Yuichi Shiraishi

List of Publications by Citations

175 papers	8,998 citations	42 h-index	94 g-index
183 ext. papers	11,417 ext. citations	7.7 avg, IF	4.96 L-index

#	Paper	IF	Citations
175	Frequent pathway mutations of splicing machinery in myelodysplasia. *Nature*, **2011**, 478, 64-9	50.4	1415
174	Integrated molecular analysis of clear-cell renal cell carcinoma. *Nature Genetics*, **2013**, 45, 860-7	36.3	723
173	Mutational landscape and clonal architecture in grade II and III gliomas. *Nature Genetics*, **2015**, 47, 458-68	36.3	543
172	Integrated molecular analysis of adult T cell leukemia/lymphoma. *Nature Genetics*, **2015**, 47, 1304-15	36.3	469
171	Whole-genome mutational landscape and characterization of noncoding and structural mutations in liver cancer. *Nature Genetics*, **2016**, 48, 500-9	36.3	423
170	Somatic RHOA mutation in angioimmunoblastic T cell lymphoma. *Nature Genetics*, **2014**, 46, 171-5	36.3	411
169	Aberrant PD-L1 expression through 3′UTR disruption in multiple cancers. *Nature*, **2016**, 534, 402-6	50.4	403
168	Age-related remodelling of oesophageal epithelia by mutated cancer drivers. *Nature*, **2019**, 565, 312-317	50.4	270
167	Dynamics of clonal evolution in myelodysplastic syndromes. *Nature Genetics*, **2017**, 49, 204-212	36.3	228
166	Inherited and Somatic Defects in DDX41 in Myeloid Neoplasms. *Cancer Cell*, **2015**, 27, 658-70	24.3	228
165	Genomic Landscape of Esophageal Squamous Cell Carcinoma in a Japanese Population. *Gastroenterology*, **2016**, 150, 1171-1182	13.3	195
164	Genetic abnormalities in myelodysplasia and secondary acute myeloid leukemia: impact on outcome of stem cell transplantation. *Blood*, **2017**, 129, 2347-2358	2.2	184
163	Acquired initiating mutations in early hematopoietic cells of CLL patients. *Cancer Discovery*, **2014**, 4, 1088-101	24.4	172
162	Genomic basis for RNA alterations in cancer. *Nature*, **2020**, 578, 129-136	50.4	148
161	Recurrent somatic mutations underlie corticotropin-independent Cushing's syndrome. *Science*, **2014**, 344, 917-20	33.3	142
160	Aberrant splicing of U12-type introns is the hallmark of ZRSR2 mutant myelodysplastic syndrome. *Nature Communications*, **2015**, 6, 6042	17.4	139
159	Whole-genome mutational landscape of liver cancers displaying biliary phenotype reveals hepatitis impact and molecular diversity. *Nature Communications*, **2015**, 6, 6120	17.4	139

158	An empirical Bayesian framework for somatic mutation detection from cancer genome sequencing data. *Nucleic Acids Research*, **2013**, 41, e89	20.1	129
157	Integrated genetic and epigenetic analysis defines novel molecular subgroups in rhabdomyosarcoma. *Nature Communications*, **2015**, 6, 7557	17.4	110
156	Integrated Multiregional Analysis Proposing a New Model of Colorectal Cancer Evolution. *PLoS Genetics*, **2016**, 12, e1005778	6	102
155	Mutations in the gene encoding the E2 conjugating enzyme UBE2T cause Fanconi anemia. *American Journal of Human Genetics*, **2015**, 96, 1001-7	11	90
154	A Simple Model-Based Approach to Inferring and Visualizing Cancer Mutation Signatures. *PLoS Genetics*, **2015**, 11, e1005657	6	87
153	Clonal evolution in myelodysplastic syndromes. *Nature Communications*, **2017**, 8, 15099	17.4	86
152	Defective Epstein-Barr virus in chronic active infection and haematological malignancy. *Nature Microbiology*, **2019**, 4, 404-413	26.6	80
