Stefan Krebs

List of Publications by Year in descending order

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		201674	214800
83	2,810	27	47
papers	citations	h-index	g-index

84	84	84	5861
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Three exposures to the spike protein of SARS-CoV-2 by either infection or vaccination elicit superior neutralizing immunity to all variants of concern. Nature Medicine, 2022, 28, 496-503.	30.7	215
2	Rapid and sensitive identification of omicron by variant-specific PCR and nanopore sequencing: paradigm for diagnostics of emerging SARS-CoV-2 variants. Medical Microbiology and Immunology, 2022, 211, 71-77.	4.8	25
3	Impaired detection of omicron by SARS-CoV-2 rapid antigen tests. Medical Microbiology and Immunology, 2022, 211, 105-117.	4.8	94
4	Detection of SARS-CoV-2-RNA in post-mortem samples of human eyes. Graefe's Archive for Clinical and Experimental Ophthalmology, 2022, 260, 1789-1797.	1.9	13
5	Should routine risk reduction procedures for the prevention and control of pandemics become a standard in all oncological outpatient clinics? The prospective COVID-19 cohort study: protect-CoV. , 2022, 39, 104.		1
6	SARS-CoV-2 Variants of Concern Hijack IFITM2 for Efficient Replication in Human Lung Cells. Journal of Virology, 2022, 96, e0059422.	3.4	21
7	Full genome sequence of bovine alphaherpesvirus 2 (BoHV-2). Archives of Virology, 2021, 166, 639-643.	2.1	3
8	Fusion gene detection by RNA sequencing complements diagnostics of acute myeloid leukemia and identifies recurring NRIP1-MIR99AHG rearrangements. Haematologica, 2021, , .	3.5	13
9	ONT-Based Draft Genome Assembly and Annotation of Alternaria atra. Molecular Plant-Microbe Interactions, 2021, 34, 870-873.	2.6	3
10	Comparison of four commercial, automated antigen tests to detect SARS-CoV-2 variants of concern. Medical Microbiology and Immunology, 2021, 210, 263-275.	4.8	47
11	Whole genome sequencing reveals a complex introgression history and the basis of adaptation to subarctic climate in wild sheep. Molecular Ecology, 2021, 30, 6701-6717.	3.9	12
12	Spatially resolved qualified sewage spot sampling to track SARS-CoV-2 dynamics in Munich - One year of experience. Science of the Total Environment, 2021, 797, 149031.	8.0	20
13	Prospective Longitudinal Serosurvey of Healthcare Workers in the First Wave of the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Pandemic in a Quaternary Care Hospital in Munich, Germany. Clinical Infectious Diseases, 2021, 73, e3055-e3065.	5.8	29
14	Distinct Morphological and Behavioural Alterations in ENU-Induced Heterozygous Trpc7K810Stop Mutant Mice. Genes, 2021, 12, 1732.	2.4	0
15	Genomic epidemiology reveals multiple introductions of SARS-CoV-2 followed by community and nosocomial spread, Germany, February to May 2020. Eurosurveillance, 2021, 26, .	7.0	11
16	Active polyâ€CA vaccination prevents microglia activation and motor deficits in a C9orf72 mouse model. EMBO Molecular Medicine, 2020, 12, e10919.	6.9	39
17	Sex-specific programming effects of parental obesity in pre-implantation embryonic development. International Journal of Obesity, 2020, 44, 1185-1190.	3.4	4
18	The clinical mutatome of core binding factor leukemia. Leukemia, 2020, 34, 1553-1562.	7.2	60

