Yuichi Shiraishi

List of Publications by Year
in descending order

174	12,896	46918 47	25716 108
papers	citations	h-index	g-index

183	183	183	21850
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Phasing analysis of lung cancer genomes using a long read sequencer. Nature Communications, 2022, 13, .	5.8	8
2	Amplified EPOR/JAK2 Genes Define a Unique Subtype of Acute Erythroid Leukemia. Blood Cancer Discovery, 2022, 3, 410-427.	2.6	7
3	Frequent mutations in HLA and related genes in extranodal NK/T cell lymphomas. Leukemia and Lymphoma, 2021, 62, 95-103.	0.6	12
4	Acquisition of monosomy 7 and a RUNX1 mutation in Pearson syndrome. Pediatric Blood and Cancer, 2021, 68, e28799.	0.8	9
5	Clonal evolution and clinical implications of genetic abnormalities in blastic transformation of chronic myeloid leukaemia. Nature Communications, 2021, 12, 2833.	5.8	39
6	Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. Cancer Cell, 2021, 39, 793-809.e8.	7.7	65
7	The Evolving Genomic Landscape of Esophageal Squamous Cell Carcinoma Under Chemoradiotherapy. Cancer Research, 2021, 81, 4926-4938.	0.4	20
8	EPOR/JAK/STAT Signaling Pathway As Therapeutic Target of Acute Erythroid Leukemia. Blood, 2021, 138, 610-610.	0.6	2
9	Clonal Evolution Pattern and Prognostic Significance of Clonal Architecture in KMT2A-Rearranged Acute Myeloid Leukemia. Blood, 2021, 138, 2358-2358.	0.6	0
10	Genome analysis of myelodysplastic syndromes among atomic bomb survivors in Nagasaki. Haematologica, 2020, 105, 358-365.	1.7	5
11	Single-cell analysis based dissection of clonality in myelofibrosis. Nature Communications, 2020, 11, 73.	5.8	46
12	Frequent mutations that converge on the NFKBIZ pathway in ulcerative colitis. Nature, 2020, 577, 260-265.	13.7	168
13	Genetic and clinical landscape of breast cancers with germline BRCA1/2 variants. Communications Biology, 2020, 3, 578.	2.0	20
14	Landscape of driver mutations and their clinical impacts in pediatric B-cell precursor acute lymphoblastic leukemia. Blood Advances, 2020, 4, 5165-5173.	2.5	33
15	Genomic basis for RNA alterations in cancer. Nature, 2020, 578, 129-136.	13.7	280
16	Post-Treatment Clone Size Predicts Survival Independently of IPSS-R and Response after Azacitidine Therapy for MDS.. Blood, 2020, 136, 12-13.	0.6	0
17	Genotype-Phenotype Relationships and Therapeutic Targets in Acute Erythroid Leukemia. Blood, 2020, 136, 17-18.	0.6	3
18	Prognostic Relevance of Genetic Abnormalities in Blastic Transformation of Chronic Myeloid Leukemia. Blood, 2020, 136, 3-4.	0.6	3

