

# Carolyn M Teschke

## List of Publications by Year in descending order

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67  
papers

1,771  
citations

257450

24  
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315739

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73  
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73  
docs citations

73  
times ranked

1150  
citing authors

#	ARTICLE	IF	CITATIONS
1	Pulse-field gradient nuclear magnetic resonance of protein translational diffusion from native to non-native states. <i>Protein Science</i> , 2022, 31, e4321.	7.6	7
2	Tryptophan Residues Are Critical for Portal Protein Assembly and Incorporation in Bacteriophage P22. <i>Viruses</i> , 2022, 14, 1400.	3.3	2
3	Intravirion DNA Can Access the Space Occupied by the Bacteriophage P22 Ejection Proteins. <i>Viruses</i> , 2021, 13, 1504.	3.3	3
4	Keeping It Together: Structures, Functions, and Applications of Viral Decoration Proteins. <i>Viruses</i> , 2020, 12, 1163.	3.3	15
5	Portal Protein: The Orchestrator of Capsid Assembly for the dsDNA Tailed Bacteriophages and Herpesviruses. <i>Annual Review of Virology</i> , 2019, 6, 141-160.	6.7	64
6	NMR Mapping of Disordered Segments from a Viral Scaffolding Protein Enclosed in a 23 MDa Procapsid. <i>Biophysical Journal</i> , 2019, 117, 1387-1392.	0.5	5
7	Of capsid structure and stability: The partnership between charged residues of E-loop and P-domain of the bacteriophage P22 coat protein. <i>Virology</i> , 2019, 534, 45-53.	2.4	6
8	A Hydrophobic Network: Intersubunit and Intercapsomer Interactions Stabilizing the Bacteriophage P22 Capsid. <i>Journal of Virology</i> , 2019, 93, .	3.4	8
9	The amazing HK97 fold: versatile results of modest differences. <i>Current Opinion in Virology</i> , 2019, 36, 9-16.	5.4	80
10	Conservation and Divergence of the I-Domain Inserted into the Ubiquitous HK97 Coat Protein Fold in P22-Like Bacteriophages. <i>Journal of Virology</i> , 2019, 93, .	3.4	4
11	Architect of Virus Assembly: the Portal Protein Nucleates Procapsid Assembly in Bacteriophage P22. <i>Journal of Virology</i> , 2019, 93, .	3.4	12
12	The phage L capsid decoration protein has a novel OB-fold and an unusual capsid binding strategy. <i>ELife</i> , 2019, 8, .	6.0	11
13	NMR assignments for monomeric phage L decoration protein. <i>Biomolecular NMR Assignments</i> , 2018, 12, 339-343.	0.8	2
14	Lessons from bacteriophages part 2: A saga of scientific breakthroughs and prospects for their use in human health. <i>PLoS Pathogens</i> , 2018, 14, e1006970.	4.7	7
15	Lessons from bacteriophages part 1: Deriving utility from protein structure, function, and evolution. <i>PLoS Pathogens</i> , 2018, 14, e1006971.	4.7	8
16	Portal protein functions akin to a DNA-sensor that couples genome-packaging to icosahedral capsid maturation. <i>Nature Communications</i> , 2017, 8, 14310.	12.8	90
17	NMR assignments for the insertion domain of bacteriophage Sf6 coat protein. <i>Biomolecular NMR Assignments</i> , 2017, 11, 35-38.	0.8	1
18	A viral scaffolding protein triggers portal ring oligomerization and incorporation during procapsid assembly. <i>Science Advances</i> , 2017, 3, e1700423.	10.3	36