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19	High conservation combined with high plasticity: genomics and evolution of Borrelia bavariensis. BMC Genomics, 2020, 21, 702.	2.8	14
20	Complete mitochondrial genomes of Karchaev goat (Capra hircus). Mitochondrial DNA Part B: Resources, 2020, 5, 3627-3628.	0.4	2
21	An improved method for high-throughput quantification of autophagy in mammalian cells. Scientific Reports, 2020, 10, 12241.	3.3	21
22	Hematopoietic stem-cell senescence and myocardial repair - Coronary artery disease genotype/phenotype analysis of post-MI myocardial regeneration response induced by CABG/CD133+ bone marrow hematopoietic stem cell treatment in RCT PERFECT Phase 3. EBioMedicine, 2020, 57, 102862.	6.1	22
23	Linkage of genetic drivers and strain-specific germline variants confound mouse cancer genome analyses. Nature Communications, 2020, 11, 4474.	12.8	1
24	The First Draft Genome Assembly of Snow Sheep (Ovis nivicola). Genome Biology and Evolution, 2020, 12, 1330-1336.	2.5	14
25	ZBTB7A prevents RUNX1-RUNX1T1-dependent clonal expansion of human hematopoietic stem and progenitor cells. Oncogene, 2020, 39, 3195-3205.	5.9	18
26	Clinical presentation and differential splicing of SRSF2, U2AF1 and SF3B1 mutations in patients with acute myeloid leukemia. Leukemia, 2020, 34, 2621-2634.	7.2	31
27	Borrelia maritima sp. nov., a novel species of the Borrelia burgdorferi sensu lato complex, occupying a basal position to North American species. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 849-856.	1.7	27
28	Multicentre comparison of quantitative PCR-based assays to detect SARS-CoV-2, Germany, March 2020. Eurosurveillance, 2020, 25, .	7.0	60
29	Allelic Imbalance of Recurrently Mutated Genes in Acute Myeloid Leukaemia. Scientific Reports, 2019, 9, 11796.	3.3	9
30	Absolute nucleosome occupancy map for the Saccharomyces cerevisiae genome. Genome Research, 2019, 29, 1996-2009.	5.5	71
31	Multi-omics insights into functional alterations of the liver in insulin-deficient diabetes mellitus. Molecular Metabolism, 2019, 26, 30-44.	6.5	26
32	PAX5 biallelic genomic alterations define a novel subgroup of B-cell precursor acute lymphoblastic leukemia. Leukemia, 2019, 33, 1895-1909.	7.2	46
33	Mild maternal hyperglycemia in INSC93S transgenic pigs causes impaired glucose tolerance and metabolic alterations in neonatal offspring. DMM Disease Models and Mechanisms, 2019, 12, .	2.4	10
34	Antigen-Specific TCR Signatures of Cytomegalovirus Infection. Journal of Immunology, 2019, 202, 979-990.	0.8	22
35	MIR sequences recruit zinc finger protein ZNF768 to expressed genes. Nucleic Acids Research, 2019, 47, 700-715.	14.5	14
36	The myelin protein PMP2 is regulated by SOX10 and drives melanoma cell invasion. Pigment Cell and Melanoma Research, 2019, 32, 424-434.	3.3	22

