Hans-Ulrich Klein

List of Publications by Year
in descending order

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		94269	60497
95	7,576	37	81
papers	citations	h-index	g-index

105	105	105	13519
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Landscape of genetic lesions in 944 patients with myelodysplastic syndromes. Leukemia, 2014, 28, 241-247.	3.3	1,291
2	Inhibition of the LSD1 (KDM1A) demethylase reactivates the all-trans-retinoic acid differentiation pathway in acute myeloid leukemia. Nature Medicine, 2012, 18, 605-611.	15.2	584
3	A molecular network of the aging human brain provides insights into the pathology and cognitive decline of Alzheimerâ€™s disease. Nature Neuroscience, 2018, 21, 811-819.	7.1	422
4	An xQTL map integrates the genetic architecture of the human brain's transcriptome and epigenome. Nature Neuroscience, 2017, 20, 1418-1426.	7.1	377
5	A multi-omic atlas of the human frontal cortex for aging and Alzheimerâ€™s disease research. Scientific Data, 2018, 5, 180142.	2.4	357
6	Inherited and Somatic Defects in DDX41 in Myeloid Neoplasms. Cancer Cell, 2015, 27, 658-670.	7.7	341
7	Next-Generation Sequencing Technology Reveals a Characteristic Pattern of Molecular Mutations in 72.8% of Chronic Myelomonocytic Leukemia by Detecting Frequent Alterations in TET2, CBL, RAS, and RUNX1. Journal of Clinical Oncology, 2010, 28, 3858-3865.	0.8	283
8	Detection of significantly differentially methylated regions in targeted bisulfite sequencing data. Bioinformatics, 2013, 29, 1647-1653.	1.8	230
9	Whole-exome sequencing identifies somatic mutations of BCOR in acute myeloid leukemia with normal karyotype. Blood, 2011, 118, 6153-6163.	0.6	227
10	Tau Activates Transposable Elements in Alzheimerâ€™s Disease. Cell Reports, 2018, 23, 2874-2880.	2.9	216
11	Meta-Analysis of the Alzheimerâ€™s Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. Cell Reports, 2020, 32, 107908.	2.9	199
12	Loss of the histone methyltransferase EZH2 induces resistance to multiple drugs in acute myeloid leukemia. Nature Medicine, 2017, 23, 69-78.	15.2	192
13	Epigenome-wide study uncovers large-scale changes in histone acetylation driven by tau pathology in aging and Alzheimerâ€™s human brains. Nature Neuroscience, 2019, 22, 37-46.	7.1	188
14	Novel Alzheimer Disease Risk Loci and Pathways in African American Individuals Using the African Genome Resources Panel. JAMA Neurology, 2021, 78, 102.	4.5	144
15	AML1-ETO requires enhanced C/D box snoRNA/RNP formation to induce self-renewal and leukaemia. Nature Cell Biology, 2017, 19, 844-855.	4.6	132
16	Multilineage dysplasia (MLD) in acute myeloid leukemia (AML) correlates with MDS-related cytogenetic abnormalities and a prior history of MDS or MDS/MPN but has no independent prognostic relevance: a comparison of 408 cases classified as â€œAML not otherwise specifiedâ€•(AML-NOS) or â€œAML with myelodysplasia-related changesâ€•(AML-MRC). Blood, 2010, 116, 2742-2751.	0.6	111
17	Multilineage dysplasia has no impact on biologic, clinicopathologic, and prognostic features of AML with mutated nucleophosmin (NPM1). Blood, 2010, 115, 3776-3786.	0.6	109
18	Genomic instability may originate from imatinib-refractory chronic myeloid leukemia stem cells. Blood, 2013, 121, 4175-4183.	0.6	105

