	3.3	92
304	Mutations in the gene encoding the E2 conjugating enzyme UBE2T cause Fanconi anemia. *American Journal of Human Genetics*, **2015**, 96, 1001-7	11	90
303	A novel cell-cycle-indicator, mVenus-p27K-, identifies quiescent cells and visualizes G0-G1 transition. *Scientific Reports*, **2014**, 4, 4012	4.9	88
302	A Simple Model-Based Approach to Inferring and Visualizing Cancer Mutation Signatures. *PLoS Genetics*, **2015**, 11, e1005657	6	87
301	Clonal evolution in myelodysplastic syndromes. *Nature Communications*, **2017**, 8, 15099	17.4	86
300	Defective Epstein-Barr virus in chronic active infection and haematological malignancy. *Nature Microbiology*, **2019**, 4, 404-413	26.6	80
299	Variegated RHOA mutations in adult T-cell leukemia/lymphoma. *Blood*, **2016**, 127, 596-604	2.2	77
298	Frequent mutations that converge on the NFKBIZ pathway in ulcerative colitis. *Nature*, **2020**, 577, 260-265	50.4	77

297	Prognostic relevance of integrated genetic profiling in adult T-cell leukemia/lymphoma. *Blood*, **2018**, 131, 215-225	2.2	76
296	Aberrant splicing and defective mRNA production induced by somatic spliceosome mutations in myelodysplasia. *Nature Communications*, **2018**, 9, 3649	17.4	76
295	Genomic landscape of liposarcoma. *Oncotarget*, **2015**, 6, 42429-44	3.3	75
294	Recurrent SPI1 (PU.1) fusions in high-risk pediatric T cell acute lymphoblastic leukemia. *Nature Genetics*, **2017**, 49, 1274-1281	36.3	74
293	Molecular heterogeneity in peripheral T-cell lymphoma, not otherwise specified revealed by comprehensive genetic profiling. *Leukemia*, **2019**, 33, 2867-2883	10.7	71
292	Haploinsufficiency of TNFAIP3 (A20) by germline mutation is involved in autoimmune lymphoproliferative syndrome. *Journal of Allergy and Clinical Immunology*, **2017**, 139, 1914-1922	11.5	69
291	Loss of function mutations in RPL27 and RPS27 identified by whole-exome sequencing in Diamond-Blackfan anaemia. *British Journal of Haematology*, **2015**, 168, 854-64	4.5	67
290	Unique mutation portraits and frequent COL2A1 gene alteration in chondrosarcoma. *Genome Research*, **2014**, 24, 1411-20	9.7	65
289	Abnormal hematopoiesis and autoimmunity in human subjects with germline IKZF1 mutations. *Journal of Allergy and Clinical Immunology*, **2017**, 140, 223-231	11.5	63
288	Whole genome sequencing discriminates hepatocellular carcinoma with intrahepatic metastasis from multi-centric tumors. *Journal of Hepatology*, **2017**, 66, 363-373	13.4	62
287	Antigen delivery targeted to tumor-associated macrophages overcomes tumor immune resistance. *Journal of Clinical Investigation*, **2019**, 129, 1278-1294	15.9	62
286	Phosphatase and tensin homolog (PTEN) mutation can cause activated phosphatidylinositol 3-kinase δ syndrome-like immunodeficiency. *Journal of Allergy and Clinical Immunology*, **2016**, 138, 1672-1680.e10	11.5	61
285	Mutational Landscape of Pediatric Acute Lymphoblastic Leukemia. *Cancer Research*, **2017**, 77, 390-400	10.1	60
284	Integrated analysis of whole genome and transcriptome sequencing reveals diverse transcriptomic aberrations driven by somatic genomic changes in liver cancers. *PLoS ONE*, **2014**, 9, e114263	3.7	58
283	Frequent structural variations involving programmed death ligands in Epstein-Barr virus-associated lymphomas. *Leukemia*, **2019**, 33, 1687-1699	10.7	57
282	Expression and clinical significance of genes frequently mutated in small cell lung cancers defined by whole exome/RNA sequencing. *Carcinogenesis*, **2015**, 36, 616-21	4.6	57
