

Peter C Fineran

List of Publications by Year in descending order

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106
papers

9,388
citations

47006

47
h-index

45317

90
g-index

120
all docs

120
docs citations

120
times ranked

7858
citing authors

#	ARTICLE	IF	CITATIONS
1	CRISPR-Cas systems are widespread accessory elements across bacterial and archaeal plasmids. <i>Nucleic Acids Research</i> , 2022, 50, 4315-4328.	14.5	44
2	High viral abundance and low diversity are associated with increased CRISPR-Cas prevalence across microbial ecosystems. <i>Current Biology</i> , 2022, 32, 220-227.e5.	3.9	23
3	A mobile restriction modification system provides phage defence and resolves an epigenetic conflict with an antagonistic endonuclease. <i>Nucleic Acids Research</i> , 2022, 50, 3348-3361.	14.5	17
4	Type I CRISPR-Cas provides robust immunity but incomplete attenuation of phage-induced cellular stress. <i>Nucleic Acids Research</i> , 2022, 50, 160-174.	14.5	12
5	PADLOC: a web server for the identification of antiviral defence systems in microbial genomes. <i>Nucleic Acids Research</i> , 2022, 50, W541-W550.	14.5	47
6	Structural rearrangements allow nucleic acid discrimination by type I-D Cascade. <i>Nature Communications</i> , 2022, 13, .	12.8	17
7	Turning down the (C)BASS: Phage-encoded inhibitors jam bacterial immune signaling. <i>Molecular Cell</i> , 2022, 82, 2185-2187.	9.7	4
8	Conquering CRISPR: how phages overcome bacterial adaptive immunity. <i>Current Opinion in Biotechnology</i> , 2021, 68, 30-36.	6.6	47
9	Identification and classification of antiviral defence systems in bacteria and archaea with PADLOC reveals new system types. <i>Nucleic Acids Research</i> , 2021, 49, 10868-10878.	14.5	92
10	Evolution of virulence in a novel family of transmissible mega-plasmids. <i>Environmental Microbiology</i> , 2021, 23, 5289-5304.	3.8	5
11	SorTn-seq: a high-throughput functional genomics approach to discovering regulators of bacterial gene expression. <i>Nature Protocols</i> , 2021, 16, 4382-4418.	12.0	7
12	The Rsm (Csr) post-transcriptional regulatory pathway coordinately controls multiple CRISPR-Cas immune systems. <i>Nucleic Acids Research</i> , 2021, 49, 9508-9525.	14.5	9
13	Crystal structure of the anti-CRISPR repressor Aca2. <i>Journal of Structural Biology</i> , 2021, 213, 107752.	2.8	6
14	The Rcs stress response inversely controls surface and CRISPR-Cas adaptive immunity to discriminate plasmids and phages. <i>Nature Microbiology</i> , 2021, 6, 162-172.	13.3	32
15	Bacterial defense islands limit viral attack. <i>Science</i> , 2021, 374, 399-400.	12.6	3
16	A jumbo phage that forms a nucleus-like structure evades CRISPR-Cas DNA targeting but is vulnerable to type III RNA-based immunity. <i>Nature Microbiology</i> , 2020, 5, 48-55.	13.3	123
17	Variation at the common polysaccharide antigen locus drives lipopolysaccharide diversity within the <i>Pseudomonas syringae</i> species complex. <i>Environmental Microbiology</i> , 2020, 22, 5356-5372.	3.8	15
18	Diverse CRISPR-Cas Complexes Require Independent Translation of Small and Large Subunits from a Single Gene. <i>Molecular Cell</i> , 2020, 80, 971-979.e7.	9.7	27