151	Frequent mutations that converge on the NFKBIZ pathway in ulcerative colitis. *Nature*, **2020**, 577, 260-265	50.4	77
150	Prognostic relevance of integrated genetic profiling in adult T-cell leukemia/lymphoma. *Blood*, **2018**, 131, 215-225	2.2	76
149	Aberrant splicing and defective mRNA production induced by somatic spliceosome mutations in myelodysplasia. *Nature Communications*, **2018**, 9, 3649	17.4	76
148	Genomic landscape of liposarcoma. *Oncotarget*, **2015**, 6, 42429-44	3.3	75
147	Recurrent SPI1 (PU.1) fusions in high-risk pediatric T cell acute lymphoblastic leukemia. *Nature Genetics*, **2017**, 49, 1274-1281	36.3	74
146	Molecular heterogeneity in peripheral T-cell lymphoma, not otherwise specified revealed by comprehensive genetic profiling. *Leukemia*, **2019**, 33, 2867-2883	10.7	71
145	Haploinsufficiency of TNFAIP3 (A20) by germline mutation is involved in autoimmune lymphoproliferative syndrome. *Journal of Allergy and Clinical Immunology*, **2017**, 139, 1914-1922	11.5	69
144	Abnormal hematopoiesis and autoimmunity in human subjects with germline IKZF1 mutations. *Journal of Allergy and Clinical Immunology*, **2017**, 140, 223-231	11.5	63
143	Whole genome sequencing discriminates hepatocellular carcinoma with intrahepatic metastasis from multi-centric tumors. *Journal of Hepatology*, **2017**, 66, 363-373	13.4	62
142	Phosphatase and tensin homolog (PTEN) mutation can cause activated phosphatidylinositol 3-kinase δ syndrome-like immunodeficiency. *Journal of Allergy and Clinical Immunology*, **2016**, 138, 1672-1680.e10	11.5	61
141	Genomic landscape and clonal evolution of acute myeloid leukemia with t(8;21): an international study on 331 patients. *Blood*, **2019**, 133, 1140-1151	2.2	61

140	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	3.7	58
139	Frequent structural variations involving programmed death ligands in Epstein-Barr virus-associated lymphomas. *Leukemia*, **2019**, 33, 1687-1699	10.7	57
138	Biallelic DICER1 mutations in sporadic pleuropulmonary blastoma. *Cancer Research*, **2014**, 74, 2742-9	10.1	56
137	Integrated molecular profiling of juvenile myelomonocytic leukemia. *Blood*, **2018**, 131, 1576-1586	2.2	51
136	A temporal shift of the evolutionary principle shaping intratumor heterogeneity in colorectal cancer. *Nature Communications*, **2018**, 9, 2884	17.4	50
135	Genomon ITDetector: a tool for somatic internal tandem duplication detection from cancer genome sequencing data. *Bioinformatics*, **2015**, 31, 116-8	7.2	46
134	Clinical utility of next-generation sequencing for inherited bone marrow failure syndromes. *Genetics in Medicine*, **2017**, 19, 796-802	8.1	45
133	Whole-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	4.5	42
132	Gene expression and risk of leukemic transformation in myelodysplasia. *Blood*, **2017**, 130, 2642-2653	2.2	40
131	GATA2 and secondary mutations in familial myelodysplastic syndromes and pediatric myeloid malignancies. *Haematologica*, **2015**, 100, e398-401	6.6	38
130	A comprehensive characterization of -acting splicing-associated variants in human cancer. *Genome Research*, **2018**, 28, 1111-1125	9.7	32
129	Frequent germline mutations of in sporadic subcutaneous panniculitis-like T-cell lymphoma. *Blood Advances*, **2019**, 3, 588-595	7.8	31
128	Characterization of HBV integration patterns and timing in liver cancer and HBV-infected livers. *Oncotarget*, **2018**, 9, 25075-25088	3.3	30
