Rotem Sorek

List of Publications by Year
in descending order

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81 papers	15,424 citations	41323 49 h-index	62565 80 g-index
94 all docs	94 docs citations	94 times ranked	15551 citing authors

#	Article	IF	Citations
1	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. Nature, 2007, 450, 560-565.	13.7	1,181
2	CRISPR â€" a widespread system that provides acquired resistance against phages in bacteria and archaea. Nature Reviews Microbiology, 2008, 6, 181-186.	13.6	789
3	Systematic discovery of antiphage defense systems in the microbial pangenome. Science, 2018, 359, .	6.0	776
4	Widespread occurrence of antisense transcription in the human genome. Nature Biotechnology, 2003, 21, 379-386.	9.4	607
5	CRISPR-Mediated Adaptive Immune Systems in Bacteria and Archaea. Annual Review of Biochemistry, 2013, 82, 237-266.	5.0	557
6	Transcriptome-wide discovery of circular RNAs in Archaea. Nucleic Acids Research, 2012, 40, 3131-3142.	6.5	482
7	Communication between viruses guides lysisâ€"lysogeny decisions. Nature, 2017, 541, 488-493.	13.7	465
8	The phageâ€host arms race: Shaping the evolution of microbes. BioEssays, 2011, 33, 43-51.	1.2	414
9	Prokaryotic transcriptomics: a new view on regulation, physiology and pathogenicity. Nature Reviews Genetics, 2010, 11, 9-16.	7.7	397
10	<scp>BREX</scp> is a novel phage resistance system widespread in microbial genomes. EMBO Journal, 2015, 34, 169-183.	3.5	395
11	Genome-Wide Experimental Determination of Barriers to Horizontal Gene Transfer. Science, 2007, 318, 1449-1452.	6.0	383
12	Evolutionary conservation of sequence and secondary structures in CRISPR repeats. Genome Biology, 2007, 8, R61.	13.9	382
13	Growth dynamics of gut microbiota in health and disease inferred from single metagenomic samples. Science, 2015, 349, 1101-1106.	6.0	382
14	Cyclic GMPâ€"AMP signalling protects bacteria against viral infection. Nature, 2019, 574, 691-695.	13.7	370
15	The pan-immune system of bacteria: antiviral defence as a community resource. Nature Reviews Microbiology, 2020, 18, 113-119.	13.6	368
16	Self-targeting by CRISPR: gene regulation or autoimmunity?. Trends in Genetics, 2010, 26, 335-340.	2.9	353
17	A single-base resolution map of an archaeal transcriptome. Genome Research, 2010, 20, 133-141.	2.4	348
18	CRISPR adaptation biases explain preference for acquisition of foreign DNA. Nature, 2015, 520, 505-510.	13.7	346

