Hiroko Tanaka

List of Publications by Year in Descending Order

141 papers	6,917 citations	40 h-index	82 g-index
147 ext. papers	8,912 ext. citations	8.8 avg, IF	4.7 L-index

#	Paper	IF	Citations
141	Unbiased Detection of Driver Mutations in Extramammary Paget Disease. *Clinical Cancer Research*, **2021**, 27, 1756-1765	12.9	10
140	EPOR/JAK/STAT Signaling Pathway As Therapeutic Target of Acute Erythroid Leukemia. *Blood*, **2021**, 138, 610-610	2.2	1
139	Alteration of the immune environment in bone marrow from children with recurrent B cell precursor acute lymphoblastic leukemia. *Cancer Science*, **2021**,	6.9	1
138	Frequent genetic alterations in immune checkpoint-related genes in intravascular large B-cell lymphoma. *Blood*, **2021**, 137, 1491-1502	2.2	19
137	Clonal evolution and clinical implications of genetic abnormalities in blastic transformation of chronic myeloid leukaemia. *Nature Communications*, **2021**, 12, 2833	17.4	7
136	Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. *Cancer Cell*, **2021**, 39, 793-809.e8	24.3	13
135	Combined landscape of single-nucleotide variants and copy number alterations in clonal hematopoiesis. *Nature Medicine*, **2021**, 27, 1239-1249	50.5	10
134	Frequent mutations in HLA and related genes in extranodal NK/T cell lymphomas. *Leukemia and Lymphoma*, **2021**, 62, 95-103	1.9	3
133	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	2.3	0
132	Molecular Classification and Tumor Microenvironment Characterization of Gallbladder Cancer by Comprehensive Genomic and Transcriptomic Analysis. *Cancers*, **2021**, 13,	6.6	3
131	Genomic analysis of multiple myeloma using targeted capture sequencing in the Japanese cohort. *British Journal of Haematology*, **2020**, 191, 755-763	4.5	
130	Landscape and function of multiple mutations within individual oncogenes. *Nature*, **2020**, 582, 95-99	50.4	41
129	Classification of primary liver cancer with immunosuppression mechanisms and correlation with genomic alterations. *EBioMedicine*, **2020**, 53, 102659	8.8	26
128	Post-Treatment Clone Size Predicts Survival Independently of IPSS-R and Response after Azacitidine Therapy for MDS.. *Blood*, **2020**, 136, 12-13	2.2	
127	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	2.2	
126	Genotype-Phenotype Relationships and Therapeutic Targets in Acute Erythroid Leukemia. *Blood*, **2020**, 136, 17-18	2.2	1
125	Prognostic Relevance of Genetic Abnormalities in Blastic Transformation of Chronic Myeloid Leukemia. *Blood*, **2020**, 136, 3-4	2.2	1

