Satoru Miyano

List of Publications by Year
in descending order

355 papers	18,206 citations	18482 62 h-index	17592 121 g-index
371 all docs	371 docs citations	371 times ranked	28753 citing authors

#	Article	IF	Citations
1	RoDiCE: robust differential protein co-expression analysis for cancer complexome. Bioinformatics, 2022, 38, 1269-1276.	4.1	1
2	Whole-genome landscape of adult T-cell leukemia/lymphoma. Blood, 2022, 139, 967-982.	1.4	44
3	Dyserythropoietic anaemia with an intronic GATA1 splicing mutation in patients suspected to have Diamondâ€Blackfan anaemia. EJHaem, 2022, 3, 163-167.	1.0	1
4	Uncovering Molecular Mechanisms of Drug Resistance via Network-Constrained Common Structure Identification. Journal of Computational Biology, 2022, , .	1.6	1
5	A high prevalence of myeloid malignancies in progeria with Werner syndrome is associated with p53 insufficiency. Experimental Hematology, 2022, 109, 11-17.	0.4	6
6	Repeated Lineage Switches in an Elderly Case of Refractory B-Cell Acute Lymphoblastic Leukemia With MLL Gene Amplification: A Case Report and Literature Review. Frontiers in Oncology, 2022, 12, 799982.	2.8	2
7	Description of longitudinal tumor evolution in a case of multiply relapsed clear cell sarcoma of the kidney. Cancer Reports, 2022, 5, e1458.	1.4	3
8	Novel TENM3â€“ALK fusion is an alternate mechanism for ALK activation in neuroblastoma. Oncogene, 2022, 41, 2789-2797.	5.9	3
9	Role of the Orphan Transporter SLC35E1 in the Nuclear Egress of Herpes Simplex Virus 1. Journal of Virology, 2022, , e0030622.	3.4	1
10	The landscape of genetic aberrations in myxofibrosarcoma. International Journal of Cancer, 2022, 151, 565-577.	5.1	13
11	Xprediction: Explainable EGFR-TKIs response prediction based on drug sensitivity specific gene networks. PLoS ONE, 2022, 17, e0261630.	2.5	1
12	Genetic Analysis of Pheochromocytoma and Paraganglioma Complicating Cyanotic Congenital Heart Disease. Journal of Clinical Endocrinology and Metabolism, 2022, 107, 2545-2555.	3.6	6
13	Abstract 6085: Clonal evolution of mammary epithelial cells into breast cancers. Cancer Research, 2022, 82, 6085-6085.	0.9	0
14	U-shaped association between abnormal serum uric acid levels and COVID-19 severity: reports from the Japan COVID-19 Task Force. International Journal of Infectious Diseases, 2022, 122, 747-754.	3.3	7
15	Amplified EPOR/JAK2 Genes Define a Unique Subtype of Acute Erythroid Leukemia. Blood Cancer Discovery, 2022, 3, 410-427.	5.0	7
16	Frequent mutations in HLA and related genes in extranodal NK/T cell lymphomas. Leukemia and Lymphoma, 2021, 62, 95-103.	1.3	12
17	Acquisition of monosomy 7 and a RUNX1 mutation in Pearson syndrome. Pediatric Blood and Cancer, 2021, 68, e28799.	1.5	9
18	Reduced-intensity conditioning is effective for hematopoietic stem cell transplantation in young pediatric patients with Diamondâ€“Blackfan anemia. Bone Marrow Transplantation, 2021, 56, 1013-1020.	2.4	10

