

Udi Qimron

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

4,476
citations

186265

28
h-index

155660

55
g-index

65
all docs

65
docs citations

65
times ranked

5132
citing authors

#	ARTICLE	IF	CITATIONS
1	A phage mechanism for selective nicking of dUMP-containing DNA. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	8
2	A continuous evolution system for contracting the host range of bacteriophage T7. Scientific Reports, 2020, 10, 307.	3.3	44
3	Phage T7 DNA mimic protein Ocr is a potent inhibitor of BREX defence. Nucleic Acids Research, 2020, 48, 5397-5406.	14.5	53
4	Optimizing DNA transduction by selection of mutations that evade bacterial defense systems. RNA Biology, 2019, 16, 595-599.	3.1	6
5	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. Nature Microbiology, 2019, 4, 1727-1736.	13.3	184
6	Activated Eosinophils Exert Antitumorigenic Activities in Colorectal Cancer. Cancer Immunology Research, 2019, 7, 388-400.	3.4	113
7	A genetic system for biasing the sex ratio in mice. EMBO Reports, 2019, 20, e48269.	4.5	15
8	A technological and regulatory outlook on CRISPR crop editing. Journal of Cellular Biochemistry, 2018, 119, 1291-1298.	2.6	53
9	T7 phage factor required for managing RpoS in <i>Escherichia coli</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5353-E5362.	7.1	36
10	CRISPR Inspirations. Cell, 2018, 173, 1560-1561.	28.9	0
11	Full shut-off of Escherichia coli RNA-polymerase by T7 phage requires a small phage-encoded DNA-binding protein. Nucleic Acids Research, 2017, 45, 7697-7707.	14.5	21
12	Extending the Host Range of Bacteriophage Particles for DNA Transduction. Molecular Cell, 2017, 66, 721-728.e3.	9.7	127
13	Crystal-clear memories of a bacterium. Science, 2017, 357, 1096-1097.	12.6	0
14	CD300f:IL-5 cross-talk inhibits adipose tissue eosinophil homing and subsequent IL-4 production. Scientific Reports, 2017, 7, 5922.	3.3	24
15	Sensitizing pathogens to antibiotics using the CRISPR-Cas system. Drug Resistance Updates, 2017, 30, 1-6.	14.4	39
16	Selection of Genetically Modified Bacteriophages Using the CRISPR-Cas System. Bio-protocol, 2017, 7, .	0.4	5
17	Adaptation in CRISPR-Cas Systems. Molecular Cell, 2016, 61, 797-808.	9.7	192
18	Repeat Size Determination by Two Molecular Rulers in the Type I-E CRISPR Array. Cell Reports, 2016, 16, 2811-2818.	6.4	27

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19	Natural selection underlies apparent stress-induced mutagenesis in a bacteriophage infection model. <i>Nature Microbiology</i> , 2016, 1, 16047.	13.3	7
20	Phenotypic heterogeneity in a bacteriophage population only appears as stress-induced mutagenesis. <i>Current Genetics</i> , 2016, 62, 771-773.	1.7	1
21	Counteracting selection for antibiotic-resistant bacteria. <i>Bacteriophage</i> , 2016, 6, e1096996.	1.9	12
22	How bacteria get spacers from invaders. <i>Nature</i> , 2015, 519, 166-167.	27.8	5
23	Temperate and lytic bacteriophages programmed to sensitize and kill antibiotic-resistant bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7267-7272.	7.1	359
24	CRISPR adaptation biases explain preference for acquisition of foreign DNA. <i>Nature</i> , 2015, 520, 505-510.	27.8	346
25	Using the CRISPR-Cas System to Positively Select Mutants in Genes Essential for Its Function. <i>Methods in Molecular Biology</i> , 2015, 1311, 233-250.	0.9	1
26	Programming Bacteriophages by Swapping Their Specificity Determinants. <i>Trends in Microbiology</i> , 2015, 23, 744-746.	7.7	14
27	Different approaches for using bacteriophages against antibiotic-resistant bacteria. <i>Bacteriophage</i> , 2014, 4, e28491.	1.9	19
28	Efficient engineering of a bacteriophage genome using the type I-E CRISPR-Cas system. <i>RNA Biology</i> , 2014, 11, 42-44.	3.1	130
29	Revealing bacterial targets of growth inhibitors encoded by bacteriophage T7. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18715-18720.	7.1	23
30	DNA motifs determining the efficiency of adaptation into the <i>Escherichia coli</i> CRISPR array. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14396-14401.	7.1	62
31	Discovery of Functional Toxin/Antitoxin Systems in Bacteria by Shotgun Cloning. <i>Molecular Cell</i> , 2013, 50, 136-148.	9.7	125
32	CRISPR adaptation in <i>Escherichia coli</i> subtypes I-E system. <i>Biochemical Society Transactions</i> , 2013, 41, 1412-1415.	3.4	10
33	Gene product 0.4 increases bacteriophage T7 competitiveness by inhibiting host cell division. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19549-19554.	7.1	46
34	New Details about Bacteriophage T7-Host Interactions. <i>Microbe Magazine</i> , 2013, 5, 117-122.	0.4	6
35	Proteins and DNA elements essential for the CRISPR adaptation process in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2012, 40, 5569-5576.	14.5	593
36	The Bacterial CRISPR/Cas System as Analog of the Mammalian Adaptive Immune System. <i>RNA Biology</i> , 2012, 9, 549-554.	3.1	23