127	Invariant patterns of clonal succession determine specific clinical features of myelodysplastic syndromes. *Nature Communications*, **2019**, 10, 5386	17.4	29
126	TERT promoter mutations and chromosome 8p loss are characteristic of nonalcoholic fatty liver disease-related hepatocellular carcinoma. *International Journal of Cancer*, **2016**, 139, 2512-8	7.5	28
125	Exome sequencing identified as a novel causative gene for Diamond-Blackfan anemia. *Haematologica*, **2017**, 102, e93-e96	6.6	25
124	Recurrent genetic defects on chromosome 5q in myeloid neoplasms. *Oncotarget*, **2017**, 8, 6483-6495	3.3	24
123	Loss of DNA Damage Response in Neuroblastoma and Utility of a PARP Inhibitor. *Journal of the National Cancer Institute*, **2017**, 109,	9.7	23

122	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	3.3	23
121	Single-cell analysis based dissection of clonality in myelofibrosis. *Nature Communications*, **2020**, 11, 73	17.4	23
120	Comprehensive analysis of genetic aberrations linked to tumorigenesis in regenerative nodules of liver cirrhosis. *Journal of Gastroenterology*, **2019**, 54, 628-640	6.9	23
119	Early detection and evolution of preleukemic clones in therapy-related myeloid neoplasms following autologous SCT. *Blood*, **2018**, 131, 1846-1857	2.2	21
118	NOTCH1 pathway activating mutations and clonal evolution in pediatric T-cell acute lymphoblastic leukemia. *Cancer Science*, **2019**, 110, 784-794	6.9	20
117	HapMuC: somatic mutation calling using heterozygous germ line variants near candidate mutations. *Bioinformatics*, **2014**, 30, 3302-9	7.2	19
116	Late-Onset Combined Immunodeficiency with a Novel IL2RG Mutation and Probable Revertant Somatic Mosaicism. *Journal of Clinical Immunology*, **2015**, 35, 610-4	5.7	18
115	PIEZO1 gene mutation in a Japanese family with hereditary high phosphatidylcholine hemolytic anemia and hemochromatosis-induced diabetes mellitus. *International Journal of Hematology*, **2016**, 104, 125-9	2.3	18
114	De Novo Mutations Activating Germline TP53 in an Inherited Bone-Marrow-Failure Syndrome. *American Journal of Human Genetics*, **2018**, 103, 440-447	11	18
113	Aberrant DNA Methylation Is Associated with a Poor Outcome in Juvenile Myelomonocytic Leukemia. *PLoS ONE*, **2015**, 10, e0145394	3.7	18
112	Molecular pathogenesis of disease progression in MLL-rearranged AML. *Leukemia*, **2019**, 33, 612-624	10.7	18
111	Genetic and transcriptional landscape of plasma cells in POEMS syndrome. *Leukemia*, **2019**, 33, 1723-1735	10.7	18
110	BRCC3 mutations in myeloid neoplasms. *Haematologica*, **2015**, 100, 1051-7	6.6	17
109	Identification of the genetic and clinical characteristics of neuroblastomas using genome-wide analysis. *Oncotarget*, **2017**, 8, 107513-107529	3.3	17
108	Common Variable Immunodeficiency Caused by FANC Mutations. *Journal of Clinical Immunology*, **2017**, 37, 434-444	5.7	15
107	Integrated Molecular Characterization of the Lethal Pediatric Cancer Pancreatoblastoma. *Cancer Research*, **2018**, 78, 865-876	10.1	15
106	Clinical and genetic features of dyskeratosis congenita, cryptic dyskeratosis congenita, and Hoyeraal-Hreidarsson syndrome in Japan. *International Journal of Hematology*, **2015**, 102, 544-52	2.3	14
105	Diagnostic challenge of Diamond-Blackfan anemia in mothers and children by whole-exome sequencing. *International Journal of Hematology*, **2017**, 105, 515-520	2.3	14

