Satoru Miyano

List of Publications by Year in Descending Order

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	Dyserythropoietic anaemia with an intronic GATA1 splicing mutation in patients suspected to have Diamond-Blackfan anaemia. *EJHaem*, **2022**, 3, 163-167	0.9	
331	Repeated Lineage Switches in an Elderly Case of Refractory B-Cell Acute Lymphoblastic Leukemia With Gene Amplification: A Case Report and Literature Review.. *Frontiers in Oncology*, **2022**, 12, 799982	5.3	0
330	Role of the Orphan Transporter SLC35E1 in the Nuclear Egress of Herpes Simplex Virus 1.. *Journal of Virology*, **2022**, e0030622	6.6	0
329	Xprediction: Explainable EGFR-TKIs response prediction based on drug sensitivity specific gene networks.. *PLoS ONE*, **2022**, 17, e0261630	3.7	0
328	DDIT: An Online Predictor for Multiple Clinical Phenotypic Drug-Disease Associations.. *Frontiers in Pharmacology*, **2021**, 12, 772026	5.6	0
327	Unbiased Detection of Driver Mutations in Extramammary Paget Disease. *Clinical Cancer Research*, **2021**, 27, 1756-1765	12.9	10
326	EPOR/JAK/STAT Signaling Pathway As Therapeutic Target of Acute Erythroid Leukemia. *Blood*, **2021**, 138, 610-610	2.2	1
325	Der(1;7)(q10;p10) Presents with a Unique Genetic Profile and Frequent ETNK1 Mutations in Myeloid Neoplasms. *Blood*, **2021**, 138, 1513-1513	2.2	0
324	Mass Cytometric Analysis Revealed Dynamic Alteration of the Tumor Immune Environment in Bone Marrow from Children with Recurrent B Cell Precursor Acute Lymphoblastic Leukemia. *Blood*, **2021**, 138, 2390-2390	2.2	
323	Clonal Evolution Pattern and Prognostic Significance of Clonal Architecture in KMT2A-Rearranged Acute Myeloid Leukemia. *Blood*, **2021**, 138, 2358-2358	2.2	
322	Enhancing breakpoint resolution with deep segmentation model: A general refinement method for read-depth based structural variant callers. *PLoS Computational Biology*, **2021**, 17, e1009186	5	
321	Whole-genome landscape of adult T-cell leukemia/lymphoma. *Blood*, **2021**,	2.2	5
320	Alteration of the immune environment in bone marrow from children with recurrent B cell precursor acute lymphoblastic leukemia. *Cancer Science*, **2021**,	6.9	1
319	Automatic sparse principal component analysis. *Canadian Journal of Statistics*, **2021**, 49, 678-697	0.4	
318	Frequent genetic alterations in immune checkpoint-related genes in intravascular large B-cell lymphoma. *Blood*, **2021**, 137, 1491-1502	2.2	19
317	Comprehensive molecular analysis of genomic profiles and PD-L1 expression in lung adenocarcinoma with a high-grade fetal adenocarcinoma component. *Translational Lung Cancer Research*, **2021**, 10, 1292-1304	4.4	3
316	Clinical significance of RAS pathway alterations in pediatric acute myeloid leukemia. *Haematologica*, **2021**,	6.6	4

315	Clonal evolution and clinical implications of genetic abnormalities in blastic transformation of chronic myeloid leukaemia. *Nature Communications*, **2021**, 12, 2833	17.4	7
314	Modeling colorectal cancer evolution. *Journal of Human Genetics*, **2021**, 66, 869-878	4.3	2
313	Functional Restoration of Bacteriomes and Viromes by Fecal Microbiota Transplantation. *Gastroenterology*, **2021**, 160, 2089-2102.e12	13.3	17
312	Application of targeted nanopore sequencing for the screening and determination of structural variants in patients with Lynch syndrome. *Journal of Human Genetics*, **2021**, 66, 1053-1060	4.3	1
311	Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. *Cancer Cell*, **2021**, 39, 793-809.e8	24.3	13
310	Combined landscape of single-nucleotide variants and copy number alterations in clonal hematopoiesis. *Nature Medicine*, **2021**, 27, 1239-1249	50.5	10
