Mikhail M Shneider

List of Publications by Year
in descending order

89	3,402	172207 29	168136 53
papers	citations	h-index	g-index

91	91	91	2704
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	PAAR-repeat proteins sharpen and diversify the type VI secretion system spike. Nature, 2013, 500, 350-353.	13.7	466
2	Structure of the T4 baseplate and its function in triggering sheath contraction. Nature, 2016, 533, 346-352.	13.7	231
3	Structural and functional similarities between the capsid proteins of bacteriophages T4 and HK97 point to a common ancestry. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7163-7168.	3.3	189
4	Contractile Tail Machines of Bacteriophages. Advances in Experimental Medicine and Biology, 2012, 726, 93-114.	0.8	170
5	The tail sheath structure of bacteriophage T4: a molecular machine for infecting bacteria. EMBO Journal, 2009, 28, 821-829.	3.5	133
6	The O-specific polysaccharide lyase from the phage LKA1 tailspike reduces Pseudomonas virulence. Scientific Reports, 2017, 7, 16302.	1.6	88
7	Function of bacteriophage G7C esterase tailspike in host cell adsorption. Molecular Microbiology, 2017, 105, 385-398.	1.2	84
8	Ability of phages to infect Acinetobacter calcoaceticusâ€Acinetobacter baumannii complex species through acquisition of different pectate lyase depolymerase domains. Environmental Microbiology, 2017, 19, 5060-5077.	1.8	81
9	Evolution of T4-related phages. Virus Genes, 1995, 11, 285-297.	0.7	80
10	Phage Pierces the Host Cell Membrane with the Iron-Loaded Spike. Structure, 2012, 20, 326-339.	1.6	77
11	Acinetobacter baumanniiK27 and K44 capsular polysaccharides have the same K unit but different structures due to the presence of distinctwzygenes in otherwise closely related K gene clusters. Glycobiology, 2016, 26, 501-508.	1.3	68
12	Structure and Function of the Branched Receptor-Binding Complex of Bacteriophage CBA120. Journal of Molecular Biology, 2019, 431, 3718-3739.	2.0	67
13	Action of a minimal contractile bactericidal nanomachine. Nature, 2020, 580, 658-662.	13.7	61
14	<scp>L</scp>isteria phage <scp>A</scp>511, a model for the contractile tail machineries of <scp>SPO</scp>1â€related bacteriophages. Molecular Microbiology, 2014, 92, 84-99.	1.2	55
15	Structure of a new pseudaminic acid-containing capsular polysaccharide of Acinetobacter baumannii LUH5550 having the KL42 capsule biosynthesis locus. Carbohydrate Research, 2015, 407, 154-157.	1.1	53
16	Structure of bacteriophage T4 gene product 11, the interface between the baseplate and short tail fibers 1 1Edited by P. E. Wright. Journal of Molecular Biology, 2000, 301, 975-985.	2.0	52
17	Structure of the capsular polysaccharide of Acinetobacter baumannii ACICU containing di-N-acetylpseudaminic acid. Carbohydrate Research, 2014, 391, 89-92.	1.1	51
18	Structural Relationship of the Lipid A Acyl Groups to Activation of Murine Toll-Like Receptor 4 by Lipopolysaccharides from Pathogenic Strains of Burkholderia mallei, Acinetobacter baumannii, and Pseudomonas aeruginosa. Frontiers in Immunology, 2015, 6, 595.	2.2	51