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37	Single-cell RNA sequencing reveals developmental heterogeneity of blastomeres during major genome activation in bovine embryos. Scientific Reports, 2018, 8, 4071.	3.3	28
38	Evolution of Cytogenetically Normal Acute Myeloid Leukemia During Therapy and Relapse: An Exome Sequencing Study of 50 Patients. Clinical Cancer Research, 2018, 24, 1716-1726.	7.0	63
39	Tyrosine-1 of RNA Polymerase II CTD Controls Global Termination of Gene Transcription in Mammals. Molecular Cell, 2018, 69, 48-61.e6.	9.7	66
40	Effects of single and combined low frequency electromagnetic fields and simulated microgravity on gene expression of human mesenchymal stem cells during chondrogenesis. Archives of Medical Science, 2018, 14, 608-616.	0.9	11
41	Remapping of the belted phenotype in cattle on BTA3 identifies a multiplication event as the candidate causal mutation. Genetics Selection Evolution, 2018, 50, 36.	3.0	7
42	Targeting tumor cell plasticity by combined inhibition of NOTCH and MAPK signaling in colon cancer. Journal of Experimental Medicine, 2018, 215, 1693-1708.	8.5	31
43	Relapse of acute myeloid leukemia after allogeneic stem cell transplantation is associated with gain of WT1 alterations and high mutation load. Haematologica, 2018, 103, e581-e584.	3.5	14
44	Comparative genomics and the nature of placozoan species. PLoS Biology, 2018, 16, e2005359.	5.6	73
45	Genome-wide measurement of local nucleosome array regularity and spacing by nanopore sequencing. Nature Structural and Molecular Biology, 2018, 25, 894-901.	8.2	68
46	Clonal heterogeneity of FLT3-ITD detected by high-throughput amplicon sequencing correlates with adverse prognosis in acute myeloid leukemia. Oncotarget, 2018, 9, 30128-30145.	1.8	33
47	Clonal Evolution of Relapsed CBFB/MYH11 Rearranged Acute Myeloid Leukemia (AML). Blood, 2018, 132, 2772-2772.	1.4	0
48	ADNP Is a Therapeutically Inducible Repressor of WNT Signaling in Colorectal Cancer. Clinical Cancer Research, 2017, 23, 2769-2780.	7.0	24
49	Transcriptome analysis of dominant-negative Brd4 mutants identifies Brd4-specific target genes of small molecule inhibitor JQ1. Scientific Reports, 2017, 7, 1684.	3.3	17
50	TTâ€seq captures enhancer landscapes immediately after Tâ€cell stimulation. Molecular Systems Biology, 2017, 13, 920.	7.2	44
51	The Munich MIDY Pig Biobank â€“ A unique resource for studying organ crosstalk in diabetes. Molecular Metabolism, 2017, 6, 931-940.	6.5	39
52	Trans-presentation of IL-6 by dendritic cells is required for the priming of pathogenic TH17 cells. Nature Immunology, 2017, 18, 74-85.	14.5	311
53	Acute myeloid leukemia with del(9q) is characterized by frequent mutations of NPM1, DNMT3A, WT1 and low expression of TLE4. Genes Chromosomes and Cancer, 2017, 56, 75-86.	2.8	15
54	EBF1 binds to EBNA2 and promotes the assembly of EBNA2 chromatin complexes in B cells. PLoS Pathogens, 2017, 13, e1006664.	4.7	25