309	Frequent mutations in HLA and related genes in extranodal NK/T cell lymphomas. *Leukemia and Lymphoma*, **2021**, 62, 95-103	1.9	3
308	Acquisition of monosomy 7 and a RUNX1 mutation in Pearson syndrome. *Pediatric Blood and Cancer* , **2021**, 68, e28799	3	2
307	Reduced-intensity conditioning is effective for hematopoietic stem cell transplantation in young pediatric patients with Diamond-Blackfan anemia. *Bone Marrow Transplantation*, **2021**, 56, 1013-1020	4.4	4
306	Association of high-risk neuroblastoma classification based on expression profiles with differentiation and metabolism. *PLoS ONE*, **2021**, 16, e0245526	3.7	3
305	Development of Philadelphia chromosome-negative acute myeloid leukemia with IDH2 and NPM1 mutations in a patient with chronic myeloid leukemia who showed a major molecular response to tyrosine kinase inhibitor therapy. *International Journal of Hematology*, **2021**, 113, 936-940	2.3	0
304	Molecular Classification and Tumor Microenvironment Characterization of Gallbladder Cancer by Comprehensive Genomic and Transcriptomic Analysis. *Cancers*, **2021**, 13,	6.6	3
303	Immunogenomic pan-cancer landscape reveals immune escape mechanisms and immunoediting histories. *Scientific Reports*, **2021**, 11, 15713	4.9	1
302	The Evolving Genomic Landscape of Esophageal Squamous Cell Carcinoma Under Chemoradiotherapy. *Cancer Research*, **2021**, 81, 4926-4938	10.1	1
301	Clinical Characteristics of Patients with Coronavirus Disease (COVID-19): Preliminary Baseline Report of Japan COVID-19 Task Force, a Nationwide Consortium to Investigate Host Genetics of COVID-19. *International Journal of Infectious Diseases*, **2021**, 113, 74-81	10.5	0
300	Description of longitudinal tumor evolution in a case of multiply relapsed clear cell sarcoma of the kidney.. *Cancer Reports*, **2021**, e1458	1.5	1
299	Novel COL4A1 mutations identified in infants with congenital hemolytic anemia in association with brain malformations. *Human Genome Variation*, **2020**, 7, 42	1.8	1
298	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

297	Successful Clinical Sequencing by Molecular Tumor Board in an Elderly Patient With Refractory S□ary Syndrome.. *JCO Precision Oncology*, **2020**, 4, 534-560	3.6	0
296	Genomic analysis of multiple myeloma using targeted capture sequencing in the Japanese cohort. *British Journal of Haematology*, **2020**, 191, 755-763	4.5	
295	Comprehensive analysis of indels in whole-genome microsatellite regions and microsatellite instability across 21 cancer types. *Genome Research*, **2020**,	9.7	29
294	Landscape and function of multiple mutations within individual oncogenes. *Nature*, **2020**, 582, 95-99	50.4	41
293	Molecular pathogenesis of progression to myeloid leukemia from TET-insufficient status. *Blood Advances*, **2020**, 4, 845-854	7.8	5
292	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
291	Classification of primary liver cancer with immunosuppression mechanisms and correlation with genomic alterations. *EBioMedicine*, **2020**, 53, 102659	8.8	26
290	Discrimination of prediction models between cold-heat and deficiency-excess patterns. *Complementary Therapies in Medicine*, **2020**, 49, 102353	3.5	6
289	Nanopore basecalling from a perspective of instance segmentation. *BMC Bioinformatics*, **2020**, 21, 136	3.6	4
288	Post-Treatment Clone Size Predicts Survival Independently of IPSS-R and Response after Azacitidine Therapy for MDS.. *Blood*, **2020**, 136, 12-13	2.2	
287	ASXL1 Mutations Predict a Poor Response to Darbepoetin Alfa in Anemic Patients with Low-Risk MDS: A Multicenter, Phase II Study. *Blood*, **2020**, 136, 28-29	2.2	
286	Genotype-Phenotype Relationships and Therapeutic Targets in Acute Erythroid Leukemia. *Blood*, **2020**, 136, 17-18	2.2	1
