

# Florian Erhard

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

2,429  
citations

361413

20  
h-index

377865

34  
g-index

44  
all docs

44  
docs citations

44  
times ranked

3722  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Hidden Enemy Within: Non-canonical Peptides in Virus-Induced Autoimmunity. <i>Frontiers in Microbiology</i> , 2022, 13, 840911.	3.5	5
2	Selective inhibition of miRNA processing by a herpesvirus-encoded miRNA. <i>Nature</i> , 2022, 605, 539-544.	27.8	23
3	Dissecting Herpes Simplex Virus 1-Induced Host Shutoff at the RNA Level. <i>Journal of Virology</i> , 2021, 95, .	3.4	25
4	Homozygous BCMA gene deletion in response to anti-BCMA CAR T cells in a patient with multiple myeloma. <i>Nature Medicine</i> , 2021, 27, 616-619.	30.7	140
5	Integrative transcription start site identification with iTiSS. <i>Bioinformatics</i> , 2021, 37, 3056-3057.	4.1	7
6	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
7	ITNâ€™VIROINF: Understanding (Harmful) Virus-Host Interactions by Linking Virology and Bioinformatics. <i>Viruses</i> , 2021, 13, 766.	3.3	5
8	The Zinc Finger Antiviral Protein ZAP Restricts Human Cytomegalovirus and Selectively Binds and Destabilizes Viral <i>UL4</i> / <i>UL5</i> Transcripts. <i>MBio</i> , 2021, 12, .	4.1	33
9	Targeted protein degradation reveals a direct role of SPT6 in RNAPII elongation and termination. <i>Molecular Cell</i> , 2021, 81, 3110-3127.e14.	9.7	38
10	SARS-CoV-2 infection triggers profibrotic macrophage responses and lung fibrosis. <i>Cell</i> , 2021, 184, 6243-6261.e27.	28.9	277
11	Single-cell transcriptional profiling of splenic fibroblasts reveals subset-specific innate immune signatures in homeostasis and during viral infection. <i>Communications Biology</i> , 2021, 4, 1355.	4.4	12
12	Identification of the Cryptic HLA-I Immunopeptidome. <i>Cancer Immunology Research</i> , 2020, 8, 1018-1026.	3.4	80
13	Herpes simplex virus blocks host transcription termination via the bimodal activities of ICP27. <i>Nature Communications</i> , 2020, 11, 293.	12.8	58
14	Integrative functional genomics decodes herpes simplex virus 1. <i>Nature Communications</i> , 2020, 11, 2038.	12.8	61
15	IL-12 from endogenous cDC1, and not vaccine DC, is required for Th1 induction. <i>JCI Insight</i> , 2020, 5, .	5.0	28
16	scSLAM-seq reveals core features of transcription dynamics in single cells. <i>Nature</i> , 2019, 571, 419-423.	27.8	153
17	A MYCâ€™GCN2â€™eIF2Î± negative feedback loop limits protein synthesis to prevent MYC-dependent apoptosis in colorectal cancer. <i>Nature Cell Biology</i> , 2019, 21, 1413-1424.	10.3	65
18	The complex of MCMV proteins and MHC class I evades NK cell control and drives the evolution of virus-specific activating Ly49 receptors. <i>Journal of Experimental Medicine</i> , 2019, 216, 1809-1827.	8.5	19

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19	Improved Ribo-seq enables identification of cryptic translation events. <i>Nature Methods</i> , 2018, 15, 363-366.	19.0	153
20	Dissecting newly transcribed and old RNA using GRAND-SLAM. <i>Bioinformatics</i> , 2018, 34, i218-i226.	4.1	79
21	Tolerogenic Transcriptional Signatures of Steady-State and Pathogen-Induced Dendritic Cells. <i>Frontiers in Immunology</i> , 2018, 9, 333.	4.8	22
22	Dicer in Macrophages Prevents Atherosclerosis by Promoting Mitochondrial Oxidative Metabolism. <i>Circulation</i> , 2018, 138, 2007-2020.	1.6	79
23	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
24	Estimating pseudocounts and fold changes for digital expression measurements. <i>Bioinformatics</i> , 2018, 34, 4054-4063.	4.1	26
25	EBF1 binds to EBNA2 and promotes the assembly of EBNA2 chromatin complexes in B cells. <i>PLoS Pathogens</i> , 2017, 13, e1006664.	4.7	25
26	Widespread disruption of host transcription termination in HSV-1 infection. <i>Nature Communications</i> , 2015, 6, 7126.	12.8	245
27	Count ratio model reveals bias affecting NGS fold changes. <i>Nucleic Acids Research</i> , 2015, 43, gkv696.	14.5	14
28	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
29	Widespread context dependency of microRNA-mediated regulation. <i>Genome Research</i> , 2014, 24, 906-919.	5.5	111
30	RIP-chip enrichment analysis. <i>Bioinformatics</i> , 2013, 29, 77-83.	4.1	12
31	Inactivation of Intergenic Enhancers by EBNA3A Initiates and Maintains Polycomb Signatures across a Chromatin Domain Encoding CXCL10 and CXCL9. <i>PLoS Pathogens</i> , 2013, 9, e1003638.	4.7	55
32	Degradation of Cellular miR-27 by a Novel, Highly Abundant Viral Transcript Is Important for Efficient Virus Replication In Vivo. <i>PLoS Pathogens</i> , 2012, 8, e1002510.	4.7	179
33	Systematic Analysis of Viral and Cellular MicroRNA Targets in Cells Latently Infected with Human $\beta$ -Herpesviruses by RISC Immunoprecipitation Assay. <i>Cell Host and Microbe</i> , 2010, 7, 324-334.	11.0	199