

Noam Stern-Ginossar

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8896471/publications.pdf>

Version: 2024-02-01

53
papers

10,441
citations

159525

30
h-index

189801

50
g-index

62
all docs

62
docs citations

62
times ranked

16425
citing authors

#	ARTICLE	IF	CITATIONS
1	Temporal dynamics of HCMV gene expression in lytic and latent infections. <i>Cell Reports</i> , 2022, 39, 110653.	2.9	19
2	Genome-wide CRISPR screens identify GATA6 as a proviral host factor for SARS-CoV-2 via modulation of ACE2. <i>Nature Communications</i> , 2022, 13, 2237.	5.8	27
3	Parsing the role of NSP1 in SARS-CoV-2 infection. <i>Cell Reports</i> , 2022, 39, 110954.	2.9	37
4	The coding capacity of SARS-CoV-2. <i>Nature</i> , 2021, 589, 125-130.	13.7	464
5	Anti-tumour immunity induces aberrant peptide presentation in melanoma. <i>Nature</i> , 2021, 590, 332-337.	13.7	81
6	ITNâ€™VIRGINF: Understanding (Harmful) Virus-Host Interactions by Linking Virology and Bioinformatics. <i>Viruses</i> , 2021, 13, 766.	1.5	5
7	SARS-CoV-2 uses a multipronged strategy to impede host protein synthesis. <i>Nature</i> , 2021, 594, 240-245.	13.7	182
8	Conflicting and ambiguous names of overlapping ORFs in the SARS-CoV-2 genome: A homology-based resolution. <i>Virology</i> , 2021, 558, 145-151.	1.1	40
9	Deciphering the principles of the RNA editing code via large-scale systematic probing. <i>Molecular Cell</i> , 2021, 81, 2374-2387.e3.	4.5	20
10	Dynamic changes in tRNA modifications and abundance during T cell activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	27
11	The integrated stress response promotes B7H6 expression. <i>Journal of Molecular Medicine</i> , 2020, 98, 135-148.	1.7	18
12	The Human Cytomegalovirus pUL145 Isoforms Act as Viral DDB1-Cullin-Associated Factors to Instruct Host Protein Degradation to Impede Innate Immunity. <i>Cell Reports</i> , 2020, 30, 2248-2260.e5.	2.9	30
13	The RNA modification N6-methyladenosine as a novel regulator of the immune system. <i>Nature Immunology</i> , 2020, 21, 501-512.	7.0	256
14	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication. <i>PLoS Pathogens</i> , 2020, 16, e1008390.	2.1	31
15	Profiling the Blood Compartment of Hematopoietic Stem Cell Transplant Patients During Human Cytomegalovirus Reactivation. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 607470.	1.8	4
16	Context-dependent functional compensation between Ythdf m⁶A reader proteins. <i>Genes and Development</i> , 2020, 34, 1373-1391.	2.7	158
17	Comprehensive annotations of human herpesvirus 6A and 6B genomes reveal novel and conserved genomic features. <i>ELife</i> , 2020, 9, .	2.8	30
18	Single cell analysis reveals human cytomegalovirus drives latently infected cells towards an anergic-like monocyte state. <i>ELife</i> , 2020, 9, .	2.8	46

