

Caroline C Friedel

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

4,847
citations

126907

33
h-index

106344

65
g-index

77
all docs

77
docs citations

77
times ranked

8174
citing authors

#	ARTICLE	IF	CITATIONS
1	Women in the European Virus Bioinformatics Center. <i>Viruses</i> , 2022, 14, 1522.	3.3	1
2	Dissecting Herpes Simplex Virus 1-Induced Host Shutoff at the RNA Level. <i>Journal of Virology</i> , 2021, 95, .	3.4	25
3	Plexin-B2 facilitates glioblastoma infiltration by modulating cell biomechanics. <i>Communications Biology</i> , 2021, 4, 145.	4.4	16
4	Diversified transcriptional responses of myeloid and glial cells in spinal cord injury shaped by HDAC3 activity. <i>Science Advances</i> , 2021, 7, .	10.3	35
5	Mechanism and consequences of herpes simplex virus 1-mediated regulation of host mRNA alternative polyadenylation. <i>PLoS Genetics</i> , 2021, 17, e1009263.	3.5	17
6	OAS1/RNase L executes RIG-I ligand-dependent tumor cell apoptosis. <i>Science Immunology</i> , 2021, 6, .	11.9	19
7	iBRET Screen of the ABCD1 Peroxisomal Network and Mutation-Induced Network Perturbations. <i>Journal of Proteome Research</i> , 2021, 20, 4366-4380.	3.7	3
8	Watchdog 2.0: New developments for reusability, reproducibility, and workflow execution. <i>GigaScience</i> , 2020, 9, .	6.4	10
9	Microglia and macrophages promote corraling, wound compaction and recovery after spinal cord injury via Plexin-B2. <i>Nature Neuroscience</i> , 2020, 23, 337-350.	14.8	146
10	Herpes simplex virus blocks host transcription termination via the bimodal activities of ICP27. <i>Nature Communications</i> , 2020, 11, 293.	12.8	58
11	Integrative functional genomics decodes herpes simplex virus 1. <i>Nature Communications</i> , 2020, 11, 2038.	12.8	61
12	CDK12 controls G1/S progression by regulating RNAPII processivity at core DNA replication genes. <i>EMBO Reports</i> , 2019, 20, e47592.	4.5	64
13	Immunostimulatory RNA leads to functional reprogramming of myeloid-derived suppressor cells in pancreatic cancer. , 2019, 7, 288.		22
14	Immune homeostasis and regulation of the interferon pathway require myeloid-derived Regnase-3. <i>Journal of Experimental Medicine</i> , 2019, 216, 1700-1723.	8.5	29
15	Gene signatures of quiescent glioblastoma cells reveal mesenchymal shift and interactions with niche microenvironment. <i>EBioMedicine</i> , 2019, 42, 252-269.	6.1	78
16	P-TEFb Activation by RBM7 Shapes a Pro-survival Transcriptional Response to Genotoxic Stress. <i>Molecular Cell</i> , 2019, 74, 254-267.e10.	9.7	73
17	MIR sequences recruit zinc finger protein ZNF768 to expressed genes. <i>Nucleic Acids Research</i> , 2019, 47, 700-715.	14.5	14
18	Comprehensive analysis of nuclear export of herpes simplex virus type 1 tegument proteins and their Epstein-Barr virus orthologs. <i>Traffic</i> , 2019, 20, 152-167.	2.7	3

