

Yuichi Shiraishi

List of Publications by Year in descending order

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Version: 2024-02-01

174
papers

12,896
citations

46918

47
h-index

25716

108
g-index

183
all docs

183
docs citations

183
times ranked

21850
citing authors

#	ARTICLE	IF	CITATIONS
1	Frequent pathway mutations of splicing machinery in myelodysplasia. <i>Nature</i> , 2011, 478, 64-69.	13.7	1,764
2	Integrated molecular analysis of clear-cell renal cell carcinoma. <i>Nature Genetics</i> , 2013, 45, 860-867.	9.4	955
3	Mutational landscape and clonal architecture in grade II and III gliomas. <i>Nature Genetics</i> , 2015, 47, 458-468.	9.4	729
4	Integrated molecular analysis of adult T cell leukemia/lymphoma. <i>Nature Genetics</i> , 2015, 47, 1304-1315.	9.4	659
5	Whole-genome mutational landscape and characterization of noncoding and structural mutations in liver cancer. <i>Nature Genetics</i> , 2016, 48, 500-509.	9.4	596
6	Somatic RHOA mutation in angioimmunoblastic T cell lymphoma. <i>Nature Genetics</i> , 2014, 46, 171-175.	9.4	542
7	Aberrant PD-L1 expression through 3' UTR disruption in multiple cancers. <i>Nature</i> , 2016, 534, 402-406.	13.7	536
8	Age-related remodelling of oesophageal epithelia by mutated cancer drivers. <i>Nature</i> , 2019, 565, 312-317.	13.7	476
9	Dynamics of clonal evolution in myelodysplastic syndromes. <i>Nature Genetics</i> , 2017, 49, 204-212.	9.4	348
10	Inherited and Somatic Defects in DDX41 in Myeloid Neoplasms. <i>Cancer Cell</i> , 2015, 27, 658-670.	7.7	341
11	Genomic basis for RNA alterations in cancer. <i>Nature</i> , 2020, 578, 129-136.	13.7	280
12	Genetic abnormalities in myelodysplasia and secondary acute myeloid leukemia: impact on outcome of stem cell transplantation. <i>Blood</i> , 2017, 129, 2347-2358.	0.6	268
13	Genomic Landscape of Esophageal Squamous Cell Carcinoma in a Japanese Population. <i>Gastroenterology</i> , 2016, 150, 1171-1182.	0.6	265
14	Acquired Initiating Mutations in Early Hematopoietic Cells of CLL Patients. <i>Cancer Discovery</i> , 2014, 4, 1088-1101.	7.7	213
15	Aberrant splicing of U12-type introns is the hallmark of ZRSR2 mutant myelodysplastic syndrome. <i>Nature Communications</i> , 2015, 6, 6042.	5.8	192
16	Whole-genome mutational landscape of liver cancers displaying biliary phenotype reveals hepatitis impact and molecular diversity. <i>Nature Communications</i> , 2015, 6, 6120.	5.8	178
17	An empirical Bayesian framework for somatic mutation detection from cancer genome sequencing data. <i>Nucleic Acids Research</i> , 2013, 41, e89-e89.	6.5	177
18	Recurrent somatic mutations underlie corticotropin-independent Cushing's syndrome. <i>Science</i> , 2014, 344, 917-920.	6.0	177

