Kenichi Yoshida

List of Publications by Year
in descending order

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212 papers	13,133 citations	38660 50 h-index	25716 108 g-index
221 all docs	221 docs citations	221 times ranked	20939 citing authors

#	Article	IF	Citations
1	Frequent pathway mutations of splicing machinery in myelodysplasia. Nature, 2011, 478, 64-69.	13.7	1,764
2	Integrated molecular analysis of clear-cell renal cell carcinoma. Nature Genetics, 2013, 45, 860-867.	9.4	955
3	Mutational landscape and clonal architecture in grade II and III gliomas. Nature Genetics, 2015, 47, 458-468.	9.4	729
4	Integrated molecular analysis of adult T cell leukemia/lymphoma. Nature Genetics, 2015, 47, 1304-1315.	9.4	659
5	Somatic RHOA mutation in angioimmunoblastic T cell lymphoma. Nature Genetics, 2014, 46, 171-175.	9.4	542
6	Aberrant PD-L1 expression through 3â€²-UTR disruption in multiple cancers. Nature, 2016, 534, 402-406.	13.7	536
7	Age-related remodelling of oesophageal epithelia by mutated cancer drivers. Nature, 2019, 565, 312-317.	13.7	476
8	Dynamics of clonal evolution in myelodysplastic syndromes. Nature Genetics, 2017, 49, 204-212.	9.4	348
9	Inherited and Somatic Defects in DDX41 in Myeloid Neoplasms. Cancer Cell, 2015, 27, 658-670.	7.7	341
10	The landscape of somatic mutations in Down syndromeâ€“related myeloid disorders. Nature Genetics, 2013, 45, 1293-1299.	9.4	324
11	Genetic abnormalities in myelodysplasia and secondary acute myeloid leukemia: impact on outcome of stem cell transplantation. Blood, 2017, 129, 2347-2358.	0.6	268
12	Acquired Initiating Mutations in Early Hematopoietic Cells of CLL Patients. Cancer Discovery, 2014, 4, 1088-1101.	7.7	213
13	Profiling of somatic mutations in acute myeloid leukemia with FLT3-ITD at diagnosis and relapse. Blood, 2015, 126, 2491-2501.	0.6	180
14	Recurrent somatic mutations underlie corticotropin-independent Cushingâ€™s syndrome. Science, 2014, 344, 917-920.	6.0	177
15	Mutation allele burden remains unchanged in chronic myelomonocytic leukaemia responding to hypomethylating agents. Nature Communications, 2016, 7, 10767.	5.8	177
16	Frequent mutations that converge on the NFKBIZ pathway in ulcerative colitis. Nature, 2020, 577, 260-265.	13.7	168
17	Defective Epsteinâ€“Barr virus in chronic active infection and haematological malignancy. Nature Microbiology, 2019, 4, 404-413.	5.9	152
18	Integrated genetic and epigenetic analysis defines novel molecular subgroups in rhabdomyosarcoma. Nature Communications, 2015, 6, 7557.	5.8	149

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19	Molecular heterogeneity in peripheral T-cell lymphoma, not otherwise specified revealed by comprehensive genetic profiling. Leukemia, 2019, 33, 2867-2883.	3.3	148
20	Aberrant splicing and defective mRNA production induced by somatic spliceosome mutations in myelodysplasia. Nature Communications, 2018, 9, 3649.	5.8	140
21	Hematopoietic lineage distribution and evolutionary dynamics of clonal hematopoiesis. Leukemia, 2018, 32, 1908-1919.	3.3	137
22	Splicing factor mutations and cancer. Wiley Interdisciplinary Reviews RNA, 2014, 5, 445-459.	3.2	126
23	Prognostic relevance of integrated genetic profiling in adult T-cell leukemia/lymphoma. Blood, 2018, 131, 215-225.	0.6	124
24	Selective production of transgenic mice using green fluorescent protein as a marker. Nature Biotechnology, 1997, 15, 458-461.	9.4	119
25	Clonal evolution in myelodysplastic syndromes. Nature Communications, 2017, 8, 15099.	5.8	118
26	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
