Hiroko Tanaka

List of Publications by Year
in descending order

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144	10,201	53660 45	37111 96
papers	citations	h-index	g-index

147	147	147	18052
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Mutational landscape and clonal architecture in grade II and III gliomas. Nature Genetics, 2015, 47, 458-468.	9.4	729
2	Integrated molecular analysis of adult T cell leukemia/lymphoma. Nature Genetics, 2015, 47, 1304-1315.	9.4	659
3	Whole-genome mutational landscape and characterization of noncoding and structural mutations in liver cancer. Nature Genetics, 2016, 48, 500-509.	9.4	596
4	Somatic RHOA mutation in angioimmunoblastic T cell lymphoma. Nature Genetics, 2014, 46, 171-175.	9.4	542
5	Aberrant PD-L1 expression through 3â€²-UTR disruption in multiple cancers. Nature, 2016, 534, 402-406.	13.7	536
6	Age-related remodelling of oesophageal epithelia by mutated cancer drivers. Nature, 2019, 565, 312-317.	13.7	476
7	Dynamics of clonal evolution in myelodysplastic syndromes. Nature Genetics, 2017, 49, 204-212.	9.4	348
8	Inherited and Somatic Defects in DDX41 in Myeloid Neoplasms. Cancer Cell, 2015, 27, 658-670.	7.7	341
9	The landscape of somatic mutations in Down syndromeâ€“related myeloid disorders. Nature Genetics, 2013, 45, 1293-1299.	9.4	324
10	Genetic abnormalities in myelodysplasia and secondary acute myeloid leukemia: impact on outcome of stem cell transplantation. Blood, 2017, 129, 2347-2358.	0.6	268
11	Genomic characterization of biliary tract cancers identifies driver genes and predisposing mutations. Journal of Hepatology, 2018, 68, 959-969.	1.8	254
12	Somatic SETBP1 mutations in myeloid malignancies. Nature Genetics, 2013, 45, 942-946.	9.4	229
13	Acquired Initiating Mutations in Early Hematopoietic Cells of CLL Patients. Cancer Discovery, 2014, 4, 1088-1101.	7.7	213
14	Exome sequencing identifies secondary mutations of SETBP1 and JAK3 in juvenile myelomonocytic leukemia. Nature Genetics, 2013, 45, 937-941.	9.4	203
15	ACTN1 Mutations Cause Congenital Macrothrombocytopenia. American Journal of Human Genetics, 2013, 92, 431-438.	2.6	186
16	Profiling of somatic mutations in acute myeloid leukemia with FLT3-ITD at diagnosis and relapse. Blood, 2015, 126, 2491-2501.	0.6	180
17	Whole-genome mutational landscape of liver cancers displaying biliary phenotype reveals hepatitis impact and molecular diversity. Nature Communications, 2015, 6, 6120.	5.8	178
18	Recurrent somatic mutations underlie corticotropin-independent Cushingâ€™s syndrome. Science, 2014, 344, 917-920.	6.0	177

