Karen L Maxwell

List of Publications by Year in Descending Order

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	A Filamentous Bacteriophage Protein Inhibits Type IV Pili To Prevent Superinfection of Pseudomonas aeruginosa.. *MBio*, **2022**, e0244121	7.8	0
67	Cyclic pyrimidines jump on the anti-phage bandwagon. *Cell*, **2021**, 184, 5691-5693	56.2	0
66	Structural and mechanistic insight into CRISPR-Cas9 inhibition by anti-CRISPR protein AcrIIC4.. *Journal of Molecular Biology*, **2021**, 434, 167420	6.5	0
65	Anti-CRISPR AcrIE2 Binds the Type I-E CRISPR-Cas Complex But Does Not Block DNA Binding. *Journal of Molecular Biology*, **2021**, 433, 166759	6.5	4
64	A phage-encoded anti-activator inhibits quorum sensing in Pseudomonas aeruginosa. *Molecular Cell* , **2021**, 81, 571-583.e6	17.6	30
63	HK97 gp74 Possesses an Helical Insertion in the Fold That Affects Its Metal Binding, Site Digestion, and Activities. *Journal of Bacteriology*, **2020**, 202,	3.5	3
62	Retrons: Complementing CRISPR in Phage Defense. *CRISPR Journal*, **2020**, 3, 226-227	2.5	3
61	Inhibition of CRISPR-Cas9 ribonucleoprotein complex assembly by anti-CRISPR AcrIIC2. *Nature Communications*, **2019**, 10, 2806	17.4	30
60	Extrachromosomal circular elements targeted by CRISPR-Cas in Dehalococcoides mccartyi are linked to mobilization of reductive dehalogenase genes. *ISME Journal*, **2019**, 13, 24-38	11.9	10
59	Anti-CRISPR AcrIIA5 Potently Inhibits All Cas9 Homologs Used for Genome Editing. *Cell Reports*, **2019**, 29, 1739-1746.e5	10.6	20
58	Meet the Anti-CRISPRs: Widespread Protein Inhibitors of CRISPR-Cas Systems. *CRISPR Journal*, **2019** , 2, 23-30	2.5	53
57	Phages Tune in to Host Cell Quorum Sensing. *Cell*, **2019**, 176, 7-8	56.2	7
56	The Diverse Impacts of Phage Morons on Bacterial Fitness and Virulence. *Advances in Virus Research* , **2019**, 103, 1-31	10.7	55
55	Anti-CRISPR: discovery, mechanism and function. *Nature Reviews Microbiology*, **2018**, 16, 12-17	22.2	200
54	Type VI secretion system baseplate. *Nature Microbiology*, **2018**, 3, 1330-1331	26.6	1
53	Potent Cas9 Inhibition in Bacterial and Human Cells by AcrIIC4 and AcrIIC5 Anti-CRISPR Proteins. *MBio*, **2018**, 9,	7.8	51
52	A chemical defence against phage infection. *Nature*, **2018**, 564, 283-286	50.4	78

51	A Unified Resource for Tracking Anti-CRISPR Names. *CRISPR Journal*, **2018**, 1, 304-305	2.5	50
50	Phage-Encoded Anti-CRISPR Defenses. *Annual Review of Genetics*, **2018**, 52, 445-464	14.5	77
49	Phage Morons Play an Important Role in Pseudomonas aeruginosa Phenotypes. *Journal of Bacteriology*, **2018**, 200,	3.5	29
48	Structure Reveals Mechanisms of Viral Suppressors that Intercept a CRISPR RNA-Guided Surveillance Complex. *Cell*, **2017**, 169, 47-57.e11	56.2	131
47	The Anti-CRISPR Story: A Battle for Survival. *Molecular Cell*, **2017**, 68, 8-14	17.6	50
46	A Broad-Spectrum Inhibitor of CRISPR-Cas9. *Cell*, **2017**, 170, 1224-1233.e15	56.2	145
45	Disabling a Type I-E CRISPR-Cas Nuclease with a Bacteriophage-Encoded Anti-CRISPR Protein. *MBio*, **2017**, 8,	7.8	42
44	Baseplate assembly of phage Mu: Defining the conserved core components of contractile-tailed phages and related bacterial systems. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 10174-9	11.5	29
43	Inactivation of CRISPR-Cas systems by anti-CRISPR proteins in diverse bacterial species. *Nature Microbiology*, **2016**, 1, 16085	26.6	203
42	The solution structure of an anti-CRISPR protein. *Nature Communications*, **2016**, 7, 13134	17.4	41
41	Prophages mediate defense against phage infection through diverse mechanisms. *ISME Journal*, **2016**, 10, 2854-2866	11.9	176
40	Phages Fight Back: Inactivation of the CRISPR-Cas Bacterial Immune System by Anti-CRISPR Proteins. *PLoS Pathogens*, **2016**, 12, e1005282	7.6	39
39	Naturally Occurring Off-Switches for CRISPR-Cas9. *Cell*, **2016**, 167, 1829-1838.e9	56.2	260
38	Multiple mechanisms for CRISPR-Cas inhibition by anti-CRISPR proteins. *Nature*, **2015**, 526, 136-9	50.4	225
37	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. *Molecular Microbiology*, **2015**, 96, 437-47	4.1	58
36	A new group of phage anti-CRISPR genes inhibits the type I-E CRISPR-Cas system of Pseudomonas aeruginosa. *MBio*, **2014**, 5, e00896	7.8	180
35	HNH proteins are a widespread component of phage DNA packaging machines. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 6022-7	11.5	59
34	A shifty chaperone for phage tail assembly. *Journal of Molecular Biology*, **2014**, 426, 1001-3	6.5	4