27	Recurrent SPI1 (PU.1) fusions in high-risk pediatric T cell acute lymphoblastic leukemia. Nature Genetics, 2017, 49, 1274-1281.	9.4	100
28	Regulation of Geminin and Cdt1 expression by E2F transcription factors. Oncogene, 2004, 23, 3802-3812.	2.6	99
29	Abnormal hematopoiesis and autoimmunity in human subjects with germline IKZF1 mutations. Journal of Allergy and Clinical Immunology, 2017, 140, 223-231.	1.5	99
30	Variegated RHOA mutations in adult T-cell leukemia/lymphoma. Blood, 2016, 127, 596-604.	0.6	98
31	Frequent structural variations involving programmed death ligands in Epstein-Barr virus-associated lymphomas. Leukemia, 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. Blood, 2019, 133, 1140-1151.	0.6	96
33	Genomic landscape of liposarcoma. Oncotarget, 2015, 6, 42429-42444.	0.8	94
34	Mechanisms of Progression of Myeloid Preleukemia to Transformed Myeloid Leukemia in Children with Down Syndrome. Cancer Cell, 2019, 36, 123-138.e10.	7.7	93
35	Two Aldehyde Clearance Systems Are Essential to Prevent Lethal Formaldehyde Accumulation in Mice and Humans. Molecular Cell, 2020, 80, 996-1012.e9.	4.5	92
36	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

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37	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
38	Frequent NFKBIE deletions are associated with poor outcome in primary mediastinal B-cell lymphoma. Blood, 2016, 128, 2666-2670.	0.6	82
39	Integrated molecular profiling of juvenile myelomonocytic leukemia. Blood, 2018, 131, 1576-1586.	0.6	78
40	The E-Id Protein Axis Specifies Adaptive Lymphoid Cell Identity and Suppresses Thymic Innate Lymphoid Cell Development. Immunity, 2017, 46, 818-834.e4.	6.6	73
41	Frequent germline mutations of HAVCR2 in sporadic subcutaneous panniculitis-like T-cell lymphoma. Blood Advances, 2019, 3, 588-595.	2.5	73
42	ATP11C is a major flippase in human erythrocytes and its defect causes congenital hemolytic anemia. Haematologica, 2016, 101, 559-565.	1.7	72
43	Gain-of-function IKBKB mutation causes human combined immune deficiency. Journal of Experimental Medicine, 2018, 215, 2715-2724.	4.2	69
44	Biallelic DICER1 Mutations in Sporadic Pleuropulmonary Blastoma. Cancer Research, 2014, 74, 2742-2749.	0.4	67
45	Clinical utility of next-generation sequencing for inherited bone marrow failure syndromes. Genetics in Medicine, 2017, 19, 796-802.	1.1	66
46	Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. Cancer Cell, 2021, 39, 793-809.e8.	7.7	65
47	Gene expression and risk of leukemic transformation in myelodysplasia. Blood, 2017, 130, 2642-2653.	0.6	64
48	Physiological Srsf2 P95H expression causes impaired hematopoietic stem cell functions and aberrant RNA splicing in mice. Blood, 2018, 131, 621-635.	0.6	64
49	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
50	Genomon ITDetector: a tool for somatic internal tandem duplication detection from cancer genome sequencing data. Bioinformatics, 2015, 31, 116-118.	1.8	58
51	Invariant patterns of clonal succession determine specific clinical features of myelodysplastic syndromes. Nature Communications, 2019, 10, 5386.	5.8	53
52	BH-protocadherin-c, a member of the cadherin superfamily, interacts with protein phosphatase 1 alpha through its intracellular domain. FEBS Letters, 1999, 460, 93-98.	1.3	52
53	Transcriptome analysis offers a comprehensive illustration of the genetic background of pediatric acute myeloid leukemia. Blood Advances, 2019, 3, 3157-3169.	2.5	51
54	Combined Cohesinâ€“RUNX1 Deficiency Synergistically Perturbs Chromatin Looping and Causes Myelodysplastic Syndromes. Cancer Discovery, 2020, 10, 836-853.	7.7	51

