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	Frequent pathway mutations of splicing machinery in myelodysplasia. Nature, 2011, 478, 64-69.	27.8	1,764
2	Integrated molecular analysis of clear-cell renal cell carcinoma. Nature Genetics, 2013, 45, 860-867.	21.4	955
3	Mutational landscape and clonal architecture in grade II and III gliomas. Nature Genetics, 2015, 47, 458-468.	21.4	729
4	Integrated molecular analysis of adult T cell leukemia/lymphoma. Nature Genetics, 2015, 47, 1304-1315.	21.4	659
5	Whole-genome mutational landscape and characterization of noncoding and structural mutations in liver cancer. Nature Genetics, 2016, 48, 500-509.	21.4	596
6	Somatic RHOA mutation in angioimmunoblastic T cell lymphoma. Nature Genetics, 2014, 46, 171-175.	21.4	542
7	Aberrant PD-L1 expression through 3â€²-UTR disruption in multiple cancers. Nature, 2016, 534, 402-406.	27.8	536
8	Age-related remodelling of oesophageal epithelia by mutated cancer drivers. Nature, 2019, 565, 312-317.	27.8	476
9	Dynamics of clonal evolution in myelodysplastic syndromes. Nature Genetics, 2017, 49, 204-212.	21.4	348
10	IDENTIFICATION OF GENETIC NETWORKS FROM A SMALL NUMBER OF GENE EXPRESSION PATTERNS UNDER THE BOOLEAN NETWORK MODEL. , 1998, , 17-28.		346
11	Inherited and Somatic Defects in DDX41 in Myeloid Neoplasms. Cancer Cell, 2015, 27, 658-670.	16.8	341
12	Genetic abnormalities in myelodysplasia and secondary acute myeloid leukemia: impact on outcome of stem cell transplantation. Blood, 2017, 129, 2347-2358.	1.4	268
13	Genomic Landscape of Esophageal Squamous Cell Carcinoma inÂa Japanese Population. Gastroenterology, 2016, 150, 1171-1182.	1.3	265
14	Genomic characterization of biliary tract cancers identifies driver genes and predisposing mutations. Journal of Hepatology, 2018, 68, 959-969.	3.7	254
15	Prognostic relevance of genetic alterations in diffuse lower-grade gliomas. Neuro-Oncology, 2018, 20, 66-77.	1.2	225
16	Acquired Initiating Mutations in Early Hematopoietic Cells of CLL Patients. Cancer Discovery, 2014, 4, 1088-1101.	9.4	213
17	Exome sequencing identifies secondary mutations of SETBP1 and JAK3 in juvenile myelomonocytic leukemia. Nature Genetics, 2013, 45, 937-941.	21.4	203
18	Aberrant splicing of U12-type introns is the hallmark of ZRSR2 mutant myelodysplastic syndrome. Nature Communications, 2015, 6, 6042.	12.8	192

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19	ACTN1 Mutations Cause Congenital Macrothrombocytopenia. American Journal of Human Genetics, 2013, 92, 431-438.	6.2	186
20	Profiling of somatic mutations in acute myeloid leukemia with FLT3-ITD at diagnosis and relapse. Blood, 2015, 126, 2491-2501.	1.4	180
21	Whole-genome mutational landscape of liver cancers displaying biliary phenotype reveals hepatitis impact and molecular diversity. Nature Communications, 2015, 6, 6120.	12.8	178
22	An empirical Bayesian framework for somatic mutation detection from cancer genome sequencing data. Nucleic Acids Research, 2013, 41, e89-e89.	14.5	177
23	Recurrent somatic mutations underlie corticotropin-independent Cushingâ€™s syndrome. Science, 2014, 344, 917-920.	12.6	177
24	Frequent mutations that converge on the NFKBIZ pathway in ulcerative colitis. Nature, 2020, 577, 260-265.	27.8	168
25	Defective Epsteinâ€“Barr virus in chronic active infection and haematological malignancy. Nature Microbiology, 2019, 4, 404-413.	13.3	152
26	Integrated genetic and epigenetic analysis defines novel molecular subgroups in rhabdomyosarcoma. Nature Communications, 2015, 6, 7557.	12.8	149
27	Molecular heterogeneity in peripheral T-cell lymphoma, not otherwise specified revealed by comprehensive genetic profiling. Leukemia, 2019, 33, 2867-2883.	7.2	148
28	Global implementation of genomic medicine: We are not alone. Science Translational Medicine, 2015, 7, 290ps13.	12.4	146
29	Algorithms for Identifying Boolean Networks and Related Biological Networks Based on Matrix Multiplication and Fingerprint Function. Journal of Computational Biology, 2000, 7, 331-343.	1.6	145