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19	Frequent mutations that converge on the NFKBIZ pathway in ulcerative colitis. <i>Nature</i> , 2020, 577, 260-265.	13.7	168
20	Defective Epstein-Barr virus in chronic active infection and haematological malignancy. <i>Nature Microbiology</i> , 2019, 4, 404-413.	5.9	152
21	Integrated genetic and epigenetic analysis defines novel molecular subgroups in rhabdomyosarcoma. <i>Nature Communications</i> , 2015, 6, 7557.	5.8	149
22	Molecular heterogeneity in peripheral T-cell lymphoma, not otherwise specified revealed by comprehensive genetic profiling. <i>Leukemia</i> , 2019, 33, 2867-2883.	3.3	148
23	Aberrant splicing and defective mRNA production induced by somatic spliceosome mutations in myelodysplasia. <i>Nature Communications</i> , 2018, 9, 3649.	5.8	140
24	Integrated Multiregional Analysis Proposing a New Model of Colorectal Cancer Evolution. <i>PLoS Genetics</i> , 2016, 12, e1005778.	1.5	134
25	Prognostic relevance of integrated genetic profiling in adult T-cell leukemia/lymphoma. <i>Blood</i> , 2018, 131, 215-225.	0.6	124
26	Clonal evolution in myelodysplastic syndromes. <i>Nature Communications</i> , 2017, 8, 15099.	5.8	118
27	A Simple Model-Based Approach to Inferring and Visualizing Cancer Mutation Signatures. <i>PLoS Genetics</i> , 2015, 11, e1005657.	1.5	118
28	Mutations in the Gene Encoding the E2 Conjugating Enzyme UBE2T Cause Fanconi Anemia. <i>American Journal of Human Genetics</i> , 2015, 96, 1001-1007.	2.6	100
29	Recurrent SPI1 (PU.1) fusions in high-risk pediatric T cell acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2017, 49, 1274-1281.	9.4	100
30	Abnormal hematopoiesis and autoimmunity in human subjects with germline IKZF1 mutations. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 140, 223-231.	1.5	99
31	Frequent structural variations involving programmed death ligands in Epstein-Barr virus-associated lymphomas. <i>Leukemia</i> , 2019, 33, 1687-1699.	3.3	98
32	Genomic landscape and clonal evolution of acute myeloid leukemia with t(8;21): an international study on 331 patients. <i>Blood</i> , 2019, 133, 1140-1151.	0.6	96
33	Genomic landscape of liposarcoma. <i>Oncotarget</i> , 2015, 6, 42429-42444.	0.8	94
34	Haploinsufficiency of TNFAIP3 (A20) by germline mutation is involved in autoimmune lymphoproliferative syndrome. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 1914-1922.	1.5	91
35	Phosphatase and tensin homolog (PTEN) mutation can cause activated phosphatidylinositol 3-kinase $\hat{\imath}$ syndrome-like immunodeficiency. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 138, 1672-1680.e10.	1.5	87
36	A temporal shift of the evolutionary principle shaping intratumor heterogeneity in colorectal cancer. <i>Nature Communications</i> , 2018, 9, 2884.	5.8	82