124	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	2.2	
123	Clinical Impacts of Germline DDX41 Mutations on Myeloid Neoplasms. *Blood*, **2020**, 136, 38-40	2.2	2
122	Whole genome sequencing analysis identifies recurrent structural alterations in esophageal squamous cell carcinoma. *PeerJ*, **2020**, 8, e9294	3.1	6
121	Frequent mutations that converge on the NFKBIZ pathway in ulcerative colitis. *Nature*, **2020**, 577, 260-265	50.4	77
120	Fusion partner-specific mutation profiles and KRAS mutations as adverse prognostic factors in MLL-rearranged AML. *Blood Advances*, **2020**, 4, 4623-4631	7.8	5
119	Genetic and clinical landscape of breast cancers with germline BRCA1/2 variants. *Communications Biology*, **2020**, 3, 578	6.7	7
118	Comprehensive genetic analysis of pediatric germ cell tumors identifies potential drug targets. *Communications Biology*, **2020**, 3, 544	6.7	3
117	Integrated multiomics analysis of hepatoblastoma unravels its heterogeneity and provides novel druggable targets. *Npj Precision Oncology*, **2020**, 4, 20	9.8	11
116	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
115	Defective Epstein-Barr virus in chronic active infection and haematological malignancy. *Nature Microbiology*, **2019**, 4, 404-413	26.6	80
114	Frequent structural variations involving programmed death ligands in Epstein-Barr virus-associated lymphomas. *Leukemia*, **2019**, 33, 1687-1699	10.7	57
113	Genomic analysis of pancreatic juice DNA assesses malignant risk of intraductal papillary mucinous neoplasm of pancreas. *Cancer Medicine*, **2019**, 8, 4565-4573	4.8	10
112	Molecular heterogeneity in peripheral T-cell lymphoma, not otherwise specified revealed by comprehensive genetic profiling. *Leukemia*, **2019**, 33, 2867-2883	10.7	71
111	Genomic Heterogeneity Within Individual Prostate Cancer Foci Impacts Predictive Biomarkers of Targeted Therapy. *European Urology Focus*, **2019**, 5, 416-424	5.1	12
110	Integrated genetic and epigenetic analysis revealed heterogeneity of acute lymphoblastic leukemia in Down syndrome. *Cancer Science*, **2019**, 110, 3358-3367	6.9	8
109	Molecular Characteristics That Predict Response to Azacitidine Therapy. *Blood*, **2019**, 134, 4246-4246	2.2	
108	Integrated Analysis of Copy-Number Alterations and Gene Mutations in 2,000 Patients with Myeloid Neoplasms. *Blood*, **2019**, 134, 4216-4216	2.2	
107	Frequent germline mutations of in sporadic subcutaneous panniculitis-like T-cell lymphoma. *Blood Advances*, **2019**, 3, 588-595	7.8	31

106	Transcriptome analysis offers a comprehensive illustration of the genetic background of pediatric acute myeloid leukemia. *Blood Advances*, **2019**, 3, 3157-3169	7.8	21
105	Invariant patterns of clonal succession determine specific clinical features of myelodysplastic syndromes. *Nature Communications*, **2019**, 10, 5386	17.4	29
104	Age-related remodelling of oesophageal epithelia by mutated cancer drivers. *Nature*, **2019**, 565, 312-317	50.4	270
103	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
102	Genetic and transcriptional landscape of plasma cells in POEMS syndrome. *Leukemia*, **2019**, 33, 1723-1735	10.7	18
101	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
100	Dysregulation of Epstein-Barr Virus Infection in Hypomorphic ZAP70 Mutation. *Journal of Infectious Diseases*, **2018**, 218, 825-834	7	10
99	Genomic characterization of biliary tract cancers identifies driver genes and predisposing mutations. *Journal of Hepatology*, **2018**, 68, 959-969	13.4	149
98	Integrated molecular profiling of juvenile myelomonocytic leukemia. *Blood*, **2018**, 131, 1576-1586	2.2	51
97	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
96	Prognostic relevance of integrated genetic profiling in adult T-cell leukemia/lymphoma. *Blood*, **2018**, 131, 215-225	2.2	76
95	Genetic heterogeneity of uncharacterized childhood autoimmune diseases with lymphoproliferation. *Pediatric Blood and Cancer*, **2018**, 65, e26831	3	12
94	A comprehensive characterization of -acting splicing-associated variants in human cancer. *Genome Research*, **2018**, 28, 1111-1125	9.7	32
93	De Novo Mutations Activating Germline TP53 in an Inherited Bone-Marrow-Failure Syndrome. *American Journal of Human Genetics*, **2018**, 103, 440-447	11	18
92	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
91	Analysis of Genomic Predispositions to Sporadic Myeloid Neoplasms Mediated By DDX41 in Japan. *Blood*, **2018**, 132, 4371-4371	2.2	
90	Integrated Molecular Characterization of the Lethal Pediatric Cancer Pancreatoblastoma. *Cancer Research*, **2018**, 78, 865-876	10.1	15
89	Characterization of HBV integration patterns and timing in liver cancer and HBV-infected livers. *Oncotarget*, **2018**, 9, 25075-25088	3.3	30