104	Novel neuroblastoma amplified sequence () mutations in a Japanese boy with fever-triggered recurrent acute liver failure. *Human Genome Variation*, **2019**, 6, 2	1.8	14
103	Hypoxic adaptation of leukemic cells infiltrating the CNS affords a therapeutic strategy targeting VEGFA. *Blood*, **2017**, 129, 3126-3129	2.2	13
102	Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. *Cancer Cell*, **2021**, 39, 793-809.e8	24.3	13
101	Genetic heterogeneity of uncharacterized childhood autoimmune diseases with lymphoproliferation. *Pediatric Blood and Cancer*, **2018**, 65, e26831	3	12
100	Recurrent mutations in -rearranged acute myeloid leukemia. *Blood Advances*, **2018**, 2, 2879-2889	7.8	12
99	ASXL2 mutations are frequently found in pediatric AML patients with t(8;21)/ RUNX1-RUNX1T1 and associated with a better prognosis. *Genes Chromosomes and Cancer*, **2017**, 56, 382-393	5	11
98	Whole-exome sequence analysis of ataxia telangiectasia-like phenotype. *Journal of the Neurological Sciences*, **2014**, 340, 86-90	3.2	11
97	Somatic mosaicism in chronic myeloid leukemia in remission. *Blood*, **2016**, 128, 2863-2866	2.2	11
96	Dysregulation of Epstein-Barr Virus Infection in Hypomorphic ZAP70 Mutation. *Journal of Infectious Diseases*, **2018**, 218, 825-834	7	10
95	Genomic basis for RNA alterations revealed by whole-genome analyses of 27 cancer types		10
94	Landscape of driver mutations and their clinical impacts in pediatric B-cell precursor acute lymphoblastic leukemia. *Blood Advances*, **2020**, 4, 5165-5173	7.8	10
93	Pathogenic mutations identified by a multimodality approach in 117 Japanese Fanconi anemia patients. *Haematologica*, **2019**, 104, 1962-1973	6.6	9
92	Clonally related diffuse large B-cell lymphoma and interdigitating dendritic cell sarcoma sharing translocation. *Haematologica*, **2018**, 103, e553-e556	6.6	9
91	mutations in pediatric acute myeloid leukemia are associated with distinct genetic features and an inferior prognosis. *Blood*, **2018**, 131, 2266-2270	2.2	8
90	Long read sequencing reveals a novel class of structural aberrations in cancers: identification and characterization of cancerous local amplifications		7
89	Genetic and clinical landscape of breast cancers with germline BRCA1/2 variants. *Communications Biology*, **2020**, 3, 578	6.7	7
88	Clonal evolution and clinical implications of genetic abnormalities in blastic transformation of chronic myeloid leukaemia. *Nature Communications*, **2021**, 12, 2833	17.4	7
87	Genomic analysis of clonal origin of Langerhans cell histiocytosis following acute lymphoblastic leukaemia. *British Journal of Haematology*, **2016**, 175, 169-72	4.5	7

86	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	3	6
85	Comprehensive Analysis of Aberrant RNA Splicing in Myelodysplastic Syndromes. *Blood*, **2014**, 124, 826-826	2.2	6
84	Genetic Predispositions to Myeloid Neoplasms Caused By Germline DDX41 Mutations. *Blood*, **2015**, 126, 2843-2843	2.2	5
83	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	11.5	5
82	Molecular studies reveal and gene fusions displaced in a case of infantile acute lymphoblastic leukemia with complex karyotype. *Oncology Letters*, **2017**, 14, 2295-2299	2.6	4
81	In Analogy to AML, MDS Can be Sub-Classified By Ancestral Mutations. *Blood*, **2014**, 124, 823-823	2.2	4
80	Paraneoplastic hypereosinophilic syndrome associated with IL3-IgH positive acute lymphoblastic leukemia. *Pediatric Blood and Cancer*, **2019**, 66, e27449	3	4