30	Aberrant splicing and defective mRNA production induced by somatic spliceosome mutations in myelodysplasia. Nature Communications, 2018, 9, 3649.	12.8	140
31	A novel cell-cycle-indicator, mVenus-p27Kâ^', identifies quiescent cells and visualizes G0â€“G1 transition. Scientific Reports, 2014, 4, 4012.	3.3	134
32	Integrated Multiregional Analysis Proposing a New Model of Colorectal Cancer Evolution. PLoS Genetics, 2016, 12, e1005778.	3.5	134
33	Circulating exosomal microRNA-203 is associated with metastasis possibly via inducing tumor-associated macrophages in colorectal cancer. Oncotarget, 2017, 8, 78598-78613.	1.8	132
34	Prognostic relevance of integrated genetic profiling in adult T-cell leukemia/lymphoma. Blood, 2018, 131, 215-225.	1.4	124
35	Clonal evolution in myelodysplastic syndromes. Nature Communications, 2017, 8, 15099.	12.8	118
36	A Simple Model-Based Approach to Inferring and Visualizing Cancer Mutation Signatures. PLoS Genetics, 2015, 11, e1005657.	3.5	118

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37	Antigen delivery targeted to tumor-associated macrophages overcomes tumor immune resistance. Journal of Clinical Investigation, 2019, 129, 1278-1294.	8.2	102
38	Mutations in the Gene Encoding the E2 Conjugating Enzyme UBE2T Cause Fanconi Anemia. American Journal of Human Genetics, 2015, 96, 1001-1007.	6.2	100
39	Recurrent SPI1 (PU.1) fusions in high-risk pediatric T cell acute lymphoblastic leukemia. Nature Genetics, 2017, 49, 1274-1281.	21.4	100
40	Abnormal hematopoiesis and autoimmunity in human subjects with germline IKZF1 mutations. Journal of Allergy and Clinical Immunology, 2017, 140, 223-231.	2.9	99
41	Variegated RHOA mutations in adult T-cell leukemia/lymphoma. Blood, 2016, 127, 596-604.	1.4	98
42	Frequent structural variations involving programmed death ligands in Epstein-Barr virus-associated lymphomas. Leukemia, 2019, 33, 1687-1699.	7.2	98
43	Genomic landscape of liposarcoma. Oncotarget, 2015, 6, 42429-42444.	1.8	94
44	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
45	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
46	Loss of function mutations in RPL27 and RPS27 identified by wholeâ€exome sequencing in Diamondâ€Blackfan anaemia. British Journal of Haematology, 2015, 168, 854-864.	2.5	87
47	Phosphatase and tensin homolog (PTEN) mutation can cause activated phosphatidylinositol 3-kinase Î´ syndromeâ€“like immunodeficiency. Journal of Allergy and Clinical Immunology, 2016, 138, 1672-1680.e10.	2.9	87
48	Unique mutation portraits and frequent COL2A1 gene alteration in chondrosarcoma. Genome Research, 2014, 24, 1411-1420.	5.5	85
49	A temporal shift of the evolutionary principle shaping intratumor heterogeneity in colorectal cancer. Nature Communications, 2018, 9, 2884.	12.8	82
50	Whole genome sequencing discriminates hepatocellular carcinoma with intrahepatic metastasis from multi-centric tumors. Journal of Hepatology, 2017, 66, 363-373.	3.7	81
51	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.	2.5	79
52	Landscape and function of multiple mutations within individual oncogenes. Nature, 2020, 582, 95-99.	27.8	79
53	Integrated molecular profiling of juvenile myelomonocytic leukemia. Blood, 2018, 131, 1576-1586.	1.4	78
54	Combined landscape of single-nucleotide variants and copy number alterations in clonal hematopoiesis. Nature Medicine, 2021, 27, 1239-1249.	30.7	78

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55	Mutational Landscape of Pediatric Acute Lymphoblastic Leukemia. Cancer Research, 2017, 77, 390-400.	0.9	77
56	Expression and clinical significance of genes frequently mutated in small cell lung cancers defined by whole exome/RNA sequencing. Carcinogenesis, 2015, 36, 616-621.	2.8	73
57	Frequent germline mutations of HAVCR2 in sporadic subcutaneous panniculitis-like T-cell lymphoma. Blood Advances, 2019, 3, 588-595.	5.2	73
58	ATP11C is a major flippase in human erythrocytes and its defect causes congenital hemolytic anemia. Haematologica, 2016, 101, 559-565.	3.5	72
59	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, 540-558.	2.9	70