#	Article	IF	Citations
19	Defective Epsteinâ€“Barr virus in chronic active infection and haematological malignancy. Nature Microbiology, 2019, 4, 404-413.	5.9	152
20	Frequent structural variations involving programmed death ligands in Epstein-Barr virus-associated lymphomas. Leukemia, 2019, 33, 1687-1699.	3.3	98
21	Molecular heterogeneity in peripheral T-cell lymphoma, not otherwise specified revealed by comprehensive genetic profiling. Leukemia, 2019, 33, 2867-2883.	3.3	148
22	Pathogenic mutations identified by a multimodality approach in 117 Japanese Fanconi anemia patients. Haematologica, 2019, 104, 1962-1973.	1.7	22
23	Comprehensive analysis of genetic aberrations linked to tumorigenesis in regenerative nodules of liver cirrhosis. Journal of Gastroenterology, 2019, 54, 628-640.	2.3	33
24	Frequent germline mutations of HAVCR2 in sporadic subcutaneous panniculitis-like T-cell lymphoma. Blood Advances, 2019, 3, 588-595.	2.5	73
25	Ring sideroblasts in AML are associated with adverse risk characteristics and have a distinct gene expression pattern. Blood Advances, 2019, 3, 3111-3122.	2.5	6
26	Invariant patterns of clonal succession determine specific clinical features of myelodysplastic syndromes. Nature Communications, 2019, 10, 5386.	5.8	53
27	Paraneoplastic hypereosinophilic syndrome associated with IL3â€IgH positive acute lymphoblastic leukemia. Pediatric Blood and Cancer, 2019, 66, e27449.	0.8	12
28	Molecular pathogenesis of disease progression in MLL-rearranged AML. Leukemia, 2019, 33, 612-624.	3.3	26
29	Age-related remodelling of oesophageal epithelia by mutated cancer drivers. Nature, 2019, 565, 312-317.	13.7	476
30	Genomic landscape and clonal evolution of acute myeloid leukemia with t(8;21): an international study on 331 patients. Blood, 2019, 133, 1140-1151.	0.6	96
31	Novel neuroblastoma amplified sequence (NBAS) mutations in a Japanese boy with fever-triggered recurrent acute liver failure. Human Genome Variation, 2019, 6, 2.	0.4	26
32	Genetic and transcriptional landscape of plasma cells in POEMS syndrome. Leukemia, 2019, 33, 1723-1735.	3.3	28
33	<scp>NOTCH</scp>1 pathway activating mutations and clonal evolution in pediatric Tâ€cell acute lymphoblastic leukemia. Cancer Science, 2019, 110, 784-794.	1.7	26
34	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.	1.5	8
35	Distinct, Ethnic, Clinical, and Genetic Characteristics of Myelodysplastic Syndromes with Der(1;7). Blood, 2019, 134, 5392-5392.	0.6	2
36	Dysregulation of Epstein-Barr Virus Infection in Hypomorphic ZAP70 Mutation. Journal of Infectious Diseases, 2018, 218, 825-834.	1.9	22

#	Article	IF	Citations
37	Integrated molecular profiling of juvenile myelomonocytic leukemia. Blood, 2018, 131, 1576-1586.	0.6	78
38	Distinct gene alterations with a high percentage of myeloperoxidase-positive leukemic blasts in de novo acute myeloid leukemia. Leukemia Research, 2018, 65, 34-41.	0.4	4
39	Early detection and evolution of preleukemic clones in therapy-related myeloid neoplasms following autologous SCT. Blood, 2018, 131, 1846-1857.	0.6	35
40	Prognostic relevance of integrated genetic profiling in adult T-cell leukemia/lymphoma. Blood, 2018, 131, 215-225.	0.6	124
41	Genetic heterogeneity of uncharacterized childhood autoimmune diseases with lymphoproliferation. Pediatric Blood and Cancer, 2018, 65, e26831.	0.8	18
42	Integrated Molecular Characterization of the Lethal Pediatric Cancer Pancreatoblastoma. Cancer Research, 2018, 78, 865-876.	0.4	25
43	Characterization of HBV integration patterns and timing in liver cancer and HBV-infected livers. Oncotarget, 2018, 9, 25075-25088.	0.8	57
44	Clonally related diffuse large B-cell lymphoma and interdigitating dendritic cell sarcoma sharing MYC translocation. Haematologica, 2018, 103, e553-e556.	1.7	14
45	Aberrant splicing and defective mRNA production induced by somatic spliceosome mutations in myelodysplasia. Nature Communications, 2018, 9, 3649.	5.8	140
46	Recurrent CCND3 mutations in MLL-rearranged acute myeloid leukemia. Blood Advances, 2018, 2, 2879-2889.	2.5	19
47	A temporal shift of the evolutionary principle shaping intratumor heterogeneity in colorectal cancer. Nature Communications, 2018, 9, 2884.	5.8	82
48	A comprehensive characterization of cis-acting splicing-associated variants in human cancer. Genome Research, 2018, 28, 1111-1125.	2.4	56
49	RUNX1 mutations in pediatric acute myeloid leukemia are associated with distinct genetic features and an inferior prognosis. Blood, 2018, 131, 2266-2270.	0.6	15
50	De Novo Mutations Activating Germline TP53 in an Inherited Bone-Marrow-Failure Syndrome. American Journal of Human Genetics, 2018, 103, 440-447.	2.6	33
51	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.	0.8	34
52	Analysis of Genomic Predispositions to Sporadic Myeloid Neoplasms Mediated By DDX41 in Japan. Blood, 2018, 132, 4371-4371.	0.6	0
53	hotsub: A batch job engine for cloud services with ETL framework. Journal of Open Source Software, 2018, 3, 1069.	2.0	0
54	Clinical utility of next-generation sequencing for inherited bone marrow failure syndromes. Genetics in Medicine, 2017, 19, 796-802.	1.1	66

