Seishi Ogawa

List of Publications by Year
in descending order

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460 papers	26,602 citations	9234 74 h-index	8138 148 g-index
475 all docs	475 docs citations	475 times ranked	32011 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	International Consensus Classification of Myeloid Neoplasms and Acute Leukemias: integrating morphologic, clinical, and genomic data. Blood, 2022, 140, 1200-1228.	0.6	814
4	Oncogenic mutations of ALK kinase in neuroblastoma. Nature, 2008, 455, 971-974.	13.7	795
5	Mutational landscape and clonal architecture in grade II and III gliomas. Nature Genetics, 2015, 47, 458-468.	9.4	729
6	Integrated molecular analysis of adult T cell leukemia/lymphoma. Nature Genetics, 2015, 47, 1304-1315.	9.4	659
7	A Robust Algorithm for Copy Number Detection Using High-Density Oligonucleotide Single Nucleotide Polymorphism Genotyping Arrays. Cancer Research, 2005, 65, 6071-6079.	0.4	593
8	Somatic RHOA mutation in angioimmunoblastic T cell lymphoma. Nature Genetics, 2014, 46, 171-175.	9.4	542
9	AML-1 is required for megakaryocytic maturation and lymphocytic differentiation, but not for maintenance of hematopoietic stem cells in adult hematopoiesis. Nature Medicine, 2004, 10, 299-304.	15.2	538
10	Aberrant PD-L1 expression through 3â€²-UTR disruption in multiple cancers. Nature, 2016, 534, 402-406.	13.7	536
11	Genomic and molecular characterization of esophageal squamous cell carcinoma. Nature Genetics, 2014, 46, 467-473.	9.4	523
12	Somatic Mutations and Clonal Hematopoiesis in Aplastic Anemia. New England Journal of Medicine, 2015, 373, 35-47.	13.9	508
13	Age-related remodelling of oesophageal epithelia by mutated cancer drivers. Nature, 2019, 565, 312-317.	13.7	476
14	Gain-of-function of mutated C-CBL tumour suppressor in myeloid neoplasms. Nature, 2009, 460, 904-908.	13.7	380
15	Clinical significance of somatic mutation in unexplained blood cytopenia. Blood, 2017, 129, 3371-3378.	0.6	379
16	Implications of TP53 allelic state for genome stability, clinical presentation and outcomes in myelodysplastic syndromes. Nature Medicine, 2020, 26, 1549-1556.	15.2	372
17	Dynamics of clonal evolution in myelodysplastic syndromes. Nature Genetics, 2017, 49, 204-212.	9.4	348
18	Inherited and Somatic Defects in DDX41 in Myeloid Neoplasms. Cancer Cell, 2015, 27, 658-670.	7.7	341

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19	Recurrent mutations in multiple components of the cohesin complex in myeloid neoplasms. Nature Genetics, 2013, 45, 1232-1237.	9.4	334
20	The landscape of somatic mutations in Down syndromeâ€“related myeloid disorders. Nature Genetics, 2013, 45, 1293-1299.	9.4	324
21	The genomic landscape of nasopharyngeal carcinoma. Nature Genetics, 2014, 46, 866-871.	9.4	317
22	SRSF2 mutations in 275 cases with chronic myelomonocytic leukemia (CMML). Blood, 2012, 120, 3080-3088.	0.6	272
23	Genetic abnormalities in myelodysplasia and secondary acute myeloid leukemia: impact on outcome of stem cell transplantation. Blood, 2017, 129, 2347-2358.	0.6	268
24	Genomic Landscape of Esophageal Squamous Cell Carcinoma inÂa Japanese Population. Gastroenterology, 2016, 150, 1171-1182.	0.6	265
25	Generation of Alveolar Epithelial Spheroids via Isolated Progenitor Cells from Human Pluripotent Stem Cells. Stem Cell Reports, 2014, 3, 394-403.	2.3	260
26	Molecular International Prognostic Scoring System for Myelodysplastic Syndromes. , 2022, 1, .		259
27	Genetics of MDS. Blood, 2019, 133, 1049-1059.	0.6	241