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55	Expression of MCM10 and TopBP1 is regulated by cell proliferation and UV irradiation via the E2F transcription factor. Oncogene, 2004, 23, 6250-6260.	2.6	50
56	Hematopoietic stem cell transplantation for progressive combined immunodeficiency and lymphoproliferation in patients with activated phosphatidylinositol-3-OH kinase Î´ syndrome type 1. Journal of Allergy and Clinical Immunology, 2019, 143, 266-275.	1.5	49
57	Frequent genetic alterations in immune checkpointâ€“related genes in intravascular large B-cell lymphoma. Blood, 2021, 137, 1491-1502.	0.6	49
58	GATA2 and secondary mutations in familial myelodysplastic syndromes and pediatric myeloid malignancies. Haematologica, 2015, 100, e398-e401.	1.7	48
59	Single-cell analysis based dissection of clonality in myelofibrosis. Nature Communications, 2020, 11, 73.	5.8	46
60	Loss of DNA Damage Response in Neuroblastoma and Utility of a PARP Inhibitor. Journal of the National Cancer Institute, 2017, 109, .	3.0	43
61	Clonal evolution and clinical implications of genetic abnormalities in blastic transformation of chronic myeloid leukaemia. Nature Communications, 2021, 12, 2833.	5.8	39
62	Germline loss-of-function SAMD9 and SAMD9L alterations in adult myelodysplastic syndromes. Blood, 2018, 132, 2309-2313.	0.6	38
63	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
64	Early detection and evolution of preleukemic clones in therapy-related myeloid neoplasms following autologous SCT. Blood, 2018, 131, 1846-1857.	0.6	35
65	The destruction box of human Geminin is critical for proliferation and tumor growth in human colon cancer cells. Oncogene, 2004, 23, 58-70.	2.6	34
66	Recurrent genetic defects on chromosome 5q in myeloid neoplasms. Oncotarget, 2017, 8, 6483-6495.	0.8	34
67	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
68	Comprehensive analysis of genetic aberrations linked to tumorigenesis in regenerative nodules of liver cirrhosis. Journal of Gastroenterology, 2019, 54, 628-640.	2.3	33
69	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
70	Fibroblast cell shape and adhesion in vitro is altered by overexpression of the 7a and 7b isoforms of protocadherin 7, but not the 7c isoform. Cellular and Molecular Biology Letters, 2003, 8, 735-41.	2.7	31
71	Exome sequencing identified RPS15A as a novel causative gene for Diamond-Blackfan anemia. Haematologica, 2017, 102, e93-e96.	1.7	30
72	Integrated multiomics analysis of hepatoblastoma unravels its heterogeneity and provides novel druggable targets. Npj Precision Oncology, 2020, 4, 20.	2.3	30

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73	Autonomous feedback loop of RUNX1-p53-CBFB in acute myeloid leukemia cells. Scientific Reports, 2017, 7, 16604.	1.6	29
74	Genetic and transcriptional landscape of plasma cells in POEMS syndrome. Leukemia, 2019, 33, 1723-1735.	3.3	28
75	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
76	Molecular pathogenesis of disease progression in MLL-rearranged AML. Leukemia, 2019, 33, 612-624.	3.3	26
77	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
78	<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
79	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
80	Integrated Molecular Characterization of the Lethal Pediatric Cancer Pancreatoblastoma. Cancer Research, 2018, 78, 865-876.	0.4	25
81	Aberrant DNA Methylation Is Associated with a Poor Outcome in Juvenile Myelomonocytic Leukemia. PLoS ONE, 2015, 10, e0145394.	1.1	25
