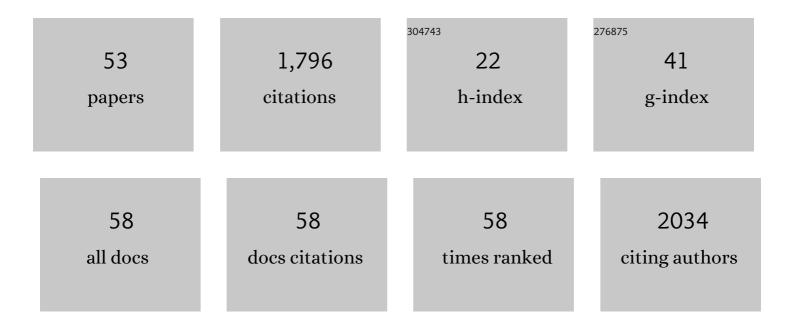
Kristin N Parent

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Metal-directed, chemically tunable assembly of one-, two- and three-dimensional crystalline protein arrays. Nature Chemistry, 2012, 4, 375-382.	13.6	332
2	P22 Coat Protein Structures Reveal a Novel Mechanism for Capsid Maturation: Stability without Auxiliary Proteins or Chemical Crosslinks. Structure, 2010, 18, 390-401.	3.3	136
3	Structural Characterization of the Dual Glycan Binding Adeno-Associated Virus Serotype 6. Journal of Virology, 2010, 84, 12945-12957.	3.4	120
4	Portal protein functions akin to a DNA-sensor that couples genome-packaging to icosahedral capsid maturation. Nature Communications, 2017, 8, 14310.	12.8	90
5	<scp>OmpA</scp> and <scp>OmpC</scp> are critical host factors for bacteriophage <scp>S</scp> f6 entry in <scp><i>S</i></scp> <i>higella</i> . Molecular Microbiology, 2014, 92, 47-60.	2.5	82
6	Human Bocavirus Capsid Structure: Insights into the Structural Repertoire of the <i>Parvoviridae</i> . Journal of Virology, 2010, 84, 5880-5889.	3.4	79
7	†Let the phage do the work': Using the phage P22 coat protein structures as a framework to understand its folding and assembly mutants. Virology, 2010, 401, 119-130.	2.4	78
8	Structural evolution of the P22-like phages: Comparison of Sf6 and P22 procapsid and virion architectures. Virology, 2012, 427, 177-188.	2.4	56
9	Electrostatic interactions govern both nucleation and elongation during phage P22 procapsid assembly. Virology, 2005, 340, 33-45.	2.4	55
10	Quantitative Analysis of Multi-component Spherical Virus Assembly: Scaffolding Protein Contributes to the Global Stability of Phage P22 Procapsids. Journal of Molecular Biology, 2006, 359, 1097-1106.	4.2	48
11	Structure of a Protozoan Virus from the Human Genitourinary Parasite Trichomonas vaginalis. MBio, 2013, 4, .	4.1	43
12	Three-Dimensional Structure of a Protozoal Double-Stranded RNA Virus That Infects the Enteric Pathogen Giardia lamblia. Journal of Virology, 2015, 89, 1182-1194.	3.4	42
13	The mitochondrial permeability transition phenomenon elucidated by cryo-EM reveals the genuine impact of calcium overload on mitochondrial structure and function. Scientific Reports, 2021, 11, 1037.	3.3	38
14	Stepwise molecular display utilizing icosahedral and helical complexes of phage coat and decoration proteins in the development of robust nanoscale display vehicles. Biomaterials, 2012, 33, 5628-5637.	11.4	35
15	Structural and Proteomic Characterization of the Initiation of Giant Virus Infection. Cell, 2020, 181, 1046-1061.e6.	28.9	35
16	Phage P22 Procapsids Equilibrate with Free Coat Protein Subunits. Journal of Molecular Biology, 2007, 365, 513-522.	4.2	34
17	Bacteriophage P22 ejects all of its internal proteins before its genome. Virology, 2015, 485, 128-134.	2.4	34
18	Breaking Symmetry in Viral Icosahedral Capsids as Seen through the Lenses of X-ray Crystallography and Cryo-Electron Microscopy. Viruses, 2018, 10, 67.	3.3	34

