

Andrey V Karlyshev

List of Publications by Year in descending order

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papers

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docs citations

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times ranked

5594
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#	ARTICLE	IF	CITATIONS
1	The genome sequence of the food-borne pathogen <i>Campylobacter jejuni</i> reveals hypervariable sequences. <i>Nature</i> , 2000, 403, 665-668.	13.7	1,869
2	Genome sequence of <i>Yersinia pestis</i> , the causative agent of plague. <i>Nature</i> , 2001, 413, 523-527.	13.7	1,144
3	Quorum sensing in <i>Aeromonas hydrophila</i> and <i>Aeromonas salmonicida</i> : identification of the LuxRI homologs AhyRI and AsaRI and their cognate N-acylhomoserine lactone signal molecules. <i>Journal of Bacteriology</i> , 1997, 179, 5271-5281.	1.0	381
4	Whole Genome Comparison of <i>Campylobacter jejuni</i> Human Isolates Using a Low-Cost Microarray Reveals Extensive Genetic Diversity. <i>Genome Research</i> , 2001, 11, 1706-1715.	2.4	278
5	Genetic and biochemical evidence of a <i>Campylobacter jejuni</i> capsular polysaccharide that accounts for Penner serotype specificity. <i>Molecular Microbiology</i> , 2002, 35, 529-541.	1.2	228
6	Biofilm formation in <i>Campylobacter jejuni</i> . <i>Microbiology (United Kingdom)</i> , 2006, 152, 387-396.	0.7	215
7	Functional analysis of the <i>Campylobacter jejuni</i> N-linked protein glycosylation pathway. <i>Molecular Microbiology</i> , 2005, 55, 1695-1703.	1.2	193
8	Adaptation of <i>Campylobacter jejuni</i> NCTC11168 to High-Level Colonization of the Avian Gastrointestinal Tract. <i>Infection and Immunity</i> , 2004, 72, 3769-3776.	1.0	162
9	The <i>Campylobacter jejuni</i> general glycosylation system is important for attachment to human epithelial cells and in the colonization of chicks. <i>Microbiology (United Kingdom)</i> , 2004, 150, 1957-1964.	0.7	162
10	Analysis of <i>Campylobacter jejuni</i> capsular loci reveals multiple mechanisms for the generation of structural diversity and the ability to form complex heptoses. <i>Molecular Microbiology</i> , 2004, 55, 90-103.	1.2	162
11	A novel paralogous gene family involved in phase-variable flagella-mediated motility in <i>Campylobacter jejuni</i> . <i>Microbiology (United Kingdom)</i> , 2002, 148, 473-480.	0.7	149
12	Multiple N-acetyl neuraminic acid synthetase (<i>neuB</i>) genes in <i>Campylobacter jejuni</i> : identification and characterization of the gene involved in sialylation of lipo-oligosaccharide. <i>Molecular Microbiology</i> , 2000, 35, 1120-1134.	1.2	128
13	Identification of N-acetylgalactosamine-containing glycoproteins PEB3 and CgpA in <i>Campylobacter jejuni</i> . <i>Molecular Microbiology</i> , 2002, 43, 497-508.	1.2	121
14	<i>Campylobacter jejuni</i> Glycosylation Island Important in Cell Charge, Legionaminic Acid Biosynthesis, and Colonization of Chickens. <i>Infection and Immunity</i> , 2009, 77, 2544-2556.	1.0	121
15	A <i>Caenorhabditis elegans</i> model of <i>Yersinia</i> infection: biofilm formation on a biotic surface. <i>Microbiology (United Kingdom)</i> , 2003, 149, 3221-3229.	0.7	120
16	Nucleotide sequence of the <i>Yersinia pestis</i> gene encoding F1 antigen and the primary structure of the protein. <i>FEBS Letters</i> , 1990, 277, 230-232.	1.3	106
17	Development and Application of an Insertional System for Gene Delivery and Expression in <i>Campylobacter jejuni</i> . <i>Applied and Environmental Microbiology</i> , 2005, 71, 4004-4013.	1.4	93
18	Expression of the envelope antigen F1 of <i>Yersinia pestis</i> is mediated by the product of <i>caf1M</i> gene having homology with the chaperone protein PapD of <i>Escherichia coli</i> . <i>FEBS Letters</i> , 1991, 286, 79-82.	1.3	91