82	Detection of the G17V RHOA Mutation in Angioimmunoblastic T-Cell Lymphoma and Related Lymphomas Using Quantitative Allele-Specific PCR. PLoS ONE, 2014, 9, e109714.	1.1	24
83	Differential expression of individual transcript variants of PD-1 and PD-L2 genes on Th-1/Th-2 status is guaranteed for prognosis prediction in PCNSL. Scientific Reports, 2019, 9, 10004.	1.6	24
84	Unbiased Detection of Driver Mutations in Extramammary Paget Disease. Clinical Cancer Research, 2021, 27, 1756-1765.	3.2	24
85	Hypoxic adaptation of leukemic cells infiltrating the CNS affords a therapeutic strategy targeting VEGFA. Blood, 2017, 129, 3126-3129.	0.6	23
86	BCL6 locus is hypermethylated in angioimmunoblastic T-cell lymphoma. International Journal of Hematology, 2017, 105, 465-469.	0.7	23
87	Identification of the genetic and clinical characteristics of neuroblastomas using genome-wide analysis. Oncotarget, 2017, 8, 107513-107529.	0.8	23
88	Dysregulation of Epstein-Barr Virus Infection in Hypomorphic ZAP70 Mutation. Journal of Infectious Diseases, 2018, 218, 825-834.	1.9	22
89	Pathogenic mutations identified by a multimodality approach in 117 Japanese Fanconi anemia patients. Haematologica, 2019, 104, 1962-1973.	1.7	22
90	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

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91	BRCC3 mutations in myeloid neoplasms. Haematologica, 2015, 100, 1051-7.	1.7	20
92	Novel DDX41 variants in Thai patients with myeloid neoplasms. International Journal of Hematology, 2020, 111, 241-246.	0.7	20
93	Genetic and clinical landscape of breast cancers with germline BRCA1/2 variants. Communications Biology, 2020, 3, 578.	2.0	20
94	Deep Sequencing in Cancer Research. Japanese Journal of Clinical Oncology, 2013, 43, 110-115.	0.6	19
95	The nicotinic cholinergic system is affected in rats with delayed carbon monoxide encephalopathy. Neuroscience Letters, 2014, 569, 33-37.	1.0	19
96	Recurrent CCND3 mutations in MLL-rearranged acute myeloid leukemia. Blood Advances, 2018, 2, 2879-2889.	2.5	19
97	Associations of complementation group, ALDH2 genotype, and clonal abnormalities with hematological outcome in Japanese patients with Fanconi anemia. Annals of Hematology, 2019, 98, 271-280.	0.8	19
98	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
99	Common Variable Immunodeficiency Caused by FANC Mutations. Journal of Clinical Immunology, 2017, 37, 434-444.	2.0	18
100	Metachronous anaplastic sarcoma of the kidney and thyroid follicular carcinoma as manifestations of DICER1 abnormalities. Human Pathology, 2017, 61, 205-209.	1.1	18
101	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
102	Genetic heterogeneity of uncharacterized childhood autoimmune diseases with lymphoproliferation. Pediatric Blood and Cancer, 2018, 65, e26831.	0.8	18
103	Conditional expression of MCM7 increases tumor growth without altering DNA replication activity. FEBS Letters, 2003, 553, 213-217.	1.3	17
104	KLF1 mutation E325K induces cell cycle arrest in erythroid cells differentiated from congenital dyserythropoietic anemia patient-specific induced pluripotent stem cells. Experimental Hematology, 2019, 73, 25-37.e8.	0.2	17
105	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
106	Integrated genetic and epigenetic analysis revealed heterogeneity of acute lymphoblastic leukemia in Down syndrome. Cancer Science, 2019, 110, 3358-3367.	1.7	15
107	Clonally related diffuse large B-cell lymphoma and interdigitating dendritic cell sarcoma sharing MYC translocation. Haematologica, 2018, 103, e553-e556.	1.7	14