28	Somatic SETBP1 mutations in myeloid malignancies. Nature Genetics, 2013, 45, 942-946.	9.4	229
29	Highly Sensitive Method for Genomewide Detection of Allelic Composition in Nonpaired, Primary Tumor Specimens by Use of Affymetrix Single-Nucleotideâ€“Polymorphism Genotyping Microarrays. American Journal of Human Genetics, 2007, 81, 114-126.	2.6	227
30	Prognostic relevance of genetic alterations in diffuse lower-grade gliomas. Neuro-Oncology, 2018, 20, 66-77.	0.6	225
31	Acquired Initiating Mutations in Early Hematopoietic Cells of CLL Patients. Cancer Discovery, 2014, 4, 1088-1101.	7.7	213
32	TP53 mutation status divides myelodysplastic syndromes with complex karyotypes into distinct prognostic subgroups. Leukemia, 2019, 33, 1747-1758.	3.3	195
33	SF3B1-mutant MDS as a distinct disease subtype: a proposal from the International Working Group for the Prognosis of MDS. Blood, 2020, 136, 157-170.	0.6	195
34	Aberrant splicing of U12-type introns is the hallmark of ZRSR2 mutant myelodysplastic syndrome. Nature Communications, 2015, 6, 6042.	5.8	192
35	ACTN1 Mutations Cause Congenital Macrothrombocytopenia. American Journal of Human Genetics, 2013, 92, 431-438.	2.6	186
36	Profiling of somatic mutations in acute myeloid leukemia with FLT3-ITD at diagnosis and relapse. Blood, 2015, 126, 2491-2501.	0.6	180

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37	An empirical Bayesian framework for somatic mutation detection from cancer genome sequencing data. Nucleic Acids Research, 2013, 41, e89-e89.	6.5	177
38	Recurrent somatic mutations underlie corticotropin-independent Cushingâ€™s syndrome. Science, 2014, 344, 917-920.	6.0	177
39	Mutation allele burden remains unchanged in chronic myelomonocytic leukaemia responding to hypomethylating agents. Nature Communications, 2016, 7, 10767.	5.8	177
40	Frequent mutations that converge on the NFKBIZ pathway in ulcerative colitis. Nature, 2020, 577, 260-265.	13.7	168
41	Role of Donor Clonal Hematopoiesis in Allogeneic Hematopoietic Stem-Cell Transplantation. Journal of Clinical Oncology, 2019, 37, 375-385.	0.8	163
42	Clonal hematopoiesis in acquired aplastic anemia. Blood, 2016, 128, 337-347.	0.6	158
43	Variant ALDH2 is associated with accelerated progression of bone marrow failure in Japanese Fanconi anemia patients. Blood, 2013, 122, 3206-3209.	0.6	156
44	Frequent loss of HLA alleles associated with copy number-neutral 6pLOH in acquired aplastic anemia. Blood, 2011, 118, 6601-6609.	0.6	153
45	Defective Epsteinâ€“Barr virus in chronic active infection and haematological malignancy. Nature Microbiology, 2019, 4, 404-413.	5.9	152
46	Integrated genetic and epigenetic analysis defines novel molecular subgroups in rhabdomyosarcoma. Nature Communications, 2015, 6, 7557.	5.8	149
47	Molecular heterogeneity in peripheral T-cell lymphoma, not otherwise specified revealed by comprehensive genetic profiling. Leukemia, 2019, 33, 2867-2883.	3.3	148
48	Gainâ€ofâ€function mutations and copy number increases of Notch2 in diffuse large Bâ€cell lymphoma. Cancer Science, 2009, 100, 920-926.	1.7	144
49	Aberrant splicing and defective mRNA production induced by somatic spliceosome mutations in myelodysplasia. Nature Communications, 2018, 9, 3649.	5.8	140
50	Hematopoietic lineage distribution and evolutionary dynamics of clonal hematopoiesis. Leukemia, 2018, 32, 1908-1919.	3.3	137
51	Integrated Multiregional Analysis Proposing a New Model of Colorectal Cancer Evolution. PLoS Genetics, 2016, 12, e1005778.	1.5	134
52	Clonal expansion in non-cancer tissues. Nature Reviews Cancer, 2021, 21, 239-256.	12.8	133