60	Gain-of-function IKBKB mutation causes human combined immune deficiency. Journal of Experimental Medicine, 2018, 215, 2715-2724.	8.5	69
61	Quantitative T cell repertoire analysis by deep cDNA sequencing of T cell receptor Î± and Î² chains using next-generation sequencing (NGS). OncoImmunology, 2014, 3, e968467.	4.6	68
62	Biallelic DICER1 Mutations in Sporadic Pleuropulmonary Blastoma. Cancer Research, 2014, 74, 2742-2749.	0.9	67
63	Circulating Tumor DNA Analysis for Liver Cancers and Its Usefulness as a Liquid Biopsy. Cellular and Molecular Gastroenterology and Hepatology, 2015, 1, 516-534.	4.5	67
64	INFERRING GENE REGULATORY NETWORKS FROM TIME-ORDERED GENE EXPRESSION DATA OF BACILLUS SUBTILIS USING DIFFERENTIAL EQUATIONS. , 2002, , .		67
65	Principal component analysis using QR decomposition. International Journal of Machine Learning and Cybernetics, 2013, 4, 679-683.	3.6	66
66	Clinical utility of next-generation sequencing for inherited bone marrow failure syndromes. Genetics in Medicine, 2017, 19, 796-802.	2.4	66
67	Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. Cancer Cell, 2021, 39, 793-809.e8.	16.8	65
68	Gene expression and risk of leukemic transformation in myelodysplasia. Blood, 2017, 130, 2642-2653.	1.4	64
69	Null space based feature selection method for gene expression data. International Journal of Machine Learning and Cybernetics, 2012, 3, 269-276.	3.6	62
70	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
71	Somatic mutations in plasma cell-free DNA are diagnostic markers for esophageal squamous cell carcinoma recurrence. Oncotarget, 2016, 7, 62280-62291.	1.8	62
72	Wholeâ€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.	2.5	60

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73	Association of single-nucleotide polymorphisms in the polymeric immunoglobulin receptor gene with immunoglobulinÂA nephropathy (IgAN) in Japanese patients. Journal of Human Genetics, 2003, 48, 293-299.	2.3	59
74	Genomon ITDetector: a tool for somatic internal tandem duplication detection from cancer genome sequencing data. Bioinformatics, 2015, 31, 116-118.	4.1	58
75	Integrated Molecular Profiling of Human Gastric Cancer Identifies DDR2 as a Potential Regulator of Peritoneal Dissemination. Scientific Reports, 2016, 6, 22371.	3.3	58
76	Characterization of HBV integration patterns and timing in liver cancer and HBV-infected livers. Oncotarget, 2018, 9, 25075-25088.	1.8	57
77	A comprehensive characterization of cis-acting splicing-associated variants in human cancer. Genome Research, 2018, 28, 1111-1125.	5.5	56
78	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
79	A feature selection method using improved regularized linear discriminant analysis. Machine Vision and Applications, 2014, 25, 775-786.	2.7	55
80	Invariant patterns of clonal succession determine specific clinical features of myelodysplastic syndromes. Nature Communications, 2019, 10, 5386.	12.8	53
81	Transcriptome analysis offers a comprehensive illustration of the genetic background of pediatric acute myeloid leukemia. Blood Advances, 2019, 3, 3157-3169.	5.2	51
82	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
83	Combined Cohesinâ€“RUNX1 Deficiency Synergistically Perturbs Chromatin Looping and Causes Myelodysplastic Syndromes. Cancer Discovery, 2020, 10, 836-853.	9.4	51
84	A novel ASXL1â€“OGT axis plays roles in H3K4 methylation and tumor suppression in myeloid malignancies. Leukemia, 2018, 32, 1327-1337.	7.2	50
85	Understanding intratumor heterogeneity by combining genome analysis and mathematical modeling. Cancer Science, 2018, 109, 884-892.	3.9	49
86	Frequent genetic alterations in immune checkpointâ€“related genes in intravascular large B-cell lymphoma. Blood, 2021, 137, 1491-1502.	1.4	49
87	GATA2 and secondary mutations in familial myelodysplastic syndromes and pediatric myeloid malignancies. Haematologica, 2015, 100, e398-e401.	3.5	48
88	Classification of primary liver cancer with immunosuppression mechanisms and correlation with genomic alterations. EBioMedicine, 2020, 53, 102659.	6.1	48
89	The Transcriptional Landscape of p53 Signalling Pathway. EBioMedicine, 2017, 20, 109-119.	6.1	47