108	DNA methylation-based classification reveals difference between pediatric T-cell acute lymphoblastic leukemia and normal thymocytes. Leukemia, 2020, 34, 1163-1168.	3.3	14

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109	Landscape Of Genetic Lesions In 944 Patients With Myelodysplastic Syndromes. Blood, 2013, 122, 521-521.	0.6	14
110	Somatic mosaicism in chronic myeloid leukemia in remission. Blood, 2016, 128, 2863-2866.	0.6	13
111	Biological Analysis of SRSF2 Mutations in Leukemogenesis. Blood, 2012, 120, 1282-1282.	0.6	13
112	The landscape of genetic aberrations in myxofibrosarcoma. International Journal of Cancer, 2022, 151, 565-577.	2.3	13
113	Whole-exome sequence analysis of ataxia telangiectasia-like phenotype. Journal of the Neurological Sciences, 2014, 340, 86-90.	0.3	12
114	Single cell genotyping of exome sequencing-identified mutations to characterize the clonal composition and evolution of inv(16) AML in a CBL mutated clonal hematopoiesis. Leukemia Research, 2016, 47, 41-46.	0.4	12
115	Genomic analysis of clonal origin of Langerhans cell histiocytosis following acute lymphoblastic leukaemia. British Journal of Haematology, 2016, 175, 169-172.	1.2	12
116	Paraneoplastic hypereosinophilic syndrome associated with IL3â€‐gH positive acute lymphoblastic leukemia. Pediatric Blood and Cancer, 2019, 66, e27449.	0.8	12
117	Frequent mutations in HLA and related genes in extranodal NK/T cell lymphomas. Leukemia and Lymphoma, 2021, 62, 95-103.	0.6	12
118	Clinical utility of target captureâ€based panel sequencing in hematological malignancies: A multicenter feasibility study. Cancer Science, 2020, 111, 3367-3378.	1.7	11
119	Association of high-risk neuroblastoma classification based on expression profiles with differentiation and metabolism. PLoS ONE, 2021, 16, e0245526.	1.1	11
120	The phenotype and clinical course of Japanese Fanconi Anaemia infants is influenced by patient, but not maternal ALDH2 genotype. British Journal of Haematology, 2016, 175, 457-461.	1.2	10
121	A founder variant in the South Asian population leads to a high prevalence ofFANCLFanconi anemia cases in India. Human Mutation, 2020, 41, 122-128.	1.1	10
122	Reduced-intensity conditioning is effective for hematopoietic stem cell transplantation in young pediatric patients with Diamondâ€“Blackfan anemia. Bone Marrow Transplantation, 2021, 56, 1013-1020.	1.3	10
123	Clinical significance of RAS pathway alterations in pediatric acute myeloid leukemia. Haematologica, 2021, , .	1.7	10
124	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
125	Comprehensive genetic analysis of pediatric germ cell tumors identifies potential drug targets. Communications Biology, 2020, 3, 544.	2.0	9
126	Acquisition of monosomy 7 and a RUNX1 mutation in Pearson syndrome. Pediatric Blood and Cancer, 2021, 68, e28799.	0.8	9

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127	Whole-exome analysis to detect congenital hemolytic anemia mimicking congenital dyserythropoietic anemia. International Journal of Hematology, 2018, 108, 306-311.	0.7	8
128	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
129	Frequent Pathway Mutations of Splicing Machinery in Myelodysplasia. Blood, 2011, 118, 458-458.	0.6	8
130	Fusion partnerâ€“specific mutation profiles and KRAS mutations as adverse prognostic factors in MLL-rearranged AML. Blood Advances, 2020, 4, 4623-4631.	2.5	7
131	Clinical Impacts of Germline DDX41 Mutations on Myeloid Neoplasms. Blood, 2020, 136, 38-40.	0.6	7
132	SRSF2 is Mutated in 47.2% (77/163) of Chronic Myelomonocytic Leukemia (CMML) and Prognostically Favorable in Cases with Concomitant RUNX1 mutations. Blood, 2011, 118, 274-274.	0.6	7
