

# Mikhail M Shneider

## List of Publications by Citations

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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	PAAR-repeat proteins sharpen and diversify the type VI secretion system spike. <i>Nature</i> , <b>2013</b> , 500, 350-353	53.4	324
82	Structural and functional similarities between the capsid proteins of bacteriophages T4 and HK97 point to a common ancestry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 7163-8	11.5	172
81	Structure of the T4 baseplate and its function in triggering sheath contraction. <i>Nature</i> , <b>2016</b> , 533, 346-350	50.4	158
80	Contractile tail machines of bacteriophages. <i>Advances in Experimental Medicine and Biology</i> , <b>2012</b> , 726, 93-114	3.6	137
79	The tail sheath structure of bacteriophage T4: a molecular machine for infecting bacteria. <i>EMBO Journal</i> , <b>2009</b> , 28, 821-9	13	108
78	Phage pierces the host cell membrane with the iron-loaded spike. <i>Structure</i> , <b>2012</b> , 20, 326-39	5.2	66
77	Evolution of T4-related phages. <i>Virus Genes</i> , <b>1995</b> , 11, 285-97	2.3	63
76	The O-specific polysaccharide lyase from the phage LKA1 tailspike reduces <i>Pseudomonas</i> virulence. <i>Scientific Reports</i> , <b>2017</b> , 7, 16302	4.9	53
75	Ability of phages to infect <i>Acinetobacter calcoaceticus</i> - <i>Acinetobacter baumannii</i> complex species through acquisition of different pectate lyase depolymerase domains. <i>Environmental Microbiology</i> , <b>2017</b> , 19, 5060-5077	5.2	52
74	Structure of bacteriophage T4 gene product 11, the interface between the baseplate and short tail fibers. <i>Journal of Molecular Biology</i> , <b>2000</b> , 301, 975-85	6.5	48
73	Listeria phage A511, a model for the contractile tail machineries of SPO1-related bacteriophages. <i>Molecular Microbiology</i> , <b>2014</b> , 92, 84-99	4.1	46
72	Function of bacteriophage G7C esterase tailspike in host cell adsorption. <i>Molecular Microbiology</i> , <b>2017</b> , 105, 385-398	4.1	45
71	Structure of the capsular polysaccharide of <i>Acinetobacter baumannii</i> ACICU containing di-N-acetylpsseudaminic acid. <i>Carbohydrate Research</i> , <b>2014</b> , 391, 89-92	2.9	45
70	Structure of the bacteriophage phi KZ lytic transglycosylase gp144. <i>Journal of Biological Chemistry</i> , <b>2008</b> , 283, 7242-50	5.4	44
69	<i>Acinetobacter baumannii</i> K27 and K44 capsular polysaccharides have the same K unit but different structures due to the presence of distinct <i>wzy</i> genes in otherwise closely related K gene clusters. <i>Glycobiology</i> , <b>2016</b> , 26, 501-8	5.8	41
68	Structure elucidation of the capsular polysaccharide of <i>Acinetobacter baumannii</i> AB5075 having the KL25 capsule biosynthesis locus. <i>Carbohydrate Research</i> , <b>2015</b> , 408, 8-11	2.9	36
67	K19 capsular polysaccharide of <i>Acinetobacter baumannii</i> is produced via a Wzy polymerase encoded in a small genomic island rather than the KL19 capsule gene cluster. <i>Microbiology (United Kingdom)</i> , <b>2016</b> , 162, 1479-1489	2.9	33