285	Prognostic Relevance of Genetic Abnormalities in Blastic Transformation of Chronic Myeloid Leukemia. *Blood*, **2020**, 136, 3-4	2.2	1
284	KRAS mutations Frequently Coexist with High-Risk MLL Fusions and Are Independent Adverse Prognostic Factors in MLL-Rearranged Acute Myeloid Leukemia. *Blood*, **2020**, 136, 28-29	2.2	
283	Clinical Impacts of Germline DDX41 Mutations on Myeloid Neoplasms. *Blood*, **2020**, 136, 38-40	2.2	2
282	Global gene network exploration based on explainable artificial intelligence approach. *PLoS ONE*, **2020**, 15, e0241508	3.7	2
281	Depressed Colorectal Cancer: A New Paradigm in Early Colorectal Cancer. *Clinical and Translational Gastroenterology*, **2020**, 11, e00269	4.2	2
280	Variant analysis of prostate cancer in Japanese patients and a new attempt to predict related biological pathways. *Oncology Reports*, **2020**, 43, 943-952	3.5	0

279	A unified simulation model for understanding the diversity of cancer evolution. *PeerJ*, **2020**, 8, e8842	3.1	2
278	Whole genome sequencing analysis identifies recurrent structural alterations in esophageal squamous cell carcinoma. *PeerJ*, **2020**, 8, e9294	3.1	6
277	DNA methylation-based classification reveals difference between pediatric T-cell acute lymphoblastic leukemia and normal thymocytes. *Leukemia*, **2020**, 34, 1163-1168	10.7	8
276	Frequent mutations that converge on the NFKBIZ pathway in ulcerative colitis. *Nature*, **2020**, 577, 260-265	50.4	77
275	Fusion partner-specific mutation profiles and KRAS mutations as adverse prognostic factors in MLL-rearranged AML. *Blood Advances*, **2020**, 4, 4623-4631	7.8	5
274	Genetic and clinical landscape of breast cancers with germline BRCA1/2 variants. *Communications Biology*, **2020**, 3, 578	6.7	7
273	Comprehensive genetic analysis of pediatric germ cell tumors identifies potential drug targets. *Communications Biology*, **2020**, 3, 544	6.7	3
272	Neoantimon: a multifunctional R package for identification of tumor-specific neoantigens. *Bioinformatics*, **2020**, 36, 4813-4816	7.2	2
271	Integrated multiomics analysis of hepatoblastoma unravels its heterogeneity and provides novel druggable targets. *Npj Precision Oncology*, **2020**, 4, 20	9.8	11
270	Genome-wide association studies and heritability analysis reveal the involvement of host genetics in the Japanese gut microbiota. *Communications Biology*, **2020**, 3, 686	6.7	5
269	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
268	Genome analysis of myelodysplastic syndromes among atomic bomb survivors in Nagasaki. *Haematologica*, **2020**, 105, 358-365	6.6	3
267	Combined Cohesin-RUNX1 Deficiency Synergistically Perturbs Chromatin Looping and Causes Myelodysplastic Syndromes. *Cancer Discovery*, **2020**, 10, 836-853	24.4	21
266	Prediction Model for Deficiency-Excess Patterns, Including Medium Pattern. *Kampo Medicine*, **2020**, 71, 315-325	0.1	
265	Replication stress triggers microsatellite destabilization and hypermutation leading to clonal expansion in vitro. *Nature Communications*, **2019**, 10, 3925	17.4	15
264	Phosphoethanolamine Accumulation Protects Cancer Cells under Glutamine Starvation through Downregulation of PCYT2. *Cell Reports*, **2019**, 29, 89-103.e7	10.6	12
263	Defective Epstein-Barr virus in chronic active infection and haematological malignancy. *Nature Microbiology*, **2019**, 4, 404-413	26.6	80
262	Frequent structural variations involving programmed death ligands in Epstein-Barr virus-associated lymphomas. *Leukemia*, **2019**, 33, 1687-1699	10.7	57

261	Robust Sample-Specific Stability Selection with Effective Error Control. *Journal of Computational Biology*, **2019**, 26, 202-217	1.7	2
