Yuichi Shiraishi

List of Publications by Year
in descending order

174 papers	12,896 citations	47006 47 h-index	25787 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. 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	Inherited and Somatic Defects in DDX41 in Myeloid Neoplasms. Cancer Cell, 2015, 27, 658-670.	16.8	341
11	Genomic basis for RNA alterations in cancer. Nature, 2020, 578, 129-136.	27.8	280
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	Acquired Initiating Mutations in Early Hematopoietic Cells of CLL Patients. Cancer Discovery, 2014, 4, 1088-1101.	9.4	213
15	Aberrant splicing of U12-type introns is the hallmark of ZRSR2 mutant myelodysplastic syndrome. Nature Communications, 2015, 6, 6042.	12.8	192
16	Whole-genome mutational landscape of liver cancers displaying biliary phenotype reveals hepatitis impact and molecular diversity. Nature Communications, 2015, 6, 6120.	12.8	178
17	An empirical Bayesian framework for somatic mutation detection from cancer genome sequencing data. Nucleic Acids Research, 2013, 41, e89-e89.	14.5	177
18	Recurrent somatic mutations underlie corticotropin-independent Cushingâ€™s syndrome. Science, 2014, 344, 917-920.	12.6	177

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19	Frequent mutations that converge on the NFKBIZ pathway in ulcerative colitis. Nature, 2020, 577, 260-265.	27.8	168
20	Defective Epsteinâ€"Barr virus in chronic active infection and haematological malignancy. Nature Microbiology, 2019, 4, 404-413.	13.3	152
21	Integrated genetic and epigenetic analysis defines novel molecular subgroups in rhabdomyosarcoma. Nature Communications, 2015, 6, 7557.	12.8	149
22	Molecular heterogeneity in peripheral T-cell lymphoma, not otherwise specified revealed by comprehensive genetic profiling. Leukemia, 2019, 33, 2867-2883.	7.2	148
23	Aberrant splicing and defective mRNA production induced by somatic spliceosome mutations in myelodysplasia. Nature Communications, 2018, 9, 3649.	12.8	140
24	Integrated Multiregional Analysis Proposing a New Model of Colorectal Cancer Evolution. PLoS Genetics, 2016, 12, e1005778.	3.5	134
25	Prognostic relevance of integrated genetic profiling in adult T-cell leukemia/lymphoma. Blood, 2018, 131, 215-225.	1.4	124
26	Clonal evolution in myelodysplastic syndromes. Nature Communications, 2017, 8, 15099.	12.8	118
27	A Simple Model-Based Approach to Inferring and Visualizing Cancer Mutation Signatures. PLoS Genetics, 2015, 11, e1005657.	3.5	118
28	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
29	Recurrent SPI1 (PU.1) fusions in high-risk pediatric T cell acute lymphoblastic leukemia. Nature Genetics, 2017, 49, 1274-1281.	21.4	100
30	Abnormal hematopoiesis and autoimmunity in human subjects with germline IKZF1 mutations. Journal of Allergy and Clinical Immunology, 2017, 140, 223-231.	2.9	99
31	Frequent structural variations involving programmed death ligands in Epstein-Barr virus-associated lymphomas. Leukemia, 2019, 33, 1687-1699.	7.2	98
32	Genomic landscape and clonal evolution of acute myeloid leukemia with t(8;21): an international study on 331 patients. Blood, 2019, 133, 1140-1151.	1.4	96
33	Genomic landscape of liposarcoma. Oncotarget, 2015, 6, 42429-42444.	1.8	94
34	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
35	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
36	A temporal shift of the evolutionary principle shaping intratumor heterogeneity in colorectal cancer. Nature Communications, 2018, 9, 2884.	12.8	82