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19	Structure of the Bacteriophage Ï†KZ Lytic Transglycosylase gp144. Journal of Biological Chemistry, 2008, 283, 7242-7250.	1.6	48
20	Structures of the K35 and K15 capsular polysaccharides of Acinetobacter baumannii LUH5535 and LUH5554 containing amino and diamino uronic acids. Carbohydrate Research, 2017, 448, 28-34.	1.1	43
21	Acinetobacter baumannii K11 and K83 capsular polysaccharides have the same 6-deoxy- l -talose-containing pentasaccharide K units but different linkages between the K units. International Journal of Biological Macromolecules, 2017, 103, 648-655.	3.6	43
22	Structure elucidation of the capsular polysaccharide of Acinetobacter baumannii AB5075 having the KL25 capsule biosynthesis locus. Carbohydrate Research, 2015, 408, 8-11.	1.1	42
23	K19 capsular polysaccharide of Acinetobacter baumannii is produced via a Wzy polymerase encoded in a small genomic island rather than the KL19 capsule gene cluster. Microbiology (United Kingdom), 2016, 162, 1479-1489.	0.7	41
24	Structure of the neutral capsular polysaccharide of Acinetobacter baumannii NIPH146 that carries the KL37 capsule gene cluster. Carbohydrate Research, 2015, 413, 12-15.	1.1	37
25	Evolution of Bacteriophage Tails: Structure of T4 Gene Product 10. Journal of Molecular Biology, 2006, 358, 912-921.	2.0	35
26	Novel Fri1-like Viruses Infecting Acinetobacter baumanniiâ€"vB_AbaP_AS11 and vB_AbaP_AS12â€"Characterization, Comparative Genomic Analysis, and Host-Recognition Strategy.. Viruses, 2017, 9, 188.	1.5	35
27	Structure and Analysis of R1 and R2 Pyocin Receptor-Binding Fibers. Viruses, 2018, 10, 427.	1.5	35
28	Structure and transformation of bacteriophage A511 baseplate and tail upon infection of Listeria Âcells. EMBO Journal, 2019, 38, .	3.5	34
29	Related structures of neutral capsular polysaccharides of Acinetobacter baumannii isolates that carry related capsule gene clusters KL43, KL47, and KL88. Carbohydrate Research, 2016, 435, 173-179.	1.1	33
30	Morphologically Different Pectobacterium brasiliense Bacteriophages PP99 and PP101: Deacetylation of O-Polysaccharide by the Tail Spike Protein of Phage PP99 Accompanies the Infection. Frontiers in Microbiology, 2019, 10, 3147.	1.5	33
31	Structure and Location of Gene Product 8 in the Bacteriophage T4 Baseplate. Journal of Molecular Biology, 2003, 328, 821-833.	2.0	32
32	K17 capsular polysaccharide produced by Acinetobacter baumannii isolate G7 contains an amide of 2-acetamido-2-deoxy-d-galacturonic acid with d-alanine. International Journal of Biological Macromolecules, 2020, 144, 857-862.	3.6	32
33	Peptidoglycan degrading activity of the broad-range Salmonella bacteriophage S-394 recombinant endolysin. Biochimie, 2014, 107, 293-299.	1.3	31
34	Structures of three different neutral polysaccharides of Acinetobacter baumannii, NIPH190, NIPH201, and NIPH615, assigned to K30, K45, and K48 capsule types, respectively, based on capsule biosynthesis gene clusters. Carbohydrate Research, 2015, 417, 81-88.	1.1	31
35	The Structure of Gene Product 6 of Bacteriophage T4, the Hinge-Pin of the Baseplate. Structure, 2009, 17, 800-808.	1.6	30
36	The KL24 gene cluster and a genomic island encoding a Wzy polymerase contribute genes needed for synthesis of the K24 capsular polysaccharide by the multiply antibiotic resistant Acinetobacter baumannii isolate RCH51. Microbiology (United Kingdom), 2017, 163, 355-363.	0.7	29