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19	Association of high-risk neuroblastoma classification based on expression profiles with differentiation and metabolism. PLoS ONE, 2021, 16, e0245526.	2.5	11
20	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.	1.6	1
21	Molecular Classification and Tumor Microenvironment Characterization of Gallbladder Cancer by Comprehensive Genomic and Transcriptomic Analysis. Cancers, 2021, 13, 733.	3.7	12
22	Frequent genetic alterations in immune checkpointâ€“related genes in intravascular large B-cell lymphoma. Blood, 2021, 137, 1491-1502.	1.4	49
23	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.	2.8	7
24	Clinical significance of RAS pathway alterations in pediatric acute myeloid leukemia. Haematologica, 2021, , .	3.5	10
25	Clonal evolution and clinical implications of genetic abnormalities in blastic transformation of chronic myeloid leukaemia. Nature Communications, 2021, 12, 2833.	12.8	39
26	Modeling colorectal cancer evolution. Journal of Human Genetics, 2021, 66, 869-878.	2.3	14
27	Functional Restoration of Bacteriomes and Viromes by Fecal Microbiota Transplantation. Gastroenterology, 2021, 160, 2089-2102.e12.	1.3	45
28	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.	2.3	12
29	Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. Cancer Cell, 2021, 39, 793-809.e8.	16.8	65
30	Combined landscape of single-nucleotide variants and copy number alterations in clonal hematopoiesis. Nature Medicine, 2021, 27, 1239-1249.	30.7	78
31	Immunogenomic pan-cancer landscape reveals immune escape mechanisms and immunoediting histories. Scientific Reports, 2021, 11, 15713.	3.3	10
32	The Evolving Genomic Landscape of Esophageal Squamous Cell Carcinoma Under Chemoradiotherapy. Cancer Research, 2021, 81, 4926-4938.	0.9	20
33	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.	3.3	24
34	Unbiased Detection of Driver Mutations in Extramammary Paget Disease. Clinical Cancer Research, 2021, 27, 1756-1765.	7.0	24
35	Enhancing breakpoint resolution with deep segmentation model: A general refinement method for read-depth based structural variant callers. PLoS Computational Biology, 2021, 17, e1009186.	3.2	0
36	Possible Role of Cytochrome P450 1B1 in the Mechanism of Gemcitabine Resistance in Pancreatic Cancer. Biomedicines, 2021, 9, 1396.	3.2	9

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37	Alteration of the immune environment in bone marrow from children with recurrent B cell precursor acute lymphoblastic leukemia. Cancer Science, 2021, , .	3.9	3
38	Automatic sparse principal component analysis. Canadian Journal of Statistics, 2021, 49, 678-697.	0.9	0
39	EPOR/JAK/STAT Signaling Pathway As Therapeutic Target of Acute Erythroid Leukemia. Blood, 2021, 138, 610-610.	1.4	2
40	Der(1;7)(q10;p10) Presents with a Unique Genetic Profile and Frequent ETNK1 Mutations in Myeloid Neoplasms. Blood, 2021, 138, 1513-1513.	1.4	2
41	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.	1.4	0
42	Clonal Evolution Pattern and Prognostic Significance of Clonal Architecture in KMT2A-Rearranged Acute Myeloid Leukemia. Blood, 2021, 138, 2358-2358.	1.4	0
43	DDIT: An Online Predictor for Multiple Clinical Phenotypic Drug-Disease Associations. Frontiers in Pharmacology, 2021, 12, 772026.	3.5	1
44	On the application of BERT models for nanopore methylation detection. , 2021, , .		7
45	IL-3 Changing Cancer Genomics and Cancer Genomic Medicine by Artificial Intelligence and Large-Scale Data Analysis. Neuro-Oncology Advances, 2021, 3, vi1-vi1.	0.7	0
46	Genome analysis of myelodysplastic syndromes among atomic bomb survivors in Nagasaki. Haematologica, 2020, 105, 358-365.	3.5	5
47	DNA methylation-based classification reveals difference between pediatric T-cell acute lymphoblastic leukemia and normal thymocytes. Leukemia, 2020, 34, 1163-1168.	7.2	14
48	Frequent mutations that converge on the NFKBIZ pathway in ulcerative colitis. Nature, 2020, 577, 260-265.	27.8	168
49	Fusion partnerâ€“specific mutation profiles and KRAS mutations as adverse prognostic factors in MLL-rearranged AML. Blood Advances, 2020, 4, 4623-4631.	5.2	7
50	Genetic and clinical landscape of breast cancers with germline BRCA1/2 variants. Communications Biology, 2020, 3, 578.	4.4	20
51	Comprehensive genetic analysis of pediatric germ cell tumors identifies potential drug targets. Communications Biology, 2020, 3, 544.	4.4	9
52	Neoantimon: a multifunctional R package for identification of tumor-specific neoantigens. Bioinformatics, 2020, 36, 4813-4816.	4.1	8
53	Integrated multiomics analysis of hepatoblastoma unravels its heterogeneity and provides novel druggable targets. Npj Precision Oncology, 2020, 4, 20.	5.4	30
54	Genome-wide association studies and heritability analysis reveal the involvement of host genetics in the Japanese gut microbiota. Communications Biology, 2020, 3, 686.	4.4	40

