

# Sebastian Kurscheid

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4735570/publications.pdf>

Version: 2024-02-01

23  
papers

2,120  
citations

394421

19  
h-index

713466

21  
g-index

23  
all docs

23  
docs citations

23  
times ranked

4269  
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiple roles of H2A.Z in regulating promoter chromatin architecture in human cells. <i>Nature Communications</i> , 2021, 12, 2524.	12.8	22
2	Gene editing of the multi-copy H2A.B gene and its importance for fertility. <i>Genome Biology</i> , 2019, 20, 23.	8.8	29
3	Long-range interactions between topologically associating domains shape the four-dimensional genome during differentiation. <i>Nature Genetics</i> , 2019, 51, 835-843.	21.4	114
4	The DNA methylome of DDR genes and benefit from RT or TMZ in IDH mutant low-grade glioma treated in EORTC 22033. <i>Acta Neuropathologica</i> , 2018, 135, 601-615.	7.7	76
5	Social network analysis of the movement of poultry to and from live bird markets in Bali and Lombok, Indonesia. <i>Transboundary and Emerging Diseases</i> , 2017, 64, 2023-2033.	3.0	8
6	Correlation of immune phenotype with IDH mutation in diffuse glioma. <i>Neuro-Oncology</i> , 2017, 19, 1460-1468.	1.2	213
7	The Histone Variant H2A.Z Is a Master Regulator of the Epithelial-Mesenchymal Transition. <i>Cell Reports</i> , 2017, 21, 943-952.	6.4	45
8	Temozolomide chemotherapy versus radiotherapy in high-risk low-grade glioma (EORTC 22033-26033): a randomised, open-label, phase 3 intergroup study. <i>Lancet Oncology</i> , The, 2016, 17, 1521-1532.	10.7	396
9	The Cardiomyocyte RNA-Binding Proteome: Links to Intermediary Metabolism and Heart Disease. <i>Cell Reports</i> , 2016, 16, 1456-1469.	6.4	128
10	Genome-wide DNA methylation detection by MethylCap-seq and Infinium HumanMethylation450 BeadChips: an independent large-scale comparison. <i>Scientific Reports</i> , 2015, 5, 15375.	3.3	17
11	Increased Levels of Macrophage Inflammatory Proteins Result in Resistance to R5-Tropic HIV-1 in a Subset of Elite Controllers. <i>Journal of Virology</i> , 2015, 89, 5502-5514.	3.4	68
12	Chromosome 7 gain and DNA hypermethylation at the HOXA10 locus are associated with expression of a stem cell related HOX-signature in glioblastoma. <i>Genome Biology</i> , 2015, 16, 16.	8.8	82
13	Rhicipcephalus microplus serine protease inhibitor family: annotation, expression and functional characterisation assessment. <i>Parasites and Vectors</i> , 2015, 8, 7.	2.5	34
14	Programmed death ligand 1 expression and tumor-infiltrating lymphocytes in glioblastoma. <i>Neuro-Oncology</i> , 2015, 17, 1064-1075.	1.2	485
15	GENETIC AND EPIGENETIC DEREGLATION ARE ASSOCIATED WITH THE ABERRANT EXPRESSION OF A STEM CELL RELATED HOX GENE SIGNATURE IN GLIOBLASTOMA. <i>Neuro-Oncology</i> , 2014, 16, iii8-iii8.	1.2	0
16	395: Epigenetic deregulation of HOXA genes associated with aberrant expression in glioblastoma. <i>European Journal of Cancer</i> , 2014, 50, S94.	2.8	0
17	Identification of Genes Critical for Resistance to Infection by West Nile Virus Using RNA-Seq Analysis. <i>Viruses</i> , 2013, 5, 1664-1681.	3.3	25
18	Postgenomic Analyses Reveal Development of Infectious <i>Anaplasma phagocytophilum</i> during Transmission from Ticks to Mice. <i>Journal of Bacteriology</i> , 2012, 194, 2238-2247.	2.2	40

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19	Enhanced Survival of Plasmodium-Infected Mosquitoes during Starvation. PLoS ONE, 2012, 7, e40556.	2.5	28
20	Gene expression evidence for off-target effects caused by RNA interference-mediated gene silencing of Ubiquitin-63E in the cattle tick Rhipicephalus microplus. International Journal for Parasitology, 2011, 41, 1001-1014.	3.1	33
21	Alterations in the Aedes aegypti Transcriptome during Infection with West Nile, Dengue and Yellow Fever Viruses. PLoS Pathogens, 2011, 7, e1002189.	4.7	180
22	Suppressive subtractive hybridization analysis of Rhipicephalus (Boophilus) microplus larval and adult transcript expression during attachment and feeding. Veterinary Parasitology, 2010, 167, 304-320.	1.8	36
23	Evidence of a tick RNAi pathway by comparative genomics and reverse genetics screen of targets with known loss-of-function phenotypes in Drosophila. BMC Molecular Biology, 2009, 10, 26.	3.0	61