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37	Reversing Bacterial Resistance to Antibiotics by Phage-Mediated Delivery of Dominant Sensitive Genes. <i>Applied and Environmental Microbiology</i> , 2012, 78, 744-751.	3.1	173
38	Experimental Definition of a Clustered Regularly Interspaced Short Palindromic Duplicon in <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2012, 423, 14-16.	4.2	46
39	High-temperature protein G is essential for activity of the <i>Escherichia coli</i> clustered regularly interspaced short palindromic repeats (CRISPR)/Cas system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20136-20141.	7.1	94
40	The <i>Escherichia coli</i> CRISPR System Protects from λ Lysogenization, Lysogens, and Prophage Induction. <i>Journal of Bacteriology</i> , 2010, 192, 6291-6294.	2.2	156
41	Mutations in the gene 5 DNA polymerase of bacteriophage T7 suppress the dominant lethal phenotype of gene 2.5 ssDNA binding protein lacking the C-terminal phenylalanine. <i>Molecular Microbiology</i> , 2009, 72, 869-880.	2.5	8
42	Mutations in the gene 5 DNA polymerase of bacteriophage T7 suppress the dominant lethal phenotype of gene 2.5 ssDNA binding protein lacking the C-terminal phenylalanine. <i>Molecular Microbiology</i> , 2009, 73, 323-323.	2.5	0
43	Inadequate inhibition of host RNA polymerase restricts T7 bacteriophage growth on hosts overexpressing <i>udk</i> . <i>Molecular Microbiology</i> , 2008, 67, 448-457.	2.5	18
44	Communication between subunits critical to DNA binding by hexameric helicase of bacteriophage T7. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8908-8913.	7.1	13
45	Gene <i>1.7</i> of bacteriophage T7 confers sensitivity of phage growth to dideoxythymidine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9373-9378.	7.1	18
46	Gene 1.7 of Bacteriophage T7 Confers Sensitivity of Phage Growth to Dideoxythymidine. <i>FASEB Journal</i> , 2008, 22, 651.5.	0.5	0
47	Dynamic DNA Helicase-DNA Polymerase Interactions Assure Processive Replication Fork Movement. <i>Molecular Cell</i> , 2007, 27, 539-549.	9.7	108
48	Genomewide screens for <i>Escherichia coli</i> genes affecting growth of T7 bacteriophage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 19039-19044.	7.1	181
49	Oligomeric States of Bacteriophage T7 Gene 4 Primase/Helicase. <i>Journal of Molecular Biology</i> , 2006, 360, 667-677.	4.2	56
50	Lethal influenza infection in the absence of the natural killer cell receptor gene <i>Ncr1</i> . <i>Nature Immunology</i> , 2006, 7, 517-523.	14.5	503
51	Primer initiation and extension by T7 DNA primase. <i>EMBO Journal</i> , 2006, 25, 2199-2208.	7.8	33
52	Role of the linker between the zinc binding domain and the polymerization domain of the bacteriophage T7 DNA primase. <i>FASEB Journal</i> , 2006, 20, A910.	0.5	0
53	Tumor Vaccination by <i>Salmonella typhimurium</i> After Transformation with a Eukaryotic Expression Vector in Mice. <i>Journal of Immunotherapy</i> , 2005, 28, 467-479.	2.4	13
54	Role of a Conserved Arginine in the Mechanism of Acetohydroxyacid Synthase. <i>Journal of Biological Chemistry</i> , 2004, 279, 24803-24812.	3.4	48

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55	Membrane-Associated Heparan Sulfate Proteoglycans Are Involved in the Recognition of Cellular Targets by NKp30 and NKp46. <i>Journal of Immunology</i> , 2004, 173, 2392-2401.	0.8	146
56	Restoration of Gene Function by Homologous Recombination: from PCR to Gene Expression in One Step. <i>Applied and Environmental Microbiology</i> , 2004, 70, 7156-7160.	3.1	5
57	Identification of <i>Salmonella typhimurium</i> genes responsible for interference with peptide presentation on MHC class I molecules: Deltayej <i>Salmonella</i> mutants induce superior CD8+ T-cell responses. <i>Cellular Microbiology</i> , 2004, 6, 1057-1070.	2.1	32
58	Non-replicating mucosal and systemic vaccines: quantitative and qualitative differences in the Ag-specific CD8+ T cell population in different tissues. <i>Vaccine</i> , 2004, 22, 1390-1394.	3.8	14
59	The mechanisms controlling NK cell autoreactivity in TAP2-deficient patients. <i>Blood</i> , 2004, 103, 1770-1778.	1.4	62
60	Reliable determination of transposon insertion site in prokaryotes by direct sequencing. <i>Journal of Microbiological Methods</i> , 2003, 54, 137-140.	1.6	9