Karen L Maxwell

List of Publications by Year
in descending order

70 papers	6,308 citations	87888 38 h-index	98798 67 g-index
74 all docs	74 docs citations	74 times ranked	5106 citing authors

#	Article	IF	Citations
1	Structural and Mechanistic Insight into CRISPR-Cas9 Inhibition by Anti-CRISPR Protein AcrIIC4. Journal of Molecular Biology, 2022, 434, 167420.	4.2	6
2	A Filamentous Bacteriophage Protein Inhibits Type IV Pili To Prevent Superinfection of Pseudomonas aeruginosa. MBio, 2022, 13, e0244121.	4.1	31
3	Gold Nanoparticle Smartphone Platform for Diagnosing Urinary Tract Infections. ACS Nanoscience Au, 2022, 2, 324-332.	4.8	7
4	Anti-CRISPR AcrIE2 Binds the Type I-E CRISPR-Cas Complex But Does Not Block DNA Binding. Journal of Molecular Biology, 2021, 433, 166759.	4.2	11
5	A phage-encoded anti-activator inhibits quorum sensing in Pseudomonas aeruginosa. Molecular Cell, 2021, 81, 571-583.e6.	9.7	80
6	Cyclic pyrimidines jump on the anti-phage bandwagon. Cell, 2021, 184, 5691-5693.	28.9	2
7	Retrons: Complementing CRISPR in Phage Defense. CRISPR Journal, 2020, 3, 226-227.	2.9	5
8	HK97 gp74 Possesses an Î±-Helical Insertion in the Î²Î²Î± Fold That Affects Its Metal Binding, cos Site Digestion, and In Vivo Activities. Journal of Bacteriology, 2020, 202, .	2.2	3
9	Extrachromosomal circular elements targeted by CRISPR-Cas in <i>Dehalococcoides mccartyi</i> are linked to mobilization of reductive dehalogenase genes. ISME Journal, 2019, 13, 24-38.	9.8	16
10	Bacterial twist to an antiviral defence. Nature, 2019, 574, 638-639.	27.8	3
11	Anti-CRISPR AcrIIA5 Potently Inhibits All Cas9 Homologs Used for Genome Editing. Cell Reports, 2019, 29, 1739-1746.e5.	6.4	35
12	Inhibition of CRISPR-Cas9 ribonucleoprotein complex assembly by anti-CRISPR AcrIIC2. Nature Communications, 2019, 10, 2806.	12.8	50
13	Meet the Anti-CRISPRs: Widespread Protein Inhibitors of CRISPR-Cas Systems. CRISPR Journal, 2019, 2, 23-30.	2.9	68
14	Phages Tune in to Host Cell Quorum Sensing. Cell, 2019, 176, 7-8.	28.9	10
15	The Diverse Impacts of Phage Morons on Bacterial Fitness and Virulence. Advances in Virus Research, 2019, 103, 1-31.	2.1	93
16	Anti-CRISPR: discovery, mechanism and function. Nature Reviews Microbiology, 2018, 16, 12-17.	28.6	288
17	Type VI secretion system baseplate. Nature Microbiology, 2018, 3, 1330-1331.	13.3	1
18	Potent Cas9 Inhibition in Bacterial and Human Cells by AcrIIC4 and AcrIIC5 Anti-CRISPR Proteins. MBio, 2018, 9, .	4.1	80

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19	A chemical defence against phage infection. Nature, 2018, 564, 283-286.	27.8	142
20	A Unified Resource for Tracking Anti-CRISPR Names. CRISPR Journal, 2018, 1, 304-305.	2.9	94
21	Phage-Encoded Anti-CRISPR Defenses. Annual Review of Genetics, 2018, 52, 445-464.	7.6	125
22	Phage Morons Play an Important Role in Pseudomonas aeruginosa Phenotypes. Journal of Bacteriology, 2018, 200, .	2.2	53
23	Structure Reveals Mechanisms of Viral Suppressors that Intercept a CRISPR RNA-Guided Surveillance Complex. Cell, 2017, 169, 47-57.e11.	28.9	191
24	The Anti-CRISPR Story: A Battle for Survival. Molecular Cell, 2017, 68, 8-14.	9.7	69
25	A Broad-Spectrum Inhibitor of CRISPR-Cas9. Cell, 2017, 170, 1224-1233.e15.	28.9	211
26	Disabling a Type I-E CRISPR-Cas Nuclease with a Bacteriophage-Encoded Anti-CRISPR Protein. MBio, 2017, 8, .	4.1	63
27	Naturally Occurring Off-Switches for CRISPR-Cas9. Cell, 2016, 167, 1829-1838.e9.	28.9	345
28	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, 10174-10179.	7.1	46
29	Inactivation of CRISPR-Cas systems by anti-CRISPR proteins in diverse bacterial species. Nature Microbiology, 2016, 1, 16085.	13.3	271
30	The solution structure of an anti-CRISPR protein. Nature Communications, 2016, 7, 13134.	12.8	48
31	Prophages mediate defense against phage infection through diverse mechanisms. ISME Journal, 2016, 10, 2854-2866.	9.8	363
32	Phages Fight Back: Inactivation of the CRISPR-Cas Bacterial Immune System by Anti-CRISPR Proteins. PLoS Pathogens, 2016, 12, e1005282.	4.7	51
33	Multiple mechanisms for CRISPRâ€"Cas inhibition by anti-CRISPR proteins. Nature, 2015, 526, 136-139.	27.8	325
34	The phage tail tape measure protein, an inner membrane protein and a periplasmic chaperone play connected roles in the genome injection process of <scp><i>E</i></scp><i>.â€‰coli</i> phage <scp>HK</scp>97. Molecular Microbiology, 2015, 96, 437-447.	2.5	89
35	A New Group of Phage Anti-CRISPR Genes Inhibits the Type I-E CRISPR-Cas System of Pseudomonas aeruginosa. MBio, 2014, 5, e00896.	4.1	224
36	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, 6022-6027.	7.1	110