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19	Frequent mutations that converge on the NFKBIZ pathway in ulcerative colitis. Nature, 2020, 577, 260-265.	13.7	168
20	Defective Epsteinâ€“Barr virus in chronic active infection and haematological malignancy. Nature Microbiology, 2019, 4, 404-413.	5.9	152
21	Integrated genetic and epigenetic analysis defines novel molecular subgroups in rhabdomyosarcoma. Nature Communications, 2015, 6, 7557.	5.8	149
22	Molecular heterogeneity in peripheral T-cell lymphoma, not otherwise specified revealed by comprehensive genetic profiling. Leukemia, 2019, 33, 2867-2883.	3.3	148
23	Prognostic relevance of integrated genetic profiling in adult T-cell leukemia/lymphoma. Blood, 2018, 131, 215-225.	0.6	124
24	Clonal evolution in myelodysplastic syndromes. Nature Communications, 2017, 8, 15099.	5.8	118
25	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
26	Recurrent SPI1 (PU.1) fusions in high-risk pediatric T cell acute lymphoblastic leukemia. Nature Genetics, 2017, 49, 1274-1281.	9.4	100
27	Abnormal hematopoiesis and autoimmunity in human subjects with germline IKZF1 mutations. Journal of Allergy and Clinical Immunology, 2017, 140, 223-231.	1.5	99
28	Variegated RHOA mutations in adult T-cell leukemia/lymphoma. Blood, 2016, 127, 596-604.	0.6	98
29	Frequent structural variations involving programmed death ligands in Epstein-Barr virus-associated lymphomas. Leukemia, 2019, 33, 1687-1699.	3.3	98
30	Genomic landscape of liposarcoma. Oncotarget, 2015, 6, 42429-42444.	0.8	94
31	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
32	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
33	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
34	Whole genome sequencing discriminates hepatocellular carcinoma with intrahepatic metastasis from multi-centric tumors. Journal of Hepatology, 2017, 66, 363-373.	1.8	81
35	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
36	Landscape and function of multiple mutations within individual oncogenes. Nature, 2020, 582, 95-99.	13.7	79

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37	Integrated molecular profiling of juvenile myelomonocytic leukemia. Blood, 2018, 131, 1576-1586.	0.6	78
38	Combined landscape of single-nucleotide variants and copy number alterations in clonal hematopoiesis. Nature Medicine, 2021, 27, 1239-1249.	15.2	78
39	Frequent germline mutations of HAVCR2 in sporadic subcutaneous panniculitis-like T-cell lymphoma. Blood Advances, 2019, 3, 588-595.	2.5	73
40	Biallelic DICER1 Mutations in Sporadic Pleuropulmonary Blastoma. Cancer Research, 2014, 74, 2742-2749.	0.4	67
41	Clinical utility of next-generation sequencing for inherited bone marrow failure syndromes. Genetics in Medicine, 2017, 19, 796-802.	1.1	66
42	Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. Cancer Cell, 2021, 39, 793-809.e8.	7.7	65
43	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
44	Characterization of HBV integration patterns and timing in liver cancer and HBV-infected livers. Oncotarget, 2018, 9, 25075-25088.	0.8	57
45	A comprehensive characterization of cis-acting splicing-associated variants in human cancer. Genome Research, 2018, 28, 1111-1125.	2.4	56
46	Invariant patterns of clonal succession determine specific clinical features of myelodysplastic syndromes. Nature Communications, 2019, 10, 5386.	5.8	53
47	Transcriptome analysis offers a comprehensive illustration of the genetic background of pediatric acute myeloid leukemia. Blood Advances, 2019, 3, 3157-3169.	2.5	51
48	Frequent genetic alterations in immune checkpointâ€“related genes in intravascular large B-cell lymphoma. Blood, 2021, 137, 1491-1502.	0.6	49
49	GATA2 and secondary mutations in familial myelodysplastic syndromes and pediatric myeloid malignancies. Haematologica, 2015, 100, e398-e401.	1.7	48
50	Classification of primary liver cancer with immunosuppression mechanisms and correlation with genomic alterations. EBioMedicine, 2020, 53, 102659.	2.7	48
51	Loss of DNA Damage Response in Neuroblastoma and Utility of a PARP Inhibitor. Journal of the National Cancer Institute, 2017, 109, .	3.0	43
52	Clonal evolution and clinical implications of genetic abnormalities in blastic transformation of chronic myeloid leukaemia. Nature Communications, 2021, 12, 2833.	5.8	39
53	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
54	Recurrent genetic defects on chromosome 5q in myeloid neoplasms. Oncotarget, 2017, 8, 6483-6495.	0.8	34