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19	Real-time Analysis of Transcription Factor Binding, Transcription, Translation, and Turnover to Display Global Events During Cellular Activation. <i>Journal of Visualized Experiments</i> , 2018, , .	0.3	1
20	Watchdog – a workflow management system for the distributed analysis of large-scale experimental data. <i>BMC Bioinformatics</i> , 2018, 19, 97.	2.6	20
21	HSV-1-induced disruption of transcription termination resembles a cellular stress response but selectively increases chromatin accessibility downstream of genes. <i>PLoS Pathogens</i> , 2018, 14, e1006954.	4.7	71
22	Rapid Genome-wide Recruitment of RNA Polymerase II Drives Transcription, Splicing, and Translation Events during T Cell Responses. <i>Cell Reports</i> , 2017, 19, 643-654.	6.4	30
23	Bioinformatics advances biology and medicine by turning big data troves into knowledge. <i>Informatik-Spektrum</i> , 2017, 40, 153-160.	1.3	2
24	Transcriptome analysis of dominant-negative Brd4 mutants identifies Brd4-specific target genes of small molecule inhibitor JQ1. <i>Scientific Reports</i> , 2017, 7, 1684.	3.3	17
25	Prediction of Poly(A) Sites by Poly(A) Read Mapping. <i>PLoS ONE</i> , 2017, 12, e0170914.	2.5	22
26	Widespread activation of antisense transcription of the host genome during herpes simplex virus 1 infection. <i>Genome Biology</i> , 2017, 18, 209.	8.8	49
27	Calpain-mediated cleavage of collapsin response mediator protein-2 drives acute axonal degeneration. <i>Scientific Reports</i> , 2016, 6, 37050.	3.3	27
28	The Hepatitis E virus intraviral interactome. <i>Scientific Reports</i> , 2015, 5, 13872.	3.3	18
29	Widespread disruption of host transcription termination in HSV-1 infection. <i>Nature Communications</i> , 2015, 6, 7126.	12.8	245
30	p53-Regulated Networks of Protein, mRNA, miRNA, and lncRNA Expression Revealed by Integrated Pulsed Stable Isotope Labeling With Amino Acids in Cell Culture (pSILAC) and Next Generation Sequencing (NGS) Analyses. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2609-2629.	3.8	59
31	RC3H1 post-transcriptionally regulates A20 mRNA and modulates the activity of the IKK/NF- κ B pathway. <i>Nature Communications</i> , 2015, 6, 7367.	12.8	99
32	ContextMap 2: fast and accurate context-based RNA-seq mapping. <i>BMC Bioinformatics</i> , 2015, 16, 122.	2.6	54
33	Metabolic Labeling of Newly Transcribed RNA for High Resolution Gene Expression Profiling of RNA Synthesis, Processing and Decay in Cell Culture. <i>Journal of Visualized Experiments</i> , 2013, , .	0.3	75
34	β 1- and α v-class integrins cooperate to regulate myosin II during rigidity sensing of fibronectin-based microenvironments. <i>Nature Cell Biology</i> , 2013, 15, 625-636.	10.3	386
35	4-thiouridine inhibits rRNA synthesis and causes a nucleolar stress response. <i>RNA Biology</i> , 2013, 10, 1623-1630.	3.1	117
36	A Systematic Analysis of Host Factors Reveals a Med23-Interferon- γ Regulatory Axis against Herpes Simplex Virus Type 1 Replication. <i>PLoS Pathogens</i> , 2013, 9, e1003514.	4.7	88