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19	The Interlaboratory RObustness of Next-generation sequencing (IRON) study: a deep sequencing investigation of TET2, CBL and KRAS mutations by an international consortium involving 10 laboratories. Leukemia, 2011, 25, 1840-1848.	3.3	96
20	Genomic landscape of liposarcoma. Oncotarget, 2015, 6, 42429-42444.	0.8	94
21	AML with translocation t(8;16)(p11;p13) demonstrates unique cytomorphological, cytogenetic, molecular and prognostic features. Leukemia, 2009, 23, 934-943.	3.3	90
22	Profiling of histone H3 lysine 9 trimethylation levels predicts transcription factor activity and survival in acute myeloid leukemia. Blood, 2010, 116, 3564-3571.	0.6	90
23	Identification of genes associated with dissociation of cognitive performance and neuropathological burden: Multistep analysis of genetic, epigenetic, and transcriptional data. PLoS Medicine, 2017, 14, e1002287.	3.9	88
24	Epigenetic dysregulation of K_{Ca}3.1 channels induces poor prognosis in lung cancer. International Journal of Cancer, 2015, 137, 1306-1317.	2.3	75
25	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. Scientific Data, 2020, 7, 340.	2.4	75
26	Genome-wide analysis of histone H3 acetylation patterns in AML identifies PRDX2 as an epigenetically silenced tumor suppressor gene. Blood, 2012, 119, 2346-2357.	0.6	72
27	Deep Sequencing in Conjunction with Expression and Functional Analyses Reveals Activation of FGFR1 in Ewing Sarcoma. Clinical Cancer Research, 2015, 21, 4935-4946.	3.2	68
28	Comparative study of unsupervised dimension reduction techniques for the visualization of microarray gene expression data. BMC Bioinformatics, 2010, 11, 567.	1.2	66
29	DNA methylation changes are a late event in acute promyelocytic leukemia and coincide with loss of transcription factor binding. Blood, 2013, 121, 178-187.	0.6	61
30	Gene expression profiling in AML with normal karyotype can predict mutations for molecular markers and allows novel insights into perturbed biological pathways. Leukemia, 2010, 24, 1216-1220.	3.3	57
31	Multiple myeloma is affected by multiple and heterogeneous somatic mutations in adhesion- and receptor tyrosine kinase signaling molecules. Blood Cancer Journal, 2013, 3, e102-e102.	2.8	51
32	Diurnal and seasonal molecular rhythms in human neocortex and their relation to Alzheimerâ€™s disease. Nature Communications, 2017, 8, 14931.	5.8	51
33	Robustness of Amplicon Deep Sequencing Underlines Its Utility in Clinical Applications. Journal of Molecular Diagnostics, 2013, 15, 473-484.	1.2	48
34	Leukemia Gene Atlas â€“ A Public Platform for Integrative Exploration of Genome-Wide Molecular Data. PLoS ONE, 2012, 7, e39148.	1.1	47
35	DNA Methyltransferase Inhibition Reverses Epigenetically Embedded Phenotypes in Lung Cancer Preferentially Affecting Polycomb Target Genes. Clinical Cancer Research, 2014, 20, 814-826.	3.2	45
36	The epigenome in Alzheimerâ€™s disease: current state and approaches for a new path to gene discovery and understanding disease mechanism. Acta Neuropathologica, 2016, 132, 503-514.	3.9	44

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37	Characterization of mitochondrial DNA quantity and quality in the human aged and Alzheimerâ€™s disease brain. Molecular Neurodegeneration, 2021, 16, 75.	4.4	44
38	Quantitative comparison of microarray experiments with published leukemia related gene expression signatures. BMC Bioinformatics, 2009, 10, 422.	1.2	40
39	Targeted next-generation sequencing detects point mutations, insertions, deletions and balanced chromosomal rearrangements as well as identifies novel leukemia-specific fusion genes in a single procedure. Leukemia, 2011, 25, 671-680.	3.3	40
40	An evaluation of methods to test predefined genomic regions for differential methylation in bisulfite sequencing data. Briefings in Bioinformatics, 2016, 17, 796-807.	3.2	40
41	Strategy for Robust Detection of Insertions, Deletions, and Point Mutations in CEBPA, a GC-Rich Content Gene, Using 454 Next-Generation Deep-Sequencing Technology. Journal of Molecular Diagnostics, 2011, 13, 129-136.	1.2	38
42	The association of epigenetic clocks in brain tissue with brain pathologies and common aging phenotypes. Neurobiology of Disease, 2021, 157, 105428.	2.1	36
43	BIN1 protein isoforms are differentially expressed in astrocytes, neurons, and microglia: neuronal and astrocyte BIN1 are implicated in tau pathology. Molecular Neurodegeneration, 2020, 15, 44.	4.4	32
44	Cancer gene prioritization by integrative analysis of mRNA expression and DNA copy number data: a comparative review. Briefings in Bioinformatics, 2013, 14, 27-35.	3.2	31
45	Integrative analysis of histone ChIP-seq and transcription data using Bayesian mixture models. Bioinformatics, 2014, 30, 1154-1162.	1.8	31
46	Genetics of Gene Expression in the Aging Human Brain Reveal TDP-43 Proteinopathy Pathophysiology. Neuron, 2020, 107, 496-508.e6.	3.8	29
47	Increased HDAC1 deposition at hematopoietic promoters in AML and its association with patient survival. Leukemia Research, 2011, 35, 620-625.	0.4	28
48	Molecular pathways of early CD105-positive erythroid cells as compared with CD34-positive common precursor cells by flow cytometric cell-sorting and gene expression profiling. Blood Cancer Journal, 2013, 3, e100-e100.	2.8	28
49	Uncovering the Role of the Methylome in Dementia and Neurodegeneration. Trends in Molecular Medicine, 2016, 22, 687-700.	3.5	25
50	Cortical Proteins and Individual Differences in Cognitive Resilience in Older Adults. Neurology, 2022, 98, .	1.5	22
51	R453Plus1Toolbox: an R/Bioconductor package for analyzing Roche 454 Sequencing data. Bioinformatics, 2011, 27, 1162-1163.	1.8	20
52	BRCC3 mutations in myeloid neoplasms. Haematologica, 2015, 100, 1051-7.	1.7	20
53	EZH2 mutations and their association with PICALMâ€MLLT10 positive acute leukaemia. British Journal of Haematology, 2012, 157, 387-390.	1.2	19
54	A New Workflow for Whole-Genome Sequencing of Single Human Cells. Human Mutation, 2014, 35, 1260-1270.	1.1	19