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37	Whole genome sequencing discriminates hepatocellular carcinoma with intrahepatic metastasis from multi-centric tumors. <i>Journal of Hepatology</i> , 2017, 66, 363-373.	1.8	81
38	Integrated Analysis of Whole Genome and Transcriptome Sequencing Reveals Diverse Transcriptomic Aberrations Driven by Somatic Genomic Changes in Liver Cancers. <i>PLoS ONE</i> , 2014, 9, e114263.	1.1	79
39	Integrated molecular profiling of juvenile myelomonocytic leukemia. <i>Blood</i> , 2018, 131, 1576-1586.	0.6	78
40	Frequent germline mutations of HAVCR2 in sporadic subcutaneous panniculitis-like T-cell lymphoma. <i>Blood Advances</i> , 2019, 3, 588-595.	2.5	73
41	Biallelic <i>DICER1</i> Mutations in Sporadic Pleuropulmonary Blastoma. <i>Cancer Research</i> , 2014, 74, 2742-2749.	0.4	67
42	Clinical utility of next-generation sequencing for inherited bone marrow failure syndromes. <i>Genetics in Medicine</i> , 2017, 19, 796-802.	1.1	66
43	Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. <i>Cancer Cell</i> , 2021, 39, 793-809.e8.	7.7	65
44	Gene expression and risk of leukemic transformation in myelodysplasia. <i>Blood</i> , 2017, 130, 2642-2653.	0.6	64
45	Whole-exome sequencing reveals the spectrum of gene mutations and the clonal evolution patterns in paediatric acute myeloid leukaemia. <i>British Journal of Haematology</i> , 2016, 175, 476-489.	1.2	60
46	Genomon ITDetector: a tool for somatic internal tandem duplication detection from cancer genome sequencing data. <i>Bioinformatics</i> , 2015, 31, 116-118.	1.8	58
47	Characterization of HBV integration patterns and timing in liver cancer and HBV-infected livers. <i>Oncotarget</i> , 2018, 9, 25075-25088.	0.8	57
48	A comprehensive characterization of <i>cis</i> -acting splicing-associated variants in human cancer. <i>Genome Research</i> , 2018, 28, 1111-1125.	2.4	56
49	Invariant patterns of clonal succession determine specific clinical features of myelodysplastic syndromes. <i>Nature Communications</i> , 2019, 10, 5386.	5.8	53
50	GATA2 and secondary mutations in familial myelodysplastic syndromes and pediatric myeloid malignancies. <i>Haematologica</i> , 2015, 100, e398-e401.	1.7	48
51	Single-cell analysis based dissection of clonality in myelofibrosis. <i>Nature Communications</i> , 2020, 11, 73.	5.8	46
52	Loss of DNA Damage Response in Neuroblastoma and Utility of a PARP Inhibitor. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	3.0	43
53	Clonal evolution and clinical implications of genetic abnormalities in blastic transformation of chronic myeloid leukaemia. <i>Nature Communications</i> , 2021, 12, 2833.	5.8	39
54	<i>TERT</i> promoter mutations and chromosome 8p loss are characteristic of nonalcoholic fatty liver disease-related hepatocellular carcinoma. <i>International Journal of Cancer</i> , 2016, 139, 2512-2518.	2.3	36

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55	Early detection and evolution of preleukemic clones in therapy-related myeloid neoplasms following autologous SCT. <i>Blood</i> , 2018, 131, 1846-1857.	0.6	35
56	Recurrent genetic defects on chromosome 5q in myeloid neoplasms. <i>Oncotarget</i> , 2017, 8, 6483-6495.	0.8	34
57	Genomic landscape of colitis-associated cancer indicates the impact of chronic inflammation and its stratification by mutations in the Wnt signaling. <i>Oncotarget</i> , 2018, 9, 969-981.	0.8	34
58	De Novo Mutations Activating Germline TP53 in an Inherited Bone-Marrow-Failure Syndrome. <i>American Journal of Human Genetics</i> , 2018, 103, 440-447.	2.6	33
59	Comprehensive analysis of genetic aberrations linked to tumorigenesis in regenerative nodules of liver cirrhosis. <i>Journal of Gastroenterology</i> , 2019, 54, 628-640.	2.3	33
60	Landscape of driver mutations and their clinical impacts in pediatric B-cell precursor acute lymphoblastic leukemia. <i>Blood Advances</i> , 2020, 4, 5165-5173.	2.5	33
61	Exome sequencing identified <i>RPS15A</i> as a novel causative gene for Diamond-Blackfan anemia. <i>Haematologica</i> , 2017, 102, e93-e96.	1.7	30
62	Genetic and transcriptional landscape of plasma cells in POEMS syndrome. <i>Leukemia</i> , 2019, 33, 1723-1735.	3.3	28
63	Late-Onset Combined Immunodeficiency with a Novel IL2RG Mutation and Probable Revertant Somatic Mosaicism. <i>Journal of Clinical Immunology</i> , 2015, 35, 610-614.	2.0	26
64	Molecular pathogenesis of disease progression in MLL-rearranged AML. <i>Leukemia</i> , 2019, 33, 612-624.	3.3	26
65	Novel neuroblastoma amplified sequence (NBAS) mutations in a Japanese boy with fever-triggered recurrent acute liver failure. <i>Human Genome Variation</i> , 2019, 6, 2.	0.4	26
66	NOTCH1 pathway activating mutations and clonal evolution in pediatric T-cell acute lymphoblastic leukemia. <i>Cancer Science</i> , 2019, 110, 784-794.	1.7	26
67	PIEZO1 gene mutation in a Japanese family with hereditary high phosphatidylcholine hemolytic anemia and hemochromatosis-induced diabetes mellitus. <i>International Journal of Hematology</i> , 2016, 104, 125-129.	0.7	25
68	Integrated Molecular Characterization of the Lethal Pediatric Cancer Pancreatoblastoma. <i>Cancer Research</i> , 2018, 78, 865-876.	0.4	25
69	Aberrant DNA Methylation Is Associated with a Poor Outcome in Juvenile Myelomonocytic Leukemia. <i>PLoS ONE</i> , 2015, 10, e0145394.	1.1	25
70	HapMuC: somatic mutation calling using heterozygous germ line variants near candidate mutations. <i>Bioinformatics</i> , 2014, 30, 3302-3309.	1.8	23
71	Hypoxic adaptation of leukemic cells infiltrating the CNS affords a therapeutic strategy targeting VEGFA. <i>Blood</i> , 2017, 129, 3126-3129.	0.6	23
72	Identification of the genetic and clinical characteristics of neuroblastomas using genome-wide analysis. <i>Oncotarget</i> , 2017, 8, 107513-107529.	0.8	23

