Claudia Pommerenke

List of Publications by Year
in descending order

65 papers	1,787 citations	471509 17 h-index	302126 39 g-index
67 all docs	67 docs citations	67 times ranked	3611 citing authors

#	Article	IF	Citations
1	The Hematopoietic TALE-Code Shows Normal Activity of IRX1 in Myeloid Progenitors and Reveals Ectopic Expression of IRX3 and IRX5 in Acute Myeloid Leukemia. International Journal of Molecular Sciences, 2022, 23, 3192.	4.1	9
2	RB1-Negative Retinal Organoids Display Proliferation of Cone Photoreceptors and Loss of Retinal Differentiation. Cancers, 2022, 14, 2166.	3.7	6
3	Downregulation of STAT3 in Epstein-Barr Virus-Positive Hodgkin Lymphoma. Biomedicines, 2022, 10, 1608.	3.2	0
4	Establishment of the TALE-code reveals aberrantly activated homeobox gene PBX1 in Hodgkin lymphoma. PLoS ONE, 2021, 16, e0246603.	2.5	16
5	NKL Homeobox Gene VENTX Is Part of a Regulatory Network in Human Conventional Dendritic Cells. International Journal of Molecular Sciences, 2021, 22, 5902.	4.1	7
6	Identification of cell lines CL-14, CL-40 and CAL-51 as suitable models for SARS-CoV-2 infection studies. PLoS ONE, 2021, 16, e0255622.	2.5	21
7	NKL Homeobox Genes NKX2-3 and NKX2-4 Deregulate Megakaryocytic-Erythroid Cell Differentiation in AML. International Journal of Molecular Sciences, 2021, 22, 11434.	4.1	7
8	Molecular Genetics of Pre-B Acute Lymphoblastic Leukemia Sister Cell Lines during Disease Progression. Current Issues in Molecular Biology, 2021, 43, 2147-2156.	2.4	0
9	DNMT3A R882H mutation in acute myeloid leukemia cell line SET-2. Leukemia Research, 2020, 88, 106270.	0.8	1
10	Aberrant expression of NKL homeobox genes HMX2 and HMX3 interferes with cell differentiation in acute myeloid leukemia. PLoS ONE, 2020, 15, e0240120.	2.5	7
11	*EZH2*-activating mutation: no reliable indicator for efficacy of methyltransferase inhibitors. Leukemia and Lymphoma, 2020, 61, 2885-2893.	1.3	1
12	Genomic deregulation of PRMT5 supports growth and stress tolerance in chronic lymphocytic leukemia. Scientific Reports, 2020, 10, 9775.	3.3	5
13	The NKL-code for innate lymphoid cells reveals deregulated expression of NKL homeobox genes HHEX and HLX in anaplastic large cell lymphoma (ALCL). Oncotarget, 2020, 11, 3208-3226.	1.8	13
14	Screening human cell lines for viral infections applying RNA-Seq data analysis. PLoS ONE, 2019, 14, e0210404.	2.5	13
15	Epstein-Barr virus (EBV) activates NKL homeobox gene HLX in DLBCL. PLoS ONE, 2019, 14, e0216898.	2.5	17
16	The LL-100 panel: 100 cell lines for blood cancer studies. Scientific Reports, 2019, 9, 8218.	3.3	74
17	Sleep Loss Disrupts Morning-to-Evening Differences in Human White Adipose Tissue Transcriptome. Journal of Clinical Endocrinology and Metabolism, 2019, 104, 1687-1696.	3.6	25
18	NKL homeobox gene activities in normal and malignant myeloid cells. PLoS ONE, 2019, 14, e0226212.	2.5	14