79	A rank-based statistical test for measuring synergistic effects between two gene sets. *Bioinformatics*, **2011**, 27, 2399-405	7.2	3
78	Landscape Of Genetic Lesions In 944 Patients With Myelodysplastic Syndromes. *Blood*, **2013**, 122, 521-521	2.2	3
77	Impact of Somatic Mutations on Outcome in Patients with MDS after Stem-Cell Transplantation. *Blood*, **2015**, 126, 711-711	2.2	3
76	Precise characterization of somatic structural variations and mobile element insertions from paired long-read sequencing data with nanomonsv		3
75	Genome analysis of myelodysplastic syndromes among atomic bomb survivors in Nagasaki. *Haematologica*, **2020**, 105, 358-365	6.6	3
74	Frequent mutations in HLA and related genes in extranodal NK/T cell lymphomas. *Leukemia and Lymphoma*, **2021**, 62, 95-103	1.9	3
73	Distinct, Ethnic, Clinical, and Genetic Characteristics of Myelodysplastic Syndromes with Der(1;7). *Blood*, **2019**, 134, 5392-5392	2.2	2
72	Mutational Spectrum Analysis of Interesting Correlation and Interrelationship Between RNA Splicing Pathway and Commonly Targeted Genes in Myelodysplastic Syndrome. *Blood*, **2011**, 118, 273-273	2.2	2
71	Somatic Mutations in Schinzel-Giedion Syndrome Gene SETBP1 Determine Progression in Myeloid Malignancies. *Blood*, **2012**, 120, 2-2	2.2	2
70	Somatic G17V Rhoa Mutation Specifies Angioimmunoblastic T-Cell Lymphoma. *Blood*, **2013**, 122, 815-815	2.2	2
69	Chronological Analysis of Clonal Evolution in Acquired Aplastic Anemia. *Blood*, **2014**, 124, 253-253	2.2	2

68	Frequent Activating Somatic Alterations in T-Cell Receptor / NF-Ƃ Signaling in Adult T-Cell Leukemia/Lymphoma. *Blood*, **2015**, 126, 113-113	2.2	2
67	Different Mutant Splicing Factors Cause Distinct Missplicing Events and Give Rise to Different Clinical Phenotypes in Myelodysplastic Syndromes. *Blood*, **2015**, 126, 139-139	2.2	2
66	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	2.2	2
65	Molecular Heterogeneity in Peripheral T-Cell Lymphoma Not Otherwise Specified Revealed By Comprehensive Mutational Profiling. *Blood*, **2016**, 128, 2927-2927	2.2	2
64	NGS-Based Copy Number Analysis in 1,185 Patients with Myeloid Neoplasms. *Blood*, **2016**, 128, 955-955	2.2	2
63	Acquisition of monosomy 7 and a RUNX1 mutation in Pearson syndrome. *Pediatric Blood and Cancer* , **2021**, 68, e28799	3	2
62	Distinct gene alterations with a high percentage of myeloperoxidase-positive leukemic blasts in de novo acute myeloid leukemia. *Leukemia Research*, **2018**, 65, 34-41	2.7	1
61	Atypical dyskeratosis congenita diagnosed using whole-exome sequencing. *Pediatrics International*, **2017**, 59, 933-935	1.2	1
60	High performance computing of a fusion gene detection pipeline on the K computer **2015**,		1
59	Genotype-Phenotype Relationships and Therapeutic Targets in Acute Erythroid Leukemia. *Blood*, **2020**, 136, 17-18	2.2	1
58	Prognostic Relevance of Genetic Abnormalities in Blastic Transformation of Chronic Myeloid Leukemia. *Blood*, **2020**, 136, 3-4	2.2	1
57	Frequent Pathway Mutations of Splicing Machinery in Myelodysplasia. *Blood*, **2011**, 118, 458-458	2.2	1
56	Whole Exome Sequencing to Predict Response to Hypomethylating Agents in MDS. *Blood*, **2012**, 120, 1698-1698	2.2	1
55	Mutation Screening Associated with Chromosome 7 Abnormalities Using Next Generation Whole Exome Sequencing. *Blood*, **2012**, 120, 173-173	2.2	1
54	ZRSR2 Mutations Cause Dysregulated RNA Splicing in MDS. *Blood*, **2014**, 124, 4609-4609	2.2	1