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19	A nucleotidyltransferase toxin inhibits growth of <i>Mycobacterium tuberculosis</i> through inactivation of tRNA acceptor stems. <i>Science Advances</i> , 2020, 6, eabb6651.	10.3	30
20	Discovery of multiple anti-CRISPRs highlights anti-defense gene clustering in mobile genetic elements. <i>Nature Communications</i> , 2020, 11, 5652.	12.8	88
21	The arms race between bacteria and their phage foes. <i>Nature</i> , 2020, 577, 327-336.	27.8	514
22	Targeting of temperate phages drives loss of type I CRISPR-Cas systems. <i>Nature</i> , 2020, 578, 149-153.	27.8	71
23	Antitoxin autoregulation of <i>M. tuberculosis</i> toxin-antitoxin expression through negative cooperativity arising from multiple inverted repeat sequences. <i>Biochemical Journal</i> , 2020, 477, 2401-2419.	3.7	9
24	Functional genomics reveals the toxin-antitoxin repertoire and AbiE activity in <i>Serratia</i> . <i>Microbial Genomics</i> , 2020, 6, .	2.0	7
25	Complete Genome Sequences of the <i>Escherichia coli</i> Donor Strains ST18 and MFD pir. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	7
26	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	13.3	184
27	Expanding the mass range for LVPD-based native top-down mass spectrometry. <i>Chemical Science</i> , 2019, 10, 7163-7171.	7.4	29
28	The autoregulator Aca2 mediates anti-CRISPR repression. <i>Nucleic Acids Research</i> , 2019, 47, 9658-9665.	14.5	49
29	Bacterial dormancy curbs phage epidemics. <i>Nature</i> , 2019, 570, 173-174.	27.8	12
30	Galk limits type I-F CRISPR-Cas expression in a CRP-dependent manner. <i>FEMS Microbiology Letters</i> , 2019, 366, .	1.8	7
31	Genome Sequence of a Jumbo Bacteriophage That Infects the Kiwifruit Phytopathogen <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	14
32	Genome-wide correlation analysis suggests different roles of CRISPR-Cas systems in the acquisition of antibiotic resistance genes in diverse species. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180384.	4.0	46
33	Different genetic and morphological outcomes for phages targeted by single or multiple CRISPR-Cas spacers. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180090.	4.0	24
34	Type I-F CRISPR-Cas resistance against virulent phages results in abortive infection and provides population-level immunity. <i>Nature Communications</i> , 2019, 10, 5526.	12.8	44
35	Bioinformatic evidence of widespread priming in type I and II CRISPR-Cas systems. <i>RNA Biology</i> , 2019, 16, 566-576.	3.1	45
36	Imprecise Spacer Acquisition Generates CRISPR-Cas Immune Diversity through Primed Adaptation. <i>Cell Host and Microbe</i> , 2019, 25, 250-260.e4.	11.0	54