90	Functional Restoration of Bacteriomes and Viromes by Fecal Microbiota Transplantation. Gastroenterology, 2021, 160, 2089-2102.e12.	1.3	45

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91	Whole-genome landscape of adult T-cell leukemia/lymphoma. Blood, 2022, 139, 967-982.	1.4	44
92	Loss of DNA Damage Response in Neuroblastoma and Utility of a PARP Inhibitor. Journal of the National Cancer Institute, 2017, 109, .	6.3	43
93	Identification of RNA-Binding Protein LARP4B as a Tumor Suppressor in Glioma. Cancer Research, 2016, 76, 2254-2264.	0.9	41
94	Integrated exome and RNA sequencing of dedifferentiated liposarcoma. Nature Communications, 2019, 10, 5683.	12.8	41
95	Lung adenocarcinoma subtypes definable by lung development-related miRNA expression profiles in association with clinicopathologic features. Carcinogenesis, 2014, 35, 2224-2231.	2.8	40
96	Elevated Î²-catenin pathway as a novel target for patients with resistance to EGF receptor targeting drugs. Scientific Reports, 2015, 5, 13076.	3.3	40
97	Characterization of T-cell Receptor Repertoire in Inflamed Tissues of Patients with CrohnÊ¼s Disease Through Deep Sequencing. Inflammatory Bowel Diseases, 2016, 22, 1275-1285.	1.9	40
98	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
99	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.	1.8	39
100	Clonal evolution and clinical implications of genetic abnormalities in blastic transformation of chronic myeloid leukaemia. Nature Communications, 2021, 12, 2833.	12.8	39
101	ALGORITHMS FOR INFERRING QUALITATIVE MODELS OF BIOLOGICAL NETWORKS. , 1999, , 293-304.		39
102	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.	5.6	38
103	A Novel Network Profiling Analysis Reveals System Changes in Epithelial-Mesenchymal Transition. PLoS ONE, 2011, 6, e20804.	2.5	38
104	Prescription of Kampo Drugs in the Japanese Health Care Insurance Program. Evidence-based Complementary and Alternative Medicine, 2013, 2013, 1-7.	1.2	38
105	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
106	TERT promoter mutations and chromosome 8p loss are characteristic of nonalcoholic fatty liver diseaseâ€related hepatocellular carcinoma. International Journal of Cancer, 2016, 139, 2512-2518.	5.1	36
107	Replication stress triggers microsatellite destabilization and hypermutation leading to clonal expansion in vitro. Nature Communications, 2019, 10, 3925.	12.8	36
108	Early detection and evolution of preleukemic clones in therapy-related myeloid neoplasms following autologous SCT. Blood, 2018, 131, 1846-1857.	1.4	35

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109	Recurrent genetic defects on chromosome 5q in myeloid neoplasms. Oncotarget, 2017, 8, 6483-6495.	1.8	34
110	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
111	Detection of APC mosaicism by next-generation sequencing in an FAP patient. Journal of Human Genetics, 2015, 60, 227-231.	2.3	33
112	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
113	Comprehensive analysis of genetic aberrations linked to tumorigenesis in regenerative nodules of liver cirrhosis. Journal of Gastroenterology, 2019, 54, 628-640.	5.1	33
114	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
115	Statistical Analysis ofHie(Cold Sensation) andHiesho(Cold Disorder) in Kampo Clinic. Evidence-based Complementary and Alternative Medicine, 2013, 2013, 1-8.	1.2	30
116	Exome sequencing identified RPS15A as a novel causative gene for Diamond-Blackfan anemia. Haematologica, 2017, 102, e93-e96.	3.5	30
117	Integrated multiomics analysis of hepatoblastoma unravels its heterogeneity and provides novel druggable targets. Npj Precision Oncology, 2020, 4, 20.	5.4	30
118	Phosphoethanolamine Accumulation Protects Cancer Cells under Glutamine Starvation through Downregulation of PCYT2. Cell Reports, 2019, 29, 89-103.e7.	6.4	29
119	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
120	Genetic and transcriptional landscape of plasma cells in POEMS syndrome. Leukemia, 2019, 33, 1723-1735.	7.2	28
121	Polynomial-time learning of elementary formal systems. New Generation Computing, 2000, 18, 217-242.	3.3	27