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19	Shigella Phages Isolated during a Dysentery Outbreak Reveal Uncommon Structures and Broad Species Diversity. Journal of Virology, 2018, 92, .	3.4	33
20	Polyhead formation in phage P22 pinpoints a region in coat protein required for conformational switching. Molecular Microbiology, 2007, 65, 1300-1310.	2.5	29
21	Cryo-reconstructions of P22 polyheads suggest that phage assembly is nucleated by trimeric interactions among coat proteins. Physical Biology, 2010, 7, 045004.	1.8	29
22	Determinants of bacteriophage P22 polyhead formation: the role of coat protein flexibility in conformational switching. Molecular Microbiology, 2010, 77, 1568-1582.	2.5	28
23	Genes affecting progression of bacteriophage P22 infection in <i>Salmonella</i> identified by transposon and single gene deletion screens. Molecular Microbiology, 2018, 108, 288-305.	2.5	28
24	Key Residues of S. flexneri OmpA Mediate Infection by Bacteriophage Sf6. Journal of Molecular Biology, 2015, 427, 1964-1976.	4.2	25
25	Three-dimensional reconstructions of the bacteriophage CUS-3 virion reveal a conserved coat protein I-domain but a distinct tailspike receptor-binding domain. Virology, 2014, 464-465, 55-66.	2.4	24
26	Virion Structure of Baboon Reovirus, a Fusogenic Orthoreovirus That Lacks an Adhesion Fiber. Journal of Virology, 2011, 85, 7483-7495.	3.4	20
27	Polyelectrolyte multilayers as anti-adhesive membrane coatings for virus concentration and recovery. Journal of Membrane Science, 2014, 469, 140-150.	8.2	20
28	Elution Is a Critical Step for Recovering Human Adenovirus 40 from Tap Water and Surface Water by Cross-Flow Ultrafiltration. Applied and Environmental Microbiology, 2016, 82, 4982-4993.	3.1	20
29	A second-site suppressor of a folding defect functions via interactions with a chaperone network to improve folding and assembly in vivo. Molecular Microbiology, 2004, 54, 1036-1050.	2.5	19
30	Emergence of a Competence-Reducing Filamentous Phage from the Genome of Acinetobacter baylyi ADP1. Journal of Bacteriology, 2016, 198, 3209-3219.	2.2	17
31	Microscopic Characterization of the Brazilian Giant Samba Virus. Viruses, 2017, 9, 30.	3.3	15
32	Modeling the Effects of Calcium Overload on Mitochondrial Ultrastructural Remodeling. Applied Sciences (Switzerland), 2021, 11, 2071.	2.5	13
33	Evolved Populations of <i>Shigella flexneri</i> Phage Sf6 Acquire Large Deletions, Altered Genomic Architecture, and Faster Life Cycles. Genome Biology and Evolution, 2016, 8, 2827-2840.	2.5	12
34	A Comparison Study of iTEP Nanoparticle-Based CTL Vaccine Carriers Revealed a Surprise Relationship between the Stability and Efficiency of the Carriers. Theranostics, 2016, 6, 666-678.	10.0	11
35	The phage L capsid decoration protein has a novel OB-fold and an unusual capsid binding strategy. ELife, 2019, 8, .	6.0	11
36	Ecology, Structure, and Evolution of <i>Shigella</i> Phages. Annual Review of Virology, 2020, 7, 121-141.	6.7	10

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37	A Concerted Mechanism for the Suppression of a Folding Defect through Interactions with Chaperones. Journal of Biological Chemistry, 2004, 279, 17473-17482.	3.4	8
38	A cornucopia of Shigella phages from the Cornhusker State. Virology, 2019, 538, 45-52.	2.4	8
39	Structure and physiology of giant DNA viruses. Current Opinion in Virology, 2021, 49, 58-67.	5.4	7
40	Students' use of chemistry core ideas to explain the structure and stability of <scp>DNA</scp> . Biochemistry and Molecular Biology Education, 2021, 49, 55-68.	1.2	6
41	Large Metabolic Rewiring from Small Genomic Changes between Strains of Shigella flexneri. Journal of Bacteriology, 2021, 203, .	2.2	6
42	GroEL/S substrate specificity based on substrate unfolding propensity. Cell Stress and Chaperones, 2007, 12, 20.	2.9	6
43	Models in the Biology Classroom: An In-Class Modeling Activity on Meiosis. American Biology Teacher, 2017, 79, 482-491.	0.2	4
44	Connecting Ideas across Courses. American Biology Teacher, 2021, 83, 303-310.	0.2	4
45	Creating and testing an activity with interdisciplinary connections: entropy to osmosis. Chemistry Education Research and Practice, 0, , .	2.5	4
46	Promotion of CTL epitope presentation by a nanoparticle with environment-responsive stability and phagolysosomal escape capacity. Journal of Controlled Release, 2020, 328, 653-664.	9.9	2
47	Shigella viruses Sf22 and KRT47 require outer membrane protein C for infection. Biochimica Et Biophysica Acta - Biomembranes, 2022, 1864, 183920.	2.6	2
48	A Gateway into Understanding the Unique Vertex of Samba Virus. Microscopy and Microanalysis, 2018, 24, 1438-1439.	0.4	1
49	Abstract 17188: Cryoem Analysis in Cardiac Isolated Mitochondria Reveals New Insights for CsA and mPTP Activation. Circulation, 2018, 138, .	1.6	1
50	Microscopic Evidence for a Stargate Structure in the Giant Virus, Samba Virus Microscopy and Microanalysis, 2016, 22, 1114-1115.	0.4	0
51	Structural Analysis of the Shigella Virus Sf14 Capsid. Microscopy and Microanalysis, 2020, 26, 1306-1306.	0.4	0
52	Structure of the Shigella flexneri podophage HRP29. Microscopy and Microanalysis, 2020, 26, 2744-2744.	0.4	0
53	Bacteriophage Receptor Proteins of Gram-Negative Bacteria. , 2021, , 175-185.		0