281	Null space based feature selection method for gene expression data. *International Journal of Machine Learning and Cybernetics*, **2012**, 3, 269-276	3.8	57
280	Biallelic DICER1 mutations in sporadic pleuropulmonary blastoma. *Cancer Research*, **2014**, 74, 2742-9	10.1	56

279	Quantitative T cell repertoire analysis by deep cDNA sequencing of T cell receptor and chains using next-generation sequencing (NGS). *OncoImmunology*, **2014**, 3, e968467	7.2	56
278	Integrated molecular profiling of juvenile myelomonocytic leukemia. *Blood*, **2018**, 131, 1576-1586	2.2	51
277	Association of single-nucleotide polymorphisms in the polymeric immunoglobulin receptor gene with immunoglobulin A nephropathy (IgAN) in Japanese patients. *Journal of Human Genetics*, **2003**, 48, 293-299	4.3	51
276	A temporal shift of the evolutionary principle shaping intratumor heterogeneity in colorectal cancer. *Nature Communications*, **2018**, 9, 2884	17.4	50
275	Circulating Tumor DNA Analysis for Liver Cancers and Its Usefulness as a Liquid Biopsy. *Cellular and Molecular Gastroenterology and Hepatology*, **2015**, 1, 516-534	7.9	48
274	A feature selection method using improved regularized linear discriminant analysis. *Machine Vision and Applications*, **2014**, 25, 775-786	2.8	48
273	ATP11C is a major flippase in human erythrocytes and its defect causes congenital hemolytic anemia. *Haematologica*, **2016**, 101, 559-65	6.6	47
272	Genomon ITDetector: a tool for somatic internal tandem duplication detection from cancer genome sequencing data. *Bioinformatics*, **2015**, 31, 116-8	7.2	46
271	Principal component analysis using QR decomposition. *International Journal of Machine Learning and Cybernetics*, **2013**, 4, 679-683	3.8	46
270	Somatic mutations in plasma cell-free DNA are diagnostic markers for esophageal squamous cell carcinoma recurrence. *Oncotarget*, **2016**, 7, 62280-62291	3.3	46
269	Clinical utility of next-generation sequencing for inherited bone marrow failure syndromes. *Genetics in Medicine*, **2017**, 19, 796-802	8.1	45
268	Comprehensive phosphoproteome analysis unravels the core signaling network that initiates the earliest synapse pathology in preclinical Alzheimer's disease brain. *Human Molecular Genetics*, **2015**, 24, 540-58	5.6	45
267	Whole-exome sequencing reveals the spectrum of gene mutations and the clonal evolution patterns in paediatric acute myeloid leukaemia. *British Journal of Haematology*, **2016**, 175, 476-489	4.5	42
266	Landscape and function of multiple mutations within individual oncogenes. *Nature*, **2020**, 582, 95-99	50.4	41
265	Gene expression and risk of leukemic transformation in myelodysplasia. *Blood*, **2017**, 130, 2642-2653	2.2	40
264	Gain-of-function mutation causes human combined immune deficiency. *Journal of Experimental Medicine*, **2018**, 215, 2715-2724	16.6	40
263	Two Aldehyde Clearance Systems Are Essential to Prevent Lethal Formaldehyde Accumulation in Mice and Humans. *Molecular Cell*, **2020**, 80, 996-1012.e9	17.6	39
262	GATA2 and secondary mutations in familial myelodysplastic syndromes and pediatric myeloid malignancies. *Haematologica*, **2015**, 100, e398-401	6.6	38

261	Integrated Molecular Profiling of Human Gastric Cancer Identifies DDR2 as a Potential Regulator of Peritoneal Dissemination. *Scientific Reports*, **2016**, 6, 22371	4.9	37
260	Prognostic impact of circulating tumor DNA status post-allogeneic hematopoietic stem cell transplantation in AML and MDS. *Blood*, **2019**, 133, 2682-2695	2.2	34