260	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
259	Classification of patients with cold sensation by a review of systems database: A single-centre observational study. *Complementary Therapies in Medicine*, **2019**, 45, 7-13	3.5	1
258	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
257	The first case of elderly -positive B-cell acute lymphoblastic leukemia. *Leukemia and Lymphoma*, **2019**, 60, 2821-2824	1.9	2
256	Molecular heterogeneity in peripheral T-cell lymphoma, not otherwise specified revealed by comprehensive genetic profiling. *Leukemia*, **2019**, 33, 2867-2883	10.7	71
255	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
254	Duplication of F1245 missense mutation due to acquired uniparental disomy associated with aggressive progression in a patient with relapsed neuroblastoma. *Oncology Letters*, **2019**, 17, 3323-3329	2.6	2
253	Sensitivity analysis of agent-based simulation utilizing massively parallel computation and interactive data visualization. *PLoS ONE*, **2019**, 14, e0210678	3.7	2
252	A Bayesian model integration for mutation calling through data partitioning. *Bioinformatics*, **2019**, 35, 4247-4254	7.2	4
251	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
250	ALPHLARD-NT: Bayesian Method for Human Leukocyte Antigen Genotyping and Mutation Calling through Simultaneous Analysis of Normal and Tumor Whole-Genome Sequence Data. *Journal of Computational Biology*, **2019**, 26, 923-937	1.7	3
249	Pathogenic mutations identified by a multimodality approach in 117 Japanese Fanconi anemia patients. *Haematologica*, **2019**, 104, 1962-1973	6.6	9
248	Genomic Heterogeneity Within Individual Prostate Cancer Foci Impacts Predictive Biomarkers of Targeted Therapy. *European Urology Focus*, **2019**, 5, 416-424	5.1	12
247	Divergent lncRNA MYMLR regulates MYC by eliciting DNA looping and promoter-enhancer interaction. *EMBO Journal*, **2019**, 38, e98441	13	16
246	Prediction of deficiency-excess pattern in Japanese Kampo medicine: Multi-centre data collection. *Complementary Therapies in Medicine*, **2019**, 45, 228-233	3.5	7
245	An Unusually Short Latent Period of Therapy-Related Myeloid Neoplasm Harboring a Rare MLL-EP300 Rearrangement: Case Report and Literature Review. *Case Reports in Hematology*, **2019**, 2019, 4532434	0.7	1
244	Integrated genetic and epigenetic analysis revealed heterogeneity of acute lymphoblastic leukemia in Down syndrome. *Cancer Science*, **2019**, 110, 3358-3367	6.9	8

243	Antigen delivery targeted to tumor-associated macrophages overcomes tumor immune resistance. *Journal of Clinical Investigation*, **2019**, 129, 1278-1294	15.9	62
242	Distinct, Ethnic, Clinical, and Genetic Characteristics of Myelodysplastic Syndromes with Der(1;7). *Blood*, **2019**, 134, 5392-5392	2.2	2
241	Genomic Analysis of Therapy-Related Myeloid Neoplasms and Tracking of the Founder Clone By Circulating Tumor DNA. *Blood*, **2019**, 134, 5393-5393	2.2	
240	Integrated Analysis of Copy-Number Alterations and Gene Mutations in 2,000 Patients with Myeloid Neoplasms. *Blood*, **2019**, 134, 4216-4216	2.2	
239	Comprehensive analysis of genetic aberrations linked to tumorigenesis in regenerative nodules of liver cirrhosis. *Journal of Gastroenterology*, **2019**, 54, 628-640	6.9	23
238	Frequent germline mutations of in sporadic subcutaneous panniculitis-like T-cell lymphoma. *Blood Advances*, **2019**, 3, 588-595	7.8	31
237	Transcriptome analysis offers a comprehensive illustration of the genetic background of pediatric acute myeloid leukemia. *Blood Advances*, **2019**, 3, 3157-3169	7.8	21
236	Invariant patterns of clonal succession determine specific clinical features of myelodysplastic syndromes. *Nature Communications*, **2019**, 10, 5386	17.4	29