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37	Reconstitution of CRISPR adaptation in vitro and its detection by PCR. <i>Methods in Enzymology</i> , 2019, 616, 411-433.	1.0	1
38	CRISPR-Cas impedes archaeal mating. <i>Nature Microbiology</i> , 2019, 4, 2-3.	13.3	1
39	Resistance is not futile: bacterial innate and CRISPR-Cas adaptive immune systems. <i>Microbiology (United Kingdom)</i> , 2019, 165, 834-841.	1.8	6
40	AbiEi Binds Cooperatively to the Type IV abiE Toxin-Antitoxin Operator Via a Positively-Charged Surface and Causes DNA Bending and Negative Autoregulation. <i>Journal of Molecular Biology</i> , 2018, 430, 1141-1156.	4.2	20
41	CRISPR-Cas-Mediated Phage Resistance Enhances Horizontal Gene Transfer by Transduction. <i>MBio</i> , 2018, 9, .	4.1	103
42	Phage-based biocontrol strategies and their application in agriculture and aquaculture. <i>Biochemical Society Transactions</i> , 2018, 46, 1605-1613.	3.4	59
43	A Unified Resource for Tracking Anti-CRISPR Names. <i>CRISPR Journal</i> , 2018, 1, 304-305.	2.9	94
44	Evolution of Pectobacterium Bacteriophage ϕ M1 To Escape Two Bifunctional Type III Toxin-Antitoxin and Abortive Infection Systems through Mutations in a Single Viral Gene. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	47
45	Spacer capture and integration by a type I-F Cas1-Cas2-3 CRISPR adaptation complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5122-E5128.	7.1	89
46	CRISPR-Cas: Adapting to change. <i>Science</i> , 2017, 356, .	12.6	323
47	Regulation of CRISPR-Cas adaptive immune systems. <i>Current Opinion in Microbiology</i> , 2017, 37, 1-7.	5.1	68
48	Type III CRISPR-Cas systems can provide redundancy to counteract viral escape from type I systems. <i>ELife</i> , 2017, 6, .	6.0	81
49	Transposon insertion libraries for the characterization of mutants from the kiwifruit pathogen <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> . <i>PLoS ONE</i> , 2017, 12, e0172790.	2.5	26
50	<i>Pectobacterium atrosepticum</i> and <i>Pectobacterium carotovorum</i> Harbor Distinct, Independently Acquired Integrative and Conjugative Elements Encoding Coronafacic Acid that Enhance Virulence on Potato Stems. <i>Frontiers in Microbiology</i> , 2016, 7, 397.	3.5	22
51	Structural plasticity and in vivo activity of Cas1 from the type I-F CRISPR-Cas system. <i>Biochemical Journal</i> , 2016, 473, 1063-1072.	3.7	8
52	CRISPRDetect: A flexible algorithm to define CRISPR arrays. <i>BMC Genomics</i> , 2016, 17, 356.	2.8	277
53	Inactivation of CRISPR-Cas systems by anti-CRISPR proteins in diverse bacterial species. <i>Nature Microbiology</i> , 2016, 1, 16085.	13.3	271
54	Quorum Sensing Controls Adaptive Immunity through the Regulation of Multiple CRISPR-Cas Systems. <i>Molecular Cell</i> , 2016, 64, 1102-1108.	9.7	183

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55	Interference-driven spacer acquisition is dominant over naive and primed adaptation in a native CRISPR-Cas system. <i>Nature Communications</i> , 2016, 7, 12853.	12.8	125
56	CRISPR-Cas gene-editing reveals RsmA and RsmC act through FlhDC to repress the SdhE flavinylation factor and control motility and prodigiosin production in <i>Serratia</i> . <i>Microbiology (United Kingdom)</i> , 2016, 162, 1047-1058.	1.8	38
57	The Cpf1 CRISPR-Cas protein expands genome-editing tools. <i>Genome Biology</i> , 2015, 16, 251.	8.8	91
58	Genome, Proteome and Structure of a T7-Like Bacteriophage of the Kiwifruit Canker Phytopathogen <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> . <i>Viruses</i> , 2015, 7, 3361-3379.	3.3	26
59	Phage ϕ Pan70, a Putative Temperate Phage, Controls <i>Pseudomonas aeruginosa</i> in Planktonic, Biofilm and Burn Mouse Model Assays. <i>Viruses</i> , 2015, 7, 4602-4623.	3.3	42
60	Regulation of the Type I-F CRISPR-Cas system by CRP-cAMP and GalM controls spacer acquisition and interference. <i>Nucleic Acids Research</i> , 2015, 43, 6038-6048.	14.5	59
61	Complete DNA Sequence of <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> , the Causal Agent of Kiwifruit Canker Disease. <i>Genome Announcements</i> , 2015, 3, .	0.8	36
62	Computational Detection of CRISPR/crRNA Targets. <i>Methods in Molecular Biology</i> , 2015, 1311, 77-89.	0.9	7
63	A century of the phage: past, present and future. <i>Nature Reviews Microbiology</i> , 2015, 13, 777-786.	28.6	537
64	Accurate computational prediction of the transcribed strand of CRISPR non-coding RNAs. <i>Bioinformatics</i> , 2014, 30, 1805-1813.	4.1	33
65	A widespread bacteriophage abortive infection system functions through a Type IV toxin-antitoxin mechanism. <i>Nucleic Acids Research</i> , 2014, 42, 4590-4605.	14.5	228
66	Priming in the Type I-F CRISPR-Cas system triggers strand-independent spacer acquisition, bi-directionally from the primed protospacer. <i>Nucleic Acids Research</i> , 2014, 42, 8516-8526.	14.5	171
67	CRISPR-Cas systems: beyond adaptive immunity. <i>Nature Reviews Microbiology</i> , 2014, 12, 317-326.	28.6	263
68	Identification of Bacteriophages for Biocontrol of the Kiwifruit Canker Phytopathogen <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 2216-2228.	3.1	101
69	Gene regulation by engineered CRISPR-Cas systems. <i>Current Opinion in Microbiology</i> , 2014, 18, 83-89.	5.1	29
70	The succinate dehydrogenase assembly factor, SdhE, is required for the flavinylation and activation of fumarate reductase in bacteria. <i>FEBS Letters</i> , 2014, 588, 414-421.	2.8	32
71	Remarkable Mechanisms in Microbes to Resist Phage Infections. <i>Annual Review of Virology</i> , 2014, 1, 307-331.	6.7	226
72	Degenerate target sites mediate rapid primed CRISPR adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1629-38.	7.1	239

