

Rotem Sorek

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

15,424
citations

41344

49
h-index

62596

80
g-index

94
all docs

94
docs citations

94
times ranked

15551
citing authors

#	ARTICLE	IF	CITATIONS
1	Bacterial gasdermins reveal an ancient mechanism of cell death. <i>Science</i> , 2022, 375, 221-225.	12.6	132
2	SnapShot: Bacterial immunity. <i>Cell</i> , 2022, 185, 578-578.e1.	28.9	45
3	Phage anti-CBASS and anti-Pycsar nucleases subvert bacterial immunity. <i>Nature</i> , 2022, 605, 522-526.	27.8	70
4	Bacterial origins of human cell-autonomous innate immune mechanisms. <i>Nature Reviews Immunology</i> , 2022, 22, 629-638.	22.7	98
5	The DarTG toxin-antitoxin system provides phage defence by ADP-ribosylating viral DNA. <i>Nature Microbiology</i> , 2022, 7, 1028-1040.	13.3	78
6	Bacteria deplete deoxynucleotides to defend against bacteriophage infection. <i>Nature Microbiology</i> , 2022, 7, 1200-1209.	13.3	58
7	Prokaryotic viperins produce diverse antiviral molecules. <i>Nature</i> , 2021, 589, 120-124.	27.8	172
8	A treasure trove of molecular scissors. <i>Science</i> , 2021, 374, 37-38.	12.6	3
9	Cyclic CMP and cyclic UMP mediate bacterial immunity against phages. <i>Cell</i> , 2021, 184, 5728-5739.e16.	28.9	156
10	Effector-mediated membrane disruption controls cell death in CBASS antiphage defense. <i>Molecular Cell</i> , 2021, 81, 5039-5051.e5.	9.7	59
11	Antiviral activity of bacterial TIR domains via immune signalling molecules. <i>Nature</i> , 2021, 600, 116-120.	27.8	159
12	The pan-immune system of bacteria: antiviral defence as a community resource. <i>Nature Reviews Microbiology</i> , 2020, 18, 113-119.	28.6	368
13	A genome assembly and the somatic genetic and epigenetic mutation rate in a wild long-lived perennial <i>Populus trichocarpa</i> . <i>Genome Biology</i> , 2020, 21, 259.	8.8	68
14	Diversity and classification of cyclic-oligonucleotide-based anti-phage signalling systems. <i>Nature Microbiology</i> , 2020, 5, 1608-1615.	13.3	160
15	Bacterial Retrons Function In Anti-Phage Defense. <i>Cell</i> , 2020, 183, 1551-1561.e12.	28.9	208
16	Abortive Infection: Bacterial Suicide as an Antiviral Immune Strategy. <i>Annual Review of Virology</i> , 2020, 7, 371-384.	6.7	247
17	STING cyclic dinucleotide sensing originated in bacteria. <i>Nature</i> , 2020, 586, 429-433.	27.8	246
18	Peptide-based quorum sensing systems in <i>Paenibacillus polymyxa</i> . <i>Life Science Alliance</i> , 2020, 3, e202000847.	2.8	11