235	Integrated exome and RNA sequencing of dedifferentiated liposarcoma. *Nature Communications*, **2019**, 10, 5683	17.4	26
234	Virtual Grid Engine: a simulated grid engine environment for large-scale supercomputers. *BMC Bioinformatics*, **2019**, 20, 591	3.6	
233	Paraneoplastic hypereosinophilic syndrome associated with IL3-IgH positive acute lymphoblastic leukemia. *Pediatric Blood and Cancer*, **2019**, 66, e27449	3	4
232	Molecular pathogenesis of disease progression in MLL-rearranged AML. *Leukemia*, **2019**, 33, 612-624	10.7	18
231	Age-related remodelling of oesophageal epithelia by mutated cancer drivers. *Nature*, **2019**, 565, 312-317	50.4	270
230	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
229	Genetic and transcriptional landscape of plasma cells in POEMS syndrome. *Leukemia*, **2019**, 33, 1723-1735	10.7	18
228	NOTCH1 pathway activating mutations and clonal evolution in pediatric T-cell acute lymphoblastic leukemia. *Cancer Science*, **2019**, 110, 784-794	6.9	20
227	Modification of cellular and humoral immunity by somatically reverted T cells in X-linked lymphoproliferative syndrome type 1. *Journal of Allergy and Clinical Immunology*, **2019**, 143, 421-424.e11	11.5	5
226	A novel ASXL1-OGT axis plays roles in H3K4 methylation and tumor suppression in myeloid malignancies. *Leukemia*, **2018**, 32, 1327-1337	10.7	33

225	Dysregulation of Epstein-Barr Virus Infection in Hypomorphic ZAP70 Mutation. *Journal of Infectious Diseases*, **2018**, 218, 825-834	7	10
224	Understanding intratumor heterogeneity by combining genome analysis and mathematical modeling. *Cancer Science*, **2018**, 109, 884-892	6.9	22
223	Azacitidine effectively reduces -mutant leukemic cell burden in secondary acute myeloid leukemia after cord blood transplantation. *Leukemia and Lymphoma*, **2018**, 59, 2755-2756	1.9	
222	Genomic characterization of biliary tract cancers identifies driver genes and predisposing mutations. *Journal of Hepatology*, **2018**, 68, 959-969	13.4	149
221	Integrated molecular profiling of juvenile myelomonocytic leukemia. *Blood*, **2018**, 131, 1576-1586	2.2	51
220	Targeting Tyro3 ameliorates a model of PGRN-mutant FTLD-TDP via tau-mediated synaptic pathology. *Nature Communications*, **2018**, 9, 433	17.4	15
219	Different clonal dynamics of chronic myeloid leukaemia between bone marrow and the central nervous system. *British Journal of Haematology*, **2018**, 183, 842-845	4.5	
218	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
217	Distinct gene alterations with a high percentage of myeloperoxidase-positive leukemic blasts in de novo acute myeloid leukemia. *Leukemia Research*, **2018**, 65, 34-41	2.7	1
216	Early detection and evolution of preleukemic clones in therapy-related myeloid neoplasms following autologous SCT. *Blood*, **2018**, 131, 1846-1857	2.2	21
215	Prognostic relevance of genetic alterations in diffuse lower-grade gliomas. *Neuro-Oncology*, **2018**, 20, 66-77	1	128
214	Adaptive NetworkProfiler for Identifying Cancer Characteristic-Specific Gene Regulatory Networks. *Journal of Computational Biology*, **2018**, 25, 130-145	1.7	4
213	Prognostic relevance of integrated genetic profiling in adult T-cell leukemia/lymphoma. *Blood*, **2018**, 131, 215-225	2.2	76
212	Genetic heterogeneity of uncharacterized childhood autoimmune diseases with lymphoproliferation. *Pediatric Blood and Cancer*, **2018**, 65, e26831	3	12
211	A temporal shift of the evolutionary principle shaping intratumor heterogeneity in colorectal cancer. *Nature Communications*, **2018**, 9, 2884	17.4	50