88	Clonally related diffuse large B-cell lymphoma and interdigitating dendritic cell sarcoma sharing translocation. *Haematologica*, **2018**, 103, e553-e556	6.6	9
87	Recurrent mutations in -rearranged acute myeloid leukemia. *Blood Advances*, **2018**, 2, 2879-2889	7.8	12
86	Clinical utility of next-generation sequencing for inherited bone marrow failure syndromes. *Genetics in Medicine*, **2017**, 19, 796-802	8.1	45
85	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
84	Genetic abnormalities in myelodysplasia and secondary acute myeloid leukemia: impact on outcome of stem cell transplantation. *Blood*, **2017**, 129, 2347-2358	2.2	184
83	Exome sequencing identified as a novel causative gene for Diamond-Blackfan anemia. *Haematologica*, **2017**, 102, e93-e96	6.6	25
82	Clonal evolution in myelodysplastic syndromes. *Nature Communications*, **2017**, 8, 15099	17.4	86
81	Common Variable Immunodeficiency Caused by FANC Mutations. *Journal of Clinical Immunology*, **2017**, 37, 434-444	5.7	15
80	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
79	Dynamics of clonal evolution in myelodysplastic syndromes. *Nature Genetics*, **2017**, 49, 204-212	36.3	228
78	Abnormal hematopoiesis and autoimmunity in human subjects with germline IKZF1 mutations. *Journal of Allergy and Clinical Immunology*, **2017**, 140, 223-231	11.5	63
77	Loss of DNA Damage Response in Neuroblastoma and Utility of a PARP Inhibitor. *Journal of the National Cancer Institute*, **2017**, 109,	9.7	23
76	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
75	Recurrent SPI1 (PU.1) fusions in high-risk pediatric T cell acute lymphoblastic leukemia. *Nature Genetics*, **2017**, 49, 1274-1281	36.3	74
74	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
73	Whole genome sequencing discriminates hepatocellular carcinoma with intrahepatic metastasis from multi-centric tumors. *Journal of Hepatology*, **2017**, 66, 363-373	13.4	62
72	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
71	Recurrent genetic defects on chromosome 5q in myeloid neoplasms. *Oncotarget*, **2017**, 8, 6483-6495	3.3	24

70	Identification of the genetic and clinical characteristics of neuroblastomas using genome-wide analysis. *Oncotarget*, **2017**, 8, 107513-107529	3.3	17
69	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
68	Variegated RHOA mutations in adult T-cell leukemia/lymphoma. *Blood*, **2016**, 127, 596-604	2.2	77
67	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
66	Genome-Wide Mutational Landscape of Infant Acute Lymphoblastic Leukemia. *Blood*, **2016**, 128, 4070-4070	2.2	
65	Transcriptome Analysis Revealed the Entire Genetic Understanding of Pediatric Acute Myeloid Leukemia with a Normal Karyotype. *Blood*, **2016**, 128, 2850-2850	2.2	
64	Identifications of Highly Aggressive Phenotype with SPI1 Overexpression in Pediatric T Cell Acute Lymphoblastic Leukemia/Lymphoma. *Blood*, **2016**, 128, 909-909	2.2	
63	Comprehensive Genetic Analysis in Cases of Juvenile Myelomonocytic Leukemia for Prognostic Estimation. *Blood*, **2016**, 128, 3159-3159	2.2	
62	Gene Expression Profiles and Methylation Analysis in Down Syndrome Related Acute Lymphoblastic Leukemia. *Blood*, **2016**, 128, 4084-4084	2.2	
61	TAL1 Super Enhancer Aberration and Stil-TAL1 Fusion in Pediatric T Cell Acute Lymphoblastic Leukemia. *Blood*, **2016**, 128, 1734-1734	2.2	
60	Structural Variations Involving Programmed Death Ligands in B-Cell and T-Cell Lymphomas. *Blood*, **2016**, 128, 4105-4105	2.2	
59	Distinctive Genetic Features of Plasma Cells in POEMS Syndrome. *Blood*, **2016**, 128, 4404-4404	2.2	
58	Genetic Profile of Acute Erythroid Leukemia. *Blood*, **2016**, 128, 40-40	2.2	
57	Landscape of Driver Mutations and Their Clinical Impacts in Pediatric Acute Lymphoblastic Leukemia. *Blood*, **2016**, 128, 912-912	2.2	
56	Whole-Genome Sequencing of Primary Central Nervous System Lymphoma and Diffuse Large B-Cell Lymphoma. *Blood*, **2016**, 128, 4112-4112	2.2	0
55	Somatic mosaicism in chronic myeloid leukemia in remission. *Blood*, **2016**, 128, 2863-2866	2.2	11
54	Aberrant PD-L1 expression through 3′UTR disruption in multiple cancers. *Nature*, **2016**, 534, 402-6	50.4	403
53	Whole-genome mutational landscape and characterization of noncoding and structural mutations in liver cancer. *Nature Genetics*, **2016**, 48, 500-9	36.3	423