259	A novel ASXL1-OGT axis plays roles in H3K4 methylation and tumor suppression in myeloid malignancies. *Leukemia*, **2018**, 32, 1327-1337	10.7	33
258	A comprehensive characterization of -acting splicing-associated variants in human cancer. *Genome Research*, **2018**, 28, 1111-1125	9.7	32
257	Lung adenocarcinoma subtypes definable by lung development-related miRNA expression profiles in association with clinicopathologic features. *Carcinogenesis*, **2014**, 35, 2224-31	4.6	32
256	Elevated catenin pathway as a novel target for patients with resistance to EGF receptor targeting drugs. *Scientific Reports*, **2015**, 5, 13076	4.9	32
255	Identification of RNA-Binding Protein LARP4B as a Tumor Suppressor in Glioma. *Cancer Research*, **2016**, 76, 2254-64	10.1	31
254	Finding module-based gene networks with state-space models - Mining high-dimensional and short time-course gene expression data. *IEEE Signal Processing Magazine*, **2007**, 24, 37-46	9.4	31
253	Frequent germline mutations of in sporadic subcutaneous panniculitis-like T-cell lymphoma. *Blood Advances*, **2019**, 3, 588-595	7.8	31
252	The Transcriptional Landscape of p53 Signalling Pathway. *EBioMedicine*, **2017**, 20, 109-119	8.8	30
251	Characterization of the T cell repertoire by deep T cell receptor sequencing in tissues and blood from patients with advanced colorectal cancer. *Oncology Letters*, **2016**, 11, 3643-3649	2.6	30
250	Characterization of HBV integration patterns and timing in liver cancer and HBV-infected livers. *Oncotarget*, **2018**, 9, 25075-25088	3.3	30
249	Clinical significance of T cell clonality and expression levels of immune-related genes in endometrial cancer. *Oncology Reports*, **2017**, 37, 2603-2610	3.5	29
248	Comprehensive analysis of indels in whole-genome microsatellite regions and microsatellite instability across 21 cancer types. *Genome Research*, **2020**,	9.7	29
247	Invariant patterns of clonal succession determine specific clinical features of myelodysplastic syndromes. *Nature Communications*, **2019**, 10, 5386	17.4	29
246	Detection of APC mosaicism by next-generation sequencing in an FAP patient. *Journal of Human Genetics*, **2015**, 60, 227-31	4.3	28
245	A novel network profiling analysis reveals system changes in epithelial-mesenchymal transition. *PLoS ONE*, **2011**, 6, e20804	3.7	28
244	Characterization of T-cell Receptor Repertoire in Inflamed Tissues of Patients with Crohn's Disease Through Deep Sequencing. *Inflammatory Bowel Diseases*, **2016**, 22, 1275-85	4.5	28

243	TERT promoter mutations and chromosome 8p loss are characteristic of nonalcoholic fatty liver disease-related hepatocellular carcinoma. *International Journal of Cancer*, **2016**, 139, 2512-8	7.5	28
242	Classification of primary liver cancer with immunosuppression mechanisms and correlation with genomic alterations. *EBioMedicine*, **2020**, 53, 102659	8.8	26
241	Statistical analysis of hie (cold sensation) and hiesho (cold disorder) in kampo clinic. *Evidence-based Complementary and Alternative Medicine*, **2013**, 2013, 398458	2.3	26
240	Integrated exome and RNA sequencing of dedifferentiated liposarcoma. *Nature Communications*, **2019**, 10, 5683	17.4	26
239	Exome sequencing identified as a novel causative gene for Diamond-Blackfan anemia. *Haematologica*, **2017**, 102, e93-e96	6.6	25
