Andrey V Karlyshev

List of Publications by Year in Descending Order

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Version: 2024-04-20

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

6,554 80 89 35 h-index g-index citations papers 7,135 4.94 95 5.5 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
89	Biotechnological and Ecological Potential of sp. nov., a Gifted Strain Isolated from the Challenger Deep of the Mariana Trench. <i>Marine Drugs</i> , 2021 , 19,	6	4
88	Complete Genome Sequence of Campylobacter jejuni Strain G1, Isolated from a Patient with Guillain-Barr Syndrome. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0050521	1.3	
87	Draft Genome Sequence of LMG 29479. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0042121	1.3	O
86	S-layer protein 2 of vaginal Lactobacillus crispatus 2029 enhances growth, differentiation, VEGF production and barrier functions in intestinal epithelial cell line Caco-2. <i>International Journal of Biological Macromolecules</i> , 2021 , 189, 410-419	7.9	1
85	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	1.9	6
84	The Effectiveness of Potential Probiotics Lactobacillus rhamnosus Vahe and Lactobacillus delbrueckii IAHAHI in Irradiated Rats Depends on the Nutritional Stage of the Host. <i>Probiotics and Antimicrobial Proteins</i> , 2020 , 12, 1439-1450	5.5	6
83	Whole Genome Sequence of 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,	6	9
82	S-layer protein 2 of Lactobacillus crispatus 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	7.9	9
81	Remarkable Features of Mitochondrial DNA of Acanthamoeba polyphaga Linc Ap-1, Revealed by Whole-Genome Sequencing. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	6
80	Cationic amphiphiles against Gardnerella vaginalis resistant strains and bacterial vaginosis-associated pathogens. <i>Pathogens and Disease</i> , 2019 , 77,	4.2	8
79	Expression of and modified genes in is not sufficient for arabinose transport. <i>Access Microbiology</i> , 2019 , 1, e000042	1	
78	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	5.7	10
77	Binding of LcrV protein from Yersinia pestis to human T-cells induces apoptosis, which is completely blocked by specific antibodies. <i>International Journal of Biological Macromolecules</i> , 2019 , 122, 1062-1070	7.9	5
76	Cohnella kolymensis sp. nov., a novel bacillus isolated from Siberian permafrost. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018 , 68, 2912-2917	2.2	9
75	The hidden perils of read mapping as a quality assessment tool in genome sequencing. <i>Scientific Reports</i> , 2017 , 7, 43149	4.9	4
74	Potential probiotic-associated traits revealed from completed high quality genome sequence of 3872. Standards in Genomic Sciences, 2017 , 12, 19		9
73	CmeABC Multidrug Efflux Pump Contributes to Antibiotic Resistance and Promotes Campylobacter jejuni Survival and Multiplication in Acanthamoeba polyphaga. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	18

(2014-2017)