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37	Acinetobacter baumannii K20 and K21 capsular polysaccharide structures establish roles for UDP-glucose dehydrogenase Ugd2, pyruvyl transferase Ptr2 and two glycosyltransferases. Glycobiology, 2018, 28, 876-884.	1.3	28
38	Host Specificity of the Dickeya Bacteriophage PP35 Is Directed by a Tail Spike Interaction With Bacterial O-Antigen, Enabling the Infection of Alternative Non-pathogenic Bacterial Host. Frontiers in Microbiology, 2018, 9, 3288.	1.5	28
39	Characterization of Pectobacterium carotovorum subsp. carotovorum Bacteriophage PP16 Prospective for Biocontrol of Potato Soft Rot. Microbiology, 2019, 88, 451-460.	0.5	27
40	Acinetobacter baumannii K116 capsular polysaccharide structure is a hybrid of the K14 and revised K37 structures. Carbohydrate Research, 2019, 484, 107774.	1.1	26
41	The K46 and K5 capsular polysaccharides produced by Acinetobacter baumannii NIPH 329 and SDF have related structures and the side-chain non-ulosonic acids are 4-O-acetylated by phage-encoded O-acetyltransferases. PLoS ONE, 2019, 14, e0218461.	1.1	26
42	Molecular architecture of bacteriophage T4. Biochemistry (Moscow), 2004, 69, 1190-1202.	0.7	23
43	Structure of an Acinetobacter Broad-Range Prophage Endolysin Reveals a C-Terminal Î±-Helix with the Proposed Role in Activity against Live Bacterial Cells. Viruses, 2018, 10, 309.	1.5	23
44	Revised structure of the capsular polysaccharide of Acinetobacter baumannii LUH5533 (serogroup O1) containing di-N-acetyllegionaminic acid. Russian Chemical Bulletin, 2015, 64, 1196-1199.	0.4	21
45	Structure of the capsular polysaccharide of Acinetobacter baumannii 1053 having the KL91 capsule biosynthesis gene locus. Carbohydrate Research, 2015, 404, 79-82.	1.1	21
46	Structure and gene cluster of the K93 capsular polysaccharide of Acinetobacter baumannii B11911 containing 5-N-Acetyl-7-N-[(R)-3-hydroxybutanoyl]pseudaminic acid. Biochemistry (Moscow), 2017, 82, 483-489.	0.7	21
47	Origin and Evolution of Studiervirinae Bacteriophages Infecting Pectobacterium: Horizontal Transfer Assists Adaptation to New Niches. Microorganisms, 2020, 8, 1707.	1.6	20
48	Preliminary Crystallographic Studies of Bacteriophage T4 Fibritin Confirm a Trimeric Coiled-Coil Structure. Virology, 1996, 219, 190-194.	1.1	19
49	Structure and gene cluster of the K125 capsular polysaccharide from Acinetobacter baumannii MAR13-1452. International Journal of Biological Macromolecules, 2018, 117, 1195-1199.	3.6	19
50	Production of the K16 capsular polysaccharide by Acinetobacter baumannii ST25 isolate D4 involves a novel glycosyltransferase encoded in the KL16 gene cluster. International Journal of Biological Macromolecules, 2019, 128, 101-106.	3.6	19
51	Structure of Bacteriophage T4 Fibritin M: a Troublesome Packing Arrangement. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 805-816.	2.5	18
52	The K90 capsular polysaccharide produced by Acinetobacter baumannii LUH5553 contains di-N-acetylpseudaminic acid and is structurally related to the K7 polysaccharide from A. baumannii LUH5533. Carbohydrate Research, 2019, 479, 1-5.	1.1	18
53	Characterization of myophage AM24 infecting Acinetobacter baumannii of the K9 capsular type. Archives of Virology, 2019, 164, 1493-1497.	0.9	18
54	From structure of the complex to understanding of the biology. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 9-16.	2.5	17

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55	Complete Genome Sequence of the Novel Giant Pseudomonas Phage PaBG. Genome Announcements, 2014, 2, .	0.8	17
56	K units of the K8 and K54 capsular polysaccharides produced by Acinetobacter baumannii BAL 097 and RCH52 have the same structure but contain different di-N-acyl derivatives of legionaminic acid and are linked differently. Carbohydrate Research, 2019, 483, 107745.	1.1	17
57	Involvement of a multifunctional rhamnosyltransferase in the synthesis of three related Acinetobacter baumannii capsular polysaccharides, K55, K74 and K85. International Journal of Biological Macromolecules, 2021, 166, 1230-1237.	3.6	17
58	The K26 capsular polysaccharide from Acinetobacter baumannii KZ-1098: Structure and cleavage by a specific phage depolymerase. International Journal of Biological Macromolecules, 2021, 191, 182-191.	3.6	16
59	Curtobacterium spp. and Curtobacterium flaccumfaciens: Phylogeny, Genomics-Based Taxonomy, Pathogenicity, and Diagnostics. Current Issues in Molecular Biology, 2022, 44, 889-927.	1.0	15
60	Crystal structure and location of gp131 in the bacteriophage phiKZ virion. Virology, 2012, 434, 257-264.	1.1	14
61	Structure of the N-acetylpseudaminic acid-containing capsular polysaccharide of Acinetobacter baumannii NIPH67. Russian Chemical Bulletin, 2016, 65, 588-591.	0.4	14
62	Structure of the K128 capsular polysaccharide produced by Acinetobacter baumannii KZ-1093 from Kazakhstan. Carbohydrate Research, 2019, 485, 107814.	1.1	13
63	The K5 capsular polysaccharide of the bacterium Acinetobacter baumannii SDF with the same K unit containing Leg5Ac7Ac as the K7 capsular polysaccharide but a different linkage between the K units. Russian Chemical Bulletin, 2019, 68, 163-167.	0.4	13
64	Genetics of biosynthesis and structure of the K53 capsular polysaccharide of Acinetobacter baumannii D23 made up of a disaccharide K unit. Microbiology (United Kingdom), 2018, 164, 1289-1292.	0.7	13
65	Autographivirinae Bacteriophage Arno 160 Infects Pectobacterium carotovorum via Depolymerization of the Bacterial O-Polysaccharide. International Journal of Molecular Sciences, 2020, 21, 3170.	1.8	12
66	Complete Genome Sequence of Acinetobacter baumannii Phage BS46. Microbiology Resource Announcements, 2020, 9, .	0.3	10
67	Pseudomonas Phage MD8: Genetic Mosaicism and Challenges of Taxonomic Classification of Lambdoid Bacteriophages. International Journal of Molecular Sciences, 2021, 22, 10350.	1.8	10
68	Correlation of Acinetobacter baumannii K144 and K86 capsular polysaccharide structures with genes at the K locus reveals the involvement of a novel multifunctional rhamnosyltransferase for structural synthesis. International Journal of Biological Macromolecules, 2021, 193, 1294-1300.	3.6	10
69	Structure and Biophysical Properties of a Triple-Stranded Beta-Helix Comprising the Central Spike of Bacteriophage T4. Viruses, 2015, 7, 4676-4706.	1.5	9
70	Genomic characteristics of vB_PpaP_PP74, a T7-like Autographivirinae bacteriophage infecting a potato pathogen of the newly proposed species Pectobacterium parmentieri. Archives of Virology, 2018, 163, 1691-1694.	0.9	9
71	Novel Acinetobacter baumannii Bacteriophage Aristophanes Encoding Structural Polysaccharide Deacetylase. Viruses, 2021, 13, 1688.	1.5	9
72	Capsule-Targeting Depolymerases Derived from Acinetobacter baumannii Prophage Regions. International Journal of Molecular Sciences, 2022, 23, 4971.	1.8	9