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73	Dysregulation of Epstein-Barr Virus Infection in Hypomorphic ZAP70 Mutation. <i>Journal of Infectious Diseases</i> , 2018, 218, 825-834.	1.9	22
74	Pathogenic mutations identified by a multimodality approach in 117 Japanese Fanconi anemia patients. <i>Haematologica</i> , 2019, 104, 1962-1973.	1.7	22
75	Clinical and genetic features of dyskeratosis congenita, cryptic dyskeratosis congenita, and Hoyeraal-Hreidarsson syndrome in Japan. <i>International Journal of Hematology</i> , 2015, 102, 544-552.	0.7	21
76	BRCC3 mutations in myeloid neoplasms. <i>Haematologica</i> , 2015, 100, 1051-7.	1.7	20
77	Genetic and clinical landscape of breast cancers with germline BRCA1/2 variants. <i>Communications Biology</i> , 2020, 3, 578.	2.0	20
78	The Evolving Genomic Landscape of Esophageal Squamous Cell Carcinoma Under Chemoradiotherapy. <i>Cancer Research</i> , 2021, 81, 4926-4938.	0.4	20
79	Recurrent CCND3 mutations in MLL-rearranged acute myeloid leukemia. <i>Blood Advances</i> , 2018, 2, 2879-2889.	2.5	19
80	<i>ASXL2</i> mutations are frequently found in pediatric AML patients with t(8;21)/ <i>RUNX1</i> and associated with a better prognosis. <i>Genes Chromosomes and Cancer</i> , 2017, 56, 382-393.	1.5	18
81	Common Variable Immunodeficiency Caused by FANC Mutations. <i>Journal of Clinical Immunology</i> , 2017, 37, 434-444.	2.0	18
82	Diagnostic challenge of Diamond-Blackfan anemia in mothers and children by whole-exome sequencing. <i>International Journal of Hematology</i> , 2017, 105, 515-520.	0.7	18
83	Genetic heterogeneity of uncharacterized childhood autoimmune diseases with lymphoproliferation. <i>Pediatric Blood and Cancer</i> , 2018, 65, e26831.	0.8	18
84	<i>RUNX1</i> mutations in pediatric acute myeloid leukemia are associated with distinct genetic features and an inferior prognosis. <i>Blood</i> , 2018, 131, 2266-2270.	0.6	15
85	Clonally related diffuse large B-cell lymphoma and interdigitating dendritic cell sarcoma sharing MYC translocation. <i>Haematologica</i> , 2018, 103, e553-e556.	1.7	14
86	Landscape Of Genetic Lesions In 944 Patients With Myelodysplastic Syndromes. <i>Blood</i> , 2013, 122, 521-521.	0.6	14
87	Somatic mosaicism in chronic myeloid leukemia in remission. <i>Blood</i> , 2016, 128, 2863-2866.	0.6	13
88	Whole-exome sequence analysis of ataxia telangiectasia-like phenotype. <i>Journal of the Neurological Sciences</i> , 2014, 340, 86-90.	0.3	12
89	Genomic analysis of clonal origin of Langerhans cell histiocytosis following acute lymphoblastic leukaemia. <i>British Journal of Haematology</i> , 2016, 175, 169-172.	1.2	12
90	Paraneoplastic hypereosinophilic syndrome associated with <i>IL3</i> positive acute lymphoblastic leukemia. <i>Pediatric Blood and Cancer</i> , 2019, 66, e27449.	0.8	12