#	Article	IF	Citations
55	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.	1.5	18
56	Genetic abnormalities in myelodysplasia and secondary acute myeloid leukemia: impact on outcome of stem cell transplantation. Blood, 2017, 129, 2347-2358.	0.6	268
57	Exome sequencing identified RPS15A as a novel causative gene for Diamond-Blackfan anemia. Haematologica, 2017, 102, e93-e96.	1.7	30
58	Hypoxic adaptation of leukemic cells infiltrating the CNS affords a therapeutic strategy targeting VEGFA. Blood, 2017, 129, 3126-3129.	0.6	23
59	Clonal evolution in myelodysplastic syndromes. Nature Communications, 2017, 8, 15099.	5.8	118
60	Common Variable Immunodeficiency Caused by FANC Mutations. Journal of Clinical Immunology, 2017, 37, 434-444.	2.0	18
61	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.	0.8	9
62	Dynamics of clonal evolution in myelodysplastic syndromes. Nature Genetics, 2017, 49, 204-212.	9.4	348
63	Abnormal hematopoiesis and autoimmunity in human subjects with germline IKZF1 mutations. Journal of Allergy and Clinical Immunology, 2017, 140, 223-231.	1.5	99
64	Gene expression and risk of leukemic transformation in myelodysplasia. Blood, 2017, 130, 2642-2653.	0.6	64
65	Loss of DNA Damage Response in Neuroblastoma and Utility of a PARP Inhibitor. Journal of the National Cancer Institute, 2017, 109, .	3.0	43
66	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.	0.8	6
67	Atypical dyskeratosis congenita diagnosed using wholeâ€exome sequencing. Pediatrics International, 2017, 59, 933-935.	0.2	2
68	Recurrent SPI1 (PU.1) fusions in high-risk pediatric T cell acute lymphoblastic leukemia. Nature Genetics, 2017, 49, 1274-1281.	9.4	100
69	Haploinsufficiency of TNFAIP3 (A20) by germline mutation is involved in autoimmune lymphoproliferative syndrome. Journal of Allergy and Clinical Immunology, 2017, 139, 1914-1922.	1.5	91
70	Whole genome sequencing discriminates hepatocellular carcinoma with intrahepatic metastasis from multi-centric tumors. Journal of Hepatology, 2017, 66, 363-373.	1.8	81
71	Diagnostic challenge of Diamondâ€“Blackfan anemia in mothers and children by whole-exome sequencing. International Journal of Hematology, 2017, 105, 515-520.	0.7	18
72	Recurrent genetic defects on chromosome 5q in myeloid neoplasms. Oncotarget, 2017, 8, 6483-6495.	0.8	34

#	Article	IF	Citations
73	Identification of the genetic and clinical characteristics of neuroblastomas using genome-wide analysis. Oncotarget, 2017, 8, 107513-107529.	0.8	23
74	A framework for generating interactive reports for cancer genome analysis. Journal of Open Source Software, 2017, 2, 457.	2.0	1
75	Somatic mosaicism in chronic myeloid leukemia in remission. Blood, 2016, 128, 2863-2866.	0.6	13
76	Aberrant PD-L1 expression through 3â€²-UTR disruption in multiple cancers. Nature, 2016, 534, 402-406.	13.7	536
77	Whole-genome mutational landscape and characterization of noncoding and structural mutations in liver cancer. Nature Genetics, 2016, 48, 500-509.	9.4	596
78	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.	2.3	36
79	Genomic analysis of clonal origin of Langerhans cell histiocytosis following acute lymphoblastic leukaemia. British Journal of Haematology, 2016, 175, 169-172.	1.2	12
80	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.	1.2	60
81	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.	1.5	87
82	Genomic Landscape of Esophageal Squamous Cell Carcinoma inÂa Japanese Population. Gastroenterology, 2016, 150, 1171-1182.	0.6	265
83	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.	0.7	25
84	Molecular Heterogeneity in Peripheral T-Cell Lymphoma Not Otherwise Specified Revealed By Comprehensive Mutational Profiling. Blood, 2016, 128, 2927-2927.	0.6	3
85	VEGFA- a New Therapeutic Target in CNS Leukemia. Blood, 2016, 128, 911-911.	0.6	6
86	NGS-Based Copy Number Analysis in 1,185 Patients with Myeloid Neoplasms. Blood, 2016, 128, 955-955.	0.6	2
87	Integrated Multiregional Analysis Proposing a New Model of Colorectal Cancer Evolution. PLoS Genetics, 2016, 12, e1005778.	1.5	134
88	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
89	Genome-Wide Mutational Landscape of Infant Acute Lymphoblastic Leukemia. Blood, 2016, 128, 4070-4070.	0.6	0
90	Transcriptome Analysis Revealed the Entire Genetic Understanding of Pediatric Acute Myeloid Leukemia with a Normal Karyotype. Blood, 2016, 128, 2850-2850.	0.6	0