53	Landscape of Genetic Alterations in Adult T-Cell Leukemia/Lymphoma. *Blood*, **2014**, 124, 75-75	2.2	1
52	Prognostic Relevance of Integrated Genetic Profiling in Adult T-Cell Leukemia/Lymphoma. *Blood*, **2015**, 126, 2643-2643	2.2	1
51	Two Novel Distinct Subtypes of Myeloid Neoplasms Molecularly Associated with Histone H3K36 Methylations. *Blood*, **2015**, 126, 2841-2841	2.2	1

50	Genetic Background of Idiopathic Bone Marrow Failure Syndromes in Children. *Blood*, **2015**, 126, 3610-3610	2.2	1
49	VEGFA- a New Therapeutic Target in CNS Leukemia. *Blood*, **2016**, 128, 911-911	2.2	1
48	EPOR/JAK/STAT Signaling Pathway As Therapeutic Target of Acute Erythroid Leukemia. *Blood*, **2021**, 138, 610-610	2.2	1
47	A framework for generating interactive reports for cancer genome analysis. *Journal of Open Source Software*, **2017**, 2, 457	5.2	1
46	Genetic Basis of Primary Central Nervous System Lymphoma. *Blood*, **2015**, 126, 2687-2687	2.2	1
45	Identification of Two New DBA Genes, RPS27 and RPL27, by Whole-Exome Sequencing in Diamond-Blackfan Anemia Patients. *Blood*, **2012**, 120, 984-984	2.2	1
44	Various Germline Congenital Disorder Genes Are Somatically Mutated in Myeloid Malignancies. *Blood*, **2012**, 120, 1405-1405	2.2	1
43	Ring sideroblasts in AML are associated with adverse risk characteristics and have a distinct gene expression pattern. *Blood Advances*, **2019**, 3, 3111-3122	7.8	1
42	The Evolving Genomic Landscape of Esophageal Squamous Cell Carcinoma Under Chemoradiotherapy. *Cancer Research*, **2021**, 81, 4926-4938	10.1	1
41	DDX41 Is a Tumor Suppressor Gene Associated with Inherited and Acquired Mutations. *Blood*, **2014**, 124, 125-125	2.2	0
40	Post-Treatment Clone Size Predicts Survival Independently of IPSS-R and Response after Azacitidine Therapy for MDS.. *Blood*, **2020**, 136, 12-13	2.2	
39	Clonal Evolution Pattern and Prognostic Significance of Clonal Architecture in KMT2A-Rearranged Acute Myeloid Leukemia. *Blood*, **2021**, 138, 2358-2358	2.2	
38	Analysis of Genomic Predispositions to Sporadic Myeloid Neoplasms Mediated By DDX41 in Japan. *Blood*, **2018**, 132, 4371-4371	2.2	
37	hotsub: A batch job engine for cloud services with ETL framework. *Journal of Open Source Software*, **2018**, 3, 1069	5.2	
36	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	2.2	
35	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	2.2	
34	Impact and Function of Somatic PHF6 Mutations in Myeloid Neoplasms. *Blood*, **2014**, 124, 3581-3581	2.2	
33	Whole-Exome Sequencing Reveals a Paucity of Somatic Gene Mutations in Aplastic Anemia and Refractory Cytopenia of Childhood. *Blood*, **2014**, 124, 4388-4388	2.2	

32	The landscape and clonal architecture in lower grade glioma.. *Journal of Clinical Oncology*, **2015**, 33, 2008-2008	2.2
31	Next-Generation Sequencing Reveal Proviral Genome and Transcriptome in Adult T-Cell Leukemia/Lymphoma. *Blood*, **2015**, 126, 3882-3882	2.2
30	Landscape of DNA Methylation and Genetic Profiles in 291 Patients with Myelodysplastic Syndromes. *Blood*, **2015**, 126, 5205-5205	2.2
29	Functional Characterization of a Novel GFI1B Mutation Causing Congenital Macrothrombocytopenia. *Blood*, **2015**, 126, 75-75	2.2
28	Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. *Blood*, **2015**, 126, 1425-1425	2.2
27	Myelodysplastic Syndrome Patients Show Mutation-Specific DNA Methylation Patterns. *Blood*, **2015**, 126, 1646-1646	2.2