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91	Frequent mutations in HLA and related genes in extranodal NK/T cell lymphomas. <i>Leukemia and Lymphoma</i> , 2021, 62, 95-103.	0.6	12
92	Constitutional abnormalities of <i>IDH1</i> combined with secondary mutations predispose a patient with Maffucci syndrome to acute lymphoblastic leukemia. <i>Pediatric Blood and Cancer</i> , 2017, 64, e26647.	0.8	9
93	Acquisition of monosomy 7 and a <i>RUNX1</i> mutation in Pearson syndrome. <i>Pediatric Blood and Cancer</i> , 2021, 68, e28799.	0.8	9
94	Impact of Somatic Mutations on Outcome in Patients with MDS after Stem-Cell Transplantation. <i>Blood</i> , 2015, 126, 711-711.	0.6	9
95	Modification of cellular and humoral immunity by somatically reverted T cells in X-linked lymphoproliferative syndrome type 1. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 421-424.e11.	1.5	8
96	Frequent Pathway Mutations of Splicing Machinery in Myelodysplasia. <i>Blood</i> , 2011, 118, 458-458.	0.6	8
97	Phasing analysis of lung cancer genomes using a long read sequencer. <i>Nature Communications</i> , 2022, 13, .	5.8	8
98	Frequent Activating Somatic Alterations in T-Cell Receptor / NF- κ B Signaling in Adult T-Cell Leukemia/Lymphoma. <i>Blood</i> , 2015, 126, 113-113.	0.6	7
99	Genetic Predispositions to Myeloid Neoplasms Caused By Germline DDX41 Mutations. <i>Blood</i> , 2015, 126, 2843-2843.	0.6	7
100	Amplified <i>EPOR</i> / <i>JAK2</i> Genes Define a Unique Subtype of Acute Erythroid Leukemia. <i>Blood Cancer Discovery</i> , 2022, 3, 410-427.	2.6	7
101	Molecular studies reveal MLL-MLLT10/AF10 and ARID5B-MLL gene fusions displaced in a case of infantile acute lymphoblastic leukemia with complex karyotype. <i>Oncology Letters</i> , 2017, 14, 2295-2299.	0.8	6
102	Ring sideroblasts in AML are associated with adverse risk characteristics and have a distinct gene expression pattern. <i>Blood Advances</i> , 2019, 3, 3111-3122.	2.5	6
103	Comprehensive Analysis of Aberrant RNA Splicing in Myelodysplastic Syndromes. <i>Blood</i> , 2014, 124, 826-826.	0.6	6
104	VEGFA- a New Therapeutic Target in CNS Leukemia. <i>Blood</i> , 2016, 128, 911-911.	0.6	6
105	Genome analysis of myelodysplastic syndromes among atomic bomb survivors in Nagasaki. <i>Haematologica</i> , 2020, 105, 358-365.	1.7	5
106	Distinct gene alterations with a high percentage of myeloperoxidase-positive leukemic blasts in de novo acute myeloid leukemia. <i>Leukemia Research</i> , 2018, 65, 34-41.	0.4	4
107	Somatic Mutations in Schinzel-Giedion Syndrome Gene SETBP1 Determine Progression in Myeloid Malignancies. <i>Blood</i> , 2012, 120, 2-2.	0.6	4
108	Chronological Analysis of Clonal Evolution in Acquired Aplastic Anemia. <i>Blood</i> , 2014, 124, 253-253.	0.6	4

