Mikhail M Shneider

List of Publications by Year in Descending Order

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83 papers	2,327 citations	26 h-index	46 g-index
91 ext. papers	2,976 ext. citations	6.3 avg, IF	4.83 L-index

#	Paper	IF	Citations
83	Curtobacterium spp. and Curtobacterium flaccumfaciens: Phylogeny, Genomics-Based Taxonomy, Pathogenicity, and Diagnostics. *Current Issues in Molecular Biology*, **2022**, 44, 889-927	2.9	1
82	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	2.9	0
81	Capsule-Targeting Depolymerases Derived from Prophage Regions.. *International Journal of Molecular Sciences*, **2022**, 23,	6.3	2
80	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**, e0150321	8.9	2
79	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, 2297-2297	7.9	1
78	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, 1294-1294	7.9	4
77	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	4	5
76	Novel Myovirus TaPaz Encoding Two Tailspike Depolymerases: Characterization and Host-Recognition Strategy. *Viruses*, **2021**, 13,	6.2	5
75	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	7.9	8
74	Novel Bacteriophage Aristophanes Encoding Structural Polysaccharide Deacetylase. *Viruses*, **2021**, 13,	6.2	4
73	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	7.9	3
72	Structure of the K87 capsular polysaccharide and KL87 gene cluster of Acinetobacter baumannii LUH5547 reveals a heptasaccharide repeating unit. *Carbohydrate Research*, **2021**, 509, 108439	2.9	2
71	Bacteriophage Arno 160 Infects via Depolymerization of the Bacterial O-Polysaccharide. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	2
70	Complete Genome Sequence of Acinetobacter baumannii Phage BS46. *Microbiology Resource Announcements*, **2020**, 9,	1.3	7
69	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	7.9	13
68	Origin and Evolution of Bacteriophages Infecting : Horizontal Transfer Assists Adaptation to New Niches. *Microorganisms*, **2020**, 8,	4.9	5
67	Action of a minimal contractile bactericidal nanomachine. *Nature*, **2020**, 580, 658-662	50.4	19

66	Structure of the K128 capsular polysaccharide produced by Acinetobacter baumannii KZ-1093 from Kazakhstan. *Carbohydrate Research*, **2019**, 485, 107814	2.9	8
65	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	7.9	12
64	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	3.7	13
63	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	2.9	11
62	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	1.7	8
61	Characterization of myophage AM24 infecting Acinetobacter baumannii of the K9 capsular type. *Archives of Virology*, **2019**, 164, 1493-1497	2.6	12
60	Characterization of Pectobacterium carotovorum subsp. carotovorum Bacteriophage PP16 Prospective for Biocontrol of Potato Soft Rot. *Microbiology*, **2019**, 88, 451-460	1.4	9
59	Acinetobacter baumannii K116 capsular polysaccharide structure is a hybrid of the K14 and revised K37 structures. *Carbohydrate Research*, **2019**, 484, 107774	2.9	13
58	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	2.9	9
57	Structure and Function of the Branched Receptor-Binding Complex of Bacteriophage CBA120. *Journal of Molecular Biology*, **2019**, 431, 3718-3739	6.5	28
56	Morphologically Different 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	5.7	8
55	Structure and transformation of bacteriophage A511 baseplate and tail upon infection of □cells. *EMBO Journal*, **2019**, 38,	13	17
54	Host Specificity of the Bacteriophage PP35 Is Directed by a Tail Spike Interaction With Bacterial -Antigen, Enabling the Infection of Alternative Non-pathogenic Bacterial Host. *Frontiers in Microbiology*, **2018**, 9, 3288	5.7	12
53	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	2.6	7
52	Draft Genome Sequence of Pectobacterium atrosepticum PB72 and Complete Genome Sequence of the Specific Bacteriophage PP90. *Genome Announcements*, **2018**, 6,		1
51	Structure of an Broad-Range Prophage Endolysin Reveals a C-Terminal □Helix with the Proposed Role in Activity against Live Bacterial Cells. *Viruses*, **2018**, 10,	6.2	11
50	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	5.8	21
49	Structure and gene cluster of the K125 capsular polysaccharide from Acinetobacter baumannii MAR13-1452. *International Journal of Biological Macromolecules*, **2018**, 117, 1195-1199	7.9	13

48	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	2.9	9
47	Structure and Analysis of R1 and R2 Pyocin Receptor-Binding Fibers. *Viruses*, **2018**, 10,	6.2	17
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	2.9	15
45	Function of bacteriophage G7C esterase tailspike in host cell adsorption. *Molecular Microbiology*, **2017**, 105, 385-398	4.1	45
44	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	2.9	19
43	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	7.9	32
42	Ability of phages to infect Acinetobacter calcoaceticus-Acinetobacter baumannii complex species through acquisition of different pectate lyase depolymerase domains. *Environmental Microbiology*, **2017**, 19, 5060-5077	5.2	52
41	Novel Fri1-like Viruses Infecting Acinetobacter baumannii-vB_AbaP_AS11 and vB_AbaP_AS12-Characterization, Comparative Genomic Analysis, and Host-Recognition Strategy. *Viruses*, **2017**, 9,	6.2	26
40	The O-specific polysaccharide lyase from the phage LKA1 tailspike reduces Pseudomonas virulence. *Scientific Reports*, **2017**, 7, 16302	4.9	53
39	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	2.9	25
38	Structure of the N-acetylpseudaminic acid-containing capsular polysaccharide of Acinetobacter baumannii NIPH67. *Russian Chemical Bulletin*, **2016**, 65, 588-591	1.7	8
37	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	2.9	25
36	Acinetobacter baumannii K27 and K44 capsular polysaccharides have the same K unit but different structures due to the presence of distinct wzy genes in otherwise closely related K gene clusters. *Glycobiology*, **2016**, 26, 501-8	5.8	41
35	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	2.9	33
34	Structure of the T4 baseplate and its function in triggering sheath contraction. *Nature*, **2016**, 533, 346-52	50.4	158
33	Structure of a new pseudaminic acid-containing capsular polysaccharide of Acinetobacter baumannii LUH5550 having the KL42 capsule biosynthesis locus. *Carbohydrate Research*, **2015**, 407, 154-7	2.9	28
32	Structure elucidation of the capsular polysaccharide of Acinetobacter baumannii AB5075 having the KL25 capsule biosynthesis locus. *Carbohydrate Research*, **2015**, 408, 8-11	2.9	36
31	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, 81-8	2.9	26