210	A comprehensive characterization of -acting splicing-associated variants in human cancer. *Genome Research*, **2018**, 28, 1111-1125	9.7	32
209	mutations in pediatric acute myeloid leukemia are associated with distinct genetic features and an inferior prognosis. *Blood*, **2018**, 131, 2266-2270	2.2	8
208	De Novo Mutations Activating Germline TP53 in an Inherited Bone-Marrow-Failure Syndrome. *American Journal of Human Genetics*, **2018**, 103, 440-447	11	18

207	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
206	Analysis of Genomic Predispositions to Sporadic Myeloid Neoplasms Mediated By DDX41 in Japan. *Blood*, **2018**, 132, 4371-4371	2.2	
205	Phenotype-based gene analysis allowed successful diagnosis of X-linked neutropenia associated with a novel WASp mutation. *Annals of Hematology*, **2018**, 97, 367-369	3	5
204	Integrated Molecular Characterization of the Lethal Pediatric Cancer Pancreatoblastoma. *Cancer Research*, **2018**, 78, 865-876	10.1	15
203	Hidden FLT3-D835Y clone in FLT3-ITD-positive acute myeloid leukemia that evolved into very late relapse with T-lymphoblastic leukemia. *Leukemia and Lymphoma*, **2018**, 59, 1490-1493	1.9	1
202	Characterization of HBV integration patterns and timing in liver cancer and HBV-infected livers. *Oncotarget*, **2018**, 9, 25075-25088	3.3	30
201	Clonally related diffuse large B-cell lymphoma and interdigitating dendritic cell sarcoma sharing translocation. *Haematologica*, **2018**, 103, e553-e556	6.6	9
200	ALPHLARD: a Bayesian method for analyzing HLA genes from whole genome sequence data. *BMC Genomics*, **2018**, 19, 790	4.5	11
199	Gain-of-function mutation causes human combined immune deficiency. *Journal of Experimental Medicine*, **2018**, 215, 2715-2724	16.6	40
198	Aberrant splicing and defective mRNA production induced by somatic spliceosome mutations in myelodysplasia. *Nature Communications*, **2018**, 9, 3649	17.4	76
197	Cell-lineage level-targeted sequencing to identify acute myeloid leukemia with myelodysplasia-related changes. *Blood Advances*, **2018**, 2, 2513-2521	7.8	7
196	Recurrent mutations in -rearranged acute myeloid leukemia. *Blood Advances*, **2018**, 2, 2879-2889	7.8	12
195	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
194	Whole-exome analysis to detect congenital hemolytic anemia mimicking congenital dyserythropoietic anemia. *International Journal of Hematology*, **2018**, 108, 306-311	2.3	4
193	Clinical utility of next-generation sequencing for inherited bone marrow failure syndromes. *Genetics in Medicine*, **2017**, 19, 796-802	8.1	45
192	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
191	Genetic abnormalities in myelodysplasia and secondary acute myeloid leukemia: impact on outcome of stem cell transplantation. *Blood*, **2017**, 129, 2347-2358	2.2	184
190	Exome sequencing identified as a novel causative gene for Diamond-Blackfan anemia. *Haematologica*, **2017**, 102, e93-e96	6.6	25

189	Hypoxic adaptation of leukemic cells infiltrating the CNS affords a therapeutic strategy targeting VEGFA. *Blood*, **2017**, 129, 3126-3129	2.2	13
188	Clonal evolution in myelodysplastic syndromes. *Nature Communications*, **2017**, 8, 15099	17.4	86
187	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
186	Common Variable Immunodeficiency Caused by FANC Mutations. *Journal of Clinical Immunology*, **2017**, 37, 434-444	5.7	15
185	The Transcriptional Landscape of p53 Signalling Pathway. *EBioMedicine*, **2017**, 20, 109-119	8.8	30
184	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
183	Identification of an immunogenic neo-epitope encoded by mouse sarcoma using CXCR3 ligand mRNAs as sensors. *OncoImmunology*, **2017**, 6, e1306617	7.2	3