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109	In Analogy to AML, MDS Can be Sub-Classified By Ancestral Mutations. Blood, 2014, 124, 823-823.	0.6	4
110	A rank-based statistical test for measuring synergistic effects between two gene sets. Bioinformatics, 2011, 27, 2399-2405.	1.8	3
111	High performance computing of a fusion gene detection pipeline on the K computer. , 2015, , .		3
112	Molecular Heterogeneity in Peripheral T-Cell Lymphoma Not Otherwise Specified Revealed By Comprehensive Mutational Profiling. Blood, 2016, 128, 2927-2927.	0.6	3
113	Genotype-Phenotype Relationships and Therapeutic Targets in Acute Erythroid Leukemia. Blood, 2020, 136, 17-18.	0.6	3
114	Prognostic Relevance of Genetic Abnormalities in Blastic Transformation of Chronic Myeloid Leukemia. Blood, 2020, 136, 3-4.	0.6	3
115	Atypical dyskeratosis congenita diagnosed using whole-exome sequencing. Pediatrics International, 2017, 59, 933-935.	0.2	2
116	Distinct, Ethnic, Clinical, and Genetic Characteristics of Myelodysplastic Syndromes with Der(1;7). Blood, 2019, 134, 5392-5392.	0.6	2
117	Mutational Spectrum Analysis of Interesting Correlation and Interrelationship Between RNA Splicing Pathway and Commonly Targeted Genes in Myelodysplastic Syndrome. Blood, 2011, 118, 273-273.	0.6	2
118	Mutation Screening Associated with Chromosome 7 Abnormalities Using Next Generation Whole Exome Sequencing. Blood, 2012, 120, 173-173.	0.6	2
119	Somatic G17V Rhoa Mutation Specifies Angioimmunoblastic T-Cell Lymphoma. Blood, 2013, 122, 815-815.	0.6	2
120	ZRSR2 Mutations Cause Dysregulated RNA Splicing in MDS. Blood, 2014, 124, 4609-4609.	0.6	2
121	Different Mutant Splicing Factors Cause Distinct Missplicing Events and Give Rise to Different Clinical Phenotypes in Myelodysplastic Syndromes. Blood, 2015, 126, 139-139.	0.6	2
122	Genetic Background of Idiopathic Bone Marrow Failure Syndromes in Children. Blood, 2015, 126, 3610-3610.	0.6	2
123	Serial Sequencing in Myelodysplastic Syndromes Reveals Dynamic Changes in Clonal Architecture and Allows for a New Prognostic Assessment of Mutations Detected in Cross-Sectional Testing. Blood, 2015, 126, 709-709.	0.6	2
124	NGS-Based Copy Number Analysis in 1,185 Patients with Myeloid Neoplasms. Blood, 2016, 128, 955-955.	0.6	2
125	EPOR/JAK/STAT Signaling Pathway As Therapeutic Target of Acute Erythroid Leukemia. Blood, 2021, 138, 610-610.	0.6	2
126	Whole Exome Sequencing to Predict Response to Hypomethylating Agents in MDS. Blood, 2012, 120, 1698-1698.	0.6	1