133	Amplified EPOR/JAK2 Genes Define a Unique Subtype of Acute Erythroid Leukemia. Blood Cancer Discovery, 2022, 3, 410-427.	2.6	7
134	Peptide binding to Geminin and inhibitory for DNA replication. Biochemical and Biophysical Research Communications, 2004, 317, 218-222.	1.0	6
135	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
136	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
137	A Possible Association Between a Nucleotideâ€Binding Domain LRRâ€Containing Protein Family PYDâ€Containing Protein 1 Mutation and an Autoinflammatory Disease Involving Liver Cirrhosis. Hepatology, 2021, 74, 2296-2299.	3.6	6
138	Comprehensive Analysis of Aberrant RNA Splicing in Myelodysplastic Syndromes. Blood, 2014, 124, 826-826.	0.6	6
139	cDNA Cloning and Chromosomal Mapping of Mouse BH-Protocadherin. DNA Sequence, 1999, 10, 43-47.	0.7	5
140	Somatic Mutations in Schinzel-Giedion Syndrome Gene SETBP1 Determine Progression in Myeloid Malignancies. Blood, 2012, 120, 2-2.	0.6	4
141	Chronological Analysis of Clonal Evolution in Acquired Aplastic Anemia. Blood, 2014, 124, 253-253.	0.6	4
142	In Analogy to AML, MDS Can be Sub-Classified By Ancestral Mutations. Blood, 2014, 124, 823-823.	0.6	4
143	Sudden Intracranial Hemorrhage in a Patient With Atypical Chronic Myeloid Leukemia in Chronic Phase. Journal of Pediatric Hematology/Oncology, 2018, 40, e553-e556.	0.3	3
144	Clonal evidence for the development of neuroblastoma with extensive copyâ€neutral loss of heterozygosity arising in a mature teratoma. Cancer Science, 2021, 112, 2921-2927.	1.7	3

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145	Optimization of prediction methods for risk assessment of pathogenic germline variants in the Japanese population. Cancer Science, 2021, 112, 3338-3348.	1.7	3
146	Prognostic Relevance of Genetic Abnormalities in Blastic Transformation of Chronic Myeloid Leukemia. Blood, 2020, 136, 3-4.	0.6	3
147	Description of longitudinal tumor evolution in a case of multiply relapsed clear cell sarcoma of the kidney. Cancer Reports, 2022, 5, e1458.	0.6	3
148	Novel TENM3â€“ALK fusion is an alternate mechanism for ALK activation in neuroblastoma. Oncogene, 2022, 41, 2789-2797.	2.6	3
149	Atypical dyskeratosis congenita diagnosed using wholeâ€exome sequencing. Pediatrics International, 2017, 59, 933-935.	0.2	2
150	Hidden FLT3-D835Y clone in FLT3-ITD-positive acute myeloid leukemia that evolved into very late relapse with T-lymphoblastic leukemia. Leukemia and Lymphoma, 2018, 59, 1490-1493.	0.6	2
151	Two siblings with familial neuroblastoma with distinct clinical phenotypes harboring an ALK germline mutation. Genes Chromosomes and Cancer, 2018, 57, 665-669.	1.5	2
152	Novel COL4A1 mutations identified in infants with congenital hemolytic anemia in association with brain malformations. Human Genome Variation, 2020, 7, 42.	0.4	2
153	Droplet digital polymerase chain reaction assay for the detection of the minor clone of KIT D816V in paediatric acute myeloid leukaemia especially showing RUNX1â€RUNX1T1 transcripts. British Journal of Haematology, 2021, 194, 414-422.	1.2	2
154	Distinct, Ethnic, Clinical, and Genetic Characteristics of Myelodysplastic Syndromes with Der(1;7). Blood, 2019, 134, 5392-5392.	0.6	2
155	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
156	Clinical â€œMUTATOMEâ€•Of Myelodysplastic Syndrome; Comparison To Primary Acute Myelogenous Leukemia. Blood, 2013, 122, 518-518.	0.6	2
157	Somatic G17V Rhoa Mutation Specifies Angioimmunoblastic T-Cell Lymphoma. Blood, 2013, 122, 815-815.	0.6	2