238	Prescription of kampo drugs in the Japanese health care insurance program. *Evidence-based Complementary and Alternative Medicine*, **2013**, 2013, 576973	2.3	25
237	Polynomial-time learning of elementary formal systems. *New Generation Computing*, **2000**, 18, 217-242	0.9	24
236	Recurrent genetic defects on chromosome 5q in myeloid neoplasms. *Oncotarget*, **2017**, 8, 6483-6495	3.3	24
235	Loss of DNA Damage Response in Neuroblastoma and Utility of a PARP Inhibitor. *Journal of the National Cancer Institute*, **2017**, 109,	9.7	23
234	Association of a single-nucleotide polymorphism in the immunoglobulin mu-binding protein 2 gene with immunoglobulin A nephropathy. *Journal of Human Genetics*, **2005**, 50, 30-35	4.3	23
233	Genomic landscape of colitis-associated cancer indicates the impact of chronic inflammation and its stratification by mutations in the Wnt signaling. *Oncotarget*, **2018**, 9, 969-981	3.3	23
232	Comprehensive analysis of genetic aberrations linked to tumorigenesis in regenerative nodules of liver cirrhosis. *Journal of Gastroenterology*, **2019**, 54, 628-640	6.9	23
231	Understanding intratumor heterogeneity by combining genome analysis and mathematical modeling. *Cancer Science*, **2018**, 109, 884-892	6.9	22
230	Early detection and evolution of preleukemic clones in therapy-related myeloid neoplasms following autologous SCT. *Blood*, **2018**, 131, 1846-1857	2.2	21
229	Transcriptome analysis offers a comprehensive illustration of the genetic background of pediatric acute myeloid leukemia. *Blood Advances*, **2019**, 3, 3157-3169	7.8	21
228	Combined Cohesin-RUNX1 Deficiency Synergistically Perturbs Chromatin Looping and Causes Myelodysplastic Syndromes. *Cancer Discovery*, **2020**, 10, 836-853	24.4	21
227	NOTCH1 pathway activating mutations and clonal evolution in pediatric T-cell acute lymphoblastic leukemia. *Cancer Science*, **2019**, 110, 784-794	6.9	20
226	Metagenome Data on Intestinal Phage-Bacteria Associations Aids the Development of Phage Therapy against Pathobionts. *Cell Host and Microbe*, **2020**, 28, 380-389.e9	23.4	19

225	HapMuC: somatic mutation calling using heterozygous germ line variants near candidate mutations. *Bioinformatics*, **2014**, 30, 3302-9	7.2	19
224	Frequent genetic alterations in immune checkpoint-related genes in intravascular large B-cell lymphoma. *Blood*, **2021**, 137, 1491-1502	2.2	19
223	Late-Onset Combined Immunodeficiency with a Novel IL2RG Mutation and Probable Revertant Somatic Mosaicism. *Journal of Clinical Immunology*, **2015**, 35, 610-4	5.7	18
222	Genome-wide screening of DNA methylation associated with lymph node metastasis in esophageal squamous cell carcinoma. *Oncotarget*, **2017**, 8, 37740-37750	3.3	18
221	PIEZO1 gene mutation in a Japanese family with hereditary high phosphatidylcholine hemolytic anemia and hemochromatosis-induced diabetes mellitus. *International Journal of Hematology*, **2016**, 104, 125-9	2.3	18
220	De Novo Mutations Activating Germline TP53 in an Inherited Bone-Marrow-Failure Syndrome. *American Journal of Human Genetics*, **2018**, 103, 440-447	11	18
219	Aberrant DNA Methylation Is Associated with a Poor Outcome in Juvenile Myelomonocytic Leukemia. *PLoS ONE*, **2015**, 10, e0145394	3.7	18
218	Molecular pathogenesis of disease progression in MLL-rearranged AML. *Leukemia*, **2019**, 33, 612-624	10.7	18
217	Genetic and transcriptional landscape of plasma cells in POEMS syndrome. *Leukemia*, **2019**, 33, 1723-1735	10.7	18
216	BRCC3 mutations in myeloid neoplasms. *Haematologica*, **2015**, 100, 1051-7	6.6	17