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127	DDX41 Is a Tumor Suppressor Gene Associated with Inherited and Acquired Mutations. Blood, 2014, 124, 125-125.	0.6	1
128	Landscape of Genetic Alterations in Adult T-Cell Leukemia/Lymphoma. Blood, 2014, 124, 75-75.	0.6	1
129	Prognostic Relevance of Integrated Genetic Profiling in Adult T-Cell Leukemia/Lymphoma. Blood, 2015, 126, 2643-2643.	0.6	1
130	Two Novel Distinct Subtypes of Myeloid Neoplasms Molecularly Associated with Histone H3K36 Methylations. Blood, 2015, 126, 2841-2841.	0.6	1
131	A framework for generating interactive reports for cancer genome analysis. Journal of Open Source Software, 2017, 2, 457.	2.0	1
132	Recurrent Mutations of Multiple Components of Cohesin Complex in Myeloid Neoplasms. Blood, 2012, 120, 782-782.	0.6	1
133	Identification of Two New DBA Genes, RPS27 and RPL27, by Whole-Exome Sequencing in Diamond-Blackfan Anemia Patients. Blood, 2012, 120, 984-984.	0.6	1
134	Various Germline Congenital Disorder Genes Are Somatic Mutated in Myeloid Malignancies. Blood, 2012, 120, 1405-1405.	0.6	1
135	Genetic Basis of Primary Central Nervous System Lymphoma. Blood, 2015, 126, 2687-2687.	0.6	1
136	Genetic Profile of Acute Erythroid Leukemia. Blood, 2016, 128, 40-40.	0.6	1
137	TET2 Mutations Revealed by Whole Genome Sequencing in Adult T-Cell Leukemia.. Blood, 2012, 120, 2697-2697.	0.6	0
138	Whole Exome Sequencing Reveals Spectrum of Gene Mutations in Pediatric AML. Blood, 2012, 120, 124-124.	0.6	0
139	Molecular Diversity Detected by Whole Exome Sequencing in Chronic Myelomonocytic Leukemia. Blood, 2012, 120, 310-310.	0.6	0
140	Mutational Spectrum of Myelodysplastic Syndrome Malignancies Revealed by Whole Exome Sequencing. Blood, 2012, 120, 307-307.	0.6	0
141	Karyotypic and Genetic Abnormalities Associated with Clonal Evolution in Paroxysmal Nocturnal Hemoglobinuria.. Blood, 2012, 120, 2371-2371.	0.6	0
142	Whole Exome Analysis Reveals Spectrum of Gene Mutations in Juvenile Myelomonocytic Leukemia. Blood, 2012, 120, 170-170.	0.6	0
143	Novel Recurrent Mutations in the Ras-Like GTP-Binding Gene Rit1 in Myeloid Malignancies. Blood, 2012, 120, 558-558.	0.6	0
144	Whole Exome Sequencing Detecting Kinesin Family Gene Defects In Myeloid Neoplasm. Blood, 2013, 122, 2762-2762.	0.6	0