52	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
51	Genomic analysis of clonal origin of Langerhans cell histiocytosis following acute lymphoblastic leukaemia. *British Journal of Haematology*, **2016**, 175, 169-72	4.5	7
50	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
49	Integrated genetic and epigenetic analysis defines novel molecular subgroups in rhabdomyosarcoma. *Nature Communications*, **2015**, 6, 7557	17.4	110
48	Inherited and Somatic Defects in DDX41 in Myeloid Neoplasms. *Cancer Cell*, **2015**, 27, 658-70	24.3	228
47	Mutational landscape and clonal architecture in grade II and III gliomas. *Nature Genetics*, **2015**, 47, 458-68	36.3	543
46	Integrated molecular analysis of adult T cell leukemia/lymphoma. *Nature Genetics*, **2015**, 47, 1304-15	36.3	469
45	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
44	GATA2 and secondary mutations in familial myelodysplastic syndromes and pediatric myeloid malignancies. *Haematologica*, **2015**, 100, e398-401	6.6	38
43	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
42	Profiling of somatic mutations in acute myeloid leukemia with FLT3-ITD at diagnosis and relapse. *Blood*, **2015**, 126, 2491-501	2.2	134
41	Mutations in the gene encoding the E2 conjugating enzyme UBE2T cause Fanconi anemia. *American Journal of Human Genetics*, **2015**, 96, 1001-7	11	90
40	BRCC3 mutations in myeloid neoplasms. *Haematologica*, **2015**, 100, 1051-7	6.6	17
39	Whole-genome mutational landscape of liver cancers displaying biliary phenotype reveals hepatitis impact and molecular diversity. *Nature Communications*, **2015**, 6, 6120	17.4	139
38	Loss of function mutations in RPL27 and RPS27 identified by whole-exome sequencing in Diamond-Blackfan anaemia. *British Journal of Haematology*, **2015**, 168, 854-64	4.5	67
37	Frequent Activating Somatic Alterations in T-Cell Receptor / NF-ß Signaling in Adult T-Cell Leukemia/Lymphoma. *Blood*, **2015**, 126, 113-113	2.2	2
36	Prognostic Relevance of Integrated Genetic Profiling in Adult T-Cell Leukemia/Lymphoma. *Blood*, **2015**, 126, 2643-2643	2.2	1
35	Two Novel Distinct Subtypes of Myeloid Neoplasms Molecularly Associated with Histone H3K36 Methylations. *Blood*, **2015**, 126, 2841-2841	2.2	1