215	Evaluation of sequence features from intrinsically disordered regions for the estimation of protein function. *PLoS ONE*, **2014**, 9, e89890	3.7	17
214	Identification of the genetic and clinical characteristics of neuroblastomas using genome-wide analysis. *Oncotarget*, **2017**, 8, 107513-107529	3.3	17
213	Functional Restoration of Bacteriomes and Viromes by Fecal Microbiota Transplantation. *Gastroenterology*, **2021**, 160, 2089-2102.e12	13.3	17
212	Characterization of the B-cell receptor repertoires in peanut allergic subjects undergoing oral immunotherapy. *Journal of Human Genetics*, **2018**, 63, 239-248	4.3	16
211	Divergent lncRNA MYMLR regulates MYC by eliciting DNA looping and promoter-enhancer interaction. *EMBO Journal*, **2019**, 38, e98441	13	16
210	Common Variable Immunodeficiency Caused by FANC Mutations. *Journal of Clinical Immunology*, **2017**, 37, 434-444	5.7	15
209	Replication stress triggers microsatellite destabilization and hypermutation leading to clonal expansion in vitro. *Nature Communications*, **2019**, 10, 3925	17.4	15
208	Targeting Tyro3 ameliorates a model of PGRN-mutant FTLD-TDP via tau-mediated synaptic pathology. *Nature Communications*, **2018**, 9, 433	17.4	15

207	Algorithms for inferring qualitative models of biological networks. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2000**, 293-304	1.3	15
206	Integrated Molecular Characterization of the Lethal Pediatric Cancer Pancreatoblastoma. *Cancer Research*, **2018**, 78, 865-876	10.1	15
205	Clinical and genetic features of dyskeratosis congenita, cryptic dyskeratosis congenita, and Hoyeraal-Hreidarsson syndrome in Japan. *International Journal of Hematology*, **2015**, 102, 544-52	2.3	14
204	Diagnostic challenge of Diamond-Blackfan anemia in mothers and children by whole-exome sequencing. *International Journal of Hematology*, **2017**, 105, 515-520	2.3	14
203	Overexpression of cohesion establishment factor DSCC1 through E2F in colorectal cancer. *PLoS ONE*, **2014**, 9, e85750	3.7	14
202	Novel neuroblastoma amplified sequence () mutations in a Japanese boy with fever-triggered recurrent acute liver failure. *Human Genome Variation*, **2019**, 6, 2	1.8	14
201	Hypoxic adaptation of leukemic cells infiltrating the CNS affords a therapeutic strategy targeting VEGFA. *Blood*, **2017**, 129, 3126-3129	2.2	13
200	Inference of gene regulatory networks incorporating multi-source biological knowledge via a state space model with L1 regularization. *PLoS ONE*, **2014**, 9, e105942	3.7	13
199	An Integrative Analysis to Identify Driver Genes in Esophageal Squamous Cell Carcinoma. *PLoS ONE*, **2015**, 10, e0139808	3.7	13
198	Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. *Cancer Cell*, **2021**, 39, 793-809.e8	24.3	13
197	The Difference between the Two Representative Kampo Formulas for Treating Dysmenorrhea: An Observational Study. *Evidence-based Complementary and Alternative Medicine*, **2016**, 2016, 3159617	2.3	13
196	Circulating tumor DNA dynamically predicts response and/or relapse in patients with hematological malignancies. *International Journal of Hematology*, **2018**, 108, 402-410	2.3	13
195	Phosphoethanolamine Accumulation Protects Cancer Cells under Glutamine Starvation through Downregulation of PCYT2. *Cell Reports*, **2019**, 29, 89-103.e7	10.6	12
194	Genetic heterogeneity of uncharacterized childhood autoimmune diseases with lymphoproliferation. *Pediatric Blood and Cancer*, **2018**, 65, e26831	3	12