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37	Deciphering the modulation of gene expression by type I and II interferons combining 4sU-tagging, translational arrest and in silico promoter analysis. <i>Nucleic Acids Research</i> , 2013, 41, 8107-8125.	14.5	31
38	Computational Analysis of Virus-Host Interactomes. <i>Methods in Molecular Biology</i> , 2013, 1064, 115-130.	0.9	3
39	Clonal Expansion Analysis of Transposon Insertions by High-Throughput Sequencing Identifies Candidate Cancer Genes in a PiggyBac Mutagenesis Screen. <i>PLoS ONE</i> , 2013, 8, e72338.	2.5	12
40	Mining RNA-Seq Data for Infections and Contaminations. <i>PLoS ONE</i> , 2013, 8, e73071.	2.5	13
41	Genome-Wide Assessment of AU-Rich Elements by the AREScore Algorithm. <i>PLoS Genetics</i> , 2012, 8, e1002433.	3.5	74
42	Real-time Transcriptional Profiling of Cellular and Viral Gene Expression during Lytic Cytomegalovirus Infection. <i>PLoS Pathogens</i> , 2012, 8, e1002908.	4.7	76
43	Detection and correction of probe-level artefacts on microarrays. <i>BMC Bioinformatics</i> , 2012, 13, 114.	2.6	6
44	Ultrashort and progressive 4sU-tagging reveals key characteristics of RNA processing at nucleotide resolution. <i>Genome Research</i> , 2012, 22, 2031-2042.	5.5	132
45	A context-based approach to identify the most likely mapping for RNA-seq experiments. <i>BMC Bioinformatics</i> , 2012, 13, S9.	2.6	14
46	A Comprehensive Evaluation of Alignment Algorithms in the Context of RNA-Seq. <i>PLoS ONE</i> , 2012, 7, e52403.	2.5	61
47	Virus-host interactomes and global models of virus-infected cells. <i>Trends in Microbiology</i> , 2011, 19, 501-508.	7.7	61
48	Quantitative proteomics of the integrin adhesome show a myosin II-dependent recruitment of LIM domain proteins. <i>EMBO Reports</i> , 2011, 12, 259-266.	4.5	315
49	The SARS-Coronavirus-Host Interactome: Identification of Cyclophilins as Target for Pan-Coronavirus Inhibitors. <i>PLoS Pathogens</i> , 2011, 7, e1002331.	4.7	367
50	HALO--a Java framework for precise transcript half-life determination. <i>Bioinformatics</i> , 2010, 26, 1264-1266.	4.1	6
51	Systematic Analysis of Viral and Cellular MicroRNA Targets in Cells Latently Infected with Human β -Herpesviruses by RISC Immunoprecipitation Assay. <i>Cell Host and Microbe</i> , 2010, 7, 324-334.	11.0	199
52	FERN -- Stochastic Simulation and Evaluation of Reaction Networks. <i>Systems Biology</i> , 2010, , 751-775.	0.1	1
53	Bootstrapping the Interactome: Unsupervised Identification of Protein Complexes in Yeast. <i>Journal of Computational Biology</i> , 2009, 16, 971-987.	1.6	85
54	Identifying the topology of protein complexes from affinity purification assays. <i>Bioinformatics</i> , 2009, 25, 2140-2146.	4.1	15

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55	Conserved principles of mammalian transcriptional regulation revealed by RNA half-life. <i>Nucleic Acids Research</i> , 2009, 37, e115-e115.	14.5	196
56	Evolutionarily Conserved Herpesviral Protein Interaction Networks. <i>PLoS Pathogens</i> , 2009, 5, e1000570.	4.7	162
57	Metabolic tagging and purification of nascent RNA: implications for transcriptomics. <i>Molecular BioSystems</i> , 2009, 5, 1271.	2.9	50
58	FERN – a Java framework for stochastic simulation and evaluation of reaction networks. <i>BMC Bioinformatics</i> , 2008, 9, 356.	2.6	26
59	ProCope – protein complex prediction and evaluation. <i>Bioinformatics</i> , 2008, 24, 2115-2116.	4.1	32
60	High-resolution gene expression profiling for simultaneous kinetic parameter analysis of RNA synthesis and decay. <i>Rna</i> , 2008, 14, 1959-1972.	3.5	380
61	Bootstrapping the Interactome: Unsupervised Identification of Protein Complexes in Yeast. <i>Lecture Notes in Computer Science</i> , 2008, , 3-16.	1.3	48
62	Influence of degree correlations on network structure and stability in protein-protein interaction networks. <i>BMC Bioinformatics</i> , 2007, 8, 297.	2.6	34
63	Analysis of Intraviral Protein-Protein Interactions of the SARS Coronavirus ORFeome. <i>PLoS ONE</i> , 2007, 2, e459.	2.5	207
64	Toward the complete interactome. <i>Nature Biotechnology</i> , 2006, 24, 614-615.	17.5	15
65	Inferring topology from clustering coefficients in protein-protein interaction networks. <i>BMC Bioinformatics</i> , 2006, 7, 519.	2.6	46
66	Reliable gene signatures for microarray classification: assessment of stability and performance. <i>Bioinformatics</i> , 2006, 22, 2356-2363.	4.1	79
67	Support vector machines for separation of mixed plant-pathogen EST collections based on codon usage. <i>Bioinformatics</i> , 2005, 21, 1383-1388.	4.1	23