158	Genetic Background of Idiopathic Bone Marrow Failure Syndromes in Children. Blood, 2015, 126, 3610-3610.	0.6	2
159	PPM1D and DNMT3A Mutations in Myelodysplasia and Clonal Hematopoiesis. Blood, 2019, 134, 1709-1709.	0.6	2
160	EPOR/JAK/STAT Signaling Pathway As Therapeutic Target of Acute Erythroid Leukemia. Blood, 2021, 138, 610-610.	0.6	2
161	ALDH2 polymorphism in patients with Diamond-Blackfan anemia in Japan. International Journal of Hematology, 2016, 103, 112-114.	0.7	1
162	Remission clone in acute myeloid leukemia shows growth advantage after chemotherapy but is distinct from leukemic clone. Experimental Hematology, 2019, 75, 26-30.	0.2	1

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163	Poor Myocardial Compaction in a Patient with Recessive MYL2 Myopathy. International Heart Journal, 2021, 62, 445-447.	0.5	1
164	Whole Exome Sequencing to Predict Response to Hypomethylating Agents in MDS. Blood, 2012, 120, 1698-1698.	0.6	1
165	Genetic Basis of Myeloid Proliferation Related to Down Syndrome. Blood, 2012, 120, 535-535.	0.6	1
166	Whole Exome Sequencing Reveals Clonal Evolution Pattern and Driver Mutations Of Relapsed Pediatric AML. Blood, 2013, 122, 1410-1410.	0.6	1
167	PRPF8 Defects Cause Missplicing In Myeloid Malignancies. Blood, 2013, 122, 2838-2838.	0.6	1
168	Spliceosomal Gene LUC7L2 Mutation Causes Missplicing and Alteration Of Gene Expression In Myeloid Neoplasms. Blood, 2013, 122, 470-470.	0.6	1
169	DDX41 Is a Tumor Suppressor Gene Associated with Inherited and Acquired Mutations. Blood, 2014, 124, 125-125.	0.6	1
170	Landscape of Genetic Alterations in Adult T-Cell Leukemia/Lymphoma. Blood, 2014, 124, 75-75.	0.6	1
171	Recurrent Mutations of Multiple Components of Cohesin Complex in Myeloid Neoplasms. Blood, 2012, 120, 782-782.	0.6	1
172	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
173	Various Germline Congenital Disorder Genes Are Somatically Mutated in Myeloid Malignancies. Blood, 2012, 120, 1405-1405.	0.6	1
174	Role Of Sf3b1 On Hematopoiesis. Blood, 2013, 122, 600-600.	0.6	1
175	Identification of Cell-Type-Specific Mutations in Angioimmunoblastic T-Cell Lymphoma. Blood, 2014, 124, 3025-3025.	0.6	1
176	Recurrent VAV1 Abnormalities in Angioimmunoblastic T Cell Lymphoma. Blood, 2016, 128, 4104-4104.	0.6	1
177	Dyserythropoietic anaemia with an intronic GATA1 splicing mutation in patients suspected to have Diamondâ€Blackfan anaemia. EJHaem, 2022, 3, 163-167.	0.4	1
178	Genomic analysis of multiple myeloma using targeted capture sequencing in the Japanese cohort. British Journal of Haematology, 2020, 191, 755-763.	1.2	0
179	Successful treatment of hepatosplenic T-cell lymphoma with fludarabine, high-dose cytarabine and subsequent unrelated umbilical cord blood transplantation. International Journal of Hematology, 2021, , 1.	0.7	0
180	Mutations of the Spliceosome Complex Genes Occur In Adult Patients but Are Very Rare In Children with Myeloid Neoplasia. Blood, 2011, 118, 2797-2797.	0.6	0

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181	Functional Analysis of SRSF2 Mutations in Myelodysplastic Syndromes and Related Disorders. Blood, 2011, 118, 1706-1706.	0.6	0
182	TET2 Mutations Revealed by Whole Genome Sequencing in Adult T-Cell Leukemia.. Blood, 2012, 120, 2697-2697.	0.6	0
183	Whole Exome Sequencing Reveals Spectrum of Gene Mutations in Pediatric AML. Blood, 2012, 120, 124-124.	0.6	0
184	Molecular Diversity Detected by Whole Exome Sequencing in Chronic Myelomonocytic Leukemia. Blood, 2012, 120, 310-310.	0.6	0
185	Mutational Spectrum of Myelodysplastic Syndrome Malignancies Revealed by Whole Exome Sequencing. Blood, 2012, 120, 307-307.	0.6	0
