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List of Publications by Year in descending order

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papers

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#	ARTICLE	IF	CITATIONS
1	Curtobacterium spp. and Curtobacterium flaccumfaciens: Phylogeny, Genomics-Based Taxonomy, Pathogenicity, and Diagnostics. <i>Current Issues in Molecular Biology</i> , 2022, 44, 889-927.	2.4	15
2	Notelidentification 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 <i>Acinetobacter baumannii</i> Res546. <i>Carbohydrate Research</i> , 2022, 513, 108531.	2.3	3
3	Capsule-Targeting Depolymerases Derived from <i>Acinetobacter baumannii</i> Prophage Regions. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4971.	4.1	9
4	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> , 2022, 10, e0150321.	3.0	7
5	Evolution of Phage Tail Sheath Protein. <i>Viruses</i> , 2022, 14, 1148.	3.3	8
6	The K89 capsular polysaccharide produced by <i>Acinetobacter baumannii</i> LUH5552 consists of a pentameric repeat-unit that includes a 3-acetamido-3,6-dideoxy-d-galactose residue. <i>International Journal of Biological Macromolecules</i> , 2022, 217, 515-521.	7.5	2
7	Involvement of a multifunctional rhamnosyltransferase in the synthesis of three related <i>Acinetobacter baumannii</i> capsular polysaccharides, K55, K74 and K85. <i>International Journal of Biological Macromolecules</i> , 2021, 166, 1230-1237.	7.5	17
8	A novel ItrA4 d-galactosyl 1-phosphate transferase is predicted to initiate synthesis of an amino sugar-lacking K92 capsular polysaccharide of <i>Acinetobacter baumannii</i> B8300. <i>Research in Microbiology</i> , 2021, 172, 103815.	2.1	8
9	Novel <i>Acinetobacter baumannii</i> Myovirus TaPaz Encoding Two Tailspike Depolymerases: Characterization and Host-Recognition Strategy. <i>Viruses</i> , 2021, 13, 978.	3.3	7
10	Novel <i>Acinetobacter baumannii</i> Bacteriophage Aristophanes Encoding Structural Polysaccharide Deacetylase. <i>Viruses</i> , 2021, 13, 1688.	3.3	9
11	Gene Analysis, Cloning, and Heterologous Expression of Protease from a Micromycete <i>Aspergillus ochraceus</i> Capable of Activating Protein C of Blood Plasma. <i>Microorganisms</i> , 2021, 9, 1936.	3.6	2
12	<i>Pseudomonas</i> Phage MD8: Genetic Mosaicism and Challenges of Taxonomic Classification of Lambdaoid Bacteriophages. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10350.	4.1	10
13	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> , 2021, 191, 182-191.	7.5	16
14	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> , 2021, 509, 108439.	2.3	7
15	Correlation of <i>Acinetobacter baumannii</i> 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> , 2021, 193, 1294-1300.	7.5	10
16	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> , 2021, 193, 2297-2303.	7.5	5
17	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> , 2020, 144, 857-862.	7.5	32
18	Origin and Evolution of Studiervirinae Bacteriophages Infecting <i>Pectobacterium</i> : Horizontal Transfer Assists Adaptation to New Niches. <i>Microorganisms</i> , 2020, 8, 1707.	3.6	20

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19	The Central Spike Complex of Bacteriophage T4 Contacts PpiD in the Periplasm of Escherichia coli. <i>Viruses</i> , 2020, 12, 1135.	3.3	4
20	Autographivirinae Bacteriophage Arno 160 Infects <i>Pectobacterium carotovorum</i> via Depolymerization of the Bacterial O-Polysaccharide. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3170.	4.1	12
21	Complete Genome Sequence of <i>Acinetobacter baumannii</i> Phage BS46. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	10
22	Action of a minimal contractile bactericidal nanomachine. <i>Nature</i> , 2020, 580, 658-662.	27.8	61
23	Characterization of <i>Pectobacterium carotovorum</i> subsp. <i>carotovorum</i> Bacteriophage PP16 Prospective for Biocontrol of Potato Soft Rot. <i>Microbiology</i> , 2019, 88, 451-460.	1.2	27
24	<i>Acinetobacter baumannii</i> K116 capsular polysaccharide structure is a hybrid of the K14 and revised K37 structures. <i>Carbohydrate Research</i> , 2019, 484, 107774.	2.3	26
25	K units of the K8 and K54 capsular polysaccharides produced by <i>Acinetobacter baumannii</i> 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> , 2019, 483, 107745.	2.3	17
26	Structure and Function of the Branched Receptor-Binding Complex of Bacteriophage CBA120. <i>Journal of Molecular Biology</i> , 2019, 431, 3718-3739.	4.2	67
27	Structure of the K128 capsular polysaccharide produced by <i>Acinetobacter baumannii</i> KZ-1093 from Kazakhstan. <i>Carbohydrate Research</i> , 2019, 485, 107814.	2.3	13
28	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> , 2019, 128, 101-106.	7.5	19
29	The K46 and K5 capsular polysaccharides produced by <i>Acinetobacter baumannii</i> NIPH 329 and SDF have related structures and the side-chain non-ulosonic acids are 4-O-acetylated by phage-encoded O-acetyltransferases. <i>PLoS ONE</i> , 2019, 14, e0218461.	2.5	26
30	The K90 capsular polysaccharide produced by <i>Acinetobacter baumannii</i> LUH5553 contains di-N-acetylpsseudaminic acid and is structurally related to the K7 polysaccharide from <i>A. baumannii</i> LUH5533. <i>Carbohydrate Research</i> , 2019, 479, 1-5.	2.3	18
31	The K5 capsular polysaccharide of the bacterium <i>Acinetobacter baumannii</i> 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> , 2019, 68, 163-167.	1.5	13
32	Characterization of myophage AM24 infecting <i>Acinetobacter baumannii</i> of the K9 capsular type. <i>Archives of Virology</i> , 2019, 164, 1493-1497.	2.1	18
33	Structure and transformation of bacteriophage A511 baseplate and tail upon infection of <i>Listeria</i> cells. <i>EMBO Journal</i> , 2019, 38, .	7.8	34
34	Morphologically Different <i>Pectobacterium brasiliense</i> Bacteriophages PP99 and PP101: Deacetylation of O-Polysaccharide by the Tail Spike Protein of Phage PP99 Accompanies the Infection. <i>Frontiers in Microbiology</i> , 2019, 10, 3147.	3.5	33
35	Genomic characteristics of vB_PpaP_PP74, a T7-like Autographivirinae bacteriophage infecting a potato pathogen of the newly proposed species <i>Pectobacterium parmentieri</i> . <i>Archives of Virology</i> , 2018, 163, 1691-1694.	2.1	9
36	Structure and Analysis of R1 and R2 Pyocin Receptor-Binding Fibers. <i>Viruses</i> , 2018, 10, 427.	3.3	35