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19	Application of High-Density Array-Based Signature-Tagged Mutagenesis To Discover Novel <i>Yersinia</i> Virulence-Associated Genes. <i>Infection and Immunity</i> , 2001, 69, 7810-7819.	1.0	91
20	<i>Galleria mellonella</i> as an alternative infection model for <i>Yersinia pseudotuberculosis</i> . <i>Microbiology (United Kingdom)</i> , 2009, 155, 1516-1522.	0.7	91
21	Single-Primer PCR Procedure for Rapid Identification of Transposon Insertion Sites. <i>BioTechniques</i> , 2000, 28, 1078-1082.	0.8	90
22	The glycome. <i>FEMS Microbiology Reviews</i> , 2005, 29, 377-390.	3.9	88
23	Commonality and Biosynthesis of the O-Methyl Phosphoramidate Capsule Modification in <i>Campylobacter jejuni</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 28566-28576.	1.6	86
24	Detection and Initial Characterization of Novel Capsular Polysaccharide among Diverse <i>Campylobacter jejuni</i> Strains Using Alcian Blue Dye. <i>Journal of Clinical Microbiology</i> , 2001, 39, 279-284.	1.8	81
25	A new gene of the ϵ' 1 operon of <i>Y. pestis</i> involved in the capsule biogenesis. <i>FEBS Letters</i> , 1992, 297, 77-80.	1.3	80
26	Demonstration of Polysaccharide Capsule in <i>Campylobacter jejuni</i> Using Electron Microscopy. <i>Infection and Immunity</i> , 2001, 69, 5921-5924.	1.0	76
27	Insect Infection Model for <i>Campylobacter jejuni</i> Reveals That O-methyl Phosphoramidate Has Insecticidal Activity. <i>Journal of Infectious Diseases</i> , 2010, 201, 100129142112076-000.	1.9	72
28	Virulent non-capsulate <i>Yersinia pestis</i> variants constructed by insertion mutagenesis. <i>Journal of Medical Microbiology</i> , 1995, 42, 264-268.	0.7	65
29	Specific high affinity binding of human interleukin 1β by Caf1A usher protein of <i>Yersinia pestis</i> . <i>FEBS Letters</i> , 1995, 371, 65-68.	1.3	64
30	Protection of particular cleavage sites of restriction endonucleases by distamycin A and actinomycin D. <i>Nucleic Acids Research</i> , 1976, 3, 2293-2302.	6.5	60
31	Caf1R gene and its role in the regulation of capsule formation of <i>Y. pestis</i> . <i>FEBS Letters</i> , 1992, 305, 37-40.	1.3	55
32	Biological Roles of the O-Methyl Phosphoramidate Capsule Modification in <i>Campylobacter jejuni</i> . <i>PLoS ONE</i> , 2014, 9, e87051.	1.1	48
33	Characterization of <i>Lactobacillus fermentum</i> UCO-979C, a probiotic strain with a potent anti- <i>Helicobacter pylori</i> activity. <i>Electronic Journal of Biotechnology</i> , 2017, 25, 75-83.	1.2	46
34	Influence of the conserved disulphide bond, exposed to the putative binding pocket, on the structure and function of the immunoglobulin-like molecular chaperone Caf1M of <i>Yersinia pestis</i> . <i>Biochemical Journal</i> , 1997, 324, 571-578.	1.7	44
35	Deciphering <i>Campylobacter jejuni</i> cell surface interactions from the genome sequence. <i>Current Opinion in Microbiology</i> , 2001, 4, 35-40.	2.3	43
36	<i>Yersinia pseudotuberculosis</i> mntH functions in intracellular manganese accumulation, which is essential for virulence and survival in cells expressing functional Nramp1. <i>Microbiology (United Kingdom)</i> , 2007, 151, 107-115.	1.0	40