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55	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
56	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
57	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
58	Exome sequencing identified RPS15A as a novel causative gene for Diamond-Blackfan anemia. Haematologica, 2017, 102, e93-e96.	1.7	30
59	Integrated multiomics analysis of hepatoblastoma unravels its heterogeneity and provides novel druggable targets. Npj Precision Oncology, 2020, 4, 20.	2.3	30
60	Genetic and transcriptional landscape of plasma cells in POEMS syndrome. Leukemia, 2019, 33, 1723-1735.	3.3	28
61	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
62	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
63	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
64	Integrated Molecular Characterization of the Lethal Pediatric Cancer Pancreatoblastoma. Cancer Research, 2018, 78, 865-876.	0.4	25
65	Unbiased Detection of Driver Mutations in Extramammary Paget Disease. Clinical Cancer Research, 2021, 27, 1756-1765.	3.2	24
66	Identification of the genetic and clinical characteristics of neuroblastomas using genome-wide analysis. Oncotarget, 2017, 8, 107513-107529.	0.8	23
67	Dysregulation of Epstein-Barr Virus Infection in Hypomorphic ZAP70 Mutation. Journal of Infectious Diseases, 2018, 218, 825-834.	1.9	22
68	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
69	Genomic analysis of pancreatic juice DNA assesses malignant risk of intraductal papillary mucinous neoplasm of pancreas. Cancer Medicine, 2019, 8, 4565-4573.	1.3	21
70	BRCC3 mutations in myeloid neoplasms. Haematologica, 2015, 100, 1051-7.	1.7	20
71	Genomic Heterogeneity Within Individual Prostate Cancer Foci Impacts Predictive Biomarkers of Targeted Therapy. European Urology Focus, 2019, 5, 416-424.	1.6	20
72	Genetic and clinical landscape of breast cancers with germline BRCA1/2 variants. Communications Biology, 2020, 3, 578.	2.0	20

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73	Recurrent CCND3 mutations in MLL-rearranged acute myeloid leukemia. Blood Advances, 2018, 2, 2879-2889.	2.5	19
74	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
75	Common Variable Immunodeficiency Caused by FANC Mutations. Journal of Clinical Immunology, 2017, 37, 434-444.	2.0	18
76	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
77	Genetic heterogeneity of uncharacterized childhood autoimmune diseases with lymphoproliferation. Pediatric Blood and Cancer, 2018, 65, e26831.	0.8	18
78	Integrated genetic and epigenetic analysis revealed heterogeneity of acute lymphoblastic leukemia in Down syndrome. Cancer Science, 2019, 110, 3358-3367.	1.7	15
79	Clonally related diffuse large B-cell lymphoma and interdigitating dendritic cell sarcoma sharing MYC translocation. Haematologica, 2018, 103, e553-e556.	1.7	14
80	Landscape Of Genetic Lesions In 944 Patients With Myelodysplastic Syndromes. Blood, 2013, 122, 521-521.	0.6	14
81	Somatic mosaicism in chronic myeloid leukemia in remission. Blood, 2016, 128, 2863-2866.	0.6	13
82	The landscape of genetic aberrations in myxofibrosarcoma. International Journal of Cancer, 2022, 151, 565-577.	2.3	13
83	Whole-exome sequence analysis of ataxia telangiectasia-like phenotype. Journal of the Neurological Sciences, 2014, 340, 86-90.	0.3	12
84	Genomic analysis of clonal origin of Langerhans cell histiocytosis following acute lymphoblastic leukaemia. British Journal of Haematology, 2016, 175, 169-172.	1.2	12
85	Frequent mutations in HLA and related genes in extranodal NK/T cell lymphomas. Leukemia and Lymphoma, 2021, 62, 95-103.	0.6	12
86	Molecular Classification and Tumor Microenvironment Characterization of Gallbladder Cancer by Comprehensive Genomic and Transcriptomic Analysis. Cancers, 2021, 13, 733.	1.7	12
87	Whole genome sequencing analysis identifies recurrent structural alterations in esophageal squamous cell carcinoma. PeerJ, 2020, 8, e9294.	0.9	12
88	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
89	Comprehensive genetic analysis of pediatric germ cell tumors identifies potential drug targets. Communications Biology, 2020, 3, 544.	2.0	9
90	Impact of Somatic Mutations on Outcome in Patients with MDS after Stem-Cell Transplantation. Blood, 2015, 126, 711-711.	0.6	9