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37	Whole genome sequencing discriminates hepatocellular carcinoma with intrahepatic metastasis from multi-centric tumors. Journal of Hepatology, 2017, 66, 363-373.	3.7	81
38	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
39	Integrated molecular profiling of juvenile myelomonocytic leukemia. Blood, 2018, 131, 1576-1586.	1.4	78
40	Frequent germline mutations of HAVCR2 in sporadic subcutaneous panniculitis-like T-cell lymphoma. Blood Advances, 2019, 3, 588-595.	5.2	73
41	Biallelic DICER1 Mutations in Sporadic Pleuropulmonary Blastoma. Cancer Research, 2014, 74, 2742-2749.	0.9	67
42	Clinical utility of next-generation sequencing for inherited bone marrow failure syndromes. Genetics in Medicine, 2017, 19, 796-802.	2.4	66
43	Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. Cancer Cell, 2021, 39, 793-809.e8.	16.8	65
44	Gene expression and risk of leukemic transformation in myelodysplasia. Blood, 2017, 130, 2642-2653.	1.4	64
45	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
46	Genomon ITDetector: a tool for somatic internal tandem duplication detection from cancer genome sequencing data. Bioinformatics, 2015, 31, 116-118.	4.1	58
47	Characterization of HBV integration patterns and timing in liver cancer and HBV-infected livers. Oncotarget, 2018, 9, 25075-25088.	1.8	57
48	A comprehensive characterization of cis-acting splicing-associated variants in human cancer. Genome Research, 2018, 28, 1111-1125.	5.5	56
49	Invariant patterns of clonal succession determine specific clinical features of myelodysplastic syndromes. Nature Communications, 2019, 10, 5386.	12.8	53
50	GATA2 and secondary mutations in familial myelodysplastic syndromes and pediatric myeloid malignancies. Haematologica, 2015, 100, e398-e401.	3.5	48
51	Single-cell analysis based dissection of clonality in myelofibrosis. Nature Communications, 2020, 11, 73.	12.8	46
52	Loss of DNA Damage Response in Neuroblastoma and Utility of a PARP Inhibitor. Journal of the National Cancer Institute, 2017, 109, .	6.3	43
53	Clonal evolution and clinical implications of genetic abnormalities in blastic transformation of chronic myeloid leukaemia. Nature Communications, 2021, 12, 2833.	12.8	39
54	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

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55	Early detection and evolution of preleukemic clones in therapy-related myeloid neoplasms following autologous SCT. Blood, 2018, 131, 1846-1857.	1.4	35
56	Recurrent genetic defects on chromosome 5q in myeloid neoplasms. Oncotarget, 2017, 8, 6483-6495.	1.8	34
57	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
58	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
59	Comprehensive analysis of genetic aberrations linked to tumorigenesis in regenerative nodules of liver cirrhosis. Journal of Gastroenterology, 2019, 54, 628-640.	5.1	33
60	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
61	Exome sequencing identified RPS15A as a novel causative gene for Diamond-Blackfan anemia. Haematologica, 2017, 102, e93-e96.	3.5	30
62	Genetic and transcriptional landscape of plasma cells in POEMS syndrome. Leukemia, 2019, 33, 1723-1735.	7.2	28
63	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
64	Molecular pathogenesis of disease progression in MLL-rearranged AML. Leukemia, 2019, 33, 612-624.	7.2	26
65	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
66	<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
67	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
68	Integrated Molecular Characterization of the Lethal Pediatric Cancer Pancreatoblastoma. Cancer Research, 2018, 78, 865-876.	0.9	25
69	Aberrant DNA Methylation Is Associated with a Poor Outcome in Juvenile Myelomonocytic Leukemia. PLoS ONE, 2015, 10, e0145394.	2.5	25
70	HapMuC: somatic mutation calling using heterozygous germ line variants near candidate mutations. Bioinformatics, 2014, 30, 3302-3309.	4.1	23
71	Hypoxic adaptation of leukemic cells infiltrating the CNS affords a therapeutic strategy targeting VEGFA. Blood, 2017, 129, 3126-3129.	1.4	23
72	Identification of the genetic and clinical characteristics of neuroblastomas using genome-wide analysis. Oncotarget, 2017, 8, 107513-107529.	1.8	23