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55	Landscape of driver mutations and their clinical impacts in pediatric B-cell precursor acute lymphoblastic leukemia. Blood Advances, 2020, 4, 5165-5173.	5.2	33
56	Novel COL4A1 mutations identified in infants with congenital hemolytic anemia in association with brain malformations. Human Genome Variation, 2020, 7, 42.	0.7	2
57	Two Aldehyde Clearance Systems Are Essential to Prevent Lethal Formaldehyde Accumulation in Mice and Humans. Molecular Cell, 2020, 80, 996-1012.e9.	9.7	92
58	Successful Clinical Sequencing by Molecular Tumor Board in an Elderly Patient With Refractory SÃ©zary Syndrome. JCO Precision Oncology, 2020, 4, 534-560.	3.0	1
59	Genomic analysis of multiple myeloma using targeted capture sequencing in the Japanese cohort. British Journal of Haematology, 2020, 191, 755-763.	2.5	0
60	Comprehensive analysis of indels in whole-genome microsatellite regions and microsatellite instability across 21 cancer types. Genome Research, 2020, 30, 334-346.	5.5	56
61	Landscape and function of multiple mutations within individual oncogenes. Nature, 2020, 582, 95-99.	27.8	79
62	Molecular pathogenesis of progression to myeloid leukemia from TET-insufficient status. Blood Advances, 2020, 4, 845-854.	5.2	11
63	Metagenome Data on Intestinal Phage-Bacteria Associations Aids the Development of Phage Therapy against Pathobionts. Cell Host and Microbe, 2020, 28, 380-389.e9.	11.0	51
64	Classification of primary liver cancer with immunosuppression mechanisms and correlation with genomic alterations. EBioMedicine, 2020, 53, 102659.	6.1	48
65	Discrimination of prediction models between cold-heat and deficiency-excess patterns. Complementary Therapies in Medicine, 2020, 49, 102353.	2.7	8
66	Nanopore basecalling from a perspective of instance segmentation. BMC Bioinformatics, 2020, 21, 136.	2.6	17
67	Combined Cohesinâ€“RUNX1 Deficiency Synergistically Perturbs Chromatin Looping and Causes Myelodysplastic Syndromes. Cancer Discovery, 2020, 10, 836-853.	9.4	51
68	Clinical Impacts of Germline DDX41 Mutations on Myeloid Neoplasms. Blood, 2020, 136, 38-40.	1.4	7
69	Global gene network exploration based on explainable artificial intelligence approach. PLoS ONE, 2020, 15, e0241508.	2.5	6
70	Depressed Colorectal Cancer: A New Paradigm in Early Colorectal Cancer. Clinical and Translational Gastroenterology, 2020, 11, e00269.	2.5	7
71	A unified simulation model for understanding the diversity of cancer evolution. PeerJ, 2020, 8, e8842.	2.0	6
72	Whole genome sequencing analysis identifies recurrent structural alterations in esophageal squamous cell carcinoma. PeerJ, 2020, 8, e9294.	2.0	12