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91	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
92	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
93	Clinical Impacts of Germline DDX41 Mutations on Myeloid Neoplasms. Blood, 2020, 136, 38-40.	0.6	7
94	Frequent Activating Somatic Alterations in T-Cell Receptor / NF-Îºb Signaling in Adult T-Cell Leukemia/Lymphoma. Blood, 2015, 126, 113-113.	0.6	7
95	Genetic Predispositions to Myeloid Neoplasms Caused By Germline DDX41 Mutations. Blood, 2015, 126, 2843-2843.	0.6	7
96	Amplified EPOR/JAK2 Genes Define a Unique Subtype of Acute Erythroid Leukemia. Blood Cancer Discovery, 2022, 3, 410-427.	2.6	7
97	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
98	Genetic Analysis of Pheochromocytoma and Paraganglioma Complicating Cyanotic Congenital Heart Disease. Journal of Clinical Endocrinology and Metabolism, 2022, 107, 2545-2555.	1.8	6
99	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
100	Chronological Analysis of Clonal Evolution in Acquired Aplastic Anemia. Blood, 2014, 124, 253-253.	0.6	4
101	In Analogy to AML, MDS Can be Sub-Classified By Ancestral Mutations. Blood, 2014, 124, 823-823.	0.6	4
102	Alteration of the immune environment in bone marrow from children with recurrent B cell precursor acute lymphoblastic leukemia. Cancer Science, 2021, , .	1.7	3
103	Genotype-Phenotype Relationships and Therapeutic Targets in Acute Erythroid Leukemia. Blood, 2020, 136, 17-18.	0.6	3
104	Prognostic Relevance of Genetic Abnormalities in Blastic Transformation of Chronic Myeloid Leukemia. Blood, 2020, 136, 3-4.	0.6	3
105	Somatic G17V Rhoa Mutation Specifies Angioimmunoblastic T-Cell Lymphoma. Blood, 2013, 122, 815-815.	0.6	2
106	Genetic Background of Idiopathic Bone Marrow Failure Syndromes in Children. Blood, 2015, 126, 3610-3610.	0.6	2
107	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
108	Comprehensive Genetic Analysis in Cases of Juvenile Myelomonocytic Leukemia for Prognostic Estimation. Blood, 2016, 128, 3159-3159.	0.6	2

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109	Whole-Genome Sequencing of Primary Central Nervous System Lymphoma and Diffuse Large B-Cell Lymphoma. Blood, 2016, 128, 4112-4112.	0.6	2
110	EPOR/JAK/STAT Signaling Pathway As Therapeutic Target of Acute Erythroid Leukemia. Blood, 2021, 138, 610-610.	0.6	2
111	Development of Philadelphia chromosome-negative acute myeloid leukemia with IDH2 and NPM1 mutations in a patient with chronic myeloid leukemia who showed a major molecular response to tyrosine kinase inhibitor therapy. International Journal of Hematology, 2021, 113, 936-940.	0.7	1
112	DDX41 Is a Tumor Suppressor Gene Associated with Inherited and Acquired Mutations. Blood, 2014, 124, 125-125.	0.6	1
113	Landscape of Genetic Alterations in Adult T-Cell Leukemia/Lymphoma. Blood, 2014, 124, 75-75.	0.6	1
114	Prognostic Relevance of Integrated Genetic Profiling in Adult T-Cell Leukemia/Lymphoma. Blood, 2015, 126, 2643-2643.	0.6	1
115	Two Novel Distinct Subtypes of Myeloid Neoplasms Molecularly Associated with Histone H3K36 Methylations. Blood, 2015, 126, 2841-2841.	0.6	1
116	Genetic Basis of Primary Central Nervous System Lymphoma. Blood, 2015, 126, 2687-2687.	0.6	1
117	Genetic Profile of Acute Erythroid Leukemia. Blood, 2016, 128, 40-40.	0.6	1
118	Genomic analysis of multiple myeloma using targeted capture sequencing in the Japanese cohort. British Journal of Haematology, 2020, 191, 755-763.	1.2	0
119	Whole Exome Analysis Reveals Spectrum of Gene Mutations in Juvenile Myelomonocytic Leukemia. Blood, 2012, 120, 170-170.	0.6	0
120	Genetic Landscapes Of Childhood T-Cell Acute Lymphoblastic Leukemia. Blood, 2013, 122, 3786-3786.	0.6	0
121	Whole Exome and Transcriptome Analyses in Pediatric T-Cell Acute Lymphoblastic Leukemia. Blood, 2014, 124, 3527-3527.	0.6	0
122	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
123	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
124	Diagnostic Efficacy of Whole-Exome Sequencing in 250 Patients with Congenital Bone Marrow Failure. Blood, 2014, 124, 4385-4385.	0.6	0
125	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
126	Next-Generation Sequencing Reveal Proviral Genome and Transcriptome in Adult T-Cell Leukemia/Lymphoma. Blood, 2015, 126, 3882-3882.	0.6	0

