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	High-fat-diet-mediated dysbiosis promotes intestinal carcinogenesis independently of obesity. Nature, 2014, 514, 508-512.	27.8	366
2	The complete genome sequence of the algal symbiont Dinoroseobacter shibae: a hitchhiker's guide to life in the sea. ISME Journal, 2010, 4, 61-77.	9.8	244
3	Genomewide Identification of Genetic Determinants of Antimicrobial Drug Resistance in Pseudomonas aeruginosa. Antimicrobial Agents and Chemotherapy, 2009, 53, 2522-2531.	3.2	108
4	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
5	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
6	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
7	The LL-100 panel: 100 cell lines for blood cancer studies. Scientific Reports, 2019, 9, 8218.	3.3	74
8	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
9	Regulatory and Metabolic Networks for the Adaptation of Pseudomonas aeruginosa Biofilms to Urinary Tract-Like Conditions. PLoS ONE, 2013, 8, e71845.	2.5	36
10	NKL homeobox gene activities in hematopoietic stem cells, T-cell development and T-cell leukemia. PLoS ONE, 2017, 12, e0171164.	2.5	33
11	KDM3B shows tumor-suppressive activity and transcriptionally regulatesHOXA1through retinoic acid response elements in acute myeloid leukemia. Leukemia and Lymphoma, 2018, 59, 204-213.	1.3	25
12	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
13	Short-Term Molecular Acclimation Processes of Legume Nodules to Increased External Oxygen Concentration. Frontiers in Plant Science, 2015, 6, 1133.	3.6	24
14	Hodgkin lymphoma cell lines: to separate the wheat from the chaff. Biological Chemistry, 2018, 399, 511-523.	2.5	23
15	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
16	The Relative Composition of the Inflammatory Infiltrate as an Additional Tool for Synovial Tissue Classification. PLoS ONE, 2013, 8, e72494.	2.5	22
17	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
18	Identification of a tumor suppressor network in T-cell leukemia. Leukemia and Lymphoma, 2017, 58, 2196-2207.	1.3	18

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19	Genomic Landscape of Primary Mediastinal B-Cell Lymphoma Cell Lines. PLoS ONE, 2015, 10, e0139663.	2.5	18
20	Th17 cytokine differentiation and loss of plasticity after SOCS1 inactivation in a cutaneous T-cell lymphoma. Oncotarget, 2016, 7, 34201-34216.	1.8	18
21	Epstein-Barr virus (EBV) activates NKL homeobox gene HLX in DLBCL. PLoS ONE, 2019, 14, e0216898.	2.5	17
22	Establishment of the TALE-code reveals aberrantly activated homeobox gene PBX1 in Hodgkin lymphoma. PLoS ONE, 2021, 16, e0246603.	2.5	16
23	NKL homeobox gene NKX2-2 is aberrantly expressed in Hodgkin lymphoma. Oncotarget, 2018, 9, 37480-37496.	1.8	16
24	ProdoNet: identification and visualization of prokaryotic gene regulatory and metabolic networks. Nucleic Acids Research, 2008, 36, W460-W464.	14.5	15
25	Next generation sequencing of sex-specific genes in the livers of obese ZSF1 rats. Genomics, 2015, 106, 204-213.	2.9	15
26	Global analysis of asymmetric RNA enrichment in oocytes reveals low conservation between closely relatedXenopusspecies. Molecular Biology of the Cell, 2015, 26, 3777-3787.	2.1	15
27	NKL homeobox gene MSX1 acts like a tumor suppressor in NK-cell leukemia. Oncotarget, 2017, 8, 66815-66832.	1.8	15
28	Deregulation of polycomb repressor complex 1 modifier AUTS2 in T-cell leukemia. Oncotarget, 2016, 7, 45398-45413.	1.8	15
29	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
30	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
31	NKL homeobox gene activities in normal and malignant myeloid cells. PLoS ONE, 2019, 14, e0226212.	2.5	14
32	Destabilization of pluripotency in the absence of Mad2l2. Cell Cycle, 2015, 14, 1596-1610.	2.6	13
33	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
34	Protein arginine methyltransferase 6 controls erythroid gene expression and differentiation of human CD34⁺ progenitor cells. Haematologica, 2018, 103, 18-29.	3.5	13
35	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
36	Screening human cell lines for viral infections applying RNA-Seq data analysis. PLoS ONE, 2019, 14, e0210404.	2.5	13

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37	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
38	Global Genotype-Phenotype Correlations in Pseudomonas aeruginosa. PLoS Pathogens, 2010, 6, e1001074.	4.7	12
39	Retinoic acid induced expression of Hnf1Î² and Fzd4 is required for pancreas development in Xenopus laevis. Development (Cambridge), 2018, 145, .	2.5	12
40	Aberrant expression of NKL homeobox gene HLX in Hodgkin lymphoma. Oncotarget, 2018, 9, 14338-14353.	1.8	12
41	Effects of repeated longâ€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
42	RBFOX2 and alternative splicing in B-cell lymphoma. Blood Cancer Journal, 2018, 8, 77.	6.2	11
43	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
44	Deregulated expression of NKL homeobox genes in T-cell lymphomas. Oncotarget, 2019, 10, 3227-3247.	1.8	10
45	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
46	Diffuse Large B Cell Lymphoma Cell Line U-2946: Model for MCL1 Inhibitor Testing. PLoS ONE, 2016, 11, e0167599.	2.5	9
47	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
48	Enhanced whole exome sequencing by higher DNA insert lengths. BMC Genomics, 2016, 17, 399.	2.8	8
49	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
50	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
51	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
52	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
53	Subclones in B-lymphoma cell lines: isogenic models for the study of gene regulation. Oncotarget, 2016, 7, 63456-63465.	1.8	6
54	RB1-Negative Retinal Organoids Display Proliferation of Cone Photoreceptors and Loss of Retinal Differentiation. Cancers, 2022, 14, 2166.	3.7	6

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55	Genomic deregulation of PRMT5 supports growth and stress tolerance in chronic lymphocytic leukemia. Scientific Reports, 2020, 10, 9775.	3.3	5
56	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
57	DSMZCellDive: Diving into high-throughput cell line data. F1000Research, 0, 11, 420.	1.6	3
58	DNMT3A R882H mutation in acute myeloid leukemia cell line SET-2. Leukemia Research, 2020, 88, 106270.	0.8	1
59	EZH2-activating mutation: no reliable indicator for efficacy of methyltransferase inhibitors. Leukemia and Lymphoma, 2020, 61, 2885-2893.	1.3	1
60	SLAMF7 in Primary Effusion Lymphoma, Target for Individualized Therapy?. Blood, 2018, 132, 5300-5300.	1.4	1
61	FOXR1 Activation in B-Cell Lymphoma. Blood, 2015, 126, 2422-2422.	1.4	0
62	Detection of Viruses in Human Cell Lines Applying Next Generation Sequencing. Blood, 2016, 128, 5093-5093.	1.4	0
63	Epigenetic Modifier Mutations in the LL-100 Panel. Blood, 2018, 132, 5271-5271.	1.4	0
64	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
65	Downregulation of STAT3 in Epstein-Barr Virus-Positive Hodgkin Lymphoma. Biomedicines, 2022, 10, 1608.	3.2	0