#	Article	IF	Citations
19	Deregulated expression of NKL homeobox genes in T-cell lymphomas. Oncotarget, 2019, 10, 3227-3247.	1.8	10
20	Effects of repeated long‑term psychosocial stress and acute cannabinoid exposure on mouse corticostriatal circuitries: Implications for neuropsychiatric disorders. CNS Neuroscience and Therapeutics, 2018, 24, 528-538.	3.9	11
21	Hodgkin lymphoma cell lines: to separate the wheat from the chaff. Biological Chemistry, 2018, 399, 511-523.	2.5	23
22	KDM3B shows tumor-suppressive activity and transcriptionally regulates *HOXA1* through retinoic acid response elements in acute myeloid leukemia. Leukemia and Lymphoma, 2018, 59, 204-213.	1.3	25
23	Protein arginine methyltransferase 6 controls erythroid gene expression and differentiation of human CD34^{+} progenitor cells. Haematologica, 2018, 103, 18-29.	3.5	13
24	A new ETV6-NTRK3 cell line model reveals MALAT1 as a novel therapeutic target - a short report. Cellular Oncology (Dordrecht), 2018, 41, 93-101.	4.4	14
25	Combined Proteomic and In Silico Target Identification Reveal a Role for 5-Lipoxygenase in Developmental Signaling Pathways. Cell Chemical Biology, 2018, 25, 1095-1106.e23.	5.2	13
26	RBFOX2 and alternative splicing in B-cell lymphoma. Blood Cancer Journal, 2018, 8, 77.	6.2	11
27	Retinoic acid induced expression of Hnf1β and Fzd4 is required for pancreas development in *Xenopus laevis*. Development (Cambridge), 2018, 145, .	2.5	12
28	Aberrant expression of NKL homeobox gene HLX in Hodgkin lymphoma. Oncotarget, 2018, 9, 14338-14353.	1.8	12
29	NKL homeobox gene NKX2-2 is aberrantly expressed in Hodgkin lymphoma. Oncotarget, 2018, 9, 37480-37496.	1.8	16
30	SLAMF7 in Primary Effusion Lymphoma, Target for Individualized Therapy?. Blood, 2018, 132, 5300-5300.	1.4	1
31	Epigenetic Modifier Mutations in the LL-100 Panel. Blood, 2018, 132, 5271-5271.	1.4	0
32	Identification of a tumor suppressor network in T-cell leukemia. Leukemia and Lymphoma, 2017, 58, 2196-2207.	1.3	18
33	Peripheral T-cell lymphoma cell line T8ML-1 highlights conspicuous targeting of PVRL2 by t(14;19)(q11.2;q13.3). Haematologica, 2017, 102, e356-e359.	3.5	3
34	NKL homeobox gene activities in hematopoietic stem cells, T-cell development and T-cell leukemia. PLoS ONE, 2017, 12, e0171164.	2.5	33
35	NKL homeobox gene MSX1 acts like a tumor suppressor in NK-cell leukemia. Oncotarget, 2017, 8, 66815-66832.	1.8	15
36	Enhanced whole exome sequencing by higher DNA insert lengths. BMC Genomics, 2016, 17, 399.	2.8	8

