

Karen L Maxwell

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

68

papers

4,588

citations

36

h-index

67

g-index

74

ext. papers

5,682

ext. citations

14.4

avg, IF

5.92

L-index

#	Paper	IF	Citations
68	Bacteriophage genes that inactivate the CRISPR/Cas bacterial immune system. <i>Nature</i> , 2013 , 493, 429-32	50.4	495
67	Naturally Occurring Off-Switches for CRISPR-Cas9. <i>Cell</i> , 2016 , 167, 1829-1838.e9	56.2	260
66	Structural proteomics of an archaeon. <i>Nature Structural Biology</i> , 2000 , 7, 903-9		247
65	Multiple mechanisms for CRISPR-Cas inhibition by anti-CRISPR proteins. <i>Nature</i> , 2015 , 526, 136-9	50.4	225
64	Inactivation of CRISPR-Cas systems by anti-CRISPR proteins in diverse bacterial species. <i>Nature Microbiology</i> , 2016 , 1, 16085	26.6	203
63	Anti-CRISPR: discovery, mechanism and function. <i>Nature Reviews Microbiology</i> , 2018 , 16, 12-17	22.2	200
62	Protein folding: defining a "standard" set of experimental conditions and a preliminary kinetic data set of two-state proteins. <i>Protein Science</i> , 2005 , 14, 602-16	6.3	181
61	A new group of phage anti-CRISPR genes inhibits the type I-E CRISPR-Cas system of <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2014 , 5, e00896	7.8	180
60	Prophages mediate defense against phage infection through diverse mechanisms. <i>ISME Journal</i> , 2016 , 10, 2854-2866	11.9	176
59	A Broad-Spectrum Inhibitor of CRISPR-Cas9. <i>Cell</i> , 2017 , 170, 1224-1233.e15	56.2	145
58	A simple in vivo assay for increased protein solubility. <i>Protein Science</i> , 1999 , 8, 1908-11	6.3	140
57	Ig-like domains on bacteriophages: a tale of promiscuity and deceit. <i>Journal of Molecular Biology</i> , 2006 , 359, 496-507	6.5	136
56	Structure Reveals Mechanisms of Viral Suppressors that Intercept a CRISPR RNA-Guided Surveillance Complex. <i>Cell</i> , 2017 , 169, 47-57.e11	56.2	131
55	Viral proteomics. <i>Microbiology and Molecular Biology Reviews</i> , 2007 , 71, 398-411	13.2	103
54	Mutagenesis of a buried polar interaction in an SH3 domain: sequence conservation provides the best prediction of stability effects. <i>Biochemistry</i> , 1998 , 37, 16172-82	3.2	85
53	Long noncontractile tail machines of bacteriophages. <i>Advances in Experimental Medicine and Biology</i> , 2012 , 726, 115-42	3.6	78
52	Viral Proteomics. <i>Microbiology and Molecular Biology Reviews</i> , 2007 , 71, 549-549	13.2	78