#	Article	IF	Citations
91	Integrated Molecular Analysis of Myelodysplastic Syndromes Using Whole Genome Sequencing. Blood, 2016, 128, 5512-5512.	0.6	0
92	Identifications of Highly Aggressive Phenotype with SPI1 Overexpression in Pediatric T Cell Acute Lymphoblastic Leukemia/Lymphoma. Blood, 2016, 128, 909-909.	0.6	0
93	Combined DNA and Transcriptome Sequencing Reveals Discrete Subtypes of Myelodysplasia. Blood, 2016, 128, 1974-1974.	0.6	0
94	Gene Expression Profiles and Methylation Analysis in Down Syndrome Related Acute Lymphoblastic Leukemia. Blood, 2016, 128, 4084-4084.	0.6	0
95	TAL1 Super Enhancer Aberration and Stil-TAL1 Fusion in Pediatric T Cell Acute Lymphoblastic Leukemia. Blood, 2016, 128, 1734-1734.	0.6	0
96	Structural Variations Involving Programmed Death Ligands in B-Cell and T-Cell Lymphomas. Blood, 2016, 128, 4105-4105.	0.6	0
97	Distinctive Genetic Features of Plasma Cells in POEMS Syndrome. Blood, 2016, 128, 4404-4404.	0.6	0
98	Genetic Profile of Acute Erythroid Leukemia. Blood, 2016, 128, 40-40.	0.6	1
99	Landscape of Driver Mutations and Their Clinical Impacts in Pediatric Acute Lymphoblastic Leukemia. Blood, 2016, 128, 912-912.	0.6	0
100	the Impact of Clonal Dynamics on Prognosis and Outcome in Myelodysplastic Syndromes. Blood, 2016, 128, 4287-4287.	0.6	0
101	High performance computing of a fusion gene detection pipeline on the K computer. , 2015, , .		3
102	Mutations in the Gene Encoding the E2 Conjugating Enzyme UBE2T Cause Fanconi Anemia. American Journal of Human Genetics, 2015, 96, 1001-1007.	2.6	100
103	Aberrant splicing of U12-type introns is the hallmark of ZRSR2 mutant myelodysplastic syndrome. Nature Communications, 2015, 6, 6042.	5.8	192
104	BRCC3 mutations in myeloid neoplasms. Haematologica, 2015, 100, 1051-7.	1.7	20
105	Whole-genome mutational landscape of liver cancers displaying biliary phenotype reveals hepatitis impact and molecular diversity. Nature Communications, 2015, 6, 6120.	5.8	178
106	Integrated genetic and epigenetic analysis defines novel molecular subgroups in rhabdomyosarcoma. Nature Communications, 2015, 6, 7557.	5.8	149
107	Inherited and Somatic Defects in DDX41 in Myeloid Neoplasms. Cancer Cell, 2015, 27, 658-670.	7.7	341
108	Mutational landscape and clonal architecture in grade II and III gliomas. Nature Genetics, 2015, 47, 458-468.	9.4	729