34	Genetic Predispositions to Myeloid Neoplasms Caused By Germline DDX41 Mutations. *Blood*, **2015**, 126, 2843-2843	2.2	5
33	Genetic Background of Idiopathic Bone Marrow Failure Syndromes in Children. *Blood*, **2015**, 126, 3610-3610	2.2	1
32	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
31	Impact of Somatic Mutations on Outcome in Patients with MDS after Stem-Cell Transplantation. *Blood*, **2015**, 126, 711-711	2.2	3
30	Genomic landscape of liposarcoma. *Oncotarget*, **2015**, 6, 42429-44	3.3	75
29	Next-Generation Sequencing Reveal Proviral Genome and Transcriptome in Adult T-Cell Leukemia/Lymphoma. *Blood*, **2015**, 126, 3882-3882	2.2	
28	Landscape of DNA Methylation and Genetic Profiles in 291 Patients with Myelodysplastic Syndromes. *Blood*, **2015**, 126, 5205-5205	2.2	
27	Genetic Basis of Primary Central Nervous System Lymphoma. *Blood*, **2015**, 126, 2687-2687	2.2	1
26	Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. *Blood*, **2015**, 126, 1425-1425	2.2	
25	TAL1 and MYB Abnormalities in Childhood T-Cell Acute Lymphoblastic Leukemia. *Blood*, **2015**, 126, 2628-2628	2.2	
24	Whole-Exome Analysis of Autoimmune Lymphoproliferative Syndrome-like Diseases. *Blood*, **2015**, 126, 1022-1022	2.2	
23	Biallelic DICER1 mutations in sporadic pleuropulmonary blastoma. *Cancer Research*, **2014**, 74, 2742-9	10.1	56
22	Recurrent somatic mutations underlie corticotropin-independent Cushing's syndrome. *Science*, **2014**, 344, 917-20	33.3	142
21	Somatic RHOA mutation in angioimmunoblastic T cell lymphoma. *Nature Genetics*, **2014**, 46, 171-5	36.3	411
20	Acquired initiating mutations in early hematopoietic cells of CLL patients. *Cancer Discovery*, **2014**, 4, 1088-101	24.4	172
19	Whole-exome sequence analysis of ataxia telangiectasia-like phenotype. *Journal of the Neurological Sciences*, **2014**, 340, 86-90	3.2	11
18	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
17	DDX41 Is a Tumor Suppressor Gene Associated with Inherited and Acquired Mutations. *Blood*, **2014**, 124, 125-125	2.2	0

16	Chronological Analysis of Clonal Evolution in Acquired Aplastic Anemia. *Blood*, **2014**, 124, 253-253	2.2	2
15	Landscape of Genetic Alterations in Adult T-Cell Leukemia/Lymphoma. *Blood*, **2014**, 124, 75-75	2.2	1
14	In Analogy to AML, MDS Can be Sub-Classified By Ancestral Mutations. *Blood*, **2014**, 124, 823-823	2.2	4
13	Whole Exome and Transcriptome Analyses in Pediatric T-Cell Acute Lymphoblastic Leukemia. *Blood*, **2014**, 124, 3527-3527	2.2	
12	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	
11	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	
10	Diagnostic Efficacy of Whole-Exome Sequencing in 250 Patients with Congenital Bone Marrow Failure. *Blood*, **2014**, 124, 4385-4385	2.2	
9	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	
8	Somatic SETBP1 mutations in myeloid malignancies. *Nature Genetics*, **2013**, 45, 942-6	36.3	178
7	Exome sequencing identifies secondary mutations of SETBP1 and JAK3 in juvenile myelomonocytic leukemia. *Nature Genetics*, **2013**, 45, 937-41	36.3	175
6	The landscape of somatic mutations in Down syndrome-related myeloid disorders. *Nature Genetics*, **2013**, 45, 1293-9	36.3	244
5	ACTN1 mutations cause congenital macrothrombocytopenia. *American Journal of Human Genetics*, **2013**, 92, 431-8	11	154
4	Landscape Of Genetic Lesions In 944 Patients With Myelodysplastic Syndromes. *Blood*, **2013**, 122, 521-52	2.2	3
3	Somatic G17V Rhoa Mutation Specifies Angioimmunoblastic T-Cell Lymphoma. *Blood*, **2013**, 122, 815-815	2.2	2
2	Genetic Landscapes Of Childhood T-Cell Acute Lymphoblastic Leukemia. *Blood*, **2013**, 122, 3786-3786	2.2	
1	Whole Exome Analysis Reveals Spectrum of Gene Mutations in Juvenile Myelomonocytic Leukemia. *Blood*, **2012**, 120, 170-170	2.2	