	Lactobacillus fermentum 3872 as a potential tool for combatting Campylobacter jejuni infections. <i>Virulence</i> , 2017 , 8, 1753-1760	4.7	20	
71	The role of apolipoprotein N-acyl transferase, Lnt, in the lipidation of factor H binding protein of Neisseria meningitidis strain MC58 and its potential as a drug target. <i>British Journal of Pharmacology</i> , 2017 , 174, 2247-2260	8.6	12	
70	Characterization of Lactobacillus fermentum UCO-979C, a probiotic strain with a potent anti-Helicobacter pylori activity. <i>Electronic Journal of Biotechnology</i> , 2017 , 25, 75-83	3.1	28	
69	YPTB3816 of Yersinia pseudotuberculosis strain IP32953 is a virulence-related metallo-oligopeptidase. <i>BMC Microbiology</i> , 2016 , 16, 282	4.5	1	
68	Draft Genome Sequence of Lactobacillus plantarum 2025. Genome Announcements, 2016, 4,		1	
67	Draft Genome Sequence of "Cohnella kolymensis" B-2846. <i>Genome Announcements</i> , 2016 , 4,		1	
66	Insight into proteomic investigations of Neisseria meningitidis serogroup C strain L91543 from analysis of its genome sequence. <i>FEMS Microbiology Letters</i> , 2015 , 362,	2.9	3	
65	Specific genetic features of Campylobacter jejuni strain G1 revealed by genome sequencing. <i>FEMS Microbiology Letters</i> , 2015 , 362,	2.9	4	
64	Campylobacter-Acanthamoeba interactions. <i>Microbiology (United Kingdom)</i> , 2015 , 161, 933-947	2.9	14	
63	Draft Genome Sequence of a Probiotic Strain, Lactobacillus fermentum UCO-979C. <i>Genome Announcements</i> , 2015 , 3,		4	
62	Lactobacillus fermentum 3872 genome sequencing reveals plasmid and chromosomal genes potentially involved in a probiotic activity. <i>FEMS Microbiology Letters</i> , 2015 , 362,	2.9	14	
61	A negative effect of Campylobacter capsule on bacterial interaction with an analogue of a host cell receptor. <i>BMC Microbiology</i> , 2014 , 14, 141	4.5	9	
	Campylobacter jejuni gene cj0511 encodes a serine peptidase essential for colonisation. FEBS Open			
60	Bio, 2014 , 4, 468-72	2.7	15	
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	Bio, 2014 , 4, 468-72	2.7 3.7		
59	Bio, 2014, 4, 468-72 Campylobacter jejuni Capsular Polysaccharide 2014, 505-521 Biological roles of the O-methyl phosphoramidate capsule modification in Campylobacter jejuni.	ŕ	3	
59 58	Bio, 2014, 4, 468-72 Campylobacter jejuni Capsular Polysaccharide 2014, 505-521 Biological roles of the O-methyl phosphoramidate capsule modification in Campylobacter jejuni. PLoS ONE, 2014, 9, e87051	ŕ	3 41	

54	Probiotic Properties of Lactobacillus crispatus 2,029: Homeostatic Interaction with Cervicovaginal Epithelial Cells and Antagonistic Activity to Genitourinary Pathogens. <i>Probiotics and Antimicrobial Proteins</i> , 2014 , 6, 165-76	5.5	30
53	Draft Genome Sequence of Lactobacillus plantarum 2165. <i>Genome Announcements</i> , 2014 , 2,		3
52	Unusual features in organisation of capsular polysaccharide-related genes of C. jejuni strain X. <i>Gene</i> , 2013 , 522, 37-45	3.8	9
51	Draft Genome Sequence of Lactobacillus jensenii Strain MD IIE-70(2). <i>Genome Announcements</i> , 2013 , 1,		2
50	Draft Genome Sequence of Lactobacillus fermentum Strain 3872. <i>Genome Announcements</i> , 2013 , 1,		12
49	Draft Genome Sequence of Corynebacterium pseudodiphtheriticum Strain 090104 "Sokolov". <i>Genome Announcements</i> , 2013 , 1,		7
48	Putative mechanisms and biological role of coccoid form formation in Campylobacter jejuni. <i>European Journal of Microbiology and Immunology</i> , 2012 , 2, 41-9	4.6	21
47	Molecular mechanisms and biological role of Campylobacter jejuni attachment to host cells. European Journal of Microbiology and Immunology, 2012 , 2, 32-40	4.6	25
46	Yersinia pseudotuberculosis mntH functions in intracellular manganese accumulation, which is essential for virulence and survival in cells expressing functional Nramp1. <i>Microbiology (United Kingdom)</i> , 2011 , 157, 1115-1122	2.9	35
45	Insect infection model for Campylobacter jejuni reveals that O-methyl phosphoramidate has insecticidal activity. <i>Journal of Infectious Diseases</i> , 2010 , 201, 776-82	7	60
44	Galleria mellonella as an alternative infection model for Yersinia pseudotuberculosis. <i>Microbiology</i> (United Kingdom), 2009 , 155, 1516-1522	2.9	80
43	Campylobacter jejuni glycosylation island important in cell charge, legionaminic acid biosynthesis, and colonization of chickens. <i>Infection and Immunity</i> , 2009 , 77, 2544-56	3.7	103
42	Campylobacter jejuni cocultured with epithelial cells reduces surface capsular polysaccharide expression. <i>Infection and Immunity</i> , 2009 , 77, 1959-67	3.7	30
41	Steps toward broad-spectrum therapeutics: discovering virulence-associated genes present in diverse human pathogens. <i>BMC Genomics</i> , 2009 , 10, 501	4.5	18
40	Commonality and biosynthesis of the O-methyl phosphoramidate capsule modification in Campylobacter jejuni. <i>Journal of Biological Chemistry</i> , 2007 , 282, 28566-28576	5.4	74
39	Biofilm formation in Campylobacter jejuni. <i>Microbiology (United Kingdom)</i> , 2006 , 152, 387-396	2.9	185
38	Analysis of Campylobacter jejuni capsular loci reveals multiple mechanisms for the generation of structural diversity and the ability to form complex heptoses. <i>Molecular Microbiology</i> , 2005 , 55, 90-103	4.1	147
37	TheCampylobacter jejuniglycome. <i>FEMS Microbiology Reviews</i> , 2005 , 29, 377-390	15.1	14