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37	A Shifty Chaperone for Phage Tail Assembly. Journal of Molecular Biology, 2014, 426, 1001-1003.	4.2	9
38	Efficacy of Bacteriophage Treatment on Pseudomonas aeruginosa Biofilms. Journal of Endodontics, 2013, 39, 364-369.	3.1	35
39	Rapid Detection of E. coli Bacteria Using Potassium-Sensitive FETs in CMOS. IEEE Transactions on Biomedical Circuits and Systems, 2013, 7, 621-630.	4.0	37
40	Bacteriophage genes that inactivate the CRISPR/Cas bacterial immune system. Nature, 2013, 493, 429-432.	27.8	689
41	A Conserved Spiral Structure for Highly Diverged Phage Tail Assembly Chaperones. Journal of Molecular Biology, 2013, 425, 2436-2449.	4.2	20
42	Tail Tip Proteins Related to Bacteriophage Î» gpL Coordinate an Iron-Sulfur Cluster. Journal of Molecular Biology, 2013, 425, 2450-2462.	4.2	23
43	The Solution Structures of Two Prophage Homologues of the Bacteriophage Î» Ea8.5 Protein Reveal a Newly Discovered Hybrid Homeodomain/Zinc-Finger Fold. Biochemistry, 2013, 52, 3612-3614.	2.5	14
44	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, 5461-5468.	2.2	18
45	The moron comes of age. Bacteriophage, 2012, 2, e23146.	1.9	52
46	Structural and Biochemical Characterization of Phage Î» FI Protein (gpFI) Reveals a Novel Mechanism of DNA Packaging Chaperone Activity. Journal of Biological Chemistry, 2012, 287, 32085-32095.	3.4	8
47	The Bacteriophage HK97 gp15 Moron Element Encodes a Novel Superinfection Exclusion Protein. Journal of Bacteriology, 2012, 194, 5012-5019.	2.2	107
48	Rapid detection of E.Coli bacteria using potassium-sensitive FETs in CMOS. , 2012, , .		28
49	The protein gp74 from the bacteriophage HK97 functions as a HNH endonuclease. Protein Science, 2012, 21, 809-818.	7.6	30
50	Long Noncontractile Tail Machines of Bacteriophages. Advances in Experimental Medicine and Biology, 2012, 726, 115-142.	1.6	101
51	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, 10168-10173.	7.1	13
52	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, 14384-14389.	7.1	37
53	The Crystal Structure of Bacteriophage HK97 gp6: Defining a Large Family of Headâ€“Tail Connector Proteins. Journal of Molecular Biology, 2010, 395, 754-768.	4.2	62
54	The Solution Structure of the C-Terminal Ig-like Domain of the Bacteriophage Î» Tail Tube Protein. Journal of Molecular Biology, 2010, 403, 468-479.	4.2	46

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55	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, 175-186.	4.2	28
56	Immunoglobulin-like domains on bacteriophage: weapons of modest damage?. Current Opinion in Microbiology, 2007, 10, 382-387.	5.1	86
57	Viral Proteomics. Microbiology and Molecular Biology Reviews, 2007, 71, 398-411.	6.6	108
58	Ig-Like Domains on Bacteriophages: A Tale of Promiscuity and Deceit. Journal of Molecular Biology, 2006, 359, 496-507.	4.2	169
59	Crystal Structure of Bacteriophage Î»cII and Its DNA Complex. Molecular Cell, 2005, 19, 259-269.	9.7	39
60	Crystal Structure of Bacteriophage Î»cII and Its DNA Complex. Molecular Cell, 2005, 19, 578.	9.7	0
61	Protein folding: Defining a â€œstandardâ€•set of experimental conditions and a preliminary kinetic data set of two-state proteins. Protein Science, 2005, 14, 602-616.	7.6	207
62	Refolding out of guanidine hydrochloride is an effective approach for high-throughput structural studies of small proteins. Protein Science, 2003, 12, 2073-2080.	7.6	39
63	The Solution Structure of the Bacteriophage Î» Headâ€"Tail Joining Protein, gpFII. Journal of Molecular Biology, 2002, 318, 1395-1404.	4.2	38
64	Protein Folding Kinetics Beyond the Î¦ 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.	4.2	75
65	The solution structure of bacteriophage Î» protein W, a small morphogenetic protein possessing a novel fold11Edited by P. E. Wright. Journal of Molecular Biology, 2001, 308, 9-14.	4.2	41
66	Structural proteomics of an archaeon. Nature Structural Biology, 2000, 7, 903-909.	9.7	272
67	Thermodynamic and Functional Characterization of Protein W from Bacteriophage Î». Journal of Biological Chemistry, 2000, 275, 18879-18886.	3.4	18
68	A simple in vivo assay for increased protein solubility. Protein Science, 1999, 8, 1908-1911.	7.6	153
69	Mutagenesis of a Buried Polar Interaction in an SH3 Domain:Â Sequence Conservation Provides the Best Prediction of Stability Effectsâ€. Biochemistry, 1998, 37, 16172-16182.	2.5	92
70	One Anti-CRISPR to Rule Them All: Potent Inhibition of Cas9 Homologs Used for Genome Editing. SSRN Electronic Journal, 0, , .	0.4	1