#	ARTICLE	IF	CITATIONS
19	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication. , 2020, 16, e1008390.		0
20	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication. , 2020, 16, e1008390.		0
21	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication. , 2020, 16, e1008390.		0
22	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication. , 2020, 16, e1008390.		0
23	Translational Control in Virus-Infected Cells. Cold Spring Harbor Perspectives in Biology, 2019, 11, a033001.	2.3	128
24	Rho-Associated Coiled-Coil Kinase 1 Translocates to the Nucleus and Inhibits Human Cytomegalovirus Propagation. Journal of Virology, 2019, 93, .	1.5	9
25	Long Noncoding RNA MALAT1 Regulates Cancer Glucose Metabolism by Enhancing mTOR-Mediated Translation of TCF7L2. Cancer Research, 2019, 79, 2480-2493.	0.4	132
26	The Transcriptome of Latent Human Cytomegalovirus. Journal of Virology, 2019, 93, .	1.5	29
27	An iPSC-Derived Myeloid Lineage Model of Herpes Virus Latency and Reactivation. Frontiers in Microbiology, 2019, 10, 2233.	1.5	18
28	m6A modification controls the innate immune response to infection by targeting type I interferons. Nature Immunology, 2019, 20, 173-182.	7.0	317
29	Defining the Transcriptional Landscape during Cytomegalovirus Latency with Single-Cell RNA Sequencing. MBio, 2018, 9, .	1.8	174
30	Decay of the Stress-Induced Ligand MICA Is Controlled by the Expression of an Alternative 3' UTR Untranslated Region. Journal of Immunology, 2018, 200, 2819-2825.	0.4	8
31	Viral Short ORFs and Their Possible Functions. Proteomics, 2018, 18, e1700255.	1.3	17
32	Virus-Induced Changes in mRNA Secondary Structure Uncover cis-Regulatory Elements that Directly Control Gene Expression. Molecular Cell, 2018, 72, 862-874.e5.	4.5	41
33	Translational control of ERK signaling through miRNA/4EHP-directed silencing. ELife, 2018, 7, .	2.8	41
34	Urea Cycle Dysregulation Generates Clinically Relevant Genomic and Biochemical Signatures. Cell, 2018, 174, 1559-1570.e22.	13.5	183
35	Cap-binding protein 4EHP effects translation silencing by microRNAs. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 5425-5430.	3.3	93
36	The m1A landscape on cytosolic and mitochondrial mRNA at single-base resolution. Nature, 2017, 551, 251-255.	13.7	440

#	ARTICLE	IF	CITATIONS
37	Global mRNA polarization regulates translation efficiency in the intestinal epithelium. <i>Science</i> , 2017, 357, 1299-1303.	6.0	140
38	RNA editing by ADAR1 leads to context-dependent transcriptome-wide changes in RNA secondary structure. <i>Nature Communications</i> , 2017, 8, 1440.	5.8	77
39	Term-seq reveals abundant ribo-regulation of antibiotics resistance in bacteria. <i>Science</i> , 2016, 352, aad9822.	6.0	294
40	Systematic discovery of cap-independent translation sequences in human and viral genomes. <i>Science</i> , 2016, 351, .	6.0	258
41	A conserved abundant cytoplasmic long noncoding RNA modulates repression by Pumilio proteins in human cells. <i>Nature Communications</i> , 2016, 7, 12209.	5.8	192
42	A systematic view on influenza induced host shutoff. <i>ELife</i> , 2016, 5, .	2.8	92
43	The Transcription and Translation Landscapes during Human Cytomegalovirus Infection Reveal Novel Host-Pathogen Interactions. <i>PLoS Pathogens</i> , 2015, 11, e1005288.	2.1	127
44	A Regression-Based Analysis of Ribosome-Profiling Data Reveals a Conserved Complexity to Mammalian Translation. <i>Molecular Cell</i> , 2015, 60, 816-827.	4.5	200
45	m ⁶ A mRNA methylation facilitates resolution of naïve pluripotency toward differentiation. <i>Science</i> , 2015, 347, 1002-1006.	6.0	1,288
46	Decoding Viral Infection by Ribosome Profiling. <i>Journal of Virology</i> , 2015, 89, 6164-6166.	1.5	19
47	Ribosome Profiling as a Tool to Decipher Viral Complexity. <i>Annual Review of Virology</i> , 2015, 2, 335-349.	3.0	26
48	Regulation of mRNA translation during mitosis. <i>ELife</i> , 2015, 4, .	2.8	138
49	Ribosome Profiling Reveals Pervasive Translation Outside of Annotated Protein-Coding Genes. <i>Cell Reports</i> , 2014, 8, 1365-1379.	2.9	591
50	KSHV 2.0: A Comprehensive Annotation of the Kaposi's Sarcoma-Associated Herpesvirus Genome Using Next-Generation Sequencing Reveals Novel Genomic and Functional Features. <i>PLoS Pathogens</i> , 2014, 10, e1003847.	2.1	264
51	Manipulation of host pathways by human cytomegalovirus: insights from genome-wide studies. <i>Seminars in Immunopathology</i> , 2014, 36, 651-658.	2.8	13
52	CRISPR-Mediated Modular RNA-Guided Regulation of Transcription in Eukaryotes. <i>Cell</i> , 2013, 154, 442-451.	13.5	3,012
53	Decoding Human Cytomegalovirus. <i>Science</i> , 2012, 338, 1088-1093.	6.0	546