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73	Dysregulation of Epstein-Barr Virus Infection in Hypomorphic ZAP70 Mutation. Journal of Infectious Diseases, 2018, 218, 825-834.	4.0	22
74	Pathogenic mutations identified by a multimodality approach in 117 Japanese Fanconi anemia patients. Haematologica, 2019, 104, 1962-1973.	3.5	22
75	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
76	BRCC3 mutations in myeloid neoplasms. Haematologica, 2015, 100, 1051-7.	3.5	20
77	Genetic and clinical landscape of breast cancers with germline BRCA1/2 variants. Communications Biology, 2020, 3, 578.	4.4	20
78	The Evolving Genomic Landscape of Esophageal Squamous Cell Carcinoma Under Chemoradiotherapy. Cancer Research, 2021, 81, 4926-4938.	0.9	20
79	Recurrent CCND3 mutations in MLL-rearranged acute myeloid leukemia. Blood Advances, 2018, 2, 2879-2889.	5.2	19
80	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
81	Common Variable Immunodeficiency Caused by FANC Mutations. Journal of Clinical Immunology, 2017, 37, 434-444.	3.8	18
82	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
83	Genetic heterogeneity of uncharacterized childhood autoimmune diseases with lymphoproliferation. Pediatric Blood and Cancer, 2018, 65, e26831.	1.5	18
84	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
85	Clonally related diffuse large B-cell lymphoma and interdigitating dendritic cell sarcoma sharing MYC translocation. Haematologica, 2018, 103, e553-e556.	3.5	14
86	Landscape Of Genetic Lesions In 944 Patients With Myelodysplastic Syndromes. Blood, 2013, 122, 521-521.	1.4	14
87	Somatic mosaicism in chronic myeloid leukemia in remission. Blood, 2016, 128, 2863-2866.	1.4	13
88	Whole-exome sequence analysis of ataxia telangiectasia-like phenotype. Journal of the Neurological Sciences, 2014, 340, 86-90.	0.6	12
89	Genomic analysis of clonal origin of Langerhans cell histiocytosis following acute lymphoblastic leukaemia. British Journal of Haematology, 2016, 175, 169-172.	2.5	12
90	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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91	Frequent mutations in HLA and related genes in extranodal NK/T cell lymphomas. Leukemia and Lymphoma, 2021, 62, 95-103.	1.3	12
92	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
93	Acquisition of monosomy 7 and a RUNX1 mutation in Pearson syndrome. Pediatric Blood and Cancer, 2021, 68, e28799.	1.5	9
94	Impact of Somatic Mutations on Outcome in Patients with MDS after Stem-Cell Transplantation. Blood, 2015, 126, 711-711.	1.4	9
95	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
96	Frequent Pathway Mutations of Splicing Machinery in Myelodysplasia. Blood, 2011, 118, 458-458.	1.4	8
97	Phasing analysis of lung cancer genomes using a long read sequencer. Nature Communications, 2022, 13, .	12.8	8
98	Frequent Activating Somatic Alterations in T-Cell Receptor / NF-Îºb Signaling in Adult T-Cell Leukemia/Lymphoma. Blood, 2015, 126, 113-113.	1.4	7
99	Genetic Predispositions to Myeloid Neoplasms Caused By Germline DDX41 Mutations. Blood, 2015, 126, 2843-2843.	1.4	7
100	Amplified EPOR/JAK2 Genes Define a Unique Subtype of Acute Erythroid Leukemia. Blood Cancer Discovery, 2022, 3, 410-427.	5.0	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. Oncology Letters, 2017, 14, 2295-2299.	1.8	6
102	Ring sideroblasts in AML are associated with adverse risk characteristics and have a distinct gene expression pattern. Blood Advances, 2019, 3, 3111-3122.	5.2	6
103	Comprehensive Analysis of Aberrant RNA Splicing in Myelodysplastic Syndromes. Blood, 2014, 124, 826-826.	1.4	6
104	VEGFA- a New Therapeutic Target in CNS Leukemia. Blood, 2016, 128, 911-911.	1.4	6
105	Genome analysis of myelodysplastic syndromes among atomic bomb survivors in Nagasaki. Haematologica, 2020, 105, 358-365.	3.5	5
106	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
107	Somatic Mutations in Schinzel-Giedion Syndrome Gene SETBP1 Determine Progression in Myeloid Malignancies. Blood, 2012, 120, 2-2.	1.4	4
108	Chronological Analysis of Clonal Evolution in Acquired Aplastic Anemia. Blood, 2014, 124, 253-253.	1.4	4