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37	Draft Genome Sequence of <i>Pectobacterium atrosepticum</i> PB72 and Complete Genome Sequence of the Specific Bacteriophage PP90. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
38	Structure of an <i>Acinetobacter</i> Broad-Range Prophage Endolysin Reveals a C-Terminal α -Helix with the Proposed Role in Activity against Live Bacterial Cells. <i>Viruses</i> , 2018, 10, 309.	3.3	23
39	<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> , 2018, 28, 876-884.	2.5	28
40	Structure and gene cluster of the K125 capsular polysaccharide from <i>Acinetobacter baumannii</i> MAR13-1452. <i>International Journal of Biological Macromolecules</i> , 2018, 117, 1195-1199.	7.5	19
41	Host Specificity of the <i>Dickeya</i> Bacteriophage PP35 Is Directed by a Tail Spike Interaction With Bacterial O-Antigen, Enabling the Infection of Alternative Non-pathogenic Bacterial Host. <i>Frontiers in Microbiology</i> , 2018, 9, 3288.	3.5	28
42	Genetics of biosynthesis and structure of the K53 capsular polysaccharide of <i>Acinetobacter baumannii</i> D23 made up of a disaccharide K unit. <i>Microbiology (United Kingdom)</i> , 2018, 164, 1289-1292.	1.8	13
43	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> , 2017, 82, 483-489.	1.5	21
44	Function of bacteriophage G7C esterase tailspike in host cell adsorption. <i>Molecular Microbiology</i> , 2017, 105, 385-398.	2.5	84
45	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> , 2017, 448, 28-34.	2.3	43
46	<i>Acinetobacter baumannii</i> K11 and K83 capsular polysaccharides have the same 6-deoxy- α -D-galactose-containing pentasaccharide K units but different linkages between the K units. <i>International Journal of Biological Macromolecules</i> , 2017, 103, 648-655.	7.5	43
47	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> , 2017, 19, 5060-5077.	3.8	81
48	The O-specific polysaccharide lyase from the phage LKA1 tailspike reduces <i>Pseudomonas</i> virulence. <i>Scientific Reports</i> , 2017, 7, 16302.	3.3	88
49	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> , 2017, 9, 188.	3.3	35
50	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> , 2017, 163, 355-363.	1.8	29
51	Structure of the T4 baseplate and its function in triggering sheath contraction. <i>Nature</i> , 2016, 533, 346-352.	27.8	231
52	Structure of the N-acetylpseudaminic acid-containing capsular polysaccharide of <i>Acinetobacter baumannii</i> NIPH67. <i>Russian Chemical Bulletin</i> , 2016, 65, 588-591.	1.5	14
53	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> , 2016, 435, 173-179.	2.3	33
54	<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> , 2016, 26, 501-508.	2.5	68