#	Article	IF	Citations
37	TLR8 regulation of LILRA3 in monocytes is abrogated in human immunodeficiency virus infection and correlates to CD4 counts and virus loads. Retrovirology, 2016, 13, 15.	2.0	10
38	Diffuse Large B Cell Lymphoma Cell Line U-2946: Model for MCL1 Inhibitor Testing. PLoS ONE, 2016, 11, e0167599.	2.5	9
39	Subclones in B-lymphoma cell lines: isogenic models for the study of gene regulation. Oncotarget, 2016, 7, 63456-63465.	1.8	6
40	Th17 cytokine differentiation and loss of plasticity after SOCS1 inactivation in a cutaneous T-cell lymphoma. Oncotarget, 2016, 7, 34201-34216.	1.8	18
41	Deregulation of polycomb repressor complex 1 modifier AUTS2 in T-cell leukemia. Oncotarget, 2016, 7, 45398-45413.	1.8	15
42	Detection of Viruses in Human Cell Lines Applying Next Generation Sequencing. Blood, 2016, 128, 5093-5093.	1.4	0
43	RNAseq expression analysis of resistant and susceptible mice after influenza A virus infection identifies novel genes associated with virus replication and important for host resistance to infection. BMC Genomics, 2015, 16, 655.	2.8	46
44	Next generation sequencing of sex-specific genes in the livers of obese ZSF1 rats. Genomics, 2015, 106, 204-213.	2.9	15
45	Destabilization of pluripotency in the absence of Mad2l2. Cell Cycle, 2015, 14, 1596-1610.	2.6	13
46	BCL6 - regulated by AhR/ARNT and wild-type MEF2B - drives expression of germinal center markers MYBL1 and LMO2. Haematologica, 2015, 100, 801-809.	3.5	13
47	Global analysis of asymmetric RNA enrichment in oocytes reveals low conservation between closely related *Xenopus* species. Molecular Biology of the Cell, 2015, 26, 3777-3787.	2.1	15
48	Short-Term Molecular Acclimation Processes of Legume Nodules to Increased External Oxygen Concentration. Frontiers in Plant Science, 2015, 6, 1133.	3.6	24
49	Genomic Landscape of Primary Mediastinal B-Cell Lymphoma Cell Lines. PLoS ONE, 2015, 10, e0139663.	2.5	18
50	FOXR1 Activation in B-Cell Lymphoma. Blood, 2015, 126, 2422-2422.	1.4	0
51	RNA-seq transcriptome profiling reveals that Medicago truncatula nodules acclimate N 2 fixation before emerging P deficiency reaches the nodules. Journal of Experimental Botany, 2014, 65, 6035-6048.	4.8	76
52	An RNA Sequencing Transcriptome Analysis Reveals Novel Insights into Molecular Aspects of the Nitrate Impact on the Nodule Activity of Medicago truncatula. Plant Physiology, 2014, 164, 400-411.	4.8	84
53	High-fat-diet-mediated dysbiosis promotes intestinal carcinogenesis independently of obesity. Nature, 2014, 514, 508-512.	27.8	366
54	Analysis of the lung transcriptome in Mycobacterium tuberculosis-infected mice reveals major differences in immune response pathways between TB-susceptible and resistant hosts. Tuberculosis, 2013, 93, 263-269.	1.9	6

#	Article	IF	Citations
55	The Relative Composition of the Inflammatory Infiltrate as an Additional Tool for Synovial Tissue Classification. PLoS ONE, 2013, 8, e72494.	2.5	22
56	Regulatory and Metabolic Networks for the Adaptation of Pseudomonas aeruginosa Biofilms to Urinary Tract-Like Conditions. PLoS ONE, 2013, 8, e71845.	2.5	36
57	Global Transcriptome Analysis in Influenza-Infected Mouse Lungs Reveals the Kinetics of Innate and Adaptive Host Immune Responses. PLoS ONE, 2012, 7, e41169.	2.5	93
58	Expression QTL mapping in regulatory and helper T cells from the BXD family of strains reveals novel cell-specific genes, gene-gene interactions and candidate genes for auto-immune disease. BMC Genomics, 2011, 12, 610.	2.8	9
59	Dynamic gene network reconstruction from gene expression data in mice after influenza A (H1N1) infection. Journal of Clinical Bioinformatics, 2011, 1, 27.	1.2	14
60	The complete genome sequence of the algal symbiont <i>Dinoroseobacter shibae</i>: a hitchhiker's guide to life in the sea. ISME Journal, 2010, 4, 61-77.	9.8	244
61	Global Genotype-Phenotype Correlations in Pseudomonas aeruginosa. PLoS Pathogens, 2010, 6, e1001074.	4.7	12
62	Evaluation of a microarray-hybridization based method applicable for discovery of single nucleotide polymorphisms (SNPs) in the Pseudomonas aeruginosa genome. BMC Genomics, 2009, 10, 29.	2.8	22
63	Genomewide Identification of Genetic Determinants of Antimicrobial Drug Resistance in <i>Pseudomonas aeruginosa</i>. Antimicrobial Agents and Chemotherapy, 2009, 53, 2522-2531.	3.2	108
64	ProdoNet: identification and visualization of prokaryotic gene regulatory and metabolic networks. Nucleic Acids Research, 2008, 36, W460-W464.	14.5	15
65	DSMZCellDive: Diving into high-throughput cell line data. F1000Research, 0, 11, 420.	1.6	3