122	Association of a single-nucleotide polymorphism in the immunoglobulinÂÎ¼-binding protein 2 gene with immunoglobulin A nephropathy. Journal of Human Genetics, 2005, 50, 30-35.	2.3	27
123	Genome-wide screening of DNA methylation associated with lymph node metastasis in esophageal squamous cell carcinoma. Oncotarget, 2017, 8, 37740-37750.	1.8	27
124	Late-Onset Combined Immunodeficiency with a Novel IL2RG Mutation and Probable Revertant Somatic Mosaicism. Journal of Clinical Immunology, 2015, 35, 610-614.	3.8	26
125	Molecular pathogenesis of disease progression in MLL-rearranged AML. Leukemia, 2019, 33, 612-624.	7.2	26
126	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

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127	<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
128	PIEZO1 gene mutation in a Japanese family with hereditary high phosphatidylcholine hemolytic anemia and hemochromatosis-induced diabetes mellitus. International Journal of Hematology, 2016, 104, 125-129.	1.6	25
129	Integrated Molecular Characterization of the Lethal Pediatric Cancer Pancreatoblastoma. Cancer Research, 2018, 78, 865-876.	0.9	25
130	Aberrant DNA Methylation Is Associated with a Poor Outcome in Juvenile Myelomonocytic Leukemia. PLoS ONE, 2015, 10, e0145394.	2.5	25
131	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
132	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
133	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
134	Unbiased Detection of Driver Mutations in Extramammary Paget Disease. Clinical Cancer Research, 2021, 27, 1756-1765.	7.0	24
135	HapMuC: somatic mutation calling using heterozygous germ line variants near candidate mutations. Bioinformatics, 2014, 30, 3302-3309.	4.1	23
136	Hypoxic adaptation of leukemic cells infiltrating the CNS affords a therapeutic strategy targeting VEGFA. Blood, 2017, 129, 3126-3129.	1.4	23
137	Targeting Tyro3 ameliorates a model of PGRN-mutant FTLD-TDP via tau-mediated synaptic pathology. Nature Communications, 2018, 9, 433.	12.8	23
138	Identification of the genetic and clinical characteristics of neuroblastomas using genome-wide analysis. Oncotarget, 2017, 8, 107513-107529.	1.8	23
139	Dysregulation of Epstein-Barr Virus Infection in Hypomorphic ZAP70 Mutation. Journal of Infectious Diseases, 2018, 218, 825-834.	4.0	22
140	Pathogenic mutations identified by a multimodality approach in 117 Japanese Fanconi anemia patients. Haematologica, 2019, 104, 1962-1973.	3.5	22
141	Clinical and genetic features of dyskeratosis congenita, cryptic dyskeratosis congenita, and Hoyeraal-Hreidarsson syndrome in Japan. International Journal of Hematology, 2015, 102, 544-552.	1.6	21
142	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
143	Overexpression of Cohesion Establishment Factor DSCC1 through E2F in Colorectal Cancer. PLoS ONE, 2014, 9, e85750.	2.5	21
144	BRCC3 mutations in myeloid neoplasms. Haematologica, 2015, 100, 1051-7.	3.5	20

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145	Genomic Heterogeneity Within Individual Prostate Cancer Foci Impacts Predictive Biomarkers of Targeted Therapy. European Urology Focus, 2019, 5, 416-424.	3.1	20
146	Genetic and clinical landscape of breast cancers with germline BRCA1/2 variants. Communications Biology, 2020, 3, 578.	4.4	20
147	The Evolving Genomic Landscape of Esophageal Squamous Cell Carcinoma Under Chemoradiotherapy. Cancer Research, 2021, 81, 4926-4938.	0.9	20
148	Recurrent CCND3 mutations in MLL-rearranged acute myeloid leukemia. Blood Advances, 2018, 2, 2879-2889.	5.2	19
149	Evaluation of Sequence Features from Intrinsically Disordered Regions for the Estimation of Protein Function. PLoS ONE, 2014, 9, e89890.	2.5	19
150	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
151	Common Variable Immunodeficiency Caused by FANC Mutations. Journal of Clinical Immunology, 2017, 37, 434-444.	3.8	18
152	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
153	Genetic heterogeneity of uncharacterized childhood autoimmune diseases with lymphoproliferation. Pediatric Blood and Cancer, 2018, 65, e26831.	1.5	18