193	Genomic Heterogeneity Within Individual Prostate Cancer Foci Impacts Predictive Biomarkers of Targeted Therapy. *European Urology Focus*, **2019**, 5, 416-424	5.1	12
192	WEIGHTED LASSO IN GRAPHICAL GAUSSIAN MODELING FOR LARGE GENE NETWORK ESTIMATION BASED ON MICROARRAY DATA **2007**,		12
191	Recurrent mutations in -rearranged acute myeloid leukemia. *Blood Advances*, **2018**, 2, 2879-2889	7.8	12
190	ASXL2 mutations are frequently found in pediatric AML patients with t(8;21)/ RUNX1-RUNX1T1 and associated with a better prognosis. *Genes Chromosomes and Cancer*, **2017**, 56, 382-393	5	11

189	Whole-exome sequence analysis of ataxia telangiectasia-like phenotype. *Journal of the Neurological Sciences*, **2014**, 340, 86-90	3.2	11
188	Integrated multiomics analysis of hepatoblastoma unravels its heterogeneity and provides novel druggable targets. *Npj Precision Oncology*, **2020**, 4, 20	9.8	11
187	Somatic mosaicism in chronic myeloid leukemia in remission. *Blood*, **2016**, 128, 2863-2866	2.2	11
186	ALPHLARD: a Bayesian method for analyzing HLA genes from whole genome sequence data. *BMC Genomics*, **2018**, 19, 790	4.5	11
185	Genomic analysis of pancreatic juice DNA assesses malignant risk of intraductal papillary mucinous neoplasm of pancreas. *Cancer Medicine*, **2019**, 8, 4565-4573	4.8	10
184	Dysregulation of Epstein-Barr Virus Infection in Hypomorphic ZAP70 Mutation. *Journal of Infectious Diseases*, **2018**, 218, 825-834	7	10
183	Sequence-specific bias correction for RNA-seq data using recurrent neural networks. *BMC Genomics* , **2017**, 18, 1044	4.5	10
182	Analysis of questionnaire for traditional medicine and development of decision support system. *Evidence-based Complementary and Alternative Medicine*, **2014**, 2014, 974139	2.3	10
181	Unbiased Detection of Driver Mutations in Extramammary Paget Disease. *Clinical Cancer Research*, **2021**, 27, 1756-1765	12.9	10
180	Landscape of driver mutations and their clinical impacts in pediatric B-cell precursor acute lymphoblastic leukemia. *Blood Advances*, **2020**, 4, 5165-5173	7.8	10
179	Combined landscape of single-nucleotide variants and copy number alterations in clonal hematopoiesis. *Nature Medicine*, **2021**, 27, 1239-1249	50.5	10
178	Reduced expression of APC-1B but not APC-1A by the deletion of promoter 1B is responsible for familial adenomatous polyposis. *Scientific Reports*, **2016**, 6, 26011	4.9	10
177	Large-scale DNA Barcode Library Generation for Biomolecule Identification in High-throughput Screens. *Scientific Reports*, **2017**, 7, 13899	4.9	9
176	Massively parallel sequencing of tenosynovial giant cell tumors reveals novel CSF1 fusion transcripts and novel somatic CBL mutations. *International Journal of Cancer*, **2019**, 145, 3276-3284	7.5	9
175	Pathogenic mutations identified by a multimodality approach in 117 Japanese Fanconi anemia patients. *Haematologica*, **2019**, 104, 1962-1973	6.6	9
174	Hybrid Petri net based modeling for biological pathway simulation. *Natural Computing*, **2011**, 10, 1099-1120	1.3	9
173	Clonally related diffuse large B-cell lymphoma and interdigitating dendritic cell sarcoma sharing translocation. *Haematologica*, **2018**, 103, e553-e556	6.6	9
172	Japanese genome-wide association study identifies a significant colorectal cancer susceptibility locus at chromosome 10p14. *Cancer Science*, **2017**, 108, 2239-2247	6.9	8