53	Cell Therapy Using Human Induced Pluripotent Stem Cell-Derived Renal Progenitors Ameliorates Acute Kidney Injury in Mice. Stem Cells Translational Medicine, 2015, 4, 980-992.	1.6	130
54	Splicing factor mutations and cancer. Wiley Interdisciplinary Reviews RNA, 2014, 5, 445-459.	3.2	126

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55	Prognostic relevance of integrated genetic profiling in adult T-cell leukemia/lymphoma. Blood, 2018, 131, 215-225.	0.6	124
56	Clonal evolution in myelodysplastic syndromes. Nature Communications, 2017, 8, 15099.	5.8	118
57	Prevalence and prognostic impact of allelic imbalances associated with leukemic transformation of Philadelphia chromosomeâ€“negative myeloproliferative neoplasms. Blood, 2010, 115, 2882-2890.	0.6	116
58	Relapse of leukemia with loss of mismatched HLA resulting from uniparental disomy after haploidentical hematopoietic stem cell transplantation. Blood, 2010, 115, 3158-3161.	0.6	105
59	A TLR3-Specific Adjuvant Relieves Innate Resistance to PD-L1 Blockade without Cytokine Toxicity in Tumor Vaccine Immunotherapy. Cell Reports, 2017, 19, 1874-1887.	2.9	104
60	Deep sequencing reveals stepwise mutation acquisition in paroxysmal nocturnal hemoglobinuria. Journal of Clinical Investigation, 2014, 124, 4529-4538.	3.9	103
61	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
62	Recurrent SPI1 (PU.1) fusions in high-risk pediatric T cell acute lymphoblastic leukemia. Nature Genetics, 2017, 49, 1274-1281.	9.4	100
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	Variegated RHOA mutations in adult T-cell leukemia/lymphoma. Blood, 2016, 127, 596-604.	0.6	98
65	Frequent structural variations involving programmed death ligands in Epstein-Barr virus-associated lymphomas. Leukemia, 2019, 33, 1687-1699.	3.3	98
66	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
67	Genomic landscape of liposarcoma. Oncotarget, 2015, 6, 42429-42444.	0.8	94
68	Regeneration of CD8Î±Î² T Cells from T-cellâ€“Derived iPSC Imparts Potent Tumor Antigen-Specific Cytotoxicity. Cancer Research, 2016, 76, 6839-6850.	0.4	93
69	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
70	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
71	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
72	Loss of function mutations in RPL27 and RPS27 identified by wholeâ€exome sequencing in Diamondâ€Blackfan anaemia. British Journal of Haematology, 2015, 168, 854-864.	1.2	87

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73	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
74	Somatic Mutations in MDS Patients Are Associated with Clinical Features and Predict Prognosis Independent of the IPSS-R: Analysis of Combined Datasets from the International Working Group for Prognosis in MDS-Molecular Committee. Blood, 2015, 126, 907-907.	0.6	85
75	Mutations of the Smad4 gene in acute myelogeneous leukemia and their functional implications in leukemogenesis. Oncogene, 2001, 20, 88-96.	2.6	83
76	Frequent NFKBIE deletions are associated with poor outcome in primary mediastinal B-cell lymphoma. Blood, 2016, 128, 2666-2670.	0.6	82
77	A temporal shift of the evolutionary principle shaping intratumor heterogeneity in colorectal cancer. Nature Communications, 2018, 9, 2884.	5.8	82
78	Highly Efficient Ex Vivo Expansion of Human Hematopoietic Stem Cells Using Delta1-Fc Chimeric Protein. Stem Cells, 2006, 24, 2456-2465.	1.4	79
79	Integrated molecular profiling of juvenile myelomonocytic leukemia. Blood, 2018, 131, 1576-1586.	0.6	78