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145	Genetic Landscapes Of Childhood T-Cell Acute Lymphoblastic Leukemia. Blood, 2013, 122, 3786-3786.	0.6	0
146	Novel Biological Effects and Distinct Patterns of Rhoa Mutations in Adult T-Cell Leukemia/Lymphoma and Angioimmunoblastic T Cell Lymphoma. Blood, 2014, 124, 2215-2215.	0.6	0
147	Clinical and Molecular Significance of Peripheral Blood Cell-Free DNA in B-Cell Lymphomas for Detection of Genetic Mutations and Correlation with Disease Status. Blood, 2014, 124, 1658-1658.	0.6	0
148	Impact and Function of Somatic PHF6 Mutations in Myeloid Neoplasms. Blood, 2014, 124, 3581-3581.	0.6	0
149	Whole-Exome Sequencing Reveals a Paucity of Somatic Gene Mutations in Aplastic Anemia and Refractory Cytopenia of Childhood. Blood, 2014, 124, 4388-4388.	0.6	0
150	The landscape and clonal architecture in lower grade glioma.. Journal of Clinical Oncology, 2015, 33, 2008-2008.	0.8	0
151	Next-Generation Sequencing Reveal Proviral Genome and Transcriptome in Adult T-Cell Leukemia/Lymphoma. Blood, 2015, 126, 3882-3882.	0.6	0
152	Landscape of DNA Methylation and Genetic Profiles in 291 Patients with Myelodysplastic Syndromes. Blood, 2015, 126, 5205-5205.	0.6	0
153	Functional Characterization of a Novel GFI1B Mutation Causing Congenital Macrothrombocytopenia. Blood, 2015, 126, 75-75.	0.6	0
154	Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. Blood, 2015, 126, 1425-1425.	0.6	0
155	Myelodysplastic Syndrome Patients Show Mutation-Specific DNA Methylation Patterns. Blood, 2015, 126, 1646-1646.	0.6	0
156	TAL1 and MYB Abnormalities in Childhood T-Cell Acute Lymphoblastic Leukemia. Blood, 2015, 126, 2628-2628.	0.6	0
157	Detection of Novel Pathogenic Gene Rearrangements in Pediatric Acute Myeloid Leukemia By RNA Sequencing. Blood, 2015, 126, 2575-2575.	0.6	0
158	Whole-Exome Analysis of Autoimmune Lymphoproliferative Syndrome-like Diseases. Blood, 2015, 126, 1022-1022.	0.6	0
159	Clinical Significance of Mutations and Copy Number Lesions on Prognosis of Patients with MDS after Unrelated Bone Marrow Transplantation. Blood, 2016, 128, 1971-1971.	0.6	0
160	Genome-Wide Mutational Landscape of Infant Acute Lymphoblastic Leukemia. Blood, 2016, 128, 4070-4070.	0.6	0
161	Transcriptome Analysis Revealed the Entire Genetic Understanding of Pediatric Acute Myeloid Leukemia with a Normal Karyotype. Blood, 2016, 128, 2850-2850.	0.6	0
162	Integrated Molecular Analysis of Myelodysplastic Syndromes Using Whole Genome Sequencing. Blood, 2016, 128, 5512-5512.	0.6	0

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163	Identifications of Highly Aggressive Phenotype with SPI1 Overexpression in Pediatric T Cell Acute Lymphoblastic Leukemia/Lymphoma. <i>Blood</i> , 2016, 128, 909-909.	0.6	0
164	Combined DNA and Transcriptome Sequencing Reveals Discrete Subtypes of Myelodysplasia. <i>Blood</i> , 2016, 128, 1974-1974.	0.6	0
165	Gene Expression Profiles and Methylation Analysis in Down Syndrome Related Acute Lymphoblastic Leukemia. <i>Blood</i> , 2016, 128, 4084-4084.	0.6	0
166	TAL1 Super Enhancer Aberration and Stil-TAL1 Fusion in Pediatric T Cell Acute Lymphoblastic Leukemia. <i>Blood</i> , 2016, 128, 1734-1734.	0.6	0
167	Structural Variations Involving Programmed Death Ligands in B-Cell and T-Cell Lymphomas. <i>Blood</i> , 2016, 128, 4105-4105.	0.6	0
168	Distinctive Genetic Features of Plasma Cells in POEMS Syndrome. <i>Blood</i> , 2016, 128, 4404-4404.	0.6	0
169	Landscape of Driver Mutations and Their Clinical Impacts in Pediatric Acute Lymphoblastic Leukemia. <i>Blood</i> , 2016, 128, 912-912.	0.6	0
170	the Impact of Clonal Dynamics on Prognosis and Outcome in Myelodysplastic Syndromes. <i>Blood</i> , 2016, 128, 4287-4287.	0.6	0
171	Analysis of Genomic Predispositions to Sporadic Myeloid Neoplasms Mediated By DDX41 in Japan. <i>Blood</i> , 2018, 132, 4371-4371.	0.6	0
172	hotsub: A batch job engine for cloud services with ETL framework. <i>Journal of Open Source Software</i> , 2018, 3, 1069.	2.0	0
173	Clonal Evolution Pattern and Prognostic Significance of Clonal Architecture in KMT2A-Rearranged Acute Myeloid Leukemia. <i>Blood</i> , 2021, 138, 2358-2358.	0.6	0
174	<i>Post-Treatment Clone Size Predicts Survival Independently of IPSS-R and Response after Azacitidine Therapy for MDS.</i>. <i>Blood</i> , 2020, 136, 12-13.	0.6	0