33	Efficacy of bacteriophage treatment on Pseudomonas aeruginosa biofilms. *Journal of Endodontics*, **2013**, 39, 364-9	4.7	30
32	Rapid detection of E. coli bacteria using potassium-sensitive FETs in CMOS. *IEEE Transactions on Biomedical Circuits and Systems*, **2013**, 7, 621-30	5.1	27
31	Bacteriophage genes that inactivate the CRISPR/Cas bacterial immune system. *Nature*, **2013**, 493, 429-32	50.4	495
30	A conserved spiral structure for highly diverged phage tail assembly chaperones. *Journal of Molecular Biology*, **2013**, 425, 2436-49	6.5	12
29	Tail tip proteins related to bacteriophage λgpL coordinate an iron-sulfur cluster. *Journal of Molecular Biology*, **2013**, 425, 2450-62	6.5	17
28	The solution structures of two prophage homologues of the bacteriophage λEa8.5 protein reveal a newly discovered hybrid homeodomain/zinc-finger fold. *Biochemistry*, **2013**, 52, 3612-4	3.2	8
27	Structural and functional studies of gpX of Escherichia coli phage P2 reveal a widespread role for LysM domains in the baseplates of contractile-tailed phages. *Journal of Bacteriology*, **2013**, 195, 5461-8	3.5	14
26	The bacteriophage HK97 gp15 moron element encodes a novel superinfection exclusion protein. *Journal of Bacteriology*, **2012**, 194, 5012-9	3.5	71
25	The protein gp74 from the bacteriophage HK97 functions as a HNH endonuclease. *Protein Science*, **2012**, 21, 809-18	6.3	23
24	Long noncontractile tail machines of bacteriophages. *Advances in Experimental Medicine and Biology* , **2012**, 726, 115-42	3.6	78
23	The moron comes of age. *Bacteriophage*, **2012**, 2, 225-228		39
22	Structural and biochemical characterization of phage λFI protein (gpFI) reveals a novel mechanism of DNA packaging chaperone activity. *Journal of Biological Chemistry*, **2012**, 287, 32085-95	5.4	5
21	Assembly mechanism is the key determinant of the dosage sensitivity of a phage structural protein. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 10168-73	11.5	11
20	Phages have adapted the same protein fold to fulfill multiple functions in virion assembly. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 14384-9	11.5	29
19	The crystal structure of bacteriophage HK97 gp6: defining a large family of head-tail connector proteins. *Journal of Molecular Biology*, **2010**, 395, 754-68	6.5	49
18	The solution structure of the C-terminal Ig-like domain of the bacteriophage λtail tube protein. *Journal of Molecular Biology*, **2010**, 403, 468-79	6.5	39
17	Viral proteomics. *Microbiology and Molecular Biology Reviews*, **2007**, 71, 398-411	13.2	103
16	Viral Proteomics. *Microbiology and Molecular Biology Reviews*, **2007**, 71, 549-549	13.2	78

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15	The NMR structure of the gpU tail-terminator protein from bacteriophage lambda: identification of sites contributing to Mg(II)-mediated oligomerization and biological function. *Journal of Molecular Biology*, **2007**, 365, 175-86	6.5	27
14	Immunoglobulin-like domains on bacteriophage: weapons of modest damage?. *Current Opinion in Microbiology*, **2007**, 10, 382-7	7.9	69
13	Ig-like domains on bacteriophages: a tale of promiscuity and deceit. *Journal of Molecular Biology*, **2006**, 359, 496-507	6.5	136
12	Crystal structure of bacteriophage lambda cII and its DNA complex. *Molecular Cell*, **2005**, 19, 259-69	17.6	34
11	Protein folding: defining a "standard" set of experimental conditions and a preliminary kinetic data set of two-state proteins. *Protein Science*, **2005**, 14, 602-16	6.3	181
10	Refolding out of guanidine hydrochloride is an effective approach for high-throughput structural studies of small proteins. *Protein Science*, **2003**, 12, 2073-80	6.3	37
9	The solution structure of the bacteriophage lambda head-tail joining protein, gpFII. *Journal of Molecular Biology*, **2002**, 318, 1395-404	6.5	31
8	Protein folding kinetics beyond the phi value: using multiple amino acid substitutions to investigate the structure of the SH3 domain folding transition state. *Journal of Molecular Biology*, **2002**, 320, 389-402	6.5	71
7	The solution structure of bacteriophage lambda protein W, a small morphogenetic protein possessing a novel fold. *Journal of Molecular Biology*, **2001**, 308, 9-14	6.5	36
6	Structural proteomics of an archaeon. *Nature Structural Biology*, **2000**, 7, 903-9		247
5	Thermodynamic and functional characterization of protein W from bacteriophage lambda. The three C-terminal residues are critical for activity. *Journal of Biological Chemistry*, **2000**, 275, 18879-86	5.4	17
4	A simple in vivo assay for increased protein solubility. *Protein Science*, **1999**, 8, 1908-11	6.3	140
3	Mutagenesis of a buried polar interaction in an SH3 domain: sequence conservation provides the best prediction of stability effects. *Biochemistry*, **1998**, 37, 16172-82	3.2	85
2	One Anti-CRISPR to Rule Them All: Potent Inhibition of Cas9 Homologs Used for Genome Editing. *SSRN Electronic Journal*,	1	1
1	Potent Cas9 inhibition in bacterial and human cells by new anti-CRISPR protein families		1