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73	Novel configurations of type I and II CRISPR-Cas systems in <i>Corynebacterium diphtheriae</i> . <i>Microbiology (United Kingdom)</i> , 2013, 159, 2118-2126.	1.8	31
74	Ribonucleases in bacterial toxin-antitoxin systems. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 523-531.	1.9	77
75	Selectivity and self-assembly in the control of a bacterial toxin by an antitoxic noncoding RNA pseudoknot. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E241-9.	7.1	57
76	Prokaryotic assembly factors for the attachment of flavin to complex II. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2013, 1827, 637-647.	1.0	21
77	CRISPR-Cas systems preferentially target the leading regions of MOB _F conjugative plasmids. <i>RNA Biology</i> , 2013, 10, 749-761.	3.1	32
78	The Conserved RGxxE Motif of the Bacterial FAD Assembly Factor SdhE Is Required for Succinate Dehydrogenase Flavinylation and Activity. <i>Biochemistry</i> , 2013, 52, 7628-7640.	2.5	21
79	Draft Genome Sequence of <i>Serratia</i> sp. Strain ATCC 39006, a Model Bacterium for Analysis of the Biosynthesis and Regulation of Prodigiosin, a Carbapenem, and Gas Vesicles. <i>Genome Announcements</i> , 2013, 1, .	0.8	19
80	The subtype F CRISPR-Cas system influences pathogenicity island retention in <i>Pectobacterium atrosepticum</i> via crRNA generation and Csy complex formation. <i>Biochemical Society Transactions</i> , 2013, 41, 1468-1474.	3.4	23
81	Cytotoxic Chromosomal Targeting by CRISPR/Cas Systems Can Reshape Bacterial Genomes and Expel or Remodel Pathogenicity Islands. <i>PLoS Genetics</i> , 2013, 9, e1003454.	3.5	297
82	YgfX (CptA) is a multimeric membrane protein that interacts with the succinate dehydrogenase assembly factor SdhE (YgfY). <i>Microbiology (United Kingdom)</i> , 2013, 159, 1352-1365.	1.8	8
83	Chromosomal targeting by CRISPR-Cas systems can contribute to genome plasticity in bacteria. <i>Mobile Genetic Elements</i> , 2013, 3, e26831.	1.8	20
84	CRISPRTarget. <i>RNA Biology</i> , 2013, 10, 817-827.	3.1	272
85	Viral Evasion of a Bacterial Suicide System by RNA-Based Molecular Mimicry Enables Infectious Altruism. <i>PLoS Genetics</i> , 2012, 8, e1003023.	3.5	108
86	Function and Regulation of Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) / CRISPR Associated (Cas) Systems. <i>Viruses</i> , 2012, 4, 2291-2311.	3.3	119
87	Viral molecular mimicry circumvents abortive infection and suppresses bacterial suicide to make hosts permissive for replication. <i>Bacteriophage</i> , 2012, 2, e23830.	1.9	9
88	SdhE Is a Conserved Protein Required for Flavinylation of Succinate Dehydrogenase in Bacteria. <i>Journal of Biological Chemistry</i> , 2012, 287, 18418-18428.	3.4	58
89	Identification and classification of bacterial Type III toxin-antitoxin systems encoded in chromosomal and plasmid genomes. <i>Nucleic Acids Research</i> , 2012, 40, 6158-6173.	14.5	129
90	Advances in Bacteriophage-Mediated Control of Plant Pathogens. <i>International Journal of Microbiology</i> , 2012, 2012, 1-11.	2.3	132

