Andrey V Karlyshev

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

#	Paper	IF	Citations
89	The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences. *Nature*, **2000**, 403, 665-8	50.4	1628
88	Genome sequence of Yersinia pestis, the causative agent of plague. *Nature*, **2001**, 413, 523-7	50.4	1003
87	Quorum sensing in Aeromonas hydrophila and Aeromonas salmonicida: identification of the LuxRI homologs AhyRI and AsaRI and their cognate N-acylhomoserine lactone signal molecules. *Journal of Bacteriology*, **1997**, 179, 5271-81	3.5	338
86	Whole genome comparison of Campylobacter jejuni human isolates using a low-cost microarray reveals extensive genetic diversity. *Genome Research*, **2001**, 11, 1706-15	9.7	246
85	Genetic and biochemical evidence of a Campylobacter jejuni capsular polysaccharide that accounts for Penner serotype specificity. *Molecular Microbiology*, **2000**, 35, 529-41	4.1	198
84	Biofilm formation in Campylobacter jejuni. *Microbiology (United Kingdom)*, **2006**, 152, 387-396	2.9	185
83	Functional analysis of the Campylobacter jejuni N-linked protein glycosylation pathway. *Molecular Microbiology*, **2005**, 55, 1695-703	4.1	165
82	Analysis of Campylobacter jejuni capsular loci reveals multiple mechanisms for the generation of structural diversity and the ability to form complex heptoses. *Molecular Microbiology*, **2005**, 55, 90-103	4.1	147
81	The Campylobacter jejuni general glycosylation system is important for attachment to human epithelial cells and in the colonization of chicks. *Microbiology (United Kingdom)*, **2004**, 150, 1957-1964	2.9	146
80	Adaptation of Campylobacter jejuni NCTC11168 to high-level colonization of the avian gastrointestinal tract. *Infection and Immunity*, **2004**, 72, 3769-76	3.7	143
79	A novel paralogous gene family involved in phase-variable flagella-mediated motility in Campylobacter jejuni. *Microbiology (United Kingdom)*, **2002**, 148, 473-480	2.9	133
78	Multiple N-acetyl neuraminic acid synthetase (neuB) genes in Campylobacter jejuni: identification and characterization of the gene involved in sialylation of lipo-oligosaccharide. *Molecular Microbiology*, **2000**, 35, 1120-34	4.1	121
77	Identification of N-acetylgalactosamine-containing glycoproteins PEB3 and CgpA in Campylobacter jejuni. *Molecular Microbiology*, **2002**, 43, 497-508	4.1	114
76	Campylobacter jejuni glycosylation island important in cell charge, legionaminic acid biosynthesis, and colonization of chickens. *Infection and Immunity*, **2009**, 77, 2544-56	3.7	103
75	A Caenorhabditis elegans model of Yersinia infection: biofilm formation on a biotic surface. *Microbiology (United Kingdom)*, **2003**, 149, 3221-3229	2.9	100
74	Nucleotide sequence of the Yersinia pestis gene encoding F1 antigen and the primary structure of the protein. Putative T and B cell epitopes. *FEBS Letters*, **1990**, 277, 230-2	3.8	87
73	Single-primer PCR procedure for rapid identification of transposon insertion sites. *BioTechniques*, **2000**, 28, 1078, 1080, 1082	2.5	83

72	Development and application of an insertional system for gene delivery and expression in Campylobacter jejuni. *Applied and Environmental Microbiology*, **2005**, 71, 4004-13	4.8	81
71	Galleria mellonella as an alternative infection model for Yersinia pseudotuberculosis. *Microbiology (United Kingdom)*, **2009**, 155, 1516-1522	2.9	80
70	Application of high-density array-based signature-tagged mutagenesis to discover novel Yersinia virulence-associated genes. *Infection and Immunity*, **2001**, 69, 7810-9	3.7	80
69	Commonality and biosynthesis of the O-methyl phosphoramidate capsule modification in Campylobacter jejuni. *Journal of Biological Chemistry*, **2007**, 282, 28566-28576	5.4	74
68	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. *FEBS Letters*, **1991**, 286, 79-82	3.8	73
67	Detection and initial characterization of novel capsular polysaccharide among diverse Campylobacter jejuni strains using alcian blue dye. *Journal of Clinical Microbiology*, **2001**, 39, 279-84	9.7	72
66	Demonstration of polysaccharide capsule in Campylobacter jejuni using electron microscopy. *Infection and Immunity*, **2001**, 69, 5921-4	3.7	70
65	The Campylobacter jejuni glycome. *FEMS Microbiology Reviews*, **2005**, 29, 377-90	15.1	67
64	A new gene of the f1 operon of Y. pestis involved in the capsule biogenesis. *FEBS Letters*, **1992**, 297, 77-80	3.8	61
63	Insect infection model for Campylobacter jejuni reveals that O-methyl phosphoramidate has insecticidal activity. *Journal of Infectious Diseases*, **2010**, 201, 776-82	7	60
62	Protection of particular cleavage sites of restriction endonucleases by distamycin A and actinomycin D. *Nucleic Acids Research*, **1976**, 3, 2293-301	20.1	56
61	Specific high affinity binding of human interleukin 1 beta by Caf1A usher protein of Yersinia pestis. *FEBS Letters*, **1995**, 371, 65-8	3.8	54
60	Virulent non-capsulate Yersinia pestis variants constructed by insertion mutagenesis. *Journal of Medical Microbiology*, **1995**, 42, 264-8	3.2	50
59	Caf1R gene and its role in the regulation of capsule formation of Y. pestis. *FEBS Letters*, **1992**, 305, 37-40	3.8	45
58	Biological roles of the O-methyl phosphoramidate capsule modification in Campylobacter jejuni. *PLoS ONE*, **2014**, 9, e87051	3.7	41
57	Deciphering Campylobacter jejuni cell surface interactions from the genome sequence. *Current Opinion in Microbiology*, **2001**, 4, 35-40	7.9	41
56	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. *Biochemical Journal*, **1997**, 324 (Pt 2), 571-8	3.8	40
55	Yersinia pseudotuberculosis mntH functions in intracellular manganese accumulation, which is essential for virulence and survival in cells expressing functional Nramp1. *Microbiology (United Kingdom)*, **2011**, 157, 1115-1122	2.9	35