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127	Landscape of DNA Methylation and Genetic Profiles in 291 Patients with Myelodysplastic Syndromes. Blood, 2015, 126, 5205-5205.	0.6	0
128	Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. Blood, 2015, 126, 1425-1425.	0.6	0
129	TAL1 and MYB Abnormalities in Childhood T-Cell Acute Lymphoblastic Leukemia. Blood, 2015, 126, 2628-2628.	0.6	0
130	Whole-Exome Analysis of Autoimmune Lymphoproliferative Syndrome-like Diseases. Blood, 2015, 126, 1022-1022.	0.6	0
131	Genome-Wide Mutational Landscape of Infant Acute Lymphoblastic Leukemia. Blood, 2016, 128, 4070-4070.	0.6	0
132	Transcriptome Analysis Revealed the Entire Genetic Understanding of Pediatric Acute Myeloid Leukemia with a Normal Karyotype. Blood, 2016, 128, 2850-2850.	0.6	0
133	Identifications of Highly Aggressive Phenotype with SPI1 Overexpression in Pediatric T Cell Acute Lymphoblastic Leukemia/Lymphoma. Blood, 2016, 128, 909-909.	0.6	0
134	Gene Expression Profiles and Methylation Analysis in Down Syndrome Related Acute Lymphoblastic Leukemia. Blood, 2016, 128, 4084-4084.	0.6	0
135	TAL1 Super Enhancer Aberration and Stil-TAL1 Fusion in Pediatric T Cell Acute Lymphoblastic Leukemia. Blood, 2016, 128, 1734-1734.	0.6	0
136	Structural Variations Involving Programmed Death Ligands in B-Cell and T-Cell Lymphomas. Blood, 2016, 128, 4105-4105.	0.6	0
137	Distinctive Genetic Features of Plasma Cells in POEMS Syndrome. Blood, 2016, 128, 4404-4404.	0.6	0
138	Landscape of Driver Mutations and Their Clinical Impacts in Pediatric Acute Lymphoblastic Leukemia. Blood, 2016, 128, 912-912.	0.6	0
139	Analysis of Genomic Predispositions to Sporadic Myeloid Neoplasms Mediated By DDX41 in Japan. Blood, 2018, 132, 4371-4371.	0.6	0
140	Molecular Characteristics That Predict Response to Azacitidine Therapy. Blood, 2019, 134, 4246-4246.	0.6	0
141	Integrated Analysis of Copy-Number Alterations and Gene Mutations in 2,000 Patients with Myeloid Neoplasms. Blood, 2019, 134, 4216-4216.	0.6	0
142	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
143	ASXL1 Mutations Predict a Poor Response to Darbepoetin Alfa in Anemic Patients with Low-Risk MDS: A Multicenter, Phase II Study. Blood, 2020, 136, 28-29.	0.6	0
144	KRAS mutations Frequently Coexist with High-Risk MLL Fusions and Are Independent Adverse Prognostic Factors in MLL-Rearranged Acute Myeloid Leukemia. Blood, 2020, 136, 28-29.	0.6	0