186	Karyotypic and Genetic Abnormalities Associated with Clonal Evolution in Paroxysmal Nocturnal Hemoglobinuria.. Blood, 2012, 120, 2371-2371.	0.6	0
187	Whole Exome Analysis Reveals Spectrum of Gene Mutations in Juvenile Myelomonocytic Leukemia. Blood, 2012, 120, 170-170.	0.6	0
188	Novel Recurrent Mutations in the Ras-Like GTP-Binding Gene Rit1 in Myeloid Malignancies. Blood, 2012, 120, 558-558.	0.6	0
189	Whole Exome Sequencing Detecting Kinesin Family Gene Defects In Myeloid Neoplasm. Blood, 2013, 122, 2762-2762.	0.6	0
190	Whole Exome Sequencing Shows a Paucity Of Somatic Gene Mutations In Pediatric Idiopathic Bone Marrow Failure Syndrome. Blood, 2013, 122, 3708-3708.	0.6	0
191	Somatic Mutations and Loss-Of-Heterozygosity Impair The DNA Repair Functions Of CUX1 in Myelodysplastic Syndromes (MDS). Blood, 2013, 122, 1246-1246.	0.6	0
192	A Novel Diagnostic Method For AITL By Detecting RHOA G17V Hotspot Mutation Using Allele-Specific Real-Time PCR. Blood, 2013, 122, 3000-3000.	0.6	0
193	Whole Exome Sequencing (â€œmutatomeâ€) Of Deletion 5q. Blood, 2013, 122, 656-656.	0.6	0
194	Whole Exome Analysis Of Germline Alterations Associated With Myelodysplastic Syndrome. Blood, 2013, 122, 2800-2800.	0.6	0
195	Genetic Landscapes Of Childhood T-Cell Acute Lymphoblastic Leukemia. Blood, 2013, 122, 3786-3786.	0.6	0
196	The Presence Of Leukemogenic Mutational Events In Paroxysmal Nocturnal Hemoglobinuria Suggests That Clonal Architecture Of Bone Marrow Failure Is Similar To Myelodysplastic Syndrome. Blood, 2013, 122, 804-804.	0.6	0
197	Clinical Features of Patients with ASXL1 and ASXL2 Mutations in Pediatric Acute Myeloid Leukemia. Blood, 2014, 124, 1024-1024.	0.6	0
198	The Clinical and Genetic Features of Dyskeratosis Congenita, Cryptic Dyskeratosis Congenita, and Hoyeraal-Hreidarsson Syndrome in Japan. Blood, 2014, 124, 1608-1608.	0.6	0

#	Article	IF	Citations
199	An Adverse Prognostic Effect of Homozygous TET2 Mutational Status on the Relapse Risk of Acute Myeloid Leukemia Patients of Normal Karyotype. Blood, 2014, 124, 1052-1052.	0.6	0
200	Whole Exome and Transcriptome Analyses in Pediatric T-Cell Acute Lymphoblastic Leukemia. Blood, 2014, 124, 3527-3527.	0.6	0
201	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
202	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
203	Impact and Function of Somatic PHF6 Mutations in Myeloid Neoplasms. Blood, 2014, 124, 3581-3581.	0.6	0
204	Diagnostic Efficacy of Whole-Exome Sequencing in 250 Patients with Congenital Bone Marrow Failure. Blood, 2014, 124, 4385-4385.	0.6	0
205	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
206	Next-Generation Sequencing Reveal Proviral Genome and Transcriptome in Adult T-Cell Leukemia/Lymphoma. Blood, 2015, 126, 3882-3882.	0.6	0
207	Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. Blood, 2015, 126, 1425-1425.	0.6	0
208	Gene Expression Profiles and Methylation Analysis in Down Syndrome Related Acute Lymphoblastic Leukemia. Blood, 2016, 128, 4084-4084.	0.6	0
209	Structural Variations Involving Programmed Death Ligands in B-Cell and T-Cell Lymphomas. Blood, 2016, 128, 4105-4105.	0.6	0
210	Analysis of Genomic Predispositions to Sporadic Myeloid Neoplasms Mediated By DDX41 in Japan. Blood, 2018, 132, 4371-4371.	0.6	0
211	Clonal Evolution Pattern and Prognostic Significance of Clonal Architecture in KMT2A-Rearranged Acute Myeloid Leukemia. Blood, 2021, 138, 2358-2358.	0.6	0
212	Abstract 6085: Clonal evolution of mammary epithelial cells into breast cancers. Cancer Research, 2022, 82, 6085-6085.	0.4	0