54	Probiotic Properties of Lactobacillus crispatus 2,029: Homeostatic Interaction with Cervicovaginal Epithelial Cells and Antagonistic Activity to Genitourinary Pathogens. *Probiotics and Antimicrobial Proteins*, **2014**, 6, 165-76	5.5	30
53	Campylobacter jejuni cocultured with epithelial cells reduces surface capsular polysaccharide expression. *Infection and Immunity*, **2009**, 77, 1959-67	3.7	30
52	Cloning and study of the genetic organization of the exe gene cluster of Aeromonas salmonicida. *Gene*, **1995**, 158, 77-82	3.8	29
51	Characterization of Lactobacillus fermentum UCO-979C, a probiotic strain with a potent anti-Helicobacter pylori activity. *Electronic Journal of Biotechnology*, **2017**, 25, 75-83	3.1	28
50	Structural and functional significance of the FGL sequence of the periplasmic chaperone Caf1M of Yersinia pestis. *Journal of Bacteriology*, **1999**, 181, 2422-9	3.5	28
49	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
48	Putative mechanisms and biological role of coccoid form formation in Campylobacter jejuni. *European Journal of Microbiology and Immunology*, **2012**, 2, 41-9	4.6	21
47	Lactobacillus fermentum 3872 as a potential tool for combatting Campylobacter jejuni infections. *Virulence*, **2017**, 8, 1753-1760	4.7	20
46	CmeABC Multidrug Efflux Pump Contributes to Antibiotic Resistance and Promotes Campylobacter jejuni Survival and Multiplication in Acanthamoeba polyphaga. *Applied and Environmental Microbiology*, **2017**, 83,	4.8	18
45	Steps toward broad-spectrum therapeutics: discovering virulence-associated genes present in diverse human pathogens. *BMC Genomics*, **2009**, 10, 501	4.5	18
44	Campylobacter jejuni gene cj0511 encodes a serine peptidase essential for colonisation. *FEBS Open Bio*, **2014**, 4, 468-72	2.7	15
43	Campylobacter-Acanthamoeba interactions. *Microbiology (United Kingdom)*, **2015**, 161, 933-947	2.9	14
42	Lactobacillus fermentum 3872 genome sequencing reveals plasmid and chromosomal genes potentially involved in a probiotic activity. *FEMS Microbiology Letters*, **2015**, 362,	2.9	14
41	TheCampylobacter jejuniglycome. *FEMS Microbiology Reviews*, **2005**, 29, 377-390	15.1	14
40	Draft Genome Sequence of Bacillus amyloliquefaciens B-1895. *Genome Announcements*, **2014**, 2,		13
39	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. *British Journal of Pharmacology*, **2017**, 174, 2247-2260	8.6	12
38	Draft Genome Sequence of Lactobacillus fermentum Strain 3872. *Genome Announcements*, **2013**, 1,		12
37	An improved physical and genetic map of Campylobacter jejuni NCTC 11168 (UA580). *Microbiology (United Kingdom)*, **1998**, 144 (Pt 2), 503-508	2.9	12