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73	Variant analysis of prostate cancer in Japanese patients and a new attempt to predict related biological pathways. Oncology Reports, 2020, 43, 943-952.	2.6	3
74	Post-Treatment Clone Size Predicts Survival Independently of IPSS-R and Response after Azacitidine Therapy for MDS.. Blood, 2020, 136, 12-13.	1.4	0
75	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.	1.4	0
76	Genotype-Phenotype Relationships and Therapeutic Targets in Acute Erythroid Leukemia. Blood, 2020, 136, 17-18.	1.4	3
77	Prognostic Relevance of Genetic Abnormalities in Blastic Transformation of Chronic Myeloid Leukemia. Blood, 2020, 136, 3-4.	1.4	3
78	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.	1.4	0
79	Prediction Model for Deficiency-Excess Patterns, Including Medium Pattern. Kampo Medicine, 2020, 71, 315-325.	0.1	0
80	Genomic Heterogeneity Within Individual Prostate Cancer Foci Impacts Predictive Biomarkers of Targeted Therapy. European Urology Focus, 2019, 5, 416-424.	3.1	20
81	Divergent lnc <scp>RNA MYMLR</scp> regulates <scp>MYC</scp> by eliciting <scp>DNA</scp> looping and promoterâ€enhancer interaction. EMBO Journal, 2019, 38, e98441.	7.8	24
82	Prediction of deficiency-excess pattern in Japanese Kampo medicine: Multi-centre data collection. Complementary Therapies in Medicine, 2019, 45, 228-233.	2.7	8
83	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, 1-6.	0.4	3
84	Integrated genetic and epigenetic analysis revealed heterogeneity of acute lymphoblastic leukemia in Down syndrome. Cancer Science, 2019, 110, 3358-3367.	3.9	15
85	Replication stress triggers microsatellite destabilization and hypermutation leading to clonal expansion in vitro. Nature Communications, 2019, 10, 3925.	12.8	36
86	Phosphoethanolamine Accumulation Protects Cancer Cells under Glutamine Starvation through Downregulation of PCYT2. Cell Reports, 2019, 29, 89-103.e7.	6.4	29
87	Defective Epsteinâ€“Barr virus in chronic active infection and haematological malignancy. Nature Microbiology, 2019, 4, 404-413.	13.3	152
88	Frequent structural variations involving programmed death ligands in Epstein-Barr virus-associated lymphomas. Leukemia, 2019, 33, 1687-1699.	7.2	98
89	Robust Sample-Specific Stability Selection with Effective Error Control. Journal of Computational Biology, 2019, 26, 202-217.	1.6	3
90	Genomic analysis of pancreatic juice DNA assesses malignant risk of intraductal papillary mucinous neoplasm of pancreas. Cancer Medicine, 2019, 8, 4565-4573.	2.8	21

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91	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.	2.7	3
92	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.	5.1	28
93	The first case of elderly TCF3-HLF-positive B-cell acute lymphoblastic leukemia. Leukemia and Lymphoma, 2019, 60, 2821-2824.	1.3	6
94	Molecular heterogeneity in peripheral T-cell lymphoma, not otherwise specified revealed by comprehensive genetic profiling. Leukemia, 2019, 33, 2867-2883.	7.2	148
95	Development of an MSI-positive colon tumor with aberrant DNA methylation in a PPAP patient. Journal of Human Genetics, 2019, 64, 729-740.	2.3	7
96	Duplication of ALK F1245 missense mutation due to acquired uniparental disomy associated with aggressive progression in a patient with relapsed neuroblastoma. Oncology Letters, 2019, 17, 3323-3329.	1.8	4
97	Sensitivity analysis of agent-based simulation utilizing massively parallel computation and interactive data visualization. PLoS ONE, 2019, 14, e0210678.	2.5	12
98	A Bayesian model integration for mutation calling through data partitioning. Bioinformatics, 2019, 35, 4247-4254.	4.1	6
99	Prognostic impact of circulating tumor DNA status postâ€“allogeneic hematopoietic stem cell transplantation in AML and MDS. Blood, 2019, 133, 2682-2695.	1.4	62
100	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.	1.6	6
101	Pathogenic mutations identified by a multimodality approach in 117 Japanese Fanconi anemia patients. Haematologica, 2019, 104, 1962-1973.	3.5	22
102	Comprehensive analysis of genetic aberrations linked to tumorigenesis in regenerative nodules of liver cirrhosis. Journal of Gastroenterology, 2019, 54, 628-640.	5.1	33
103	Frequent germline mutations of HAVCR2 in sporadic subcutaneous panniculitis-like T-cell lymphoma. Blood Advances, 2019, 3, 588-595.	5.2	73
104	Transcriptome analysis offers a comprehensive illustration of the genetic background of pediatric acute myeloid leukemia. Blood Advances, 2019, 3, 3157-3169.	5.2	51
105	Invariant patterns of clonal succession determine specific clinical features of myelodysplastic syndromes. Nature Communications, 2019, 10, 5386.	12.8	53
106	Integrated exome and RNA sequencing of dedifferentiated liposarcoma. Nature Communications, 2019, 10, 5683.	12.8	41
107	Virtual Grid Engine: a simulated grid engine environment for large-scale supercomputers. BMC Bioinformatics, 2019, 20, 591.	2.6	0
108	Paraneoplastic hypereosinophilic syndrome associated with IL3â€“IgH positive acute lymphoblastic leukemia. Pediatric Blood and Cancer, 2019, 66, e27449.	1.5	12