171	Gene set differential analysis of time course expression profiles via sparse estimation in functional logistic model with application to time-dependent biomarker detection. *Biostatistics*, **2016**, 17, 235-48	3.7	8
170	mutations in pediatric acute myeloid leukemia are associated with distinct genetic features and an inferior prognosis. *Blood*, **2018**, 131, 2266-2270	2.2	8
169	Integrated genetic and epigenetic analysis revealed heterogeneity of acute lymphoblastic leukemia in Down syndrome. *Cancer Science*, **2019**, 110, 3358-3367	6.9	8
168	Recursive Random Lasso (RRLasso) for Identifying Anti-Cancer Drug Targets. *PLoS ONE*, **2015**, 10, e0141869	3.7	8
167	DNA methylation-based classification reveals difference between pediatric T-cell acute lymphoblastic leukemia and normal thymocytes. *Leukemia*, **2020**, 34, 1163-1168	10.7	8
166	phyC: Clustering cancer evolutionary trees. *PLoS Computational Biology*, **2017**, 13, e1005509	5	7
165	Prediction of deficiency-excess pattern in Japanese Kampo medicine: Multi-centre data collection. *Complementary Therapies in Medicine*, **2019**, 45, 228-233	3.5	7
164	Transcriptional profiling of hematopoietic stem cells by high-throughput sequencing. *International Journal of Hematology*, **2009**, 89, 24-33	2.3	7
163	INFERRING GENE REGULATORY NETWORKS FROM TIME-ORDERED GENE EXPRESSION DATA OF BACILLUS SUBTILIS USING DIFFERENTIAL EQUATIONS **2002**,		7
162	Robust prediction of anti-cancer drug sensitivity and sensitivity-specific biomarker. *PLoS ONE*, **2014**, 9, e108990	3.7	7
161	Genetic and clinical landscape of breast cancers with germline BRCA1/2 variants. *Communications Biology*, **2020**, 3, 578	6.7	7
160	Clonal evolution and clinical implications of genetic abnormalities in blastic transformation of chronic myeloid leukaemia. *Nature Communications*, **2021**, 12, 2833	17.4	7
159	Genomic analysis of clonal origin of Langerhans cell histiocytosis following acute lymphoblastic leukaemia. *British Journal of Haematology*, **2016**, 175, 169-72	4.5	7
158	Cell-lineage level-targeted sequencing to identify acute myeloid leukemia with myelodysplasia-related changes. *Blood Advances*, **2018**, 2, 2513-2521	7.8	7
157	Constitutional abnormalities of IDH1 combined with secondary mutations predispose a patient with Maffucci syndrome to acute lymphoblastic leukemia. *Pediatric Blood and Cancer*, **2017**, 64, e26647	3	6
156	Discrimination of prediction models between cold-heat and deficiency-excess patterns. *Complementary Therapies in Medicine*, **2020**, 49, 102353	3.5	6
155	Comprehensive Analysis of Aberrant RNA Splicing in Myelodysplastic Syndromes. *Blood*, **2014**, 124, 826-826	2.2	6
154	Whole genome sequencing analysis identifies recurrent structural alterations in esophageal squamous cell carcinoma. *PeerJ*, **2020**, 8, e9294	3.1	6

153	Development of an MSI-positive colon tumor with aberrant DNA methylation in a PPAP patient. *Journal of Human Genetics*, **2019**, 64, 729-740	4.3	5
152	Molecular pathogenesis of progression to myeloid leukemia from TET-insufficient status. *Blood Advances*, **2020**, 4, 845-854	7.8	5
151	PARAMETER ESTIMATION OF IN SILICO BIOLOGICAL PATHWAYS WITH PARTICLE FILTERING TOWARDS A PETASCALE COMPUTING **2008**,		5
150	Genetic Predispositions to Myeloid Neoplasms Caused By Germline DDX41 Mutations. *Blood*, **2015**, 126, 2843-2843	2.2	5
149	Identification of a p53-repressed gene module in breast cancer cells. *Oncotarget*, **2017**, 8, 55821-55836	3.3	5
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