154	The Difference between the Two Representative Kampo Formulas for Treating Dysmenorrhea: An Observational Study. Evidence-based Complementary and Alternative Medicine, 2016, 2016, 1-10.	1.2	17
155	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.	3.3	17
156	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
157	Nanopore basecalling from a perspective of instance segmentation. BMC Bioinformatics, 2020, 21, 136.	2.6	17
158	An Integrative Analysis to Identify Driver Genes in Esophageal Squamous Cell Carcinoma. PLoS ONE, 2015, 10, e0139808.	2.5	17
159	ALPHLARD: a Bayesian method for analyzing HLA genes from whole genome sequence data. BMC Genomics, 2018, 19, 790.	2.8	16
160	Recursive Random Lasso (RRLasso) for Identifying Anti-Cancer Drug Targets. PLoS ONE, 2015, 10, e0141869.	2.5	15
161	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
162	Integrated genetic and epigenetic analysis revealed heterogeneity of acute lymphoblastic leukemia in Down syndrome. Cancer Science, 2019, 110, 3358-3367.	3.9	15

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163	Inference of Gene Regulatory Networks Incorporating Multi-Source Biological Knowledge via a State Space Model with L1 Regularization. PLoS ONE, 2014, 9, e105942.	2.5	15
164	WEIGHTED LASSO IN GRAPHICAL GAUSSIAN MODELING FOR LARGE GENE NETWORK ESTIMATION BASED ON MICROARRAY DATA. , 2007, , .		14
165	Hybrid Petri net based modeling for biological pathway simulation. Natural Computing, 2011, 10, 1099-1120.	3.0	14
166	Large-scale DNA Barcode Library Generation for Biomolecule Identification in High-throughput Screens. Scientific Reports, 2017, 7, 13899.	3.3	14
167	Sequence-specific bias correction for RNA-seq data using recurrent neural networks. BMC Genomics, 2017, 18, 1044.	2.8	14
168	Clonally related diffuse large B-cell lymphoma and interdigitating dendritic cell sarcoma sharing MYC translocation. Haematologica, 2018, 103, e553-e556.	3.5	14
169	DNA methylation-based classification reveals difference between pediatric T-cell acute lymphoblastic leukemia and normal thymocytes. Leukemia, 2020, 34, 1163-1168.	7.2	14
170	Modeling colorectal cancer evolution. Journal of Human Genetics, 2021, 66, 869-878.	2.3	14
171	Landscape Of Genetic Lesions In 944 Patients With Myelodysplastic Syndromes. Blood, 2013, 122, 521-521.	1.4	14
172	PARAMETER ESTIMATION OF IN SILICO BIOLOGICAL PATHWAYS WITH PARTICLE FILTERING TOWARDS A PETASCALE COMPUTING. , 2008, , .		13
173	Somatic mosaicism in chronic myeloid leukemia in remission. Blood, 2016, 128, 2863-2866.	1.4	13
174	The landscape of genetic aberrations in myxofibrosarcoma. International Journal of Cancer, 2022, 151, 565-577.	5.1	13
175	Analysis of Questionnaire for Traditional Medicine and Development of Decision Support System. Evidence-based Complementary and Alternative Medicine, 2014, 2014, 1-8.	1.2	12
176	Whole-exome sequence analysis of ataxia telangiectasia-like phenotype. Journal of the Neurological Sciences, 2014, 340, 86-90.	0.6	12
177	Genomic analysis of clonal origin of Langerhans cell histiocytosis following acute lymphoblastic leukaemia. British Journal of Haematology, 2016, 175, 169-172.	2.5	12
178	phyC: Clustering cancer evolutionary trees. PLoS Computational Biology, 2017, 13, e1005509.	3.2	12
179	Sensitivity analysis of agent-based simulation utilizing massively parallel computation and interactive data visualization. PLoS ONE, 2019, 14, e0210678.	2.5	12
180	Paraneoplastic hypereosinophilic syndrome associated with IL3â€‹gH positive acute lymphoblastic leukemia. Pediatric Blood and Cancer, 2019, 66, e27449.	1.5	12

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181	Frequent mutations in HLA and related genes in extranodal NK/T cell lymphomas. Leukemia and Lymphoma, 2021, 62, 95-103.	1.3	12
182	Molecular Classification and Tumor Microenvironment Characterization of Gallbladder Cancer by Comprehensive Genomic and Transcriptomic Analysis. Cancers, 2021, 13, 733.	3.7	12
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