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55	A cortical immune network map identifies distinct microglial transcriptional programs associated with Î²-amyloid and Tau pathologies. Translational Psychiatry, 2021, 11, 50.	2.4	19
56	Atlas of RNA editing events affecting protein expression in aged and Alzheimerâ€™s disease human brain tissue. Nature Communications, 2021, 12, 7035.	5.8	19
57	Integrative Analyses for Omics Data: A Bayesian Mixture Model to Assess the Concordance of ChIP-chip and ChIP-seq Measurements. Journal of Toxicology and Environmental Health - Part A: Current Issues, 2012, 75, 461-470.	1.1	15
58	Proximal and distal effects of genetic susceptibility to multiple sclerosis on the T cell epigenome. Nature Communications, 2021, 12, 7078.	5.8	15
59	Cortical proteins may provide motor resilience in older adults. Scientific Reports, 2021, 11, 11311.	1.6	14
60	Landscape Of Genetic Lesions In 944 Patients With Myelodysplastic Syndromes. Blood, 2013, 122, 521-521.	0.6	14
61	Identification of CAR As a Novel Mediator of Erythroid Differentiation and Migration That Is Specifically Downregulated in Erythropoietic Progenitor Cells in Patients with MDS. Blood, 2014, 124, 1570-1570.	0.6	14
62	CD34+ gene expression profiling of individual children with very severe aplastic anemia indicates a pathogenic role of integrin receptors and the proapoptotic death ligand TRAIL. Haematologica, 2012, 97, 1304-1311.	1.7	13
63	Endoplasmic reticulum protein GliPR1 regulates G protein signaling and the cell cycle and is overexpressed in AML. Oncology Reports, 2013, 30, 2254-2262.	1.2	13
64	Characterization of ZC3H15 as a potential TRAF-2-interacting protein implicated in the NFÎºB pathway and overexpressed in AML. International Journal of Oncology, 2013, 43, 246-254.	1.4	12
65	Prognosis in patients with MDS or AML and bone marrow blasts between 10% and 30% is not associated with blast counts but depends on cytogenetic and molecular genetic characteristics. Leukemia, 2011, 25, 1361-1364.	3.3	11
66	Considerations for integrative multiâ€omic approaches to explore Alzheimer's disease mechanisms. Brain Pathology, 2020, 30, 984-991.	2.1	11
67	Bayesian integrative analysis of epigenomic and transcriptomic data identifies Alzheimer's disease candidate genes and networks. PLoS Computational Biology, 2020, 16, e1007771.	1.5	10
68	Epigenomic features related to microglia are associated with attenuated effect of APOE Îµ4 on Alzheimer's disease risk in humans. Alzheimer's and Dementia, 2022, 18, 688-699.	0.4	9
69	Rheumatoid arthritis-associated RBPJ polymorphism alters memory CD4⁺T cells. Human Molecular Genetics, 2016, 25, 404-417.	1.4	8
70	UNC5C variants are associated with cerebral amyloid angiopathy. Neurology: Genetics, 2017, 3, e176.	0.9	8
71	MS AHI1 genetic risk promotes IFNÎ³ ⁺ CD4 ⁺ T cells. Neurology: Neuroimmunology and NeuroInflammation, 2018, 5, e414.	3.1	6
72	Integrative analysis of multiple genomic variables using a hierarchical Bayesian model. Bioinformatics, 2017, 33, 3220-3227.	1.8	5