66	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. <i>International Journal of Biological Macromolecules</i> , <b>2017</b> , 103, 648-655	7.9	32
65	Evolution of bacteriophage tails: Structure of T4 gene product 10. <i>Journal of Molecular Biology</i> , <b>2006</b> , 358, 912-21	6.5	32
64	Structure and location of gene product 8 in the bacteriophage T4 baseplate. <i>Journal of Molecular Biology</i> , <b>2003</b> , 328, 821-33	6.5	30
63	Structural Relationship of the Lipid A Acyl Groups to Activation of Murine Toll-Like Receptor 4 by Lipopolysaccharides from Pathogenic Strains of <i>Burkholderia mallei</i> , <i>Acinetobacter baumannii</i> , and <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Immunology</i> , <b>2015</b> , 6, 595	8.4	29
62	Structure of the neutral capsular polysaccharide of <i>Acinetobacter baumannii</i> NIPH146 that carries the KL37 capsule gene cluster. <i>Carbohydrate Research</i> , <b>2015</b> , 413, 12-5	2.9	29
61	Structure of a new pseudaminic acid-containing capsular polysaccharide of <i>Acinetobacter baumannii</i> LUH5550 having the KL42 capsule biosynthesis locus. <i>Carbohydrate Research</i> , <b>2015</b> , 407, 154-7-9	7.9	28
60	Structure and Function of the Branched Receptor-Binding Complex of Bacteriophage CBA120. <i>Journal of Molecular Biology</i> , <b>2019</b> , 431, 3718-3739	6.5	28
59	Structures of three different neutral polysaccharides of <i>Acinetobacter baumannii</i> , NIPH190, NIPH201, and NIPH615, assigned to K30, K45, and K48 capsule types, respectively, based on capsule biosynthesis gene clusters. <i>Carbohydrate Research</i> , <b>2015</b> , 417, 81-8	2.9	26
58	Novel Fri1-like Viruses Infecting <i>Acinetobacter baumannii</i> -vB_AbaP_AS11 and vB_AbaP_AS12-Characterization, Comparative Genomic Analysis, and Host-Recognition Strategy. <i>Viruses</i> , <b>2017</b> , 9,	6.2	26
57	Peptidoglycan degrading activity of the broad-range <i>Salmonella</i> bacteriophage S-394 recombinant endolysin. <i>Biochimie</i> , <b>2014</b> , 107 Pt B, 293-9	4.6	26
56	The structure of gene product 6 of bacteriophage T4, the hinge-pin of the baseplate. <i>Structure</i> , <b>2009</b> , 17, 800-8	5.2	26
55	Related structures of neutral capsular polysaccharides of <i>Acinetobacter baumannii</i> isolates that carry related capsule gene clusters KL43, KL47, and KL88. <i>Carbohydrate Research</i> , <b>2016</b> , 435, 173-179	2.9	25
54	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 <i>Acinetobacter baumannii</i> isolate RCH51. <i>Microbiology (United Kingdom)</i> , <b>2017</b> , 163, 355-363	2.9	25
53	Molecular architecture of bacteriophage T4. <i>Biochemistry (Moscow)</i> , <b>2004</b> , 69, 1190-202	2.9	22
52	<i>Acinetobacter baumannii</i> K20 and K21 capsular polysaccharide structures establish roles for UDP-glucose dehydrogenase Ugd2, pyruvyl transferase Ptr2 and two glycosyltransferases. <i>Glycobiology</i> , <b>2018</b> , 28, 876-884	5.8	21
51	Structures of the K35 and K15 capsular polysaccharides of <i>Acinetobacter baumannii</i> LUH5535 and LUH5554 containing amino and diamino uronic acids. <i>Carbohydrate Research</i> , <b>2017</b> , 448, 28-34	2.9	19
50	Structure of the capsular polysaccharide of <i>Acinetobacter baumannii</i> 1053 having the KL91 capsule biosynthesis gene locus. <i>Carbohydrate Research</i> , <b>2015</b> , 404, 79-82	2.9	19
49	Action of a minimal contractile bactericidal nanomachine. <i>Nature</i> , <b>2020</b> , 580, 658-662	50.4	19