51	A chemical defence against phage infection. <i>Nature</i> , 2018 , 564, 283-286	50.4	78
50	Phage-Encoded Anti-CRISPR Defenses. <i>Annual Review of Genetics</i> , 2018 , 52, 445-464	14.5	77
49	The bacteriophage HK97 gp15 moron element encodes a novel superinfection exclusion protein. <i>Journal of Bacteriology</i> , 2012 , 194, 5012-9	3.5	71
48	Protein folding kinetics beyond the phi value: using multiple amino acid substitutions to investigate the structure of the SH3 domain folding transition state. <i>Journal of Molecular Biology</i> , 2002 , 320, 389-402	6.5	71
47	Immunoglobulin-like domains on bacteriophage: weapons of modest damage?. <i>Current Opinion in Microbiology</i> , 2007 , 10, 382-7	7.9	69
46	HNH proteins are a widespread component of phage DNA packaging machines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 6022-7	11.5	59
45	The phage tail tape measure protein, an inner membrane protein and a periplasmic chaperone play connected roles in the genome injection process of E. coli phage HK97. <i>Molecular Microbiology</i> , 2015 , 96, 437-47	4.1	58
44	The Diverse Impacts of Phage Morons on Bacterial Fitness and Virulence. <i>Advances in Virus Research</i> , 2019 , 103, 1-31	10.7	55
43	Meet the Anti-CRISPRs: Widespread Protein Inhibitors of CRISPR-Cas Systems. <i>CRISPR Journal</i> , 2019 , 2, 23-30	2.5	53
42	Potent Cas9 Inhibition in Bacterial and Human Cells by AcrIIc4 and AcrIIc5 Anti-CRISPR Proteins. <i>MBio</i> , 2018 , 9,	7.8	51
41	The Anti-CRISPR Story: A Battle for Survival. <i>Molecular Cell</i> , 2017 , 68, 8-14	17.6	50
40	A Unified Resource for Tracking Anti-CRISPR Names. <i>CRISPR Journal</i> , 2018 , 1, 304-305	2.5	50
39	The crystal structure of bacteriophage HK97 gp6: defining a large family of head-tail connector proteins. <i>Journal of Molecular Biology</i> , 2010 , 395, 754-68	6.5	49
38	Disabling a Type I-E CRISPR-Cas Nuclease with a Bacteriophage-Encoded Anti-CRISPR Protein. <i>MBio</i> , 2017 , 8,	7.8	42
37	The solution structure of an anti-CRISPR protein. <i>Nature Communications</i> , 2016 , 7, 13134	17.4	41
36	The solution structure of the C-terminal Ig-like domain of the bacteriophage tail tube protein. <i>Journal of Molecular Biology</i> , 2010 , 403, 468-79	6.5	39
35	The moron comes of age. <i>Bacteriophage</i> , 2012 , 2, 225-228		39
34	Phages Fight Back: Inactivation of the CRISPR-Cas Bacterial Immune System by Anti-CRISPR Proteins. <i>PLoS Pathogens</i> , 2016 , 12, e1005282	7.6	39

33	Refolding out of guanidine hydrochloride is an effective approach for high-throughput structural studies of small proteins. <i>Protein Science</i> , 2003 , 12, 2073-80	6.3	37
32	The solution structure of bacteriophage lambda protein W, a small morphogenetic protein possessing a novel fold. <i>Journal of Molecular Biology</i> , 2001 , 308, 9-14	6.5	36
31	Crystal structure of bacteriophage lambda cII and its DNA complex. <i>Molecular Cell</i> , 2005 , 19, 259-69	17.6	34
30	The solution structure of the bacteriophage lambda head-tail joining protein, gpII. <i>Journal of Molecular Biology</i> , 2002 , 318, 1395-404	6.5	31
29	Inhibition of CRISPR-Cas9 ribonucleoprotein complex assembly by anti-CRISPR AcrIIC2. <i>Nature Communications</i> , 2019 , 10, 2806	17.4	30
28	Efficacy of bacteriophage treatment on <i>Pseudomonas aeruginosa</i> biofilms. <i>Journal of Endodontics</i> , 2013 , 39, 364-9	4.7	30
27	A phage-encoded anti-activator inhibits quorum sensing in <i>Pseudomonas aeruginosa</i> . <i>Molecular Cell</i> , 2021 , 81, 571-583.e6	17.6	30
26	Baseplate assembly of phage Mu: Defining the conserved core components of contractile-tailed phages and related bacterial systems. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 10174-9	11.5	29
25	Phages have adapted the same protein fold to fulfill multiple functions in virion assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 14384-9	11.5	29
24	Phage Morons Play an Important Role in <i>Pseudomonas aeruginosa</i> Phenotypes. <i>Journal of Bacteriology</i> , 2018 , 200,	3.5	29
23	Rapid detection of <i>E. coli</i> bacteria using potassium-sensitive FETs in CMOS. <i>IEEE Transactions on Biomedical Circuits and Systems</i> , 2013 , 7, 621-30	5.1	27
22	The NMR structure of the gpU tail-terminator protein from bacteriophage lambda: identification of sites contributing to Mg(II)-mediated oligomerization and biological function. <i>Journal of Molecular Biology</i> , 2007 , 365, 175-86	6.5	27
21	The protein gp74 from the bacteriophage HK97 functions as a HNH endonuclease. <i>Protein Science</i> , 2012 , 21, 809-18	6.3	23
20	Anti-CRISPR AcrIIA5 Potently Inhibits All Cas9 Homologs Used for Genome Editing. <i>Cell Reports</i> , 2019 , 29, 1739-1746.e5	10.6	20
19	Tail tip proteins related to bacteriophage λ gpL coordinate an iron-sulfur cluster. <i>Journal of Molecular Biology</i> , 2013 , 425, 2450-62	6.5	17
18	Thermodynamic and functional characterization of protein W from bacteriophage lambda. The three C-terminal residues are critical for activity. <i>Journal of Biological Chemistry</i> , 2000 , 275, 18879-86	5.4	17
17	Structural and functional studies of gpX of <i>Escherichia coli</i> phage P2 reveal a widespread role for LysM domains in the baseplates of contractile-tailed phages. <i>Journal of Bacteriology</i> , 2013 , 195, 5461-8	3.5	14
16	A conserved spiral structure for highly diverged phage tail assembly chaperones. <i>Journal of Molecular Biology</i> , 2013 , 425, 2436-49	6.5	12