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109	Molecular pathogenesis of disease progression in MLL-rearranged AML. Leukemia, 2019, 33, 612-624.	7.2	26
110	Age-related remodelling of oesophageal epithelia by mutated cancer drivers. Nature, 2019, 565, 312-317.	27.8	476
111	Novel neuroblastoma amplified sequence (NBAS) mutations in a Japanese boy with fever-triggered recurrent acute liver failure. Human Genome Variation, 2019, 6, 2.	0.7	26
112	Genetic and transcriptional landscape of plasma cells in POEMS syndrome. Leukemia, 2019, 33, 1723-1735.	7.2	28
113	<scp>NOTCH</scp>1 pathway activating mutations and clonal evolution in pediatric Tâ€cell acute lymphoblastic leukemia. Cancer Science, 2019, 110, 784-794.	3.9	26
114	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.	2.9	8
115	Antigen delivery targeted to tumor-associated macrophages overcomes tumor immune resistance. Journal of Clinical Investigation, 2019, 129, 1278-1294.	8.2	102
116	Distinct, Ethnic, Clinical, and Genetic Characteristics of Myelodysplastic Syndromes with Der(1;7). Blood, 2019, 134, 5392-5392.	1.4	2
117	Genomic Analysis of Therapy-Related Myeloid Neoplasms and Tracking of the Founder Clone By Circulating Tumor DNA. Blood, 2019, 134, 5393-5393.	1.4	0
118	Integrated Analysis of Copy-Number Alterations and Gene Mutations in 2,000 Patients with Myeloid Neoplasms. Blood, 2019, 134, 4216-4216.	1.4	0
119	A novel ASXL1â€“OGT axis plays roles in H3K4 methylation and tumor suppression in myeloid malignancies. Leukemia, 2018, 32, 1327-1337.	7.2	50
120	Dysregulation of Epstein-Barr Virus Infection in Hypomorphic ZAP70 Mutation. Journal of Infectious Diseases, 2018, 218, 825-834.	4.0	22
121	Understanding intratumor heterogeneity by combining genome analysis and mathematical modeling. Cancer Science, 2018, 109, 884-892.	3.9	49
122	Azacitidine effectively reduces TP53-mutant leukemic cell burden in secondary acute myeloid leukemia after cord blood transplantation. Leukemia and Lymphoma, 2018, 59, 2755-2756.	1.3	0
123	Genomic characterization of biliary tract cancers identifies driver genes and predisposing mutations. Journal of Hepatology, 2018, 68, 959-969.	3.7	254
124	Integrated molecular profiling of juvenile myelomonocytic leukemia. Blood, 2018, 131, 1576-1586.	1.4	78
125	Targeting Tyro3 ameliorates a model of PGRN-mutant FTLD-TDP via tau-mediated synaptic pathology. Nature Communications, 2018, 9, 433.	12.8	23
126	Different clonal dynamics of chronic myeloid leukaemia between bone marrow and the central nervous system. British Journal of Haematology, 2018, 183, 842-845.	2.5	0