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73	A novel ItrA4 d-galactosyl 1-phosphate transferase is predicted to initiate synthesis of an amino sugar-lacking K92 capsular polysaccharide of Acinetobacter baumannii B8300. Research in Microbiology, 2021, 172, 103815.	1.0	8
74	Evolution of Phage Tail Sheath Protein. Viruses, 2022, 14, 1148.	1.5	8
75	Transformation of a fragment of beta-structural bacteriophage T4 adhesin to stable alpha-helical trimer. Biochemistry (Moscow), 2000, 65, 1346-1351.	0.7	7
76	Properties of bacteriophage T4 baseplate protein encoded by gene 8. Biochemistry (Moscow), 2001, 66, 693-697.	0.7	7
77	Novel Acinetobacter baumannii Myovirus TaPaz Encoding Two Tailspike Depolymerases: Characterization and Host-Recognition Strategy. Viruses, 2021, 13, 978.	1.5	7
78	Structure of the K87 capsular polysaccharide and KL87 gene cluster of Acinetobacter baumannii LUH5547 reveals a heptasaccharide repeating unit. Carbohydrate Research, 2021, 509, 108439.	1.1	7
79	Involvement of a Phage-Encoded Wzy Protein in the Polymerization of K127 Units To Form the Capsular Polysaccharide of Acinetobacter baumannii Isolate 36-1454. Microbiology Spectrum, 2022, 10, e0150321.	1.2	7
80	The K139 capsular polysaccharide produced by Acinetobacter baumannii MAR17-1041 belongs to a group of related structures including K14, K37 and K116. International Journal of Biological Macromolecules, 2021, 193, 2297-2303.	3.6	5
81	The Central Spike Complex of Bacteriophage T4 Contacts PpiD in the Periplasm of Escherichia coli. Viruses, 2020, 12, 1135.	1.5	4
82	The tail sheath structure of bacteriophage T4: a molecular machine for infecting bacteria. EMBO Journal, 2012, 31, 3507-3507.	3.5	3
83	NoteIdentification of 5,7-diacetamido-3,5,7,9-tetradeoxy-d-glycero-l-manno-non-2-ulosonic acid (di-N-acetyl-8-epipseudaminic acid) in the capsular polysaccharide of Acinetobacter baumannii Res546. Carbohydrate Research, 2022, 513, 108531.	1.1	3
84	Functional Role of the N-Terminal Domain of Bacteriophage T4-Gene Product 11. Biochemistry (Moscow), 2005, 70, 1111-1118.	0.7	2
85	Draft Genome Sequence of Pectobacterium atrosepticum PB72 and Complete Genome Sequence of the Specific Bacteriophage PP90. Genome Announcements, 2018, 6, .	0.8	2
86	Gene Analysis, Cloning, and Heterologous Expression of Protease from a Micromycete Aspergillus ochraceus Capable of Activating Protein C of Blood Plasma. Microorganisms, 2021, 9, 1936.	1.6	2
87	The K89 capsular polysaccharide produced by Acinetobacter baumannii LUH5552 consists of a pentameric repeat-unit that includes a 3-acetamido-3,6-dideoxy-d-galactose residue. International Journal of Biological Macromolecules, 2022, 217, 515-521.	3.6	2
88	Central spike proteins of contractile ejection systems. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C579-C579.	0.0	0
89	Crystal structure of gpV - the bacteriophage P2 cell-puncturing device. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s24-s25.	0.3	0