36	Procedure for the investigation of bacterial genomes: random shot-gun cloning, sample sequencing and mutagenesis of Campylobacter jejuni. *BioTechniques*, **1999**, 26, 50-2, 54, 56	2.5	11
35	Post genome analysis of Campylobacter jejuni. *Journal of Applied Microbiology*, **2001**, 90, 36S-44S	4.7	10
34	Variant Signal Peptides of Vaccine Antigen, FHbp, Impair Processing Affecting Surface Localization and Antibody-Mediated Killing in Most Meningococcal Isolates. *Frontiers in Microbiology*, **2019**, 10, 2847	5.7	10
33	Potential probiotic-associated traits revealed from completed high quality genome sequence of 3872. *Standards in Genomic Sciences*, **2017**, 12, 19		9
32	Whole Genome Sequence of MT1.1 Isolated from the Challenger Deep of the Mariana Trench Reveals Phenazine Biosynthesis Locus and Environmental Adaptation Factors. *Marine Drugs*, **2020**, 18,	6	9
31	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. *International Journal of Biological Macromolecules*, **2020**, 150, 400-412	7.9	9
30	A negative effect of Campylobacter capsule on bacterial interaction with an analogue of a host cell receptor. *BMC Microbiology*, **2014**, 14, 141	4.5	9
29	Unusual features in organisation of capsular polysaccharide-related genes of C. jejuni strain X. *Gene* , **2013**, 522, 37-45	3.8	9
28	Cohnella kolymensis sp. nov., a novel bacillus isolated from Siberian permafrost. *International Journal of Systematic and Evolutionary Microbiology*, **2018**, 68, 2912-2917	2.2	9
27	Cationic amphiphiles against Gardnerella vaginalis resistant strains and bacterial vaginosis-associated pathogens. *Pathogens and Disease*, **2019**, 77,	4.2	8
26	Draft Genome Sequence of Bacillus subtilis strain KATMIRA1933. *Genome Announcements*, **2014**, 2,		8
25	Draft Genome Sequence of Corynebacterium pseudodiphtheriticum Strain 090104 "Sokolov". *Genome Announcements*, **2013**, 1,		7
24	Regulation of restriction endonuclease activity with antibiotics. *Advances in Enzyme Regulation*, **1978**, 17, 307-21		7
23	Remarkable Features of Mitochondrial DNA of Acanthamoeba polyphaga Linc Ap-1, Revealed by Whole-Genome Sequencing. *Microbiology Resource Announcements*, **2019**, 8,	1.3	6
22	Whole genome sequencing of four bacterial strains from South Shetland Trench revealing biosynthetic and environmental adaptation gene clusters. *Marine Genomics*, **2020**, 54, 100782	1.9	6
21	The Effectiveness of Potential Probiotics Lactobacillus rhamnosus Vahe and Lactobacillus delbrueckii IAHAHI in Irradiated Rats Depends on the Nutritional Stage of the Host. *Probiotics and Antimicrobial Proteins*, **2020**, 12, 1439-1450	5.5	6
20	Study of the intergenic exeF-exeG region and its application as a simple preliminary test for Aeromonas spp. *FEMS Microbiology Letters*, **1996**, 137, 37-44	2.9	5
19	Binding of LcrV protein from Yersinia pestis to human T-cells induces apoptosis, which is completely blocked by specific antibodies. *International Journal of Biological Macromolecules*, **2019**, 122, 1062-1070	7.9	5

18	The hidden perils of read mapping as a quality assessment tool in genome sequencing. *Scientific Reports*, **2017**, 7, 43149	4.9	4
17	Specific genetic features of Campylobacter jejuni strain G1 revealed by genome sequencing. *FEMS Microbiology Letters*, **2015**, 362,	2.9	4
16	Draft Genome Sequence of a Probiotic Strain, Lactobacillus fermentum UCO-979C. *Genome Announcements*, **2015**, 3,		4
15	Signature-tagged mutagenesis of Yersinia pestis. *Advances in Experimental Medicine and Biology*, **2003**, 529, 39-41	3.6	4
14	Biotechnological and Ecological Potential of sp. nov., a Gifted Strain Isolated from the Challenger Deep of the Mariana Trench. *Marine Drugs*, **2021**, 19,	6	4
13	Insight into proteomic investigations of Neisseria meningitidis serogroup C strain L91543 from analysis of its genome sequence. *FEMS Microbiology Letters*, **2015**, 362,	2.9	3
12	Campylobacter jejuni Capsular Polysaccharide **2014**, 505-521		3
11	Draft Genome Sequence of Lactobacillus crispatus 2029. *Genome Announcements*, **2014**, 2,		3
10	Draft Genome Sequence of Lactobacillus plantarum 2165. *Genome Announcements*, **2014**, 2,		3
9	Draft Genome Sequence of Lactobacillus jensenii Strain MD IIE-70(2). *Genome Announcements*, **2013** , 1,		2
8	YPTB3816 of Yersinia pseudotuberculosis strain IP32953 is a virulence-related metallo-oligopeptidase. *BMC Microbiology*, **2016**, 16, 282	4.5	1
7	Draft Genome Sequence of Lactobacillus plantarum 2025. *Genome Announcements*, **2016**, 4,		1
6	Draft Genome Sequence of "Cohnella kolymensis" B-2846. *Genome Announcements*, **2016**, 4,		1
5	S-layer protein 2 of vaginal Lactobacillus crispatus 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	7.9	1
4	Draft Genome Sequence of LMG 29479. *Microbiology Resource Announcements*, **2021**, 10, e0042121	1.3	0
3	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	2.8	
2	Expression of and modified genes in is not sufficient for arabinose transport. *Access Microbiology*, **2019**, 1, e000042	1	
1	Complete Genome Sequence of Campylobacter jejuni Strain G1, Isolated from a Patient with Guillain-Barré Syndrome. *Microbiology Resource Announcements*, **2021**, 10, e0050521	1.3	