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19	Measurement of the accurate mass of a 50ÅMDa infectious virus. <i>Rapid Communications in Mass Spectrometry</i> , 2016, 30, 1957-1962.	1.5	46
20	Localization of the Houdinisome (Ejection Proteins) inside the Bacteriophage P22 Virion by Bubblegram Imaging. <i>MBio</i> , 2016, 7, .	4.1	27
21	Contextual Role of a Salt Bridge in the Phage P22 Coat Protein I-Domain. <i>Journal of Biological Chemistry</i> , 2016, 291, 11359-11372.	3.4	4
22	Acquiring Structural Information on Virus Particles with Charge Detection Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1028-1036.	2.8	42
23	Mechanism of Protein Denaturation: Partial Unfolding of the P22 Coat Protein I-Domain by Urea Binding. <i>Biophysical Journal</i> , 2015, 109, 2666-2677.	0.5	15
24	NMR assignments for the insertion domain of bacteriophage CUS-3 coat protein. <i>Biomolecular NMR Assignments</i> , 2015, 9, 333-336.	0.8	5
25	A method to investigate protein association with intact sealed mycobacterial membrane vesicles. <i>Analytical Biochemistry</i> , 2015, 485, 109-111.	2.4	0
26	Nature's favorite building block: Deciphering folding and capsid assembly of proteins with the HK97-fold. <i>Virology</i> , 2015, 479-480, 487-497.	2.4	92
27	A Molecular Staple: D-Loops in the I Domain of Bacteriophage P22 Coat Protein Make Important Intercapsomer Contacts Required for Procapsid Assembly. <i>Journal of Virology</i> , 2015, 89, 10569-10579.	3.4	17
28	ADP-dependent Conformational Changes Distinguish <i>Mycobacterium tuberculosis</i> SecA2 from SecA1. <i>Journal of Biological Chemistry</i> , 2014, 289, 2307-2317.	3.4	11
29	Highly Specific Salt Bridges Govern Bacteriophage P22 Icosahedral Capsid Assembly: Identification of the Site in Coat Protein Responsible for Interaction with Scaffolding Protein. <i>Journal of Virology</i> , 2014, 88, 5287-5297.	3.4	24
30	Multiple Functional Roles of the Accessory I-Domain of Bacteriophage P22 Coat Protein Revealed by NMR Structure and CryoEM Modeling. <i>Structure</i> , 2014, 22, 830-841.	3.3	40
31	An Intramolecular Chaperone Inserted in Bacteriophage P22 Coat Protein Mediates Its Chaperonin-independent Folding. <i>Journal of Biological Chemistry</i> , 2013, 288, 33772-33783.	3.4	14
32	NMR assignments for the telokin-like domain of bacteriophage P22 coat protein. <i>Biomolecular NMR Assignments</i> , 2013, 7, 257-260.	0.8	7
33	Themes and Variations of Viral Small Terminase Proteins. <i>Structure</i> , 2012, 20, 1291-1292.	3.3	5
34	Unraveling the Role of the C-terminal Helix Turn Helix of the Coat-binding Domain of Bacteriophage P22 Scaffolding Protein. <i>Journal of Biological Chemistry</i> , 2012, 287, 33766-33780.	3.4	26
35	Stepwise molecular display utilizing icosahedral and helical complexes of phage coat and decoration proteins in the development of robust nanoscale display vehicles. <i>Biomaterials</i> , 2012, 33, 5628-5637.	11.4	35
36	The energetic contributions of scaffolding and coat proteins to the assembly of bacteriophage procapsids. <i>Virology</i> , 2012, 428, 64-69.	2.4	17