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127	Characterization of the B-cell receptor repertoires in peanut allergic subjects undergoing oral immunotherapy. Journal of Human Genetics, 2018, 63, 239-248.	2.3	24
128	Distinct gene alterations with a high percentage of myeloperoxidase-positive leukemic blasts in de novo acute myeloid leukemia. Leukemia Research, 2018, 65, 34-41.	0.8	4
129	Early detection and evolution of preleukemic clones in therapy-related myeloid neoplasms following autologous SCT. Blood, 2018, 131, 1846-1857.	1.4	35
130	Prognostic relevance of genetic alterations in diffuse lower-grade gliomas. Neuro-Oncology, 2018, 20, 66-77.	1.2	225
131	Adaptive NetworkProfiler for Identifying Cancer Characteristic-Specific Gene Regulatory Networks. Journal of Computational Biology, 2018, 25, 130-145.	1.6	5
132	Prognostic relevance of integrated genetic profiling in adult T-cell leukemia/lymphoma. Blood, 2018, 131, 215-225.	1.4	124
133	Genetic heterogeneity of uncharacterized childhood autoimmune diseases with lymphoproliferation. Pediatric Blood and Cancer, 2018, 65, e26831.	1.5	18
134	Phenotype-based gene analysis allowed successful diagnosis of X-linked neutropenia associated with a novel WASp mutation. Annals of Hematology, 2018, 97, 367-369.	1.8	10
135	Integrated Molecular Characterization of the Lethal Pediatric Cancer Pancreatoblastoma. Cancer Research, 2018, 78, 865-876.	0.9	25
136	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.	1.3	2
137	Virtual Grid Engine: Accelerating thousands of omics sample analyses using large-scale supercomputers. , 2018, , .		0
138	Characterization of HBV integration patterns and timing in liver cancer and HBV-infected livers. Oncotarget, 2018, 9, 25075-25088.	1.8	57
139	Clonally related diffuse large B-cell lymphoma and interdigitating dendritic cell sarcoma sharing MYC translocation. Haematologica, 2018, 103, e553-e556.	3.5	14
140	ALPHLARD: a Bayesian method for analyzing HLA genes from whole genome sequence data. BMC Genomics, 2018, 19, 790.	2.8	16
141	Gain-of-function IKBKB mutation causes human combined immune deficiency. Journal of Experimental Medicine, 2018, 215, 2715-2724.	8.5	69
142	Aberrant splicing and defective mRNA production induced by somatic spliceosome mutations in myelodysplasia. Nature Communications, 2018, 9, 3649.	12.8	140
143	Cell-lineage levelâ€“targeted sequencing to identify acute myeloid leukemia with myelodysplasia-related changes. Blood Advances, 2018, 2, 2513-2521.	5.2	10
144	Recurrent CCND3 mutations in MLL-rearranged acute myeloid leukemia. Blood Advances, 2018, 2, 2879-2889.	5.2	19

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145	Circulating tumor DNA dynamically predicts response and/or relapse in patients with hematological malignancies. International Journal of Hematology, 2018, 108, 402-410.	1.6	17
146	Whole-exome analysis to detect congenital hemolytic anemia mimicking congenital dyserythropoietic anemia. International Journal of Hematology, 2018, 108, 306-311.	1.6	8
147	A temporal shift of the evolutionary principle shaping intratumor heterogeneity in colorectal cancer. Nature Communications, 2018, 9, 2884.	12.8	82
148	A comprehensive characterization of cis-acting splicing-associated variants in human cancer. Genome Research, 2018, 28, 1111-1125.	5.5	56
149	RUNX1 mutations in pediatric acute myeloid leukemia are associated with distinct genetic features and an inferior prognosis. Blood, 2018, 131, 2266-2270.	1.4	15
150	De Novo Mutations Activating Germline TP53 in an Inherited Bone-Marrow-Failure Syndrome. American Journal of Human Genetics, 2018, 103, 440-447.	6.2	33
151	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.	1.8	34
152	Analysis of Genomic Predispositions to Sporadic Myeloid Neoplasms Mediated By DDX41 in Japan. Blood, 2018, 132, 4371-4371.	1.4	0
153	Clinical utility of next-generation sequencing for inherited bone marrow failure syndromes. Genetics in Medicine, 2017, 19, 796-802.	2.4	66
154	ASXL2 mutations are frequently found in pediatric AML patients with t(8;21)/ RUNX1â€RUNX1T1 and associated with a better prognosis. Genes Chromosomes and Cancer, 2017, 56, 382-393.	2.8	18
155	Genetic abnormalities in myelodysplasia and secondary acute myeloid leukemia: impact on outcome of stem cell transplantation. Blood, 2017, 129, 2347-2358.	1.4	268
156	Exome sequencing identified RPS15A as a novel causative gene for Diamond-Blackfan anemia. Haematologica, 2017, 102, e93-e96.	3.5	30
157	Hypoxic adaptation of leukemic cells infiltrating the CNS affords a therapeutic strategy targeting VEGFA. Blood, 2017, 129, 3126-3129.	1.4	23
158	Clonal evolution in myelodysplastic syndromes. Nature Communications, 2017, 8, 15099.	12.8	118
159	Clinical significance of T cell clonality and expression levels of immune-related genes in endometrial cancer. Oncology Reports, 2017, 37, 2603-2610.	2.6	38
160	Common Variable Immunodeficiency Caused by FANC Mutations. Journal of Clinical Immunology, 2017, 37, 434-444.	3.8	18
161	The Transcriptional Landscape of p53 Signalling Pathway. EBioMedicine, 2017, 20, 109-119.	6.1	47
162	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.	1.5	9