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19	CRISPRâ€“Cas adaptation: insights into the mechanism of action. Nature Reviews Microbiology, 2016, 14, 67-76.	13.6	324
20	Term-seq reveals abundant ribo-regulation of antibiotics resistance in bacteria. Science, 2016, 352, aad9822.	6.0	294
21	In search of antisense. Trends in Biochemical Sciences, 2004, 29, 88-94.	3.7	277
22	Transcriptome-Wide Mapping of 5-methylcytidine RNA Modifications in Bacteria, Archaea, and Yeast Reveals m5C within Archaeal mRNAs. PLoS Genetics, 2013, 9, e1003602.	1.5	274
23	Comparative transcriptomics of pathogenic and nonâ€pathogenic Listeria species. Molecular Systems Biology, 2012, 8, 583.	3.2	269
24	Genomic island variability facilitates Prochlorococcusâ€“virus coexistence. Nature, 2011, 474, 604-608.	13.7	267
25	Abortive Infection: Bacterial Suicide as an Antiviral Immune Strategy. Annual Review of Virology, 2020, 7, 371-384.	3.0	247
26	STING cyclic dinucleotide sensing originated in bacteria. Nature, 2020, 586, 429-433.	13.7	246
27	The Single-Nucleotide Resolution Transcriptome of Pseudomonas aeruginosa Grown in Body Temperature. PLoS Pathogens, 2012, 8, e1002945.	2.1	240
28	DISARM is a widespread bacterial defence system with broad anti-phage activities. Nature Microbiology, 2018, 3, 90-98.	5.9	225
29	Bacterial Retrons Function In Anti-Phage Defense. Cell, 2020, 183, 1551-1561.e12.	13.5	208
30	CRISPR targeting reveals a reservoir of common phages associated with the human gut microbiome. Genome Research, 2012, 22, 1985-1994.	2.4	185
31	Validation of two ribosomal RNA removal methods for microbial metatranscriptomics. Nature Methods, 2010, 7, 807-812.	9.0	184
32	Contemporary Phage Biology: From Classic Models to New Insights. Cell, 2018, 172, 1260-1270.	13.5	176
33	Prokaryotic viperins produce diverse antiviral molecules. Nature, 2021, 589, 120-124.	13.7	172
34	Diversity and classification of cyclic-oligonucleotide-based anti-phage signalling systems. Nature Microbiology, 2020, 5, 1608-1615.	5.9	160
35	Antiviral activity of bacterial TIR domains via immune signalling molecules. Nature, 2021, 600, 116-120.	13.7	159
36	Cyclic CMP and cyclic UMP mediate bacterial immunity against phages. Cell, 2021, 184, 5728-5739.e16.	13.5	156

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37	The excludon: a new concept in bacterial antisense RNA-mediated gene regulation. Nature Reviews Microbiology, 2013, 11, 75-82.	13.6	152
38	Sequestration of a two-component response regulator by a riboswitch-regulated noncoding RNA. Science, 2014, 345, 940-943.	6.0	145
39	Bacterial gasdermins reveal an ancient mechanism of cell death. Science, 2022, 375, 221-225.	6.0	132
40	Discovery of Functional Toxin/Antitoxin Systems in Bacteria by Shotgun Cloning. Molecular Cell, 2013, 50, 136-148.	4.5	125
41	Optimality and sub-optimality in a bacterial growth law. Nature Communications, 2017, 8, 14123.	5.8	102
42	Bacterial origins of human cell-autonomous innate immune mechanisms. Nature Reviews Immunology, 2022, 22, 629-638.	10.6	98
43	High-resolution RNA 3â€²-ends mapping of bacterial Rho-dependent transcripts. Nucleic Acids Research, 2018, 46, 6797-6805.	6.5	88
44	Transcriptome dynamics of a broad host-range cyanophage and its hosts. ISME Journal, 2016, 10, 1437-1455.	4.4	84
45	The DarTG toxin-antitoxin system provides phage defence by ADP-ribosylating viral DNA. Nature Microbiology, 2022, 7, 1028-1040.	5.9	78
46	Widespread Utilization of Peptide Communication in Phages Infecting Soil and Pathogenic Bacteria. Cell Host and Microbe, 2019, 25, 746-755.e5.	5.1	77
47	A Global Transcriptional Switch between the Attack and Growth Forms of Bdellovibrio bacteriovorus. PLoS ONE, 2013, 8, e61850.	1.1	76
48	A vast collection of microbial genes that are toxic to bacteria. Genome Research, 2012, 22, 802-809.	2.4	71
49	Phage anti-CBASS and anti-Pycsar nucleases subvert bacterial immunity. Nature, 2022, 605, 522-526.	13.7	70
50	A genome assembly and the somatic genetic and epigenetic mutation rate in a wild long-lived perennial Populus trichocarpa. Genome Biology, 2020, 21, 259.	3.8	68
51	Differential Translation Tunes Uneven Production of Operon-Encoded Proteins. Cell Reports, 2013, 4, 938-944.	2.9	64
52	Extensive reshaping of bacterial operons by programmed mRNA decay. PLoS Genetics, 2018, 14, e1007354.	1.5	60
53	Effector-mediated membrane disruption controls cell death in CBASS antiphage defense. Molecular Cell, 2021, 81, 5039-5051.e5.	4.5	59
54	Widespread formation of alternative 3â€² UTR isoforms via transcription termination in archaea. Nature Microbiology, 2016, 1, 16143.	5.9	58