(2000-2005)

36	Functional analysis of the Campylobacter jejuni N-linked protein glycosylation pathway. <i>Molecular Microbiology</i> , 2005 , 55, 1695-703	4.1	165
35	The Campylobacter jejuni glycome. FEMS Microbiology Reviews, 2005 , 29, 377-90	15.1	67
34	Development and application of an insertional system for gene delivery and expression in Campylobacter jejuni. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 4004-13	4.8	81
33	Adaptation of Campylobacter jejuni NCTC11168 to high-level colonization of the avian gastrointestinal tract. <i>Infection and Immunity</i> , 2004 , 72, 3769-76	3.7	143
32	The Campylobacter jejuni 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	2.9	146
31	A Caenorhabditis elegans model of Yersinia infection: biofilm formation on a biotic surface. <i>Microbiology (United Kingdom)</i> , 2003 , 149, 3221-3229	2.9	100
30	Signature-tagged mutagenesis of Yersinia pestis. <i>Advances in Experimental Medicine and Biology</i> , 2003 , 529, 39-41	3.6	4
29	Identification of N-acetylgalactosamine-containing glycoproteins PEB3 and CgpA in Campylobacter jejuni. <i>Molecular Microbiology</i> , 2002 , 43, 497-508	4.1	114
28	Further strategies for signature-tagged mutagenesis and the application of oligonucleotide microarrays for the quantification of DNA-tagged strains. <i>Methods in Microbiology</i> , 2002 , 33, 167-184	2.8	
27	A novel paralogous gene family involved in phase-variable flagella-mediated motility in Campylobacter jejuni. <i>Microbiology (United Kingdom)</i> , 2002 , 148, 473-480	2.9	133
26	Post genome analysis of Campylobacter jejuni. <i>Journal of Applied Microbiology</i> , 2001 , 90, 36S-44S	4.7	10
25	Genome sequence of Yersinia pestis, the causative agent of plague. <i>Nature</i> , 2001 , 413, 523-7	50.4	1003
24	Demonstration of polysaccharide capsule in Campylobacter jejuni using electron microscopy. <i>Infection and Immunity</i> , 2001 , 69, 5921-4	3.7	70
23	Detection and initial characterization of novel capsular polysaccharide among diverse Campylobacter jejuni strains using alcian blue dye. <i>Journal of Clinical Microbiology</i> , 2001 , 39, 279-84	9.7	72
22	Application of high-density array-based signature-tagged mutagenesis to discover novel Yersinia virulence-associated genes. <i>Infection and Immunity</i> , 2001 , 69, 7810-9	3.7	80
21	Whole genome comparison of Campylobacter jejuni human isolates using a low-cost microarray reveals extensive genetic diversity. <i>Genome Research</i> , 2001 , 11, 1706-15	9.7	246
20	Deciphering Campylobacter jejuni cell surface interactions from the genome sequence. <i>Current Opinion in Microbiology</i> , 2001 , 4, 35-40	7.9	41
19	Genetic and biochemical evidence of a Campylobacter jejuni capsular polysaccharide that accounts for Penner serotype specificity. <i>Molecular Microbiology</i> , 2000 , 35, 529-41	4.1	198