30	Structure of the capsular polysaccharide of Acinetobacter baumannii 1053 having the KL91 capsule biosynthesis gene locus. *Carbohydrate Research*, **2015**, 404, 79-82	2.9	19
29	Structure and Biophysical Properties of a Triple-Stranded Beta-Helix Comprising the Central Spike of Bacteriophage T4. *Viruses*, **2015**, 7, 4676-706	6.2	5
28	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	8.4	29
27	Structure of the neutral capsular polysaccharide of Acinetobacter baumannii NIPH146 that carries the KL37 capsule gene cluster. *Carbohydrate Research*, **2015**, 413, 12-5	2.9	29
26	Revised structure of the capsular polysaccharide of Acinetobacter baumannii LUH5533 (serogroup O1) containing di-N-acetyllegionaminic acid. *Russian Chemical Bulletin*, **2015**, 64, 1196-1199	1.7	15
25	Listeria phage A511, a model for the contractile tail machineries of SPO1-related bacteriophages. *Molecular Microbiology*, **2014**, 92, 84-99	4.1	46
24	Structure of the capsular polysaccharide of Acinetobacter baumannii ACICU containing di-N-acetylpseudaminic acid. *Carbohydrate Research*, **2014**, 391, 89-92	2.9	45
23	Complete Genome Sequence of the Novel Giant Pseudomonas Phage PaBG. *Genome Announcements*, **2014**, 2,		15
22	Peptidoglycan degrading activity of the broad-range Salmonella bacteriophage S-394 recombinant endolysin. *Biochimie*, **2014**, 107 Pt B, 293-9	4.6	26
21	PAAR-repeat proteins sharpen and diversify the type VI secretion system spike. *Nature*, **2013**, 500, 350-353	50.4	324
20	Phage pierces the host cell membrane with the iron-loaded spike. *Structure*, **2012**, 20, 326-39	5.2	66
19	Crystal structure and location of gp131 in the bacteriophage phiKZ virion. *Virology*, **2012**, 434, 257-64	3.6	14
18	Contractile tail machines of bacteriophages. *Advances in Experimental Medicine and Biology*, **2012**, 726, 93-114	3.6	137
17	The tail sheath structure of bacteriophage T4: a molecular machine for infecting bacteria. *EMBO Journal*, **2012**, 31, 3507-3507	13	3
16	The structure of gene product 6 of bacteriophage T4, the hinge-pin of the baseplate. *Structure*, **2009**, 17, 800-8	5.2	26
15	The tail sheath structure of bacteriophage T4: a molecular machine for infecting bacteria. *EMBO Journal*, **2009**, 28, 821-9	13	108
14	Structure of the bacteriophage phi KZ lytic transglycosylase gp144. *Journal of Biological Chemistry*, **2008**, 283, 7242-50	5.4	44
13	From structure of the complex to understanding of the biology. *Acta Crystallographica Section D: Biological Crystallography*, **2007**, 63, 9-16		14

12	Evolution of bacteriophage tails: Structure of T4 gene product 10. *Journal of Molecular Biology*, **2006**, 358, 912-21	6.5	32
11	Functional role of the N-terminal domain of bacteriophage T4 gene product 11. *Biochemistry (Moscow)*, **2005**, 70, 1111-8	2.9	1
10	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, 7163-8	11.5	172
9	Molecular architecture of bacteriophage T4. *Biochemistry (Moscow)*, **2004**, 69, 1190-202	2.9	22
8	Structure and location of gene product 8 in the bacteriophage T4 baseplate. *Journal of Molecular Biology*, **2003**, 328, 821-33	6.5	30
7	Properties of bacteriophage T4 baseplate protein encoded by gene 8. *Biochemistry (Moscow)*, **2001**, 66, 693-7	2.9	5
6	Transformation of a fragment of beta-structural bacteriophage T4 adhesin to stable alpha-helical trimer. *Biochemistry (Moscow)*, **2000**, 65, 1346-51	2.9	6
5	Structure of bacteriophage T4 gene product 11, the interface between the baseplate and short tail fibers. *Journal of Molecular Biology*, **2000**, 301, 975-85	6.5	48
4	Structure of bacteriophage T4 fibritin M: a troublesome packing arrangement. *Acta Crystallographica Section D: Biological Crystallography*, **1998**, 54, 805-16		17
3	Preliminary crystallographic studies of bacteriophage T4 fibritin confirm a trimeric coiled-coil structure. *Virology*, **1996**, 219, 190-4	3.6	18
2	Evolution of T4-related phages. *Virus Genes*, **1995**, 11, 285-97	2.3	63
1	Crystal Structure of the putative tail fiber protein gp53 from the Acinetobacter baumannii bacteriophage AP22		1