Kristin N Parent

List of Publications by Year
in descending order

53	1,796	304743	276875
papers	citations	22 h-index	41 g-index

58	58	58	2034
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Shigella viruses Sf22 and KRT47 require outer membrane protein C for infection. Biochimica Et Biophysica Acta - Biomembranes, 2022, 1864, 183920.	2.6	2
2	Bacteriophage Receptor Proteins of Gram-Negative Bacteria. , 2021, , 175-185.		0
3	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
4	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
5	Modeling the Effects of Calcium Overload on Mitochondrial Ultrastructural Remodeling. Applied Sciences (Switzerland), 2021, 11, 2071.	2.5	13
6	Connecting Ideas across Courses. American Biology Teacher, 2021, 83, 303-310.	0.2	4
7	Large Metabolic Rewiring from Small Genomic Changes between Strains of Shigella flexneri. Journal of Bacteriology, 2021, 203, .	2.2	6
8	Structure and physiology of giant DNA viruses. Current Opinion in Virology, 2021, 49, 58-67.	5.4	7
9	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
10	Structural Analysis of the Shigella Virus Sf14 Capsid. Microscopy and Microanalysis, 2020, 26, 1306-1306.	0.4	0
11	Structure of the Shigella flexneri podophage HRP29. Microscopy and Microanalysis, 2020, 26, 2744-2744.	0.4	0
12	Ecology, Structure, and Evolution of Shigella Phages. Annual Review of Virology, 2020, 7, 121-141.	6.7	10
13	Structural and Proteomic Characterization of the Initiation of Giant Virus Infection. Cell, 2020, 181, 1046-1061.e6.	28.9	35
14	A cornucopia of Shigella phages from the Cornhusker State. Virology, 2019, 538, 45-52.	2.4	8
15	The phage L capsid decoration protein has a novel OB-fold and an unusual capsid binding strategy. ELife, 2019, 8, .	6.0	11
16	Genes affecting progression of bacteriophage P22 infection in Salmonella identified by transposon and single gene deletion screens. Molecular Microbiology, 2018, 108, 288-305.	2.5	28
17	Shigella Phages Isolated during a Dysentery Outbreak Reveal Uncommon Structures and Broad Species Diversity. Journal of Virology, 2018, 92, .	3.4	33
18	A Gateway into Understanding the Unique Vertex of Samba Virus. Microscopy and Microanalysis, 2018, 24, 1438-1439.	0.4	1

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19	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
20	Abstract 17188: Cryoem Analysis in Cardiac Isolated Mitochondria Reveals New Insights for CsA and mPTP Activation. Circulation, 2018, 138, .	1.6	1
21	Portal protein functions akin to a DNA-sensor that couples genome-packaging to icosahedral capsid maturation. Nature Communications, 2017, 8, 14310.	12.8	90
22	Models in the Biology Classroom: An In-Class Modeling Activity on Meiosis. American Biology Teacher, 2017, 79, 482-491.	0.2	4
23	Microscopic Characterization of the Brazilian Giant Samba Virus. Viruses, 2017, 9, 30.	3.3	15
24	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
25	Microscopic Evidence for a Stargate Structure in the Giant Virus, Samba Virus.. Microscopy and Microanalysis, 2016, 22, 1114-1115.	0.4	0
26	Emergence of a Competence-Reducing Filamentous Phage from the Genome of Acinetobacter baylyi ADP1. Journal of Bacteriology, 2016, 198, 3209-3219.	2.2	17
27	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
28	Evolved Populations ofShigella flexneriPhage Sf6 Acquire Large Deletions, Altered Genomic Architecture, and Faster Life Cycles. Genome Biology and Evolution, 2016, 8, 2827-2840.	2.5	12
29	Key Residues of S. flexneri OmpA Mediate Infection by Bacteriophage Sf6. Journal of Molecular Biology, 2015, 427, 1964-1976.	4.2	25
30	Bacteriophage P22 ejects all of its internal proteins before its genome. Virology, 2015, 485, 128-134.	2.4	34
31	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
32	<scp>OmpA</scp> and <scp>OmpC</scp> are critical host factors for bacteriophage <scp>S</scp>f6 entry in <scp>S</scp>higella. Molecular Microbiology, 2014, 92, 47-60.	2.5	82
33	Polyelectrolyte multilayers as anti-adhesive membrane coatings for virus concentration and recovery. Journal of Membrane Science, 2014, 469, 140-150.	8.2	20
34	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
35	Structure of a Protozoan Virus from the Human Genitourinary Parasite Trichomonas vaginalis. MBio, 2013, 4, .	4.1	43
36	Metal-directed, chemically tunable assembly of one-, two- and three-dimensional crystalline protein arrays. Nature Chemistry, 2012, 4, 375-382.	13.6	332

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37	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
38	Structural evolution of the P22-like phages: Comparison of Sf6 and P22 procapsid and virion architectures. Virology, 2012, 427, 177-188.	2.4	56
39	Virion Structure of Baboon Reovirus, a Fusogenic Orthoreovirus That Lacks an Adhesion Fiber. Journal of Virology, 2011, 85, 7483-7495.	3.4	20
40	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
41	â€˜Let the phage do the workâ€™: 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
42	Determinants of bacteriophage P22 polyhead formation: the role of coat protein flexibility in conformational switching. Molecular Microbiology, 2010, 77, 1568-1582.	2.5	28
43	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
44	Human Bocavirus Capsid Structure: Insights into the Structural Repertoire of the Parvoviridae. Journal of Virology, 2010, 84, 5880-5889.	3.4	79
45	Structural Characterization of the Dual Glycan Binding Adeno-Associated Virus Serotype 6. Journal of Virology, 2010, 84, 12945-12957.	3.4	120
46	Phage P22 Procapsids Equilibrate with Free Coat Protein Subunits. Journal of Molecular Biology, 2007, 365, 513-522.	4.2	34
47	Polyhead formation in phage P22 pinpoints a region in coat protein required for conformational switching. Molecular Microbiology, 2007, 65, 1300-1310.	2.5	29
48	GroEL/S substrate specificity based on substrate unfolding propensity. Cell Stress and Chaperones, 2007, 12, 20.	2.9	6
49	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
50	Electrostatic interactions govern both nucleation and elongation during phage P22 procapsid assembly. Virology, 2005, 340, 33-45.	2.4	55
51	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
52	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
53	Creating and testing an activity with interdisciplinary connections: entropy to osmosis. Chemistry Education Research and Practice, 0, , .	2.5	4