

# Tim Nicolai Siegel

## List of Publications by Year in descending order

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Version: 2024-02-01

34  
papers

2,471  
citations

279798

23  
h-index

377865

34  
g-index

37  
all docs

37  
docs citations

37  
times ranked

2032  
citing authors

#	ARTICLE	IF	CITATIONS
1	Four histone variants mark the boundaries of polycistronic transcription units in <i>Trypanosoma brucei</i> . <i>Genes and Development</i> , 2009, 23, 1063-1076.	5.9	312
2	Genome-wide analysis of mRNA abundance in two life-cycle stages of <i>Trypanosoma brucei</i> and identification of splicing and polyadenylation sites. <i>Nucleic Acids Research</i> , 2010, 38, 4946-4957.	14.5	276
3	Evidence for a Shared Nuclear Pore Complex Architecture That Is Conserved from the Last Common Eukaryotic Ancestor. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2119-2130.	3.8	200
4	Comparative ribosome profiling reveals extensive translational complexity in different <i>Trypanosoma brucei</i> life cycle stages. <i>Nucleic Acids Research</i> , 2014, 42, 3623-3637.	14.5	154
5	Genome organization and DNA accessibility control antigenic variation in trypanosomes. <i>Nature</i> , 2018, 563, 121-125.	27.8	151
6	Strand-specific RNA-Seq reveals widespread and developmentally regulated transcription of natural antisense transcripts in <i>Plasmodium falciparum</i> . <i>BMC Genomics</i> , 2014, 15, 150.	2.8	93
7	Two thymidine hydroxylases differentially regulate the formation of glucosylated DNA at regions flanking polymerase II polycistronic transcription units throughout the genome of <i>Trypanosoma brucei</i> . <i>Nucleic Acids Research</i> , 2010, 38, 3923-3935.	14.5	84
8	Analysis of the <i>Trypanosoma brucei</i> cell cycle by quantitative DAPI imaging. <i>Molecular and Biochemical Parasitology</i> , 2008, 160, 171-174.	1.1	78
9	Histone H3 trimethylated at lysine 4 is enriched at probable transcription start sites in <i>Trypanosoma brucei</i> . <i>Molecular and Biochemical Parasitology</i> , 2010, 172, 141-144.	1.1	77
10	Systematic Study of Sequence Motifs for RNA trans Splicing in <i>Trypanosoma brucei</i> . <i>Molecular and Cellular Biology</i> , 2005, 25, 9586-9594.	2.3	76
11	Novel insights into RNP granules by employing the trypanosome's microtubule skeleton as a molecular sieve. <i>Nucleic Acids Research</i> , 2015, 43, 8013-8032.	14.5	74
12	Two essential MYST family proteins display distinct roles in histone H4K10 acetylation and telomeric silencing in trypanosomes. <i>Molecular Microbiology</i> , 2008, 69, 1054-1068.	2.5	73
13	Exonuclease-mediated degradation of nascent RNA silences genes linked to severe malaria. <i>Nature</i> , 2014, 513, 431-435.	27.8	73
14	Gene expression in <i>Trypanosoma brucei</i> : lessons from high-throughput RNA sequencing. <i>Trends in Parasitology</i> , 2011, 27, 434-441.	3.3	71
15	PfAlbas constitute a new eukaryotic DNA/RNA-binding protein family in malaria parasites. <i>Nucleic Acids Research</i> , 2012, 40, 3066-3077.	14.5	70
16	Regulation of transcription termination by glucosylated hydroxymethyluracil, base J, in <i>Leishmania major</i> and <i>Trypanosoma brucei</i> . <i>Nucleic Acids Research</i> , 2014, 42, 9717-9729.	14.5	68
17	Genetic promoters can drive RNA polymerase II transcription and deposition of H2A.Z in African trypanosomes. <i>EMBO Journal</i> , 2017, 36, 2581-2594.	7.8	68
18	Histone H3 Variant Regulates RNA Polymerase II Transcription Termination and Dual Strand Transcription of siRNA Loci in <i>Trypanosoma brucei</i> . <i>PLoS Genetics</i> , 2016, 12, e1005758.	3.5	55

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19	Acetylation of histone H4K4 is cell cycle regulated and mediated by HAT3 in <i>Trypanosoma brucei</i> . <i>Molecular Microbiology</i> , 2008, 67, 762-771.	2.5	54
20	Noncoding RNAs as emerging regulators of <i>Plasmodium falciparum</i> virulence gene expression. <i>Current Opinion in Microbiology</i> , 2014, 20, 153-161.	5.1	52
21	Spatial integration of transcription and splicing in a dedicated compartment sustains monogenic antigen expression in African trypanosomes. <i>Nature Microbiology</i> , 2021, 6, 289-300.	13.3	50
22	Efficient and specific oligo-based depletion of rRNA. <i>Scientific Reports</i> , 2019, 9, 12281.	3.3	44
23	Promoter occupancy of the basal class I transcription factor A differs strongly between active and silent VSG expression sites in <i>Trypanosoma brucei</i> . <i>Nucleic Acids Research</i> , 2014, 42, 3164-3176.	14.5	35
24	Distinct roles for H4 and H2A.Z acetylation in RNA transcription in African trypanosomes. <i>Nature Communications</i> , 2020, 11, 1498.	12.8	35
25	Comparative ribosome profiling uncovers a dominant role for translational control in <i>Toxoplasma gondii</i> . <i>BMC Genomics</i> , 2017, 18, 961.	2.8	23
26	Exploiting CRISPR-Cas9 technology to investigate individual histone modifications. <i>Nucleic Acids Research</i> , 2018, 46, e106-e106.	14.5	22
27	Ribosome Profiling Reveals HSP90 Inhibitor Effects on Stage-Specific Protein Synthesis in <i>Leishmania donovani</i> . <i>MSystems</i> , 2018, 3, .	3.8	20
28	Base J represses genes at the end of polycistronic gene clusters in <i>Leishmania major</i> by promoting RNAP II termination. <i>Molecular Microbiology</i> , 2016, 101, 559-574.	2.5	18
29	H2B.V demarcates divergent strand-switch regions, some tDNA loci, and genome compartments in <i>Trypanosoma cruzi</i> and affects parasite differentiation and host cell invasion. <i>PLoS Pathogens</i> , 2022, 18, e1009694.	4.7	15
30	Genome-wide Chromatin Immunoprecipitation-Sequencing in <i>Plasmodium</i> . <i>Methods in Molecular Biology</i> , 2012, 923, 321-333.	0.9	14
31	Genome-wide analysis of chromatin structures in <i>Trypanosoma brucei</i> using high-resolution MNase-ChIP-seq. <i>Experimental Parasitology</i> , 2017, 180, 2-12.	1.2	10
32	Allele-specific assembly of a eukaryotic genome corrects apparent frameshifts and reveals a lack of nonsense-mediated mRNA decay. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab082.	3.2	10
33	Fragment Ion Patchwork Quantification for Measuring Site-Specific Acetylation Degrees. <i>Analytical Chemistry</i> , 2015, 87, 9939-9945.	6.5	7
34	Cell-to-Cell Heterogeneity in Trypanosomes. <i>Annual Review of Microbiology</i> , 2021, 75, 107-128.	7.3	4