48	Preliminary crystallographic studies of bacteriophage T4 fibritin confirm a trimeric coiled-coil structure. <i>Virology</i> , <b>1996</b> , 219, 190-4	3.6	18
47	Structure of bacteriophage T4 fibritin M: a troublesome packing arrangement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>1998</b> , 54, 805-16		17
46	Structure and transformation of bacteriophage A511 baseplate and tail upon infection of $\lambda$ cells. <i>EMBO Journal</i> , <b>2019</b> , 38,	13	17
45	Structure and Analysis of R1 and R2 Pyocin Receptor-Binding Fibers. <i>Viruses</i> , <b>2018</b> , 10,	6.2	17
44	Structure and Gene Cluster of the K93 Capsular Polysaccharide of <i>Acinetobacter baumannii</i> B11911 Containing 5-N-Acetyl-7-N-[(R)-3-hydroxybutanoyl]pseudaminic Acid. <i>Biochemistry (Moscow)</i> , <b>2017</b> , 82, 483-489	2.9	15
43	Revised structure of the capsular polysaccharide of <i>Acinetobacter baumannii</i> LUH5533 (serogroup O1) containing di-N-acetyllegionaminic acid. <i>Russian Chemical Bulletin</i> , <b>2015</b> , 64, 1196-1199	1.7	15
42	Complete Genome Sequence of the Novel Giant <i>Pseudomonas</i> Phage PaBG. <i>Genome Announcements</i> , <b>2014</b> , 2,		15
41	Crystal structure and location of gp131 in the bacteriophage phiKZ virion. <i>Virology</i> , <b>2012</b> , 434, 257-64	3.6	14
40	From structure of the complex to understanding of the biology. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2007</b> , 63, 9-16		14
39	The K46 and K5 capsular polysaccharides produced by <i>Acinetobacter baumannii</i> NIPH 329 and SDF have related structures and the side-chain non-ulonic acids are 4-O-acetylated by phage-encoded O-acetyltransferases. <i>PLoS ONE</i> , <b>2019</b> , 14, e0218461	3.7	13
38	Structure and gene cluster of the K125 capsular polysaccharide from <i>Acinetobacter baumannii</i> MAR13-1452. <i>International Journal of Biological Macromolecules</i> , <b>2018</b> , 117, 1195-1199	7.9	13
37	<i>Acinetobacter baumannii</i> K116 capsular polysaccharide structure is a hybrid of the K14 and revised K37 structures. <i>Carbohydrate Research</i> , <b>2019</b> , 484, 107774	2.9	13
36	K17 capsular polysaccharide produced by <i>Acinetobacter baumannii</i> isolate G7 contains an amide of 2-acetamido-2-deoxy-d-galacturonic acid with d-alanine. <i>International Journal of Biological Macromolecules</i> , <b>2020</b> , 144, 857-862	7.9	13
35	Production of the K16 capsular polysaccharide by <i>Acinetobacter baumannii</i> ST25 isolate D4 involves a novel glycosyltransferase encoded in the KL16 gene cluster. <i>International Journal of Biological Macromolecules</i> , <b>2019</b> , 128, 101-106	7.9	12
34	Characterization of myophage AM24 infecting <i>Acinetobacter baumannii</i> of the K9 capsular type. <i>Archives of Virology</i> , <b>2019</b> , 164, 1493-1497	2.6	12
33	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. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 3288	5.7	12
32	The K90 capsular polysaccharide produced by <i>Acinetobacter baumannii</i> LUH5553 contains di-N-acetylpsudaminic acid and is structurally related to the K7 polysaccharide from <i>A. baumannii</i> LUH5533. <i>Carbohydrate Research</i> , <b>2019</b> , 479, 1-5	2.9	11
31	Structure of an Broad-Range Prophage Endolysin Reveals a C-Terminal $\beta$ -Helix with the Proposed Role in Activity against Live Bacterial Cells. <i>Viruses</i> , <b>2018</b> , 10,	6.2	11

30	Characterization of Pectobacterium carotovorum subsp. carotovorum Bacteriophage PP16 Prospective for Biocontrol of Potato Soft Rot. <i>Microbiology</i> , <b>2019</b> , 88, 451-460	1.4	9
29	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. <i>Carbohydrate Research</i> , <b>2019</b> , 483, 107745	2.9	9
28	Genetics of biosynthesis and structure of the K53 capsular polysaccharide of Acinetobacter baumannii D23 made up of a disaccharide K unit. <i>Microbiology (United Kingdom)</i> , <b>2018</b> , 164, 1289-1292	2.9	9
27	Structure of the K128 capsular polysaccharide produced by Acinetobacter baumannii KZ-1093 from Kazakhstan. <i>Carbohydrate Research</i> , <b>2019</b> , 485, 107814	2.9	8
26	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. <i>Russian Chemical Bulletin</i> , <b>2019</b> , 68, 163-167	1.7	8
25	Structure of the N-acetyl pseudaminic acid-containing capsular polysaccharide of Acinetobacter baumannii NIPH67. <i>Russian Chemical Bulletin</i> , <b>2016</b> , 65, 588-591	1.7	8
24	Morphologically Different Bacteriophages PP99 and PP101: Deacetylation of O-Polysaccharide by the Tail Spike Protein of Phage PP99 Accompanies the Infection. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 3147	5.7	8
23	Involvement of a multifunctional rhamnosyltransferase in the synthesis of three related Acinetobacter baumannii capsular polysaccharides, K55, K74 and K85. <i>International Journal of Biological Macromolecules</i> , <b>2021</b> , 166, 1230-1237	7.9	8
22	Complete Genome Sequence of Acinetobacter baumannii Phage BS46. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,	1.3	7
21	Genomic characteristics of vB_PpaP_PP74, a T7-like Autographivirinae bacteriophage infecting a potato pathogen of the newly proposed species Pectobacterium parmentieri. <i>Archives of Virology</i> , <b>2018</b> , 163, 1691-1694	2.6	7
20	Transformation of a fragment of beta-structural bacteriophage T4 adhesin to stable alpha-helical trimer. <i>Biochemistry (Moscow)</i> , <b>2000</b> , 65, 1346-51	2.9	6
19	Structure and Biophysical Properties of a Triple-Stranded Beta-Helix Comprising the Central Spike of Bacteriophage T4. <i>Viruses</i> , <b>2015</b> , 7, 4676-706	6.2	5
18	Properties of bacteriophage T4 baseplate protein encoded by gene 8. <i>Biochemistry (Moscow)</i> , <b>2001</b> , 66, 693-7	2.9	5
17	Origin and Evolution of Bacteriophages Infecting : Horizontal Transfer Assists Adaptation to New Niches. <i>Microorganisms</i> , <b>2020</b> , 8,	4.9	5
16	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. <i>Research in Microbiology</i> , <b>2021</b> , 172, 103815	4	5
15	Novel Myovirus TaPaz Encoding Two Tailspike Depolymerases: Characterization and Host-Recognition Strategy. <i>Viruses</i> , <b>2021</b> , 13,	6.2	5
14	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. <i>International Journal of Biological Macromolecules</i> , <b>2021</b> , 193, 1294-1294	7.9	4
13	Novel Bacteriophage Aristophanes Encoding Structural Polysaccharide Deacetylase. <i>Viruses</i> , <b>2021</b> , 13,	6.2	4