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37	Conformational Changes in Bacteriophage P22 Scaffolding Protein Induced by Interaction with Coat Protein. <i>Journal of Molecular Biology</i> , 2011, 410, 226-240.	4.2	17
38	Bacteriophage P22 capsid size determination: Roles for the coat protein telokin-like domain and the scaffolding protein amino-terminus. <i>Virology</i> , 2011, 417, 418-429.	2.4	24
39	Decoding bacteriophage P22 assembly: Identification of two charged residues in scaffolding protein responsible for coat protein interaction. <i>Virology</i> , 2011, 421, 1-11.	2.4	40
40	P22 Coat Protein Structures Reveal a Novel Mechanism for Capsid Maturation: Stability without Auxiliary Proteins or Chemical Crosslinks. <i>Structure</i> , 2010, 18, 390-401.	3.3	136
41	“Let the phage do the work™”: Using the phage P22 coat protein structures as a framework to understand its folding and assembly mutants. <i>Virology</i> , 2010, 401, 119-130.	2.4	78
42	Determinants of bacteriophage P22 polyhead formation: the role of coat protein flexibility in conformational switching. <i>Molecular Microbiology</i> , 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. <i>Physical Biology</i> , 2010, 7, 045004.	1.8	29
44	ATPase Activity of <i>Mycobacterium tuberculosis</i> SecA1 and SecA2 Proteins and Its Importance for SecA2 Function in Macrophages. <i>Journal of Bacteriology</i> , 2008, 190, 4880-4887.	2.2	50
45	Phage P22 Procapsids Equilibrate with Free Coat Protein Subunits. <i>Journal of Molecular Biology</i> , 2007, 365, 513-522.	4.2	34
46	Polyhead formation in phage P22 pinpoints a region in coat protein required for conformational switching. <i>Molecular Microbiology</i> , 2007, 65, 1300-1310.	2.5	29
47	GroEL/S substrate specificity based on substrate unfolding propensity. <i>Cell Stress and Chaperones</i> , 2007, 12, 20.	2.9	6
48	Quantitative Analysis of Multi-component Spherical Virus Assembly: Scaffolding Protein Contributes to the Global Stability of Phage P22 Procapsids. <i>Journal of Molecular Biology</i> , 2006, 359, 1097-1106.	4.2	48
49	Molecular Glue to Cement a Phage. <i>Structure</i> , 2006, 14, 803-804.	3.3	0
50	Electrostatic interactions govern both nucleation and elongation during phage P22 procapsid assembly. <i>Virology</i> , 2005, 340, 33-45.	2.4	55
51	A Concerted Mechanism for the Suppression of a Folding Defect through Interactions with Chaperones. <i>Journal of Biological Chemistry</i> , 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. <i>Molecular Microbiology</i> , 2004, 54, 1036-1050.	2.5	19
53	SecA Folding Kinetics: A Large Dimeric Protein Rapidly Forms Multiple Native States. <i>Journal of Molecular Biology</i> , 2004, 341, 199-214.	4.2	15
54	Folding of phage P22 coat protein monomers: kinetic and thermodynamic properties. <i>Virology</i> , 2003, 313, 184-197.	2.4	27

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55	Rapid Unfolding of a Domain Populates an Aggregation-prone Intermediate that can be Recognized by GroEL. <i>Journal of Molecular Biology</i> , 2003, 332, 937-951.	4.2	13
56	Penton Release from P22 Heat-Expanded Capsids Suggests Importance of Stabilizing Penton-Hexon Interactions during Capsid Maturation. <i>Biophysical Journal</i> , 2003, 84, 2585-2592.	0.5	88
57	Alleviation of a Defect in Protein Folding by Increasing the Rate of Subunit Assembly. <i>Journal of Biological Chemistry</i> , 2001, 276, 25372-25377.	3.4	8
58	Folding Defects Caused by Single Amino Acid Substitutions in a Subunit Are Not Alleviated by Assembly. <i>Biochemistry</i> , 2000, 39, 1142-1151.	2.5	15
59	GroEL binds a late folding intermediate of phage P22 coat protein. <i>Cell Stress and Chaperones</i> , 2000, 5, 163.	2.9	10
60	Single Amino Acid Substitutions Globally Suppress the Folding Defects of Temperature-sensitive Folding Mutants of Phage P22 Coat Protein. <i>Journal of Biological Chemistry</i> , 1999, 274, 22217-22224.	3.4	30
61	Aggregation and Assembly of Phage P22 Temperature-Sensitive Coat Protein Mutants in Vitro Mimic the in Vivo Phenotype. <i>Biochemistry</i> , 1999, 38, 2873-2881.	2.5	21
62	GroEL and GroES Control of Substrate Flux in the in Vivo Folding Pathway of Phage P22 Coat Protein. <i>Journal of Biological Chemistry</i> , 1998, 273, 27236-27244.	3.4	24
63	The Folded Conformation of Phage P22 Coat Protein Is Affected by Amino Acid Substitutions That Lead to a Cold-Sensitive Phenotype. <i>Biochemistry</i> , 1997, 36, 3971-3980.	2.5	6
64	The Chaperonins. <i>Cell Stress and Chaperones</i> , 1997, 2, 72.	2.9	0
65	Interactions between Coat and Scaffolding Proteins of Phage P22 Are Altered in Vitro by Amino Acid Substitutions in Coat Protein That Cause a Cold-Sensitive Phenotype. <i>Biochemistry</i> , 1996, 35, 14831-14840.	2.5	22
66	Inhibition of viral capsid assembly by 1,1'-bis(4-anilinonaphthalene-5-sulfonic acid). <i>Biochemistry</i> , 1993, 32, 10658-10665.	2.5	66
67	Folding and assembly of oligomeric proteins in <i>Escherichia coli</i> . <i>Current Opinion in Biotechnology</i> , 1992, 3, 468-473.	6.6	32