26	TAL1 and MYB Abnormalities in Childhood T-Cell Acute Lymphoblastic Leukemia. *Blood*, **2015**, 126, 2628-2628	2.2
25	Detection of Novel Pathogenic Gene Rearrangements in Pediatric Acute Myeloid Leukemia By RNA Sequencing. *Blood*, **2015**, 126, 2575-2575	2.2
24	Whole-Exome Analysis of Autoimmune Lymphoproliferative Syndrome-like Diseases. *Blood*, **2015**, 126, 1022-1022	2.2
23	Clinical Significance of Mutations and Copy Number Lesions on Prognosis of Patients with MDS after Unrelated Bone Marrow Transplantation. *Blood*, **2016**, 128, 1971-1971	2.2
22	Genome-Wide Mutational Landscape of Infant Acute Lymphoblastic Leukemia. *Blood*, **2016**, 128, 4070-4070	2.2
21	Transcriptome Analysis Revealed the Entire Genetic Understanding of Pediatric Acute Myeloid Leukemia with a Normal Karyotype. *Blood*, **2016**, 128, 2850-2850	2.2
20	Integrated Molecular Analysis of Myelodysplastic Syndromes Using Whole Genome Sequencing. *Blood*, **2016**, 128, 5512-5512	2.2
19	Identifications of Highly Aggressive Phenotype with SPI1 Overexpression in Pediatric T Cell Acute Lymphoblastic Leukemia/Lymphoma. *Blood*, **2016**, 128, 909-909	2.2
18	Combined DNA and Transcriptome Sequencing Reveals Discrete Subtypes of Myelodysplasia. *Blood*, **2016**, 128, 1974-1974	2.2
17	Gene Expression Profiles and Methylation Analysis in Down Syndrome Related Acute Lymphoblastic Leukemia. *Blood*, **2016**, 128, 4084-4084	2.2
16	TAL1 Super Enhancer Aberration and Stil-TAL1 Fusion in Pediatric T Cell Acute Lymphoblastic Leukemia. *Blood*, **2016**, 128, 1734-1734	2.2
15	Structural Variations Involving Programmed Death Ligands in B-Cell and T-Cell Lymphomas. *Blood*, **2016**, 128, 4105-4105	2.2

14	Distinctive Genetic Features of Plasma Cells in POEMS Syndrome. *Blood*, **2016**, 128, 4404-4404	2.2
13	Genetic Profile of Acute Erythroid Leukemia. *Blood*, **2016**, 128, 40-40	2.2
12	Landscape of Driver Mutations and Their Clinical Impacts in Pediatric Acute Lymphoblastic Leukemia. *Blood*, **2016**, 128, 912-912	2.2
11	the Impact of Clonal Dynamics on Prognosis and Outcome in Myelodysplastic Syndromes. *Blood*, **2016**, 128, 4287-4287	2.2
10	TET2 Mutations Revealed by Whole Genome Sequencing in Adult T-Cell Leukemia.. *Blood*, **2012**, 120, 2697-2697	2.2
9	Whole Exome Sequencing Reveals Spectrum of Gene Mutations in Pediatric AML. *Blood*, **2012**, 120, 124-124	2.2
8	Molecular Diversity Detected by Whole Exome Sequencing in Chronic Myelomonocytic Leukemia. *Blood*, **2012**, 120, 310-310	2.2
7	Recurrent Mutations of Multiple Components of Cohesin Complex in Myeloid Neoplasms. *Blood*, **2012**, 120, 782-782	2.2
6	Mutational Spectrum of Myelodysplastic Syndrome Malignancies Revealed by Whole Exome Sequencing. *Blood*, **2012**, 120, 307-307	2.2
5	Karyotypic and Genetic Abnormalities Associated with Clonal Evolution in Paroxysmal Nocturnal Hemoglobinuria.. *Blood*, **2012**, 120, 2371-2371	2.2
4	Whole Exome Analysis Reveals Spectrum of Gene Mutations in Juvenile Myelomonocytic Leukemia. *Blood*, **2012**, 120, 170-170	2.2
3	Novel Recurrent Mutations in the Ras-Like GTP-Binding Gene Rit1 in Myeloid Malignancies. *Blood*, **2012**, 120, 558-558	2.2
2	Whole Exome Sequencing Detecting Kinesin Family Gene Defects In Myeloid Neoplasm. *Blood*, **2013**, 122, 2762-2762	2.2
1	Genetic Landscapes Of Childhood T-Cell Acute Lymphoblastic Leukemia. *Blood*, **2013**, 122, 3786-3786	2.2