12	The tail sheath structure of bacteriophage T4: a molecular machine for infecting bacteria. <i>EMBO Journal</i> , <b>2012</b> , 31, 3507-3507	13	3
11	The K26 capsular polysaccharide from <i>Acinetobacter baumannii</i> KZ-1098: Structure and cleavage by a specific phage depolymerase. <i>International Journal of Biological Macromolecules</i> , <b>2021</b> , 191, 182-191	7.9	3
10	Bacteriophage Arno 160 Infects via Depolymerization of the Bacterial O-Polysaccharide. <i>International Journal of Molecular Sciences</i> , <b>2020</b> , 21,	6.3	2
9	Structure of the K87 capsular polysaccharide and KL87 gene cluster of <i>Acinetobacter baumannii</i> LUH5547 reveals a heptasaccharide repeating unit. <i>Carbohydrate Research</i> , <b>2021</b> , 509, 108439	2.9	2
8	Capsule-Targeting Depolymerases Derived from Prophage Regions.. <i>International Journal of Molecular Sciences</i> , <b>2022</b> , 23,	6.3	2
7	Involvement of a Phage-Encoded Wzy Protein in the Polymerization of K127 Units To Form the Capsular Polysaccharide of <i>Acinetobacter baumannii</i> Isolate 36-1454.. <i>Microbiology Spectrum</i> , <b>2022</b> , e0150321	8.9	2
6	Draft Genome Sequence of <i>Pectobacterium atrosepticum</i> PB72 and Complete Genome Sequence of the Specific Bacteriophage PP90. <i>Genome Announcements</i> , <b>2018</b> , 6,		1
5	Functional role of the N-terminal domain of bacteriophage T4 gene product 11. <i>Biochemistry (Moscow)</i> , <b>2005</b> , 70, 1111-8	2.9	1
4	The K139 capsular polysaccharide produced by <i>Acinetobacter baumannii</i> MAR17-1041 belongs to a group of related structures including K14, K37 and K116. <i>International Journal of Biological Macromolecules</i> , <b>2021</b> , 193, 2297-2297	7.9	1
3	Crystal Structure of the putative tail fiber protein gp53 from the <i>Acinetobacter baumannii</i> bacteriophage AP22		1
2	<i>Curtobacterium</i> spp. and <i>Curtobacterium flaccumfaciens</i> : Phylogeny, Genomics-Based Taxonomy, Pathogenicity, and Diagnostics. <i>Current Issues in Molecular Biology</i> , <b>2022</b> , 44, 889-927	2.9	1
1	Note Identification of 5,7-diacetamido-3,5,7,9-tetra-deoxy-d-glycero-l-manno-non-2-ulosonic acid (di-N-acetyl-8-epipseudaminic acid) in the capsular polysaccharide of <i>Acinetobacter baumannii</i> Res546.. <i>Carbohydrate Research</i> , <b>2022</b> , 513, 108531	2.9	0