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37	Probiotic Properties of <i>Lactobacillus crispatus</i> 2,029: Homeostatic Interaction with Cervicovaginal Epithelial Cells and Antagonistic Activity to Genitourinary Pathogens. <i>Probiotics and Antimicrobial Proteins</i> , 2014, 6, 165-176.	1.9	41
38	<i>Campylobacter jejuni</i> Cocultured with Epithelial Cells Reduces Surface Capsular Polysaccharide Expression. <i>Infection and Immunity</i> , 2009, 77, 1959-1967.	1.0	37
39	<i>Lactobacillus fermentum</i> 3872 as a potential tool for combatting <i>Campylobacter jejuni</i> infections. <i>Virulence</i> , 2017, 8, 1753-1760.	1.8	36
40	CmeABC Multidrug Efflux Pump Contributes to Antibiotic Resistance and Promotes <i>Campylobacter jejuni</i> Survival and Multiplication in <i>Acanthamoeba polyphaga</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	34
41	Cloning and study of the genetic organization of the <i>exe</i> gene cluster of <i>Aeromonas salmonicida</i> . <i>Gene</i> , 1995, 158, 77-82.	1.0	32
42	Molecular mechanisms and biological role of <i>Campylobacter jejuni</i> attachment to host cells. <i>European Journal of Microbiology and Immunology</i> , 2012, 2, 32-40.	1.5	31
43	Structural and Functional Significance of the FGL Sequence of the Periplasmic Chaperone Caf1M of <i>Yersinia pestis</i> . <i>Journal of Bacteriology</i> , 1999, 181, 2422-2429.	1.0	30
44	Putative mechanisms and biological role of coccoid form formation in <i>Campylobacter jejuni</i> . <i>European Journal of Microbiology and Immunology</i> , 2012, 2, 41-49.	1.5	27
45	The <i>Campylobacter jejuni</i> glycome. <i>FEMS Microbiology Reviews</i> , 2005, 29, 377-390.	3.9	24
46	<i>Campylobacter jejuni</i> gene <i>cj0511</i> encodes a serine peptidase essential for colonisation. <i>FEBS Open Bio</i> , 2014, 4, 468-472.	1.0	23
47	<i>Lactobacillus fermentum</i> 3872 genome sequencing reveals plasmid and chromosomal genes potentially involved in a probiotic activity. <i>FEMS Microbiology Letters</i> , 2015, 362, .	0.7	21
48	<i>Campylobacter</i> – <i>Acanthamoeba</i> interactions. <i>Microbiology (United Kingdom)</i> , 2015, 161, 933-947.	0.7	21
49	Potential probiotic-associated traits revealed from completed high quality genome sequence of <i>Lactobacillus fermentum</i> 3872. <i>Standards in Genomic Sciences</i> , 2017, 12, 19.	1.5	21
50	An improved physical and genetic map of <i>Campylobacter jejuni</i> NCTC 11168 (UA580). <i>Microbiology (United Kingdom)</i> , 1998, 144, 503-508.	0.7	19
51	Steps toward broad-spectrum therapeutics: discovering virulence-associated genes present in diverse human pathogens. <i>BMC Genomics</i> , 2009, 10, 501.	1.2	18
52	S-layer protein 2 of <i>Lactobacillus crispatus</i> 2029, its structural and immunomodulatory characteristics and roles in protective potential of the whole bacteria against foodborne pathogens. <i>International Journal of Biological Macromolecules</i> , 2020, 150, 400-412.	3.6	17
53	The role of apolipoprotein N-acyl transferase, Lnt, in the lipidation of factor H binding protein of <i>Neisseria meningitidis</i> strain MC58 and its potential as a drug target. <i>British Journal of Pharmacology</i> , 2017, 174, 2247-2260.	2.7	16
54	<i>Cohnella kolymensis</i> sp. nov., a novel bacillus isolated from Siberian permafrost. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2912-2917.	0.8	16