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91	Memory of viral infections by CRISPR-Cas adaptive immune systems: Acquisition of new information. <i>Virology</i> , 2012, 434, 202-209.	2.4	188
92	In Vivo Protein Interactions and Complex Formation in the <i>Pectobacterium atrosepticum</i> Subtype I-F CRISPR/Cas System. <i>PLoS ONE</i> , 2012, 7, e49549.	2.5	69
93	Csy4 is responsible for CRISPR RNA processing in <i>Pectobacterium atrosepticum</i> . <i>RNA Biology</i> , 2011, 8, 517-528.	3.1	101
94	A processed noncoding RNA regulates an altruistic bacterial antiviral system. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 185-190.	8.2	115
95	PigS and PigP Regulate Prodigiosin Biosynthesis in <i>Serratia</i> via Differential Control of Divergent Operons, Which Include Predicted Transporters of Sulfur-Containing Molecules. <i>Journal of Bacteriology</i> , 2011, 193, 1076-1085.	2.2	54
96	Mutagenesis and Functional Characterization of the RNA and Protein Components of the <i>toxIN</i> Abortive Infection and Toxin-Antitoxin Locus of <i>Erwinia</i> . <i>Journal of Bacteriology</i> , 2009, 191, 6029-6039.	2.2	73
97	The PhoBR two-component system regulates antibiotic biosynthesis in <i>Serratia</i> in response to phosphate. <i>BMC Microbiology</i> , 2009, 9, 112.	3.3	38
98	The phage abortive infection system, ToxIN, functions as a protein-RNA toxin-antitoxin pair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 894-899.	7.1	445
99	Integrated regulation involving quorum sensing, a two-component system, a GGDEF/EAL domain protein and a post-transcriptional regulator controls swarming and RhlA-dependent surfactant biosynthesis in <i>Serratia</i> . <i>Environmental Microbiology</i> , 2008, 10, 1202-1217.	3.8	65
100	PigZ, a TetR/AcrR family repressor, modulates secondary metabolism via the expression of a putative four-component resistance-modulation-cell division efflux pump, ZrpADBC, in <i>Serratia</i> sp. ATCC 39006. <i>Molecular Microbiology</i> , 2008, 69, 418-435.	2.5	36
101	Virulence and Prodigiosin Antibiotic Biosynthesis in <i>Serratia</i> Are Regulated Pleiotropically by the GGDEF/EAL Domain Protein, PigX. <i>Journal of Bacteriology</i> , 2007, 189, 7653-7662.	2.2	64
102	Anticancer and immunosuppressive properties of bacterial prodiginines. <i>Future Microbiology</i> , 2007, 2, 605-618.	2.0	175
103	Biotechnological exploitation of bacteriophage research. <i>Trends in Biotechnology</i> , 2007, 25, 7-15.	9.3	141
104	The biosynthesis and regulation of bacterial prodiginines. <i>Nature Reviews Microbiology</i> , 2006, 4, 887-899.	28.6	425
105	Biosynthesis of tripyrrole and β -lactam secondary metabolites in <i>Serratia</i> : integration of quorum sensing with multiple new regulatory components in the control of prodigiosin and carbapenem antibiotic production. <i>Molecular Microbiology</i> , 2005, 56, 1495-1517.	2.5	125
106	A GntR family transcriptional regulator (PigT) controls gluconate-mediated repression and defines a new, independent pathway for regulation of the tripyrrole antibiotic, prodigiosin, in <i>Serratia</i> . <i>Microbiology (United Kingdom)</i> , 2005, 151, 3833-3845.	1.8	77