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109	In Analogy to AML, MDS Can be Sub-Classified By Ancestral Mutations. Blood, 2014, 124, 823-823.	1.4	4
110	A rank-based statistical test for measuring synergistic effects between two gene sets. Bioinformatics, 2011, 27, 2399-2405.	4.1	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.	1.4	3
113	Genotype-Phenotype Relationships and Therapeutic Targets in Acute Erythroid Leukemia. Blood, 2020, 136, 17-18.	1.4	3
114	Prognostic Relevance of Genetic Abnormalities in Blastic Transformation of Chronic Myeloid Leukemia. Blood, 2020, 136, 3-4.	1.4	3
115	Atypical dyskeratosis congenita diagnosed using wholeâ€exome sequencing. Pediatrics International, 2017, 59, 933-935.	0.5	2
116	Distinct, Ethnic, Clinical, and Genetic Characteristics of Myelodysplastic Syndromes with Der(1;7). Blood, 2019, 134, 5392-5392.	1.4	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.	1.4	2
118	Mutation Screening Associated with Chromosome 7 Abnormalities Using Next Generation Whole Exome Sequencing. Blood, 2012, 120, 173-173.	1.4	2
119	Somatic G17V Rhoa Mutation Specifies Angioimmunoblastic T-Cell Lymphoma. Blood, 2013, 122, 815-815.	1.4	2
120	ZRSR2 Mutations Cause Dysregulated RNA Splicing in MDS. Blood, 2014, 124, 4609-4609.	1.4	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.	1.4	2
122	Genetic Background of Idiopathic Bone Marrow Failure Syndromes in Children. Blood, 2015, 126, 3610-3610.	1.4	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.	1.4	2
124	NGS-Based Copy Number Analysis in 1,185 Patients with Myeloid Neoplasms. Blood, 2016, 128, 955-955.	1.4	2
125	EPOR/JAK/STAT Signaling Pathway As Therapeutic Target of Acute Erythroid Leukemia. Blood, 2021, 138, 610-610.	1.4	2
126	Whole Exome Sequencing to Predict Response to Hypomethylating Agents in MDS. Blood, 2012, 120, 1698-1698.	1.4	1

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127	DDX41 Is a Tumor Suppressor Gene Associated with Inherited and Acquired Mutations. Blood, 2014, 124, 125-125.	1.4	1
128	Landscape of Genetic Alterations in Adult T-Cell Leukemia/Lymphoma. Blood, 2014, 124, 75-75.	1.4	1
129	Prognostic Relevance of Integrated Genetic Profiling in Adult T-Cell Leukemia/Lymphoma. Blood, 2015, 126, 2643-2643.	1.4	1
130	Two Novel Distinct Subtypes of Myeloid Neoplasms Molecularly Associated with Histone H3K36 Methylations. Blood, 2015, 126, 2841-2841.	1.4	1
131	A framework for generating interactive reports for cancer genome analysis. Journal of Open Source Software, 2017, 2, 457.	4.6	1
132	Recurrent Mutations of Multiple Components of Cohesin Complex in Myeloid Neoplasms. Blood, 2012, 120, 782-782.	1.4	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.	1.4	1
134	Various Germline Congenital Disorder Genes Are Somatically Mutated in Myeloid Malignancies. Blood, 2012, 120, 1405-1405.	1.4	1
135	Genetic Basis of Primary Central Nervous System Lymphoma. Blood, 2015, 126, 2687-2687.	1.4	1
136	Genetic Profile of Acute Erythroid Leukemia. Blood, 2016, 128, 40-40.	1.4	1
137	TET2 Mutations Revealed by Whole Genome Sequencing in Adult T-Cell Leukemia.. Blood, 2012, 120, 2697-2697.	1.4	0
138	Whole Exome Sequencing Reveals Spectrum of Gene Mutations in Pediatric AML. Blood, 2012, 120, 124-124.	1.4	0
139	Molecular Diversity Detected by Whole Exome Sequencing in Chronic Myelomonocytic Leukemia. Blood, 2012, 120, 310-310.	1.4	0
140	Mutational Spectrum of Myelodysplastic Syndrome Malignancies Revealed by Whole Exome Sequencing. Blood, 2012, 120, 307-307.	1.4	0
141	Karyotypic and Genetic Abnormalities Associated with Clonal Evolution in Paroxysmal Nocturnal Hemoglobinuria.. Blood, 2012, 120, 2371-2371.	1.4	0
142	Whole Exome Analysis Reveals Spectrum of Gene Mutations in Juvenile Myelomonocytic Leukemia. Blood, 2012, 120, 170-170.	1.4	0
143	Novel Recurrent Mutations in the Ras-Like GTP-Binding Gene Rit1 in Myeloid Malignancies. Blood, 2012, 120, 558-558.	1.4	0
144	Whole Exome Sequencing Detecting Kinesin Family Gene Defects In Myeloid Neoplasm. Blood, 2013, 122, 2762-2762.	1.4	0