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55	Splicing stimulates siRNA formation at Drosophila DNA double-strand breaks. PLoS Genetics, 2017, 13, e1006861.	3.5	15
56	Detection of two non-synonymous SNPs in SLC45A2 on BTA20 as candidate causal mutations for oculocutaneous albinism in Braunvieh cattle. Genetics Selection Evolution, 2017, 49, 73.	3.0	17
57	Standardized, systemic phenotypic analysis reveals kidney dysfunction as main alteration of Kctd1 I27N mutant mice. Journal of Biomedical Science, 2017, 24, 57.	7.0	8
58	SP001ALTERATIONS OF ION TRANSPORTERS IN CELLS OF THICK ASCENDING LIMB IN AUTOSOMAL DOMINANT TUBULOINTERSTITIAL KIDNEY DISEASE - UMOD. Nephrology Dialysis Transplantation, 2016, 31, i86-i86.	0.7	2
59	Recurrent evolution of host and vector association in bacteria of the Borrelia burgdorferi sensu lato species complex. BMC Genomics, 2016, 17, 734.	2.8	42
60	ZBTB7A mutations in acute myeloid leukaemia with t(8;21) translocation. Nature Communications, 2016, 7, 11733.	12.8	45
61	The 1.78-kb insertion in the 3â€²-untranslated region of RXFP2 does not segregate with horn status in sheep breeds with variable horn status. Genetics Selection Evolution, 2016, 48, 78.	3.0	22
62	Mitochondrial genomes of the freshwater sponges Spongilla lacustris and Ephydatia cf. muelleri. Mitochondrial DNA Part B: Resources, 2016, 1, 250-251.	0.4	5
63	TRAPLINE: a standardized and automated pipeline for RNA sequencing data analysis, evaluation and annotation. BMC Bioinformatics, 2016, 17, 21.	2.6	35
64	Young woman with mild bone marrow dysplasia, GATA2 and ASXL1 mutation treated with allogeneic hematopoietic stem cell transplantation. Leukemia Research Reports, 2015, 4, 72-75.	0.4	10
65	Remodeling of the Nuclear Envelope and Lamina during Bovine Preimplantation Development and Its Functional Implications. PLoS ONE, 2015, 10, e0124619.	2.5	26
66	Integrative Analysis of MicroRNA and mRNA Data Reveals an Orchestrated Function of MicroRNAs in Skeletal Myocyte Differentiation in Response to TNF-Î± or IGF1. PLoS ONE, 2015, 10, e0135284.	2.5	21
67	Tumor Necrosis Factor Alpha and Insulin-Like Growth Factor 1 Induced Modifications of the Gene Expression Kinetics of Differentiating Skeletal Muscle Cells. PLoS ONE, 2015, 10, e0139520.	2.5	15
68	Lack of Rybp in Mouse Embryonic Stem Cells Impairs Cardiac Differentiation. Stem Cells and Development, 2015, 24, 2193-2205.	2.1	18
69	Effects of the glucagon-like peptide-1 receptor agonist liraglutide in juvenile transgenic pigs modeling a pre-diabetic condition. Journal of Translational Medicine, 2015, 13, 73.	4.4	24
70	NGS population genetics analyses reveal divergent evolution of a Lyme Borreliosis agent in Europe and Asia. Ticks and Tick-borne Diseases, 2015, 6, 344-351.	2.7	43
71	GATA2 deficiency in children and adults with severe pulmonary alveolar proteinosis and hematologic disorders. BMC Pulmonary Medicine, 2015, 15, 87.	2.0	63
72	Comparing effects of perfusion and hydrostatic pressure on gene profiles of human chondrocyte.. Journal of Biotechnology, 2015, 210, 59-65.	3.8	16

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73	Parapoxvirus (PPV) of red deer reveals subclinical infection and confirms a unique species. Journal of General Virology, 2015, 96, 1446-1462.	2.9	27
74	Mutational spectrum of adult T-ALL. Oncotarget, 2015, 6, 2754-2766.	1.8	98
75	Genomic Profiling Reveals Gain of Mutations in Histone Methylation Regulators in Relapsed Adult B Cell Precursor ALL. Blood, 2015, 126, 2625-2625.	1.4	0
76	Evidence for a role of E-cadherin in suppressing liver carcinogenesis in mice and men. Carcinogenesis, 2014, 35, 1855-1862.	2.8	28
77	Isolated trisomy 13 defines a homogeneous AML subgroup with high frequency of mutations in spliceosome genes and poor prognosis. Blood, 2014, 124, 1304-1311.	1.4	81
78	Comparative and retrospective molecular analysis of Parapoxvirus (PPV) isolates. Virus Research, 2014, 181, 11-21.	2.2	41
79	Genome activation in bovine embryos: Review of the literature and new insights from RNA sequencing experiments. Animal Reproduction Science, 2014, 149, 46-58.	1.5	113
80	Programming and Isolation of Highly Pure Physiologically and Pharmacologically Functional Sinus-Nodal Bodies from Pluripotent Stem Cells. Stem Cell Reports, 2014, 2, 592-605.	4.8	81
81	Acute Myeloid Leukemia With Isolated Trisomy 13 Is a Genetically Homogenous Entity With a High Frequency Of Mutations In Genes Encoding Components Of The Splicing Machinery and Extremely Poor Prognosis. Blood, 2013, 122, 608-608.	1.4	5
82	FAT1 Expression and Mutation Status In Adult Acute Lymphoblastic Leukemia. Blood, 2013, 122, 2564-2564.	1.4	0
83	Unbalanced Translocation t(5;17) Resulting In a TP53 Loss As Recurrent Aberration In Myelodysplastic Syndrome With Complex Karyotype. Blood, 2013, 122, 4949-4949.	1.4	0