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55	Draft Genome Sequence of <i>Bacillus amyloliquefaciens</i> B-1895. <i>Genome Announcements</i> , 2014, 2, .	0.8	15
56	Whole Genome Sequence of <i>Dermacoccus abyssi</i> MT1.1 Isolated from the Challenger Deep of the Mariana Trench Reveals Phenazine Biosynthesis Locus and Environmental Adaptation Factors. <i>Marine Drugs</i> , 2020, 18, 131.	2.2	15
57	Post genome analysis of <i>Campylobacter jejuni</i> . <i>Journal of Applied Microbiology</i> , 2001, 90, 36S-44S.	1.4	14
58	Draft Genome Sequence of <i>Lactobacillus fermentum</i> Strain 3872. <i>Genome Announcements</i> , 2013, 1, .	0.8	13
59	The Effectiveness of Potential Probiotics <i>Lactobacillus rhamnosus</i> Vahe and <i>Lactobacillus delbrueckii</i> IAHAH1 in Irradiated Rats Depends on the Nutritional Stage of the Host. <i>Probiotics and Antimicrobial Proteins</i> , 2020, 12, 1439-1450.	1.9	13
60	Draft Genome Sequence of <i>Corynebacterium pseudodiphtheriticum</i> Strain 090104 "Sokolov". <i>Genome Announcements</i> , 2013, 1, .	0.8	12
61	A negative effect of <i>Campylobacter</i> capsule on bacterial interaction with an analogue of a host cell receptor. <i>BMC Microbiology</i> , 2014, 14, 141.	1.3	12
62	Variant Signal Peptides of Vaccine Antigen, FHbp, Impair Processing Affecting Surface Localization and Antibody-Mediated Killing in Most Meningococcal Isolates. <i>Frontiers in Microbiology</i> , 2019, 10, 2847.	1.5	12
63	Procedure for the Investigation of Bacterial Genomes: Random Shot-Gun Cloning, Sample Sequencing and Mutagenesis of <i>Campylobacter jejuni</i> . <i>BioTechniques</i> , 1999, 26, 50-56.	0.8	11
64	Unusual features in organisation of capsular polysaccharide-related genes of <i>C. jejuni</i> strain X. <i>Gene</i> , 2013, 522, 37-45.	1.0	11
65	Whole genome sequencing of four bacterial strains from South Shetland Trench revealing biosynthetic and environmental adaptation gene clusters. <i>Marine Genomics</i> , 2020, 54, 100782.	0.4	11
66	Biotechnological and Ecological Potential of <i>Micromonospora provocatoris</i> sp. nov., a Gifted Strain Isolated from the Challenger Deep of the Mariana Trench. <i>Marine Drugs</i> , 2021, 19, 243.	2.2	10
67	Draft Genome Sequence of <i>Bacillus subtilis</i> strain KATMIRA1933. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
68	Cationic amphiphiles against <i>Gardnerella vaginalis</i> resistant strains and bacterial vaginosis-associated pathogens. <i>Pathogens and Disease</i> , 2019, 77, .	0.8	9
69	Regulation of restriction endonuclease activity with antibiotics. <i>Advances in Enzyme Regulation</i> , 1979, 17, 307-321.	2.9	8
70	Remarkable Features of Mitochondrial DNA of <i>Acanthamoeba polyphaga</i> Linc Ap-1, Revealed by Whole-Genome Sequencing. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	8
71	Study of the intergenic <i>exf</i> - <i>exg</i> region and its application as a simple preliminary test for <i>Aeromonas</i> spp.. <i>FEMS Microbiology Letters</i> , 1996, 137, 37-44.	0.7	6
72	Insight into proteomic investigations of <i>Neisseria meningitidis</i> serogroup C strain L91543 from analysis of its genome sequence. <i>FEMS Microbiology Letters</i> , 2015, 362, .	0.7	6