#	Article	IF	Citations
109	Integrated molecular analysis of adult T cell leukemia/lymphoma. Nature Genetics, 2015, 47, 1304-1315.	9.4	659
110	Clinical and genetic features of dyskeratosis congenita, cryptic dyskeratosis congenita, and Hoyeraal-Hreidarsson syndrome in Japan. International Journal of Hematology, 2015, 102, 544-552.	0.7	21
111	GATA2 and secondary mutations in familial myelodysplastic syndromes and pediatric myeloid malignancies. Haematologica, 2015, 100, e398-e401.	1.7	48
112	Late-Onset Combined Immunodeficiency with a Novel IL2RG Mutation and Probable Revertant Somatic Mosaicism. Journal of Clinical Immunology, 2015, 35, 610-614.	2.0	26
113	Genomon ITDetector: a tool for somatic internal tandem duplication detection from cancer genome sequencing data. Bioinformatics, 2015, 31, 116-118.	1.8	58
114	Frequent Activating Somatic Alterations in T-Cell Receptor / NF-Î²b Signaling in Adult T-Cell Leukemia/Lymphoma. Blood, 2015, 126, 113-113.	0.6	7
115	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
116	Prognostic Relevance of Integrated Genetic Profiling in Adult T-Cell Leukemia/Lymphoma. Blood, 2015, 126, 2643-2643.	0.6	1
117	Two Novel Distinct Subtypes of Myeloid Neoplasms Molecularly Associated with Histone H3K36 Methylations. Blood, 2015, 126, 2841-2841.	0.6	1
118	Genetic Predispositions to Myeloid Neoplasms Caused By Germline DDX41 Mutations. Blood, 2015, 126, 2843-2843.	0.6	7
119	Genetic Background of Idiopathic Bone Marrow Failure Syndromes in Children. Blood, 2015, 126, 3610-3610.	0.6	2
120	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
121	Impact of Somatic Mutations on Outcome in Patients with MDS after Stem-Cell Transplantation. Blood, 2015, 126, 711-711.	0.6	9
122	A Simple Model-Based Approach to Inferring and Visualizing Cancer Mutation Signatures. PLoS Genetics, 2015, 11, e1005657.	1.5	118
123	Aberrant DNA Methylation Is Associated with a Poor Outcome in Juvenile Myelomonocytic Leukemia. PLoS ONE, 2015, 10, e0145394.	1.1	25
124	Genomic landscape of liposarcoma. Oncotarget, 2015, 6, 42429-42444.	0.8	94
125	The landscape and clonal architecture in lower grade glioma.. Journal of Clinical Oncology, 2015, 33, 2008-2008.	0.8	0
126	Next-Generation Sequencing Reveal Proviral Genome and Transcriptome in Adult T-Cell Leukemia/Lymphoma. Blood, 2015, 126, 3882-3882.	0.6	0

#	Article	IF	Citations
127	Landscape of DNA Methylation and Genetic Profiles in 291 Patients with Myelodysplastic Syndromes. Blood, 2015, 126, 5205-5205.	0.6	0
128	Functional Characterization of a Novel GFI1B Mutation Causing Congenital Macrothrombocytopenia. Blood, 2015, 126, 75-75.	0.6	0
129	Genetic Basis of Primary Central Nervous System Lymphoma. Blood, 2015, 126, 2687-2687.	0.6	1
130	Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. Blood, 2015, 126, 1425-1425.	0.6	0
131	Myelodysplastic Syndrome Patients Show Mutation-Specific DNA Methylation Patterns. Blood, 2015, 126, 1646-1646.	0.6	0
132	TAL1 and MYB Abnormalities in Childhood T-Cell Acute Lymphoblastic Leukemia. Blood, 2015, 126, 2628-2628.	0.6	0
133	Detection of Novel Pathogenic Gene Rearrangements in Pediatric Acute Myeloid Leukemia By RNA Sequencing. Blood, 2015, 126, 2575-2575.	0.6	0
134	Whole-Exome Analysis of Autoimmune Lymphoproliferative Syndrome-like Diseases. Blood, 2015, 126, 1022-1022.	0.6	0
135	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.	1.1	79
136	HapMuC: somatic mutation calling using heterozygous germ line variants near candidate mutations. Bioinformatics, 2014, 30, 3302-3309.	1.8	23
137	Biallelic DICER1 Mutations in Sporadic Pleuropulmonary Blastoma. Cancer Research, 2014, 74, 2742-2749.	0.4	67
138	Recurrent somatic mutations underlie corticotropin-independent Cushingâ€™s syndrome. Science, 2014, 344, 917-920.	6.0	177
139	Somatic RHOA mutation in angioimmunoblastic T cell lymphoma. Nature Genetics, 2014, 46, 171-175.	9.4	542
140	Acquired Initiating Mutations in Early Hematopoietic Cells of CLL Patients. Cancer Discovery, 2014, 4, 1088-1101.	7.7	213
141	Whole-exome sequence analysis of ataxia telangiectasia-like phenotype. Journal of the Neurological Sciences, 2014, 340, 86-90.	0.3	12
142	DDX41 Is a Tumor Suppressor Gene Associated with Inherited and Acquired Mutations. Blood, 2014, 124, 125-125.	0.6	1
143	Chronological Analysis of Clonal Evolution in Acquired Aplastic Anemia. Blood, 2014, 124, 253-253.	0.6	4
144	ZRSR2 Mutations Cause Dysregulated RNA Splicing in MDS. Blood, 2014, 124, 4609-4609.	0.6	2