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19	Successful Brincidofovir Treatment of Metagenomics-detected Adenovirus Infection in a Severely Ill Signal Transducer and Activator of Transcription-1-deficient Patient. <i>Pediatric Infectious Disease Journal</i> , 2019, 38, 297-299.	2.0	7
20	Cyclic GMP-AMP signalling protects bacteria against viral infection. <i>Nature</i> , 2019, 574, 691-695.	27.8	370
21	Widespread Utilization of Peptide Communication in Phages Infecting Soil and Pathogenic Bacteria. <i>Cell Host and Microbe</i> , 2019, 25, 746-755.e5.	11.0	77
22	A <i>rhlI</i> 5' UTR-Derived sRNA Regulates RhlR-Dependent Quorum Sensing in <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2019, 10, .	4.1	40
23	Contemporary Phage Biology: From Classic Models to New Insights. <i>Cell</i> , 2018, 172, 1260-1270.	28.9	176
24	High-resolution RNA 3'-ends mapping of bacterial Rho-dependent transcripts. <i>Nucleic Acids Research</i> , 2018, 46, 6797-6805.	14.5	88
25	Systematic discovery of antiphage defense systems in the microbial pangenome. <i>Science</i> , 2018, 359, .	12.6	776
26	Quantitative species-level ecology of reef fish larvae via metabarcoding. <i>Nature Ecology and Evolution</i> , 2018, 2, 306-316.	7.8	56
27	DISARM is a widespread bacterial defence system with broad anti-phage activities. <i>Nature Microbiology</i> , 2018, 3, 90-98.	13.3	225
28	HflXr, a homolog of a ribosome-splitting factor, mediates antibiotic resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 13359-13364.	7.1	41
29	Bacterial Noncoding RNAs Excised from within Protein-Coding Transcripts. <i>MBio</i> , 2018, 9, .	4.1	46
30	Viruses cooperate to defeat bacteria. <i>Nature</i> , 2018, 559, 482-484.	27.8	15
31	Extensive reshaping of bacterial operons by programmed mRNA decay. <i>PLoS Genetics</i> , 2018, 14, e1007354.	3.5	60
32	Communication between viruses guides lysis-lysogeny decisions. <i>Nature</i> , 2017, 541, 488-493.	27.8	465
33	Vesicles Spread Susceptibility to Phages. <i>Cell</i> , 2017, 168, 13-15.	28.9	39
34	Optimality and sub-optimality in a bacterial growth law. <i>Nature Communications</i> , 2017, 8, 14123.	12.8	102
35	Regulation of antibiotic-resistance by non-coding RNAs in bacteria. <i>Current Opinion in Microbiology</i> , 2017, 36, 111-117.	5.1	33
36	Intracellular signaling in CRISPR-Cas defense. <i>Science</i> , 2017, 357, 550-551.	12.6	10

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37	Computational prediction of regulatory, premature transcription termination in bacteria. <i>Nucleic Acids Research</i> , 2017, 45, 886-893.	14.5	30
38	Evidence for a cytoplasmic pool of ribosome-free mRNAs encoding inner membrane proteins in <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2017, 12, e0183862.	2.5	12
39	Term-seq reveals abundant ribo-regulation of antibiotics resistance in bacteria. <i>Science</i> , 2016, 352, aad9822.	12.6	294
40	Comparative transcriptomics across the prokaryotic tree of life. <i>Nucleic Acids Research</i> , 2016, 44, W46-W53.	14.5	35
41	Repeat Size Determination by Two Molecular Rulers in the Type I-E CRISPR Array. <i>Cell Reports</i> , 2016, 16, 2811-2818.	6.4	27
42	CRISPR-Cas: Spacer Diversity Determines the Efficiency of Defense. <i>Current Biology</i> , 2016, 26, R683-R685.	3.9	1
43	Widespread formation of alternative 3' UTR isoforms via transcription termination in archaea. <i>Nature Microbiology</i> , 2016, 1, 16143.	13.3	58
44	Natural selection underlies apparent stress-induced mutagenesis in a bacteriophage infection model. <i>Nature Microbiology</i> , 2016, 1, 16047.	13.3	7
45	CRISPR-Cas adaptation: insights into the mechanism of action. <i>Nature Reviews Microbiology</i> , 2016, 14, 67-76.	28.6	324
46	Transcriptome dynamics of a broad host-range cyanophage and its hosts. <i>ISME Journal</i> , 2016, 10, 1437-1455.	9.8	84
47	Growth dynamics of gut microbiota in health and disease inferred from single metagenomic samples. <i>Science</i> , 2015, 349, 1101-1106.	12.6	382
48	CRISPR adaptation biases explain preference for acquisition of foreign DNA. <i>Nature</i> , 2015, 520, 505-510.	27.8	346
49	<scp>BREX</scp> is a novel phage resistance system widespread in microbial genomes. <i>EMBO Journal</i> , 2015, 34, 169-183.	7.8	395
50	Sequestration of a two-component response regulator by a riboswitch-regulated noncoding RNA. <i>Science</i> , 2014, 345, 940-943.	12.6	145
51	High-resolution metagenomics. <i>Nature Biotechnology</i> , 2014, 32, 750-751.	17.5	13
52	The excludon: a new concept in bacterial antisense RNA-mediated gene regulation. <i>Nature Reviews Microbiology</i> , 2013, 11, 75-82.	28.6	152
53	Differential Translation Tunes Uneven Production of Operon-Encoded Proteins. <i>Cell Reports</i> , 2013, 4, 938-944.	6.4	64
54	Holding a grudge. <i>RNA Biology</i> , 2013, 10, 900-906.	3.1	12