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73	The hidden perils of read mapping as a quality assessment tool in genome sequencing. Scientific Reports, 2017, 7, 43149.	1.6	5
74	Binding of LcrV protein from <i>Yersinia pestis</i> to human T-cells induces apoptosis, which is completely blocked by specific antibodies. International Journal of Biological Macromolecules, 2019, 122, 1062-1070.	3.6	5
75	S-layer protein 2 of vaginal <i>Lactobacillus crispatus</i> 2029 enhances growth, differentiation, VEGF production and barrier functions in intestinal epithelial cell line Caco-2. International Journal of Biological Macromolecules, 2021, 189, 410-419.	3.6	5
76	Signature-tagged Mutagenesis of <i>Yersinia pestis</i> . Advances in Experimental Medicine and Biology, 2004, 529, 39-42.	0.8	4
77	Draft Genome Sequence of <i>Lactobacillus crispatus</i> 2029. Genome Announcements, 2014, 2, .	0.8	4
78	Draft Genome Sequence of a Probiotic Strain, <i>Lactobacillus fermentum</i> UCO-979C. Genome Announcements, 2015, 3, .	0.8	4
79	Specific genetic features of <i>Campylobacter jejuni</i> strain G1 revealed by genome sequencing. FEMS Microbiology Letters, 2015, 362, 1-3.	0.7	4
80	Draft Genome Sequence of <i>Lactobacillus jensenii</i> Strain MD IIE-70(2). Genome Announcements, 2013, 1, .	0.8	3
81	Draft Genome Sequence of <i>Lactobacillus plantarum</i> 2165. Genome Announcements, 2014, 2, .	0.8	3
82	<i>Campylobacter jejuni</i> Capsular Polysaccharide. , 0, , 505-521.		3
83	Whole-Genome Sequencing of Xanthomonadaceae Strain Alg18-2.2, Isolated from the Saline Lake Gudzhirganskoe in the Republic of Buryatia, Russia. Microbiology Resource Announcements, 2019, 8, .	0.3	2
84	Draft Genome Sequence of <i>Lactobacillus plantarum</i> 2025. Genome Announcements, 2016, 4, .	0.8	1
85	Draft Genome Sequence of <i>Cohnella kolyensis</i> B-2846. Genome Announcements, 2016, 4, .	0.8	1
86	YPTB3816 of <i>Yersinia pseudotuberculosis</i> strain IP32953 is a virulence-related metallo-oligopeptidase. BMC Microbiology, 2016, 16, 282.	1.3	1
87	Complete Genome Sequence of <i>Campylobacter jejuni</i> Strain G1, Isolated from a Patient with Guillain-Barré Syndrome. Microbiology Resource Announcements, 2021, 10, e0050521.	0.3	1
88	Draft Genome Sequence of <i>Coralloluteibacterium stylophorae</i> LMG 29479 T. Microbiology Resource Announcements, 2021, 10, e0042121.	0.3	1
89	Complete Genome Sequencing of <i>Campylobacter jejuni</i> Strain X Reveals the Presence of pVir- and pTet-like Plasmids. Microbiology Resource Announcements, 0, , .	0.3	1
90	Further strategies for signature-tagged mutagenesis and the application of oligonucleotide microarrays for the quantification of DNA-tagged strains. Methods in Microbiology, 2002, 33, 167-184.	0.4	0

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91	Draft Genome Sequence of <i>Lactobacillus gasseri</i> Strain 2016. <i>Genome Announcements</i> , 2013, 1, .	0.8	0
92	Draft Genome Sequence of <i>Enterococcus faecalis</i> MB5259. <i>Genome Announcements</i> , 2014, 2, .	0.8	0
93	Draft Genome Sequence of <i>Lactobacillus rhamnosus</i> 2166. <i>Genome Announcements</i> , 2014, 2, .	0.8	0
94	Expression of <i>Escherichia coli</i> <i>araE</i> and modified <i>lacY</i> genes in <i>Campylobacter jejuni</i> is not sufficient for arabinose transport. <i>Access Microbiology</i> , 2019, 1, e000042.	0.2	0