80	Combined landscape of single-nucleotide variants and copy number alterations in clonal hematopoiesis. Nature Medicine, 2021, 27, 1239-1249.	15.2	78
81	Mutational Landscape of Pediatric Acute Lymphoblastic Leukemia. Cancer Research, 2017, 77, 390-400.	0.4	77
82	Neoantigen Load, Antigen Presentation Machinery, and Immune Signatures Determine Prognosis in Clear Cell Renal Cell Carcinoma. Cancer Immunology Research, 2016, 4, 463-471.	1.6	76
83	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
84	Frequent germline mutations of HAVCR2 in sporadic subcutaneous panniculitis-like T-cell lymphoma. Blood Advances, 2019, 3, 588-595.	2.5	73
85	ATP11C is a major flippase in human erythrocytes and its defect causes congenital hemolytic anemia. Haematologica, 2016, 101, 559-565.	1.7	72
86	Gain-of-function IKBKB mutation causes human combined immune deficiency. Journal of Experimental Medicine, 2018, 215, 2715-2724.	4.2	69
87	The U2AF1S34F mutation induces lineage-specific splicing alterations in myelodysplastic syndromes. Journal of Clinical Investigation, 2017, 127, 2206-2221.	3.9	69
88	Biallelic DICER1 Mutations in Sporadic Pleuropulmonary Blastoma. Cancer Research, 2014, 74, 2742-2749.	0.4	67
89	KLF5 Regulates the Integrity and Oncogenicity of Intestinal Stem Cells. Cancer Research, 2014, 74, 2882-2891.	0.4	66
90	Clinical utility of next-generation sequencing for inherited bone marrow failure syndromes. Genetics in Medicine, 2017, 19, 796-802.	1.1	66

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91	Early diagnosis of central nervous system aspergillosis using polymerase chain reaction, latex agglutination test, and enzyme-linked immunosorbent assay. British Journal of Haematology, 1999, 106, 536-537.	1.2	65
92	Spliceosomal gene aberrations are rare, coexist with oncogenic mutations, and are unlikely to exert a driver effect in childhood MDS and JMML. Blood, 2012, 119, e96-e99.	0.6	65
93	Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. Cancer Cell, 2021, 39, 793-809.e8.	7.7	65
94	Gene expression and risk of leukemic transformation in myelodysplasia. Blood, 2017, 130, 2642-2653.	0.6	64
95	Physiological Srsf2 P95H expression causes impaired hematopoietic stem cell functions and aberrant RNA splicing in mice. Blood, 2018, 131, 621-635.	0.6	64
96	Highly immunogenic cancer cells require activation of the WNT pathway for immunological escape. Science Immunology, 2021, 6, eabc6424.	5.6	64
97	North American ATLL has a distinct mutational and transcriptional profile and responds to epigenetic therapies. Blood, 2018, 132, 1507-1518.	0.6	63
98	Telomere attrition and candidate gene mutations preceding monosomy 7 in aplastic anemia. Blood, 2015, 125, 706-709.	0.6	60
99	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
100	Genomon ITDetector: a tool for somatic internal tandem duplication detection from cancer genome sequencing data. Bioinformatics, 2015, 31, 116-118.	1.8	58
101	A comprehensive characterization of cis-acting splicing-associated variants in human cancer. Genome Research, 2018, 28, 1111-1125.	2.4	56
102	Favorable outcome of patients who have 13q deletion: a suggestion for revision of the WHO 'MDS-U' designation. Haematologica, 2012, 97, 1845-1849.	1.7	54
103	Biochemical and Epigenetic Insights into L-2-Hydroxyglutarate, a Potential Therapeutic Target in Renal Cancer. Clinical Cancer Research, 2018, 24, 6433-6446.	3.2	54
104	Invariant patterns of clonal succession determine specific clinical features of myelodysplastic syndromes. Nature Communications, 2019, 10, 5386.	5.8	53