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55	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> , 2016, 162, 1479-1489.	1.8	41
56	Structure and Biophysical Properties of a Triple-Stranded Beta-Helix Comprising the Central Spike of Bacteriophage T4. <i>Viruses</i> , 2015, 7, 4676-4706.	3.3	9
57	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> , 2015, 6, 595.	4.8	51
58	Structure of the neutral capsular polysaccharide of <i>Acinetobacter baumannii</i> NIPH146 that carries the KL37 capsule gene cluster. <i>Carbohydrate Research</i> , 2015, 413, 12-15.	2.3	37
59	Revised structure of the capsular polysaccharide of <i>Acinetobacter baumannii</i> LUH5533 (serogroup O1) containing di-N-acetylglucosaminic acid. <i>Russian Chemical Bulletin</i> , 2015, 64, 1196-1199.	1.5	21
60	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> , 2015, 407, 154-157.	2.3	53
61	Structure elucidation of the capsular polysaccharide of <i>Acinetobacter baumannii</i> AB5075 having the KL25 capsule biosynthesis locus. <i>Carbohydrate Research</i> , 2015, 408, 8-11.	2.3	42
62	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> , 2015, 417, 81-88.	2.3	31
63	Structure of the capsular polysaccharide of <i>Acinetobacter baumannii</i> 1053 having the KL91 capsule biosynthesis gene locus. <i>Carbohydrate Research</i> , 2015, 404, 79-82.	2.3	21
64	Complete Genome Sequence of the Novel Giant <i>Pseudomonas</i> Phage PaBG. <i>Genome Announcements</i> , 2014, 2, .	0.8	17
65	Peptidoglycan degrading activity of the broad-range <i>Salmonella</i> bacteriophage S-394 recombinant endolysin. <i>Biochimie</i> , 2014, 107, 293-299.	2.6	31
66	<i>Escherichia coli</i> phage λ C, a model for the contractile tail machineries of λ -related bacteriophages. <i>Molecular Microbiology</i> , 2014, 92, 84-99.	2.5	55
67	Structure of the capsular polysaccharide of <i>Acinetobacter baumannii</i> ACICU containing di-N-acetylglucosaminic acid. <i>Carbohydrate Research</i> , 2014, 391, 89-92.	2.3	51
68	Central spike proteins of contractile ejection systems. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C579-C579.	0.1	0
69	PAAR-repeat proteins sharpen and diversify the type VI secretion system spike. <i>Nature</i> , 2013, 500, 350-353.	27.8	466
70	The tail sheath structure of bacteriophage T4: a molecular machine for infecting bacteria. <i>EMBO Journal</i> , 2012, 31, 3507-3507.	7.8	3
71	Crystal structure and location of gp131 in the bacteriophage phiKZ virion. <i>Virology</i> , 2012, 434, 257-264.	2.4	14
72	Contractile Tail Machines of Bacteriophages. <i>Advances in Experimental Medicine and Biology</i> , 2012, 726, 93-114.	1.6	170

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73	Phage Pierces the Host Cell Membrane with the Iron-Loaded Spike. <i>Structure</i> , 2012, 20, 326-339.	3.3	77
74	Crystal structure of gpV - the bacteriophage P2 cell-puncturing device. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2010, 66, s24-s25.	0.3	0
75	The Structure of Gene Product 6 of Bacteriophage T4, the Hinge-Pin of the Baseplate. <i>Structure</i> , 2009, 17, 800-808.	3.3	30
76	The tail sheath structure of bacteriophage T4: a molecular machine for infecting bacteria. <i>EMBO Journal</i> , 2009, 28, 821-829.	7.8	133
77	Structure of the Bacteriophage ϕ KZ Lytic Transglycosylase gp144. <i>Journal of Biological Chemistry</i> , 2008, 283, 7242-7250.	3.4	48
78	From structure of the complex to understanding of the biology. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 9-16.	2.5	17
79	Evolution of Bacteriophage Tails: Structure of T4 Gene Product 10. <i>Journal of Molecular Biology</i> , 2006, 358, 912-921.	4.2	35
80	Functional Role of the N-Terminal Domain of Bacteriophage T4-Gene Product 11. <i>Biochemistry (Moscow)</i> , 2005, 70, 1111-1118.	1.5	2
81	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> , 2005, 102, 7163-7168.	7.1	189
82	Molecular architecture of bacteriophage T4. <i>Biochemistry (Moscow)</i> , 2004, 69, 1190-1202.	1.5	23
83	Structure and Location of Gene Product 8 in the Bacteriophage T4 Baseplate. <i>Journal of Molecular Biology</i> , 2003, 328, 821-833.	4.2	32
84	Properties of bacteriophage T4 baseplate protein encoded by gene 8. <i>Biochemistry (Moscow)</i> , 2001, 66, 693-697.	1.5	7
85	Transformation of a fragment of beta-structural bacteriophage T4 adhesin to stable alpha-helical trimer. <i>Biochemistry (Moscow)</i> , 2000, 65, 1346-1351.	1.5	7
86	Structure of bacteriophage T4 gene product 11, the interface between the baseplate and short tail fibers 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 2000, 301, 975-985.	4.2	52
87	Structure of Bacteriophage T4 Fibrin M: a Troublesome Packing Arrangement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 805-816.	2.5	18
88	Preliminary Crystallographic Studies of Bacteriophage T4 Fibrin Confirm a Trimeric Coiled-Coil Structure. <i>Virology</i> , 1996, 219, 190-194.	2.4	19
89	Evolution of T4-related phages. <i>Virus Genes</i> , 1995, 11, 285-297.	1.6	80