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55	Discovery of Functional Toxin/Antitoxin Systems in Bacteria by Shotgun Cloning. <i>Molecular Cell</i> , 2013, 50, 136-148.	9.7	125
56	CRISPR-Mediated Adaptive Immune Systems in Bacteria and Archaea. <i>Annual Review of Biochemistry</i> , 2013, 82, 237-266.	11.1	557
57	Transcriptome-Wide Mapping of 5-methylcytidine RNA Modifications in Bacteria, Archaea, and Yeast Reveals m5C within Archaeal mRNAs. <i>PLoS Genetics</i> , 2013, 9, e1003602.	3.5	274
58	Computational evaluation of cellular metabolic costs successfully predicts genes whose expression is deleterious. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19166-19171.	7.1	21
59	A Global Transcriptional Switch between the Attack and Growth Forms of <i>Bdellovibrio bacteriovorus</i> . <i>PLoS ONE</i> , 2013, 8, e61850.	2.5	76
60	The Single-Nucleotide Resolution Transcriptome of <i>Pseudomonas aeruginosa</i> Grown in Body Temperature. <i>PLoS Pathogens</i> , 2012, 8, e1002945.	4.7	240
61	RNA-seq analysis of small RNPs in <i>Trypanosoma brucei</i> reveals a rich repertoire of non-coding RNAs. <i>Nucleic Acids Research</i> , 2012, 40, 1282-1298.	14.5	32
62	PanDaTox. <i>Bioengineered</i> , 2012, 3, 218-221.	3.2	8
63	A vast collection of microbial genes that are toxic to bacteria. <i>Genome Research</i> , 2012, 22, 802-809.	5.5	71
64	Transcriptome-wide discovery of circular RNAs in Archaea. <i>Nucleic Acids Research</i> , 2012, 40, 3131-3142.	14.5	482
65	Comparative transcriptomics of pathogenic and non-pathogenic <i>Listeria</i> species. <i>Molecular Systems Biology</i> , 2012, 8, 583.	7.2	269
66	CRISPR targeting reveals a reservoir of common phages associated with the human gut microbiome. <i>Genome Research</i> , 2012, 22, 1985-1994.	5.5	185
67	Bacterial genomes: from regulatory complexity to engineering. <i>Current Opinion in Microbiology</i> , 2011, 14, 577-578.	5.1	3
68	Genomic island variability facilitates <i>Prochlorococcus</i> –virus coexistence. <i>Nature</i> , 2011, 474, 604-608.	27.8	267
69	The phage–host arms race: Shaping the evolution of microbes. <i>BioEssays</i> , 2011, 33, 43-51.	2.5	414
70	Self-targeting by CRISPR: gene regulation or autoimmunity?. <i>Trends in Genetics</i> , 2010, 26, 335-340.	6.7	353
71	Validation of two ribosomal RNA removal methods for microbial metatranscriptomics. <i>Nature Methods</i> , 2010, 7, 807-812.	19.0	184
72	Prokaryotic transcriptomics: a new view on regulation, physiology and pathogenicity. <i>Nature Reviews Genetics</i> , 2010, 11, 9-16.	16.3	397

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73	A single-base resolution map of an archaeal transcriptome. <i>Genome Research</i> , 2010, 20, 133-141.	5.5	348
74	Mutation Detection with Next-Generation Resequencing through a Mediator Genome. <i>PLoS ONE</i> , 2010, 5, e15628.	2.5	45
75	Ribosomal protein genes form a barrier to horizontal gene transfer. <i>FASEB Journal</i> , 2009, 23, LB206.	0.5	0
76	CRISPR – a widespread system that provides acquired resistance against phages in bacteria and archaea. <i>Nature Reviews Microbiology</i> , 2008, 6, 181-186.	28.6	789
77	Evolutionary conservation of sequence and secondary structures in CRISPR repeats. <i>Genome Biology</i> , 2007, 8, R61.	9.6	382
78	Genome-Wide Experimental Determination of Barriers to Horizontal Gene Transfer. <i>Science</i> , 2007, 318, 1449-1452.	12.6	383
79	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. <i>Nature</i> , 2007, 450, 560-565.	27.8	1,181
80	In search of antisense. <i>Trends in Biochemical Sciences</i> , 2004, 29, 88-94.	7.5	277
81	Widespread occurrence of antisense transcription in the human genome. <i>Nature Biotechnology</i> , 2003, 21, 379-386.	17.5	607