105	Derivation of functional mature neutrophils from human embryonic stem cells. Blood, 2009, 113, 6584-6592.	0.6	51
106	Transcriptome analysis offers a comprehensive illustration of the genetic background of pediatric acute myeloid leukemia. Blood Advances, 2019, 3, 3157-3169.	2.5	51
107	Combined Cohesinâ€“RUNX1 Deficiency Synergistically Perturbs Chromatin Looping and Causes Myelodysplastic Syndromes. Cancer Discovery, 2020, 10, 836-853.	7.7	51
108	Origins of myelodysplastic syndromes after aplastic anemia. Blood, 2017, 130, 1953-1957.	0.6	50

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109	Oncogenic mutations of ALK in neuroblastoma. Cancer Science, 2011, 102, 302-308.	1.7	49
110	Extensive gene deletions in Japanese patients with Diamond-Blackfan anemia. Blood, 2012, 119, 2376-2384.	0.6	49
111	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
112	Frequent genetic alterations in immune checkpointâ€“related genes in intravascular large B-cell lymphoma. Blood, 2021, 137, 1491-1502.	0.6	49
113	GATA2 and secondary mutations in familial myelodysplastic syndromes and pediatric myeloid malignancies. Haematologica, 2015, 100, e398-e401.	1.7	48
114	The BRG1/SOX9 axis is critical for acinar cellâ€“derived pancreatic tumorigenesis. Journal of Clinical Investigation, 2018, 128, 3475-3489.	3.9	48
115	Pseudouridine-modified tRNA fragments repress aberrant protein synthesis and predict leukaemic progression in myelodysplastic syndrome. Nature Cell Biology, 2022, 24, 299-306.	4.6	47
116	Evolutionary basis of HLA-DPB1 alleles affects acute GVHD in unrelated donor stem cell transplantation. Blood, 2018, 131, 808-817.	0.6	46
117	Single-cell analysis based dissection of clonality in myelofibrosis. Nature Communications, 2020, 11, 73.	5.8	46
118	Genetic profiling of myeloproliferative disorders by single-nucleotide polymorphism oligonucleotide microarray. Experimental Hematology, 2008, 36, 1471-1479.	0.2	44
119	Prognostic analysis according to the 2017 ELN risk stratification by genetics in adult acute myeloid leukemia patients treated in the Japan Adult Leukemia Study Group (JALSG) AML201 study. Leukemia Research, 2018, 66, 20-27.	0.4	44
120	Whole-genome landscape of adult T-cell leukemia/lymphoma. Blood, 2022, 139, 967-982.	0.6	44
121	Loss of DNA Damage Response in Neuroblastoma and Utility of a PARP Inhibitor. Journal of the National Cancer Institute, 2017, 109, .	3.0	43
122	Integration of Recurrent Somatic Mutations with Clinical Outcomes: A Pooled Analysis of 1049 Patients with Clear Cell Renal Cell Carcinoma. European Urology Focus, 2017, 3, 421-427.	1.6	43
123	Genomewide screening of DNA copy number changes in chronic myelogenous leukemia with the use of high-resolution array-based comparative genomic hybridization. Genes Chromosomes and Cancer, 2006, 45, 482-494.	1.5	41
124	The transcription factor E2A activates multiple enhancers that drive Rag expression in developing T and B cells. Science Immunology, 2020, 5, .	5.6	41
125	Somatic mutations in lymphocytes in patients with immune-mediated aplastic anemia. Leukemia, 2021, 35, 1365-1379.	3.3	41
126	Wholeâ€genome profiling of chromosomal aberrations in hepatoblastoma using highâ€density singleâ€nucleotide polymorphism genotyping microarrays. Cancer Science, 2008, 99, 564-570.	1.7	39

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127	Clonal evolution and clinical implications of genetic abnormalities in blastic transformation of chronic myeloid leukaemia. Nature Communications, 2021, 12, 2833.	5.8	39
