Stefan Bonn

List of Publications by Year in descending order

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STEEAN RONN

#	Article	IF	CITATIONS
1	Th17 cell plasticity towards a T-bet-dependent Th1 phenotype is required for bacterial control in Staphylococcus aureus infection. PLoS Pathogens, 2022, 18, e1010430.	2.1	12
2	Deep Learning-Based Bias Transfer for Overcoming Laboratory Differences of Microscopic Images. Lecture Notes in Computer Science, 2021, , 322-336.	1.0	1
3	Interactive gene networks with KNIT. Bioinformatics, 2021, 37, 276-278.	1.8	0
4	Clonal expansion and activation of tissue-resident memory-like T _H 17 cells expressing GM-CSF in the lungs of patients with severe COVID-19. Science Immunology, 2021, 6, .	5.6	125
5	Algorithmic advances in machine learning for single-cell expression analysis. Current Opinion in Systems Biology, 2021, 25, 27-33.	1.3	20
6	Deep learning–based molecular morphometrics for kidney biopsies. JCI Insight, 2021, 6, .	2.3	31
7	Single-cell biology to decode the immune cellular composition of kidney inflammation. Cell and Tissue Research, 2021, 385, 435-443.	1.5	5
8	Bias-invariant RNA-sequencing metadata annotation. GigaScience, 2021, 10, .	3.3	5
9	Protein Phosphorylation in Depolarized Synaptosomes: Dissecting Primary Effects of Calcium from Synaptic Vesicle Cycling. Molecular and Cellular Proteomics, 2021, 20, 100061.	2.5	11
10	Organ-specific small non-coding RNA responses in domestic (Sudani) ducks experimentally infected with highly pathogenic avian influenza virus (H5N1). RNA Biology, 2020, 17, 112-124.	1.5	15
11	SEAweb: the small RNA Expression Atlas web application. Nucleic Acids Research, 2020, 48, D204-D219.	6.5	15
12	Realistic in silico generation and augmentation of single-cell RNA-seq data using generative adversarial networks. Nature Communications, 2020, 11, 166.	5.8	118
13	Neuropathology of patients with COVID-19 in Germany: a post-mortem case series. Lancet Neurology, The, 2020, 19, 919-929.	4.9	957
14	Pathogen-induced tissue-resident memory T _H 17 (T _{RM} 17) cells amplify autoimmune kidney disease. Science Immunology, 2020, 5, .	5.6	58
15	Deep learning–based cell composition analysis from tissue expression profiles. Science Advances, 2020, 6, eaba2619.	4.7	113
16	SUMOylation controls the neurodevelopmental function of the transcription factor Zbtb20. Journal of Neurochemistry, 2020, 154, 647-661.	2.1	12
17	Explainable Deep Learning for Augmentation of Small RNA Expression Profiles. Journal of Computational Biology, 2020, 27, 234-247.	0.8	9
18	Violent aggression predicted by multiple pre-adult environmental hits. Molecular Psychiatry, 2019, 24, 1549-1564.	4.1	23

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19	Tagger—A Swiss army knife for multiomics to dissect cell type–specific mechanisms of gene expression in mice. PLoS Biology, 2019, 17, e3000374.	2.6	12
20	Deep Learning and Random Forest-Based Augmentation of sRNA Expression Profiles. Lecture Notes in Computer Science, 2019, , 159-170.	1.0	5
21	RNA editing alterations define manifestation of prion diseases. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19727-19735.	3.3	17
22	The long noncoding RNA <i>neuroLNC</i> regulates presynaptic activity by interacting with the neurodegeneration-associated protein TDP-43. Science Advances, 2019, 5, eaay2670.	4.7	38
23	Epigenetic alterations in longevity regulators, reduced life span, and exacerbated aging-related pathology in old father offspring mice. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2348-E2357.	3.3	102
24	Oasis 2: improved online analysis of small RNA-seq data. BMC Bioinformatics, 2018, 19, 54.	1.2	70
25	OTTO: a new strategy to extract mental disease-relevant combinations of GWAS hits from individuals. Molecular Psychiatry, 2018, 23, 476-486.	4.1	17
26	The codon sequences predict protein lifetimes and other parameters of the protein life cycle in the mouse brain. Scientific Reports, 2018, 8, 16913.	1.6	17
27	Precisely measured protein lifetimes in the mouse brain reveal differences across tissues and subcellular fractions. Nature Communications, 2018, 9, 4230.	5.8	219
28	Targeting myelin lipid metabolism as a potential therapeutic strategy in a model of CMT1A neuropathy. Nature Communications, 2018, 9, 3025.	5.8	71
29	Genome-wide association study results for educational attainment aid in identifying genetic heterogeneity of schizophrenia. Nature Communications, 2018, 9, 3078.	5.8	64
30	Regional and subtype-dependent miRNA signatures in sporadic Creutzfeldt-Jakob disease are accompanied by alterations in miRNA silencing machinery and biogenesis. PLoS Pathogens, 2018, 14, e1006802.	2.1	26
31	RNF40 regulates gene expression in an epigenetic context-dependent manner. Genome Biology, 2017, 18, 32.	3.8	41
32	Sodium butyrate rescues dopaminergic cells from alpha-synuclein-induced transcriptional deregulation and DNA damage. Human Molecular Genetics, 2017, 26, 2231-2246.	1.4	121
33	A novel method for culturing stellate astrocytes reveals spatially distinct Ca2+ signaling and vesicle recycling in astrocytic processes. Journal of General Physiology, 2017, 149, 149-170.	0.9	27
34	Severe DCM phenotype of patient harboring RBM20 mutation S635A can be modeled by patient-specific induced pluripotent stem cell-derived cardiomyocytes. Journal of Molecular and Cellular Cardiology, 2017, 113, 9-21.	0.9	84
35	Altered Ca2+ homeostasis induces Calpain-Cathepsin axis activation in sporadic Creutzfeldt-Jakob disease. Acta Neuropathologica Communications, 2017, 5, 35.	2.4	31
36	The landscape of human mutually exclusive splicing. Molecular Systems Biology, 2017, 13, 959.	3.2	53

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37	Endophilin-A Deficiency Induces the Foxo3a-Fbxo32 Network in the Brain and Causes Dysregulation of Autophagy and the Ubiquitin-Proteasome System. Cell Reports, 2016, 17, 1071-1086.	2.9	100
38	TAp73 is a central transcriptional regulator of airway multiciliogenesis. Genes and Development, 2016, 30, 1300-1312.	2.7	112
39	DNA methylation changes in plasticity genes accompany the formation and maintenance of memory. Nature Neuroscience, 2016, 19, 102-110.	7.1	307
40	Genome-wide chromatin and gene expression profiling during memory formation and maintenance in adult mice. Scientific Data, 2016, 3, 160090.	2.4	7
41	Oasis: online analysis of small RNA deep sequencing data. Bioinformatics, 2015, 31, 2205-2207.	1.8	61