18	Multiple N-acetyl neuraminic acid synthetase (neuB) genes in Campylobacter jejuni: identification and characterization of the gene involved in sialylation of lipo-oligosaccharide. <i>Molecular Microbiology</i> , 2000 , 35, 1120-34	4.1	121
17	The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences. <i>Nature</i> , 2000 , 403, 665-8	50.4	1628
16	Single-primer PCR procedure for rapid identification of transposon insertion sites. <i>BioTechniques</i> , 2000 , 28, 1078, 1080, 1082	2.5	83
15	Procedure for the investigation of bacterial genomes: random shot-gun cloning, sample sequencing and mutagenesis of Campylobacter jejuni. <i>BioTechniques</i> , 1999 , 26, 50-2, 54, 56	2.5	11
14	Structural and functional significance of the FGL sequence of the periplasmic chaperone Caf1M of Yersinia pestis. <i>Journal of Bacteriology</i> , 1999 , 181, 2422-9	3.5	28
13	An improved physical and genetic map of Campylobacter jejuni NCTC 11168 (UA580). <i>Microbiology</i> (United Kingdom), 1998 , 144 (Pt 2), 503-508	2.9	12
12	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 Yersinia pestis. <i>Biochemical Journal</i> , 1997 , 324 (Pt 2), 571-8	3.8	40
11	Quorum sensing in Aeromonas hydrophila and Aeromonas salmonicida: identification of the LuxRI homologs AhyRI and AsaRI and their cognate N-acylhomoserine lactone signal molecules. <i>Journal of Bacteriology</i> , 1997 , 179, 5271-81	3.5	338
10	Study of the intergenic exeF-exeG region and its application as a simple preliminary test for Aeromonas spp. <i>FEMS Microbiology Letters</i> , 1996 , 137, 37-44	2.9	5
9	Virulent non-capsulate Yersinia pestis variants constructed by insertion mutagenesis. <i>Journal of Medical Microbiology</i> , 1995 , 42, 264-8	3.2	50
8	Cloning and study of the genetic organization of the exe gene cluster of Aeromonas salmonicida. <i>Gene</i> , 1995 , 158, 77-82	3.8	29
7	Specific high affinity binding of human interleukin 1 beta by Caf1A usher protein of Yersinia pestis. <i>FEBS Letters</i> , 1995 , 371, 65-8	3.8	54
6	A new gene of the f1 operon of Y. pestis involved in the capsule biogenesis. <i>FEBS Letters</i> , 1992 , 297, 77-80	3.8	61
5	Caf1R gene and its role in the regulation of capsule formation of Y. pestis. FEBS Letters, 1992 , 305, 37-4	10 3.8	45
4	Expression of the envelope antigen F1 of Yersinia pestis is mediated by the product of caf1M gene having homology with the chaperone protein PapD of Escherichia coli. <i>FEBS Letters</i> , 1991 , 286, 79-82	3.8	73
3	Nucleotide sequence of the Yersinia pestis gene encoding F1 antigen and the primary structure of the protein. Putative T and B cell epitopes. <i>FEBS Letters</i> , 1990 , 277, 230-2	3.8	87
2	Regulation of restriction endonuclease activity with antibiotics. <i>Advances in Enzyme Regulation</i> , 1978 , 17, 307-21		7
1	Protection of particular cleavage sites of restriction endonucleases by distamycin A and actinomycin D. <i>Nucleic Acids Research</i> , 1976 , 3, 2293-301	20.1	56