128	SNP array analysis of tyrosine kinase inhibitor-resistant chronic myeloid leukemia identifies heterogeneous secondary genomic alterations. Blood, 2010, 115, 1049-1053.	0.6	38
129	Germline loss-of-function SAMD9 and SAMD9L alterations in adult myelodysplastic syndromes. Blood, 2018, 132, 2309-2313.	0.6	38
130	Recurrent RARB Translocations in Acute Promyelocytic Leukemia Lacking RARA Translocation. Cancer Research, 2018, 78, 4452-4458.	0.4	37
131	Splicing factor mutations in myelodysplasia. International Journal of Hematology, 2012, 96, 438-442.	0.7	36
132	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
133	Significance of perivascular tumour cells defined by CD109 expression in progression of glioma. Journal of Pathology, 2017, 243, 468-480.	2.1	36
134	Dasatinib Is an Effective Treatment for Angioimmunoblastic T-cell Lymphoma. Cancer Research, 2020, 80, 1875-1884.	0.4	36
135	Early detection and evolution of preleukemic clones in therapy-related myeloid neoplasms following autologous SCT. Blood, 2018, 131, 1846-1857.	0.6	35
136	Clinical and genetic characteristics of congenital sideroblastic anemia: comparison with myelodysplastic syndrome with ring sideroblast (MDS-RS). Annals of Hematology, 2013, 92, 1-9.	0.8	34
137	Recurrent genetic defects on chromosome 5q in myeloid neoplasms. Oncotarget, 2017, 8, 6483-6495.	0.8	34
138	Single-Nucleotide Polymorphism Array Karyotyping in Clinical Practice: Where, When, and How?. Seminars in Oncology, 2012, 39, 13-25.	0.8	33
139	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
140	Comprehensive analysis of genetic aberrations linked to tumorigenesis in regenerative nodules of liver cirrhosis. Journal of Gastroenterology, 2019, 54, 628-640.	2.3	33
141	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
142	Somatic Mutations and Clonal Hematopoiesis in Aplastic Anemia. New England Journal of Medicine, 2015, 373, 1673-1676.	13.9	32
143	LUBAC accelerates B-cell lymphomagenesis by conferring resistance to genotoxic stress on B cells. Blood, 2020, 136, 684-697.	0.6	32
144	Deregulated Intracellular Signaling by Mutated c-CBL in Myeloid Neoplasms. Clinical Cancer Research, 2010, 16, 3825-3831.	3.2	31

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145	Genome-wide surveillance of mismatched alleles for graft-versus-host disease in stem cell transplantation. Blood, 2015, 126, 2752-2763.	0.6	31
146	Profiling the inhibitory receptors LAG-3, TIM-3, and TIGIT in renal cell carcinoma reveals malignancy. Nature Communications, 2021, 12, 5547.	5.8	31
147	Molecular characterization of the recurrent unbalanced translocation der(1;7)(q10;p10). Blood, 2003, 102, 2597-2604.	0.6	30
148	Adult Tâ€cell leukemia cells are characterized by abnormalities of <scp>Helios</scp> expression that promote T cell growth. Cancer Science, 2013, 104, 1097-1106.	1.7	30
149	Variegated RHOA mutations in human cancers. Experimental Hematology, 2016, 44, 1123-1129.	0.2	30
150	Exome sequencing identified RPS15A as a novel causative gene for Diamond-Blackfan anemia. Haematologica, 2017, 102, e93-e96.	1.7	30
151	Integrated multiomics analysis of hepatoblastoma unravels its heterogeneity and provides novel druggable targets. Npj Precision Oncology, 2020, 4, 20.	2.3	30
152	Autonomous feedback loop of RUNX1-p53-CBFB in acute myeloid leukemia cells. Scientific Reports, 2017, 7, 16604.	1.6	29
153	Identification of a SRC-like tyrosine kinase gene,FRK, fused withETV6 in a patient with acute myelogenous leukemia carrying a t(6;12)(q21;p13) translocation. Genes Chromosomes and Cancer, 2005, 42, 269-279.	1.5	28