182	Dynamics of clonal evolution in myelodysplastic syndromes. *Nature Genetics*, **2017**, 49, 204-212	36.3	228
181	Abnormal hematopoiesis and autoimmunity in human subjects with germline IKZF1 mutations. *Journal of Allergy and Clinical Immunology*, **2017**, 140, 223-231	11.5	63
180	Large-scale DNA Barcode Library Generation for Biomolecule Identification in High-throughput Screens. *Scientific Reports*, **2017**, 7, 13899	4.9	9
179	Japanese genome-wide association study identifies a significant colorectal cancer susceptibility locus at chromosome 10p14. *Cancer Science*, **2017**, 108, 2239-2247	6.9	8
178	Gene expression and risk of leukemic transformation in myelodysplasia. *Blood*, **2017**, 130, 2642-2653	2.2	40
177	Loss of DNA Damage Response in Neuroblastoma and Utility of a PARP Inhibitor. *Journal of the National Cancer Institute*, **2017**, 109,	9.7	23
176	phyC: Clustering cancer evolutionary trees. *PLoS Computational Biology*, **2017**, 13, e1005509	5	7
175	Genome-wide screening of DNA methylation associated with lymph node metastasis in esophageal squamous cell carcinoma. *Oncotarget*, **2017**, 8, 37740-37750	3.3	18
174	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
173	Identification of a p53 target, CD137L, that mediates growth suppression and immune response of osteosarcoma cells. *Scientific Reports*, **2017**, 7, 10739	4.9	3
172	Requirement of glycosylation machinery in TLR responses revealed by CRISPR/Cas9 screening. *International Immunology*, **2017**, 29, 347-355	4.9	4

171	Molecular studies reveal and gene fusions displaced in a case of infantile acute lymphoblastic leukemia with complex karyotype. *Oncology Letters*, **2017**, 14, 2295-2299	2.6	4
170	Recurrent SPI1 (PU.1) fusions in high-risk pediatric T cell acute lymphoblastic leukemia. *Nature Genetics*, **2017**, 49, 1274-1281	36.3	74
169	Sequence-specific bias correction for RNA-seq data using recurrent neural networks. *BMC Genomics* , **2017**, 18, 1044	4.5	10
168	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
167	Whole genome sequencing discriminates hepatocellular carcinoma with intrahepatic metastasis from multi-centric tumors. *Journal of Hepatology*, **2017**, 66, 363-373	13.4	62
166	Interaction-Based Feature Selection for Uncovering Cancer Driver Genes Through Copy Number-Driven Expression Level. *Journal of Computational Biology*, **2017**, 24, 138-152	1.7	2
165	Mutational Landscape of Pediatric Acute Lymphoblastic Leukemia. *Cancer Research*, **2017**, 77, 390-400	10.1	60
164	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
163	Reconstruction of high read-depth signals from low-depth whole genome sequencing data using deep learning **2017**,		1
162	Recurrent genetic defects on chromosome 5q in myeloid neoplasms. *Oncotarget*, **2017**, 8, 6483-6495	3.3	24
161	Identification of a p53-repressed gene module in breast cancer cells. *Oncotarget*, **2017**, 8, 55821-55836	3.3	5
160	Identification of the genetic and clinical characteristics of neuroblastomas using genome-wide analysis. *Oncotarget*, **2017**, 8, 107513-107529	3.3	17
159	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
158	Variegated RHOA mutations in adult T-cell leukemia/lymphoma. *Blood*, **2016**, 127, 596-604	2.2	77
157	Predicting Japanese Kampo formulas by analyzing database of medical records: a preliminary observational study. *BMC Medical Informatics and Decision Making*, **2016**, 16, 118	3.6	4
156	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
155	Genomic Landscape of Esophageal Squamous Cell Carcinoma in´a Japanese Population. *Gastroenterology*, **2016**, 150, 1171-1182	13.3	195
154	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

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