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55	Bacteria deplete deoxynucleotides to defend against bacteriophage infection. Nature Microbiology, 2022, 7, 1200-1209.	5.9	58
56	Quantitative species-level ecology of reef fish larvae via metabarcoding. Nature Ecology and Evolution, 2018, 2, 306-316.	3.4	56
57	Bacterial Noncoding RNAs Excised from within Protein-Coding Transcripts. MBio, 2018, 9, .	1.8	46
58	Mutation Detection with Next-Generation Resequencing through a Mediator Genome. PLoS ONE, 2010, 5, e15628.	1.1	45
59	SnapShot: Bacterial immunity. Cell, 2022, 185, 578-578.e1.	13.5	45
60	HflXr, a homolog of a ribosome-splitting factor, mediates antibiotic resistance. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 13359-13364.	3.3	41
61	A rhlI 5â€² UTR-Derived sRNA Regulates RhlR-Dependent Quorum Sensing in Pseudomonas aeruginosa. MBio, 2019, 10, .	1.8	40
62	Vesicles Spread Susceptibility to Phages. Cell, 2017, 168, 13-15.	13.5	39
63	Comparative transcriptomics across the prokaryotic tree of life. Nucleic Acids Research, 2016, 44, W46-W53.	6.5	35
64	Regulation of antibiotic-resistance by non-coding RNAs in bacteria. Current Opinion in Microbiology, 2017, 36, 111-117.	2.3	33
65	RNA-seq analysis of small RNPs in Trypanosoma brucei reveals a rich repertoire of non-coding RNAs. Nucleic Acids Research, 2012, 40, 1282-1298.	6.5	32
66	Computational prediction of regulatory, premature transcription termination in bacteria. Nucleic Acids Research, 2017, 45, 886-893.	6.5	30
67	Repeat Size Determination by Two Molecular Rulers in the Type I-E CRISPR Array. Cell Reports, 2016, 16, 2811-2818.	2.9	27
68	Computational evaluation of cellular metabolic costs successfully predicts genes whose expression is deleterious. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19166-19171.	3.3	21
69	Viruses cooperate to defeat bacteria. Nature, 2018, 559, 482-484.	13.7	15
70	High-resolution metagenomics. Nature Biotechnology, 2014, 32, 750-751.	9.4	13
71	Holding a grudge. RNA Biology, 2013, 10, 900-906.	1.5	12
72	Evidence for a cytoplasmic pool of ribosome-free mRNAs encoding inner membrane proteins in Escherichia coli. PLoS ONE, 2017, 12, e0183862.	1.1	12

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73	Peptide-based quorum sensing systems in Paenibacillus polymyxa. Life Science Alliance, 2020, 3, e202000847.	1.3	11
74	Intracellular signaling in CRISPR-Cas defense. Science, 2017, 357, 550-551.	6.0	10
75	PanDaTox. Bioengineered, 2012, 3, 218-221.	1.4	8
76	Natural selection underlies apparent stress-induced mutagenesis in a bacteriophage infection model. Nature Microbiology, 2016, 1, 16047.	5.9	7
77	Successful Brincidofovir Treatment of Metagenomics-detected Adenovirus Infection in a Severely Ill Signal Transducer and Activator of Transcription-1-deficient Patient. Pediatric Infectious Disease Journal, 2019, 38, 297-299.	1.1	7
78	Bacterial genomes: from regulatory complexity to engineering. Current Opinion in Microbiology, 2011, 14, 577-578.	2.3	3
79	A treasure trove of molecular scissors. Science, 2021, 374, 37-38.	6.0	3
80	CRISPRâ€“Cas: Spacer Diversity Determines the Efficiency of Defense. Current Biology, 2016, 26, R683-R685.	1.8	1
81	Ribosomal protein genes form a barrier to horizontal gene transfer. FASEB Journal, 2009, 23, LB206.	0.2	0