154	Genetic and transcriptional landscape of plasma cells in POEMS syndrome. Leukemia, 2019, 33, 1723-1735.	3.3	28
155	Two novel high-risk adult B-cell acute lymphoblastic leukemia subtypes with high expression of CDX2 and IDH1/2 mutations. Blood, 2022, 139, 1850-1862.	0.6	28
156	Infection perturbs Bach2- and Bach1-dependent erythroid lineage â€˜choiceâ€™ to cause anemia. Nature Immunology, 2018, 19, 1059-1070.	7.0	27
157	RNA fusions involving CD28 are rare in peripheral T-cell lymphomas and concentrate mainly in those derived from follicular helper T cells. Haematologica, 2018, 103, e360-e363.	1.7	27
158	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
159	Molecular pathogenesis of disease progression in MLL-rearranged AML. Leukemia, 2019, 33, 612-624.	3.3	26
160	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
161	<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
162	High-risk HLA alleles for severe acute graft- versus -host disease and mortality in unrelated donor bone marrow transplantation. Haematologica, 2016, 101, 491-498.	1.7	25

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163	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
164	Integrated Molecular Characterization of the Lethal Pediatric Cancer Pancreatoblastoma. Cancer Research, 2018, 78, 865-876.	0.4	25
165	Aberrant DNA Methylation Is Associated with a Poor Outcome in Juvenile Myelomonocytic Leukemia. PLoS ONE, 2015, 10, e0145394.	1.1	25
166	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
167	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
168	Clinical Characteristics of Patients with Coronavirus Disease (COVID-19): Preliminary Baseline Report of Japan COVID-19 Task Force, a Nationwide Consortium to Investigate Host Genetics of COVID-19. International Journal of Infectious Diseases, 2021, 113, 74-81.	1.5	24
169	Unbiased Detection of Driver Mutations in Extramammary Paget Disease. Clinical Cancer Research, 2021, 27, 1756-1765.	3.2	24
170	Hepatoblastoma in a Patient with Sotos Syndrome. Journal of Pediatrics, 2009, 155, 937-939.	0.9	23
171	HapMuC: somatic mutation calling using heterozygous germ line variants near candidate mutations. Bioinformatics, 2014, 30, 3302-3309.	1.8	23
172	Clinical significance and origin of leukocytes that lack HLA-A allele expression in patients with acquired aplastic anemia. Experimental Hematology, 2016, 44, 931-939.e3.	0.2	23
173	Hypoxic adaptation of leukemic cells infiltrating the CNS affords a therapeutic strategy targeting VEGFA. Blood, 2017, 129, 3126-3129.	0.6	23
174	BCL6 locus is hypermethylated in angioimmunoblastic T-cell lymphoma. International Journal of Hematology, 2017, 105, 465-469.	0.7	23
175	Identification of the genetic and clinical characteristics of neuroblastomas using genome-wide analysis. Oncotarget, 2017, 8, 107513-107529.	0.8	23
176	Dysregulation of Epstein-Barr Virus Infection in Hypomorphic ZAP70 Mutation. Journal of Infectious Diseases, 2018, 218, 825-834.	1.9	22
177	Myelodysplastic Syndrome-Associated SRSF2 Mutations Cause Splicing Changes by Altering Binding Motif Sequences. Frontiers in Genetics, 2019, 10, 338.	1.1	22
178	Pathogenic mutations identified by a multimodality approach in 117 Japanese Fanconi anemia patients. Haematologica, 2019, 104, 1962-1973.	1.7	22
179	Genetic analysis of a case of Helicobacter pylori-uninfected intramucosal gastric cancer in a family with hereditary diffuse gastric cancer. Gastric Cancer, 2019, 22, 892-898.	2.7	22
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