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73	Integration of GWAS and brain transcriptomic analyses in a multiethnic sample of 35,245 older adults identifies DCDC2 gene as predictor of episodic memory maintenance. Alzheimer's and Dementia, 2022, 18, 1797-1811.	0.4	5
74	Proteome-Wide Discovery of Cortical Proteins That May Provide Motor Resilience to Offset the Negative Effects of Pathologies in Older Adults. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2023, 78, 494-503.	1.7	4
75	Mitochondrial respiratory chain protein co-regulation in the human brain. Heliyon, 2022, 8, e09353.	1.4	4
76	Integrative Analysis of Histone ChIPâ€seq and RNAâ€seq Data. Current Protocols in Human Genetics, 2016, 90, 20.3.1-20.3.16.	3.5	3
77	Epigenomic features related to microglia are associated with attenuated effect of APOE Îµ4 on Alzheimerâ€™s disease risk in humans. Alzheimer's and Dementia, 2020, 16, e043533.	0.4	2
78	Robust and Sensitive Detection of Insertions, Deletions and Point Mutations In CEBPA, a GC-Rich Content Gene, Using 454 Next-Generation Deep-Sequencing (NGS).. Blood, 2010, 116, 1657-1657.	0.6	1
79	DDX41 Is a Tumor Suppressor Gene Associated with Inherited and Acquired Mutations. Blood, 2014, 124, 125-125.	0.6	1
80	Two Novel Distinct Subtypes of Myeloid Neoplasms Molecularly Associated with Histone H3K36 Methylations. Blood, 2015, 126, 2841-2841.	0.6	1
81	Targeted Next-Generation Sequencing and Genome-Wide High-Resolution Copy Number DNA Arrays Allow the Identification of Five Novel RUNX1 Fusions In Hematological Malignancies.. Blood, 2010, 116, 1193-1193.	0.6	1
82	Multiâ€region brain transcriptomes uncover two subtypes of aging individuals with differences in the impact of APOEe4. Alzheimer's and Dementia, 2021, 17, e057240.	0.4	1
83	How do we measure the epigenome(s)?. Multiple Sclerosis Journal, 2018, 24, 446-448.	1.4	0
84	P3â€136: MODULE QUANTITATIVE TRAIT LOCI ANALYSIS IMPLICATES TMEM106B AND RBFOX1 AS KEY BRAIN TRANSCRIPTOME REGULATORS IN OLDER ADULTS. Alzheimer's and Dementia, 2018, 14, P1120.	0.4	0
85	Global Identification of Genomic Structural Variants In Childhood ETV6/RUNX1 (TEL/AML1) Acute Lymphoblastic Leukemias by Mate-Pair Massively Parallel Sequencing.. Blood, 2010, 116, 3364-3364.	0.6	0
86	The Interlaboratory RObustness of Next-Generation Sequencing (IRON) Study: Deep-Sequencing Investigating TET2, CBL, and KRAS Mutations In 4464 Amplicons by An International Group Involving 8 Laboratories.. Blood, 2010, 116, 1665-1665.	0.6	0
87	Targeted Next-Generation Sequencing (NGS) Enables a Broad Screening of 95 Molecular Mutations In a One-Step Approach and Detects Recurrent Mutations In AML with a Normal Karyotype In MYH11 and NOTCH1. Blood, 2010, 116, 175-175.	0.6	0
88	EZH2 Mutations Can Be Detected in 23% of t(10;11)(p13;q14)/PICALM-MLLT10 Positive Acute Leukemias,. Blood, 2011, 118, 3440-3440.	0.6	0
89	Whole Genome Amplification with Subsequent High Throughput Sequencing Allows Comprehensive Genome-Wide Analysis of Single Leukemic Cells. Blood, 2011, 118, 1437-1437.	0.6	0
90	Histone H3 Methylation Mediates All-Trans-Retinoic Acid Responsiveness in Acute Myeloid Leukemia. Blood, 2011, 118, 224-224.	0.6	0

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91	Identification of the PML-RARÎ± Associated DNA Methylome Using Reduced Representation Bisulfite Sequencing in Primary Patient Samples. Blood, 2011, 118, 2436-2436.	0.6	0
92	Abnormal Expression Of The Major Coxsackie-Adenovirus Receptor CAR On Immature Dysplastic CD105+ Erythroid Progenitor Cells In Patients With MDS and Related Bone Marrow Neoplasms. Blood, 2013, 122, 2818-2818.	0.6	0
93	Abstract 4430: Loss of the histone methyltransferase EZH2 induces chemoresistance in acute myeloid leukemia (AML). , 2015, , .		0
94	Abstract A2-20: Integrative study of genomic alterations in liposarcoma. , 2015, , .		0
95	Cell type-specific Alzheimer's disease polygenic risk scores are associated with distinct disease processes in preclinical Alzheimer's disease.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e055304.	0.4	0