#	Article	IF	Citations
145	Landscape of Genetic Alterations in Adult T-Cell Leukemia/Lymphoma. Blood, 2014, 124, 75-75.	0.6	1
146	In Analogy to AML, MDS Can be Sub-Classified By Ancestral Mutations. Blood, 2014, 124, 823-823.	0.6	4
147	Comprehensive Analysis of Aberrant RNA Splicing in Myelodysplastic Syndromes. Blood, 2014, 124, 826-826.	0.6	6
148	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
149	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
150	Impact and Function of Somatic PHF6 Mutations in Myeloid Neoplasms. Blood, 2014, 124, 3581-3581.	0.6	0
151	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
152	Integrated molecular analysis of clear-cell renal cell carcinoma. Nature Genetics, 2013, 45, 860-867.	9.4	955
153	An empirical Bayesian framework for somatic mutation detection from cancer genome sequencing data. Nucleic Acids Research, 2013, 41, e89-e89.	6.5	177
154	Landscape Of Genetic Lesions In 944 Patients With Myelodysplastic Syndromes. Blood, 2013, 122, 521-521.	0.6	14
155	Somatic G17V Rhoa Mutation Specifies Angioimmunoblastic T-Cell Lymphoma. Blood, 2013, 122, 815-815.	0.6	2
156	Whole Exome Sequencing Detecting Kinesin Family Gene Defects In Myeloid Neoplasm. Blood, 2013, 122, 2762-2762.	0.6	0
157	Genetic Landscapes Of Childhood T-Cell Acute Lymphoblastic Leukemia. Blood, 2013, 122, 3786-3786.	0.6	0
158	Whole Exome Sequencing to Predict Response to Hypomethylating Agents in MDS. Blood, 2012, 120, 1698-1698.	0.6	1
159	Mutation Screening Associated with Chromosome 7 Abnormalities Using Next Generation Whole Exome Sequencing. Blood, 2012, 120, 173-173.	0.6	2
160	Somatic Mutations in Schinzel-Giedion Syndrome Gene SETBP1 Determine Progression in Myeloid Malignancies. Blood, 2012, 120, 2-2.	0.6	4
161	TET2 Mutations Revealed by Whole Genome Sequencing in Adult T-Cell Leukemia.. Blood, 2012, 120, 2697-2697.	0.6	0
162	Whole Exome Sequencing Reveals Spectrum of Gene Mutations in Pediatric AML. Blood, 2012, 120, 124-124.	0.6	0

#	Article	IF	Citations
163	Molecular Diversity Detected by Whole Exome Sequencing in Chronic Myelomonocytic Leukemia. Blood, 2012, 120, 310-310.	0.6	0
164	Recurrent Mutations of Multiple Components of Cohesin Complex in Myeloid Neoplasms. Blood, 2012, 120, 782-782.	0.6	1
165	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
166	Mutational Spectrum of Myelodysplastic Syndrome Malignancies Revealed by Whole Exome Sequencing. Blood, 2012, 120, 307-307.	0.6	0
167	Karyotypic and Genetic Abnormalities Associated with Clonal Evolution in Paroxysmal Nocturnal Hemoglobinuria.. Blood, 2012, 120, 2371-2371.	0.6	0
168	Whole Exome Analysis Reveals Spectrum of Gene Mutations in Juvenile Myelomonocytic Leukemia. Blood, 2012, 120, 170-170.	0.6	0
169	Various Germline Congenital Disorder Genes Are Somatically Mutated in Myeloid Malignancies. Blood, 2012, 120, 1405-1405.	0.6	1
170	Novel Recurrent Mutations in the Ras-Like GTP-Binding Gene Rit1 in Myeloid Malignancies. Blood, 2012, 120, 558-558.	0.6	0
171	Frequent pathway mutations of splicing machinery in myelodysplasia. Nature, 2011, 478, 64-69.	13.7	1,764
172	A rank-based statistical test for measuring synergistic effects between two gene sets. Bioinformatics, 2011, 27, 2399-2405.	1.8	3
173	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
174	Frequent Pathway Mutations of Splicing Machinery in Myelodysplasia. Blood, 2011, 118, 458-458.	0.6	8