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145	Genetic Landscapes Of Childhood T-Cell Acute Lymphoblastic Leukemia. Blood, 2013, 122, 3786-3786.	1.4	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.	1.4	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.	1.4	0
148	Impact and Function of Somatic PHF6 Mutations in Myeloid Neoplasms. Blood, 2014, 124, 3581-3581.	1.4	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.	1.4	0
150	The landscape and clonal architecture in lower grade glioma.. Journal of Clinical Oncology, 2015, 33, 2008-2008.	1.6	0
151	Next-Generation Sequencing Reveal Proviral Genome and Transcriptome in Adult T-Cell Leukemia/Lymphoma. Blood, 2015, 126, 3882-3882.	1.4	0
152	Landscape of DNA Methylation and Genetic Profiles in 291 Patients with Myelodysplastic Syndromes. Blood, 2015, 126, 5205-5205.	1.4	0
153	Functional Characterization of a Novel GFI1B Mutation Causing Congenital Macrothrombocytopenia. Blood, 2015, 126, 75-75.	1.4	0
154	Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. Blood, 2015, 126, 1425-1425.	1.4	0
155	Myelodysplastic Syndrome Patients Show Mutation-Specific DNA Methylation Patterns. Blood, 2015, 126, 1646-1646.	1.4	0
156	TAL1 and MYB Abnormalities in Childhood T-Cell Acute Lymphoblastic Leukemia. Blood, 2015, 126, 2628-2628.	1.4	0
157	Detection of Novel Pathogenic Gene Rearrangements in Pediatric Acute Myeloid Leukemia By RNA Sequencing. Blood, 2015, 126, 2575-2575.	1.4	0
158	Whole-Exome Analysis of Autoimmune Lymphoproliferative Syndrome-like Diseases. Blood, 2015, 126, 1022-1022.	1.4	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.	1.4	0
160	Genome-Wide Mutational Landscape of Infant Acute Lymphoblastic Leukemia. Blood, 2016, 128, 4070-4070.	1.4	0
161	Transcriptome Analysis Revealed the Entire Genetic Understanding of Pediatric Acute Myeloid Leukemia with a Normal Karyotype. Blood, 2016, 128, 2850-2850.	1.4	0
162	Integrated Molecular Analysis of Myelodysplastic Syndromes Using Whole Genome Sequencing. Blood, 2016, 128, 5512-5512.	1.4	0

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163	Identifications of Highly Aggressive Phenotype with SPI1 Overexpression in Pediatric T Cell Acute Lymphoblastic Leukemia/Lymphoma. Blood, 2016, 128, 909-909.	1.4	0
164	Combined DNA and Transcriptome Sequencing Reveals Discrete Subtypes of Myelodysplasia. Blood, 2016, 128, 1974-1974.	1.4	0
165	Gene Expression Profiles and Methylation Analysis in Down Syndrome Related Acute Lymphoblastic Leukemia. Blood, 2016, 128, 4084-4084.	1.4	0
166	TAL1 Super Enhancer Aberration and Stil-TAL1 Fusion in Pediatric T Cell Acute Lymphoblastic Leukemia. Blood, 2016, 128, 1734-1734.	1.4	0
167	Structural Variations Involving Programmed Death Ligands in B-Cell and T-Cell Lymphomas. Blood, 2016, 128, 4105-4105.	1.4	0
168	Distinctive Genetic Features of Plasma Cells in POEMS Syndrome. Blood, 2016, 128, 4404-4404.	1.4	0
169	Landscape of Driver Mutations and Their Clinical Impacts in Pediatric Acute Lymphoblastic Leukemia. Blood, 2016, 128, 912-912.	1.4	0
170	the Impact of Clonal Dynamics on Prognosis and Outcome in Myelodysplastic Syndromes. Blood, 2016, 128, 4287-4287.	1.4	0
171	Analysis of Genomic Predispositions to Sporadic Myeloid Neoplasms Mediated By DDX41 in Japan. Blood, 2018, 132, 4371-4371.	1.4	0
172	hotsub: A batch job engine for cloud services with ETL framework. Journal of Open Source Software, 2018, 3, 1069.	4.6	0
173	Clonal Evolution Pattern and Prognostic Significance of Clonal Architecture in KMT2A-Rearranged Acute Myeloid Leukemia. Blood, 2021, 138, 2358-2358.	1.4	0
174	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