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163	Identification of an immunogenic neo-epitope encoded by mouse sarcoma using CXCR3 ligand mRNAs as sensors. OncoImmunology, 2017, 6, e1306617.	4.6	5
164	Dynamics of clonal evolution in myelodysplastic syndromes. Nature Genetics, 2017, 49, 204-212.	21.4	348
165	Abnormal hematopoiesis and autoimmunity in human subjects with germline IKZF1 mutations. Journal of Allergy and Clinical Immunology, 2017, 140, 223-231.	2.9	99
166	Large-scale DNA Barcode Library Generation for Biomolecule Identification in High-throughput Screens. Scientific Reports, 2017, 7, 13899.	3.3	14
167	Japanese genomeâ€wide association study identifies a significant colorectal cancer susceptibility locus at chromosome 10p14. Cancer Science, 2017, 108, 2239-2247.	3.9	10
168	Gene expression and risk of leukemic transformation in myelodysplasia. Blood, 2017, 130, 2642-2653.	1.4	64
169	Loss of DNA Damage Response in Neuroblastoma and Utility of a PARP Inhibitor. Journal of the National Cancer Institute, 2017, 109, .	6.3	43
170	Identification of a p53 target, CD137L, that mediates growth suppression and immune response of osteosarcoma cells. Scientific Reports, 2017, 7, 10739.	3.3	3
171	Requirement of glycosylation machinery in TLR responses revealed by CRISPR/Cas9 screening. International Immunology, 2017, 29, 347-355.	4.0	9
172	Molecular studies reveal MLL-MLLT10/AF10 and ARID5B-MLL gene fusions displaced in a case of infantile acute lymphoblastic leukemia with complex karyotype. Oncology Letters, 2017, 14, 2295-2299.	1.8	6
173	Recurrent SPI1 (PU.1) fusions in high-risk pediatric T cell acute lymphoblastic leukemia. Nature Genetics, 2017, 49, 1274-1281.	21.4	100
174	Sequence-specific bias correction for RNA-seq data using recurrent neural networks. BMC Genomics, 2017, 18, 1044.	2.8	14
175	Haploinsufficiency of TNFAIP3 (A20) by germline mutation is involved in autoimmune lymphoproliferative syndrome. Journal of Allergy and Clinical Immunology, 2017, 139, 1914-1922.	2.9	91
176	Whole genome sequencing discriminates hepatocellular carcinoma with intrahepatic metastasis from multi-centric tumors. Journal of Hepatology, 2017, 66, 363-373.	3.7	81
177	Interaction-Based Feature Selection for Uncovering Cancer Driver Genes Through Copy Number-Driven Expression Level. Journal of Computational Biology, 2017, 24, 138-152.	1.6	3
178	Mutational Landscape of Pediatric Acute Lymphoblastic Leukemia. Cancer Research, 2017, 77, 390-400.	0.9	77
179	Diagnostic challenge of Diamondâ€“Blackfan anemia in mothers and children by whole-exome sequencing. International Journal of Hematology, 2017, 105, 515-520.	1.6	18
180	Reconstruction of high read-depth signals from low-depth whole genome sequencing data using deep learning. , 2017, , .		1

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