15	Assembly mechanism is the key determinant of the dosage sensitivity of a phage structural protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 10168-73	11.5	11
14	Extrachromosomal circular elements targeted by CRISPR-Cas in <i>Dehalococcoides mccartyi</i> are linked to mobilization of reductive dehalogenase genes. <i>ISME Journal</i> , 2019 , 13, 24-38	11.9	10
13	The solution structures of two prophage homologues of the bacteriophage λ Ea8.5 protein reveal a newly discovered hybrid homeodomain/zinc-finger fold. <i>Biochemistry</i> , 2013 , 52, 3612-4	3.2	8
12	Phages Tune in to Host Cell Quorum Sensing. <i>Cell</i> , 2019 , 176, 7-8	56.2	7
11	Structural and biochemical characterization of phage λ FI protein (gpFI) reveals a novel mechanism of DNA packaging chaperone activity. <i>Journal of Biological Chemistry</i> , 2012 , 287, 32085-95	5.4	5
10	A shifty chaperone for phage tail assembly. <i>Journal of Molecular Biology</i> , 2014 , 426, 1001-3	6.5	4
9	Anti-CRISPR AcrIE2 Binds the Type I-E CRISPR-Cas Complex But Does Not Block DNA Binding. <i>Journal of Molecular Biology</i> , 2021 , 433, 166759	6.5	4
8	HK97 gp74 Possesses an α -Helical Insertion in the λ -Fold That Affects Its Metal Binding, Site Digestion, and Activities. <i>Journal of Bacteriology</i> , 2020 , 202,	3.5	3
7	Retrons: Complementing CRISPR in Phage Defense. <i>CRISPR Journal</i> , 2020 , 3, 226-227	2.5	3
6	One Anti-CRISPR to Rule Them All: Potent Inhibition of Cas9 Homologs Used for Genome Editing. <i>SSRN Electronic Journal</i> ,	1	1
5	Potent Cas9 inhibition in bacterial and human cells by new anti-CRISPR protein families		1
4	Type VI secretion system baseplate. <i>Nature Microbiology</i> , 2018 , 3, 1330-1331	26.6	1
3	A Filamentous Bacteriophage Protein Inhibits Type IV Pili To Prevent Superinfection of <i>Pseudomonas aeruginosa</i> .. <i>MBio</i> , 2022 , e0244121	7.8	0
2	Cyclic pyrimidines jump on the anti-phage bandwagon. <i>Cell</i> , 2021 , 184, 5691-5693	56.2	0
1	Structural and mechanistic insight into CRISPR-Cas9 inhibition by anti-CRISPR protein AcrIIC4.. <i>Journal of Molecular Biology</i> , 2021 , 434, 167420	6.5	0