

# Yong-Joon Cho

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/8708637/yong-joon-cho-publications-by-citations.pdf>  
**Version:** 2024-04-05

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.  
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

60 papers	5,431 citations	18 h-index	62 g-index
62 ext. papers	5,957 ext. citations	4.2 avg, IF	5.06 L-index

#	Paper	IF	Citations
60	Introducing EzTaxon-e: a prokaryotic 16S rRNA gene sequence database with phylotypes that represent uncultured species. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2012</b> , 62, 716-721	2.2	4480
59	EzEditor: a versatile sequence alignment editor for both rRNA- and protein-coding genes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2014</b> , 64, 689-691	2.2	109
58	Duplex-specific nuclease efficiently removes rRNA for prokaryotic RNA-seq. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, e140	20.1	93
57	Complete genome sequence of <i>Vibrio vulnificus</i> MO6-24/O. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 2062-3	3.5	55
56	Profiling bacterial community in upper respiratory tracts. <i>BMC Infectious Diseases</i> , <b>2014</b> , 14, 583	4	48
55	The genome sequence of <i>Mycobacterium massiliense</i> strain CIP 108297 suggests the independent taxonomic status of the <i>Mycobacterium abscessus</i> complex at the subspecies level. <i>PLoS ONE</i> , <b>2013</b> , 8, e81560	3.7	44
54	A defect in iron uptake enhances the susceptibility of <i>Cryptococcus neoformans</i> to azole antifungal drugs. <i>Fungal Genetics and Biology</i> , <b>2012</b> , 49, 955-66	3.9	41
53	Genomic evolution of <i>Vibrio cholerae</i> . <i>Current Opinion in Microbiology</i> , <b>2010</b> , 13, 646-51	7.9	39
52	Genome sequence of <i>Escherichia coli</i> J53, a reference strain for genetic studies. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 3742-3	3.5	36
51	Complete Genome Sequence of Middle East Respiratory Syndrome Coronavirus KOR/KNIH/002_05_2015, Isolated in South Korea. <i>Genome Announcements</i> , <b>2015</b> , 3,		35
50	Whole genome sequencing analysis of the cutaneous pathogenic yeast <i>Malassezia restricta</i> and identification of the major lipase expressed on the scalp of patients with dandruff. <i>Mycoses</i> , <b>2017</b> , 60, 188-197	5.2	34
49	A vanillin derivative causes mitochondrial dysfunction and triggers oxidative stress in <i>Cryptococcus neoformans</i> . <i>PLoS ONE</i> , <b>2014</b> , 9, e89122	3.7	32
48	Synthesis of gamma-glutamylcysteine as a major low-molecular-weight thiol in lactic acid bacteria <i>Leuconostoc</i> spp. <i>Biochemical and Biophysical Research Communications</i> , <b>2008</b> , 369, 1047-51	3.4	28
47	Draft genome sequence of <i>Mycobacterium abscessus</i> subsp. <i>bolletii</i> BD(T). <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 2756-7	3.5	27
46	Understanding the Mechanism of Action of the Anti-Dandruff Agent Zinc Pyrithione against <i>Malassezia restricta</i> . <i>Scientific Reports</i> , <b>2018</b> , 8, 12086	4.9	23
45	Complete genome sequence analysis of <i>Leuconostoc kimchii</i> IMSNU 11154. <i>Journal of Bacteriology</i> , <b>2010</b> , 192, 3844-5	3.5	23
44	Functional screening of a metagenomic library reveals operons responsible for enhanced intestinal colonization by gut commensal microbes. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 3829-38	4.8	20

43	Time-resolved pathogenic gene expression analysis of the plant pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>BMC Genomics</i> , <b>2016</b> , 17, 345	4.5	19
42	Toll-like receptor 9 mediates oral bacteria-induced IL-8 expression in gingival epithelial cells. <i>Immunology and Cell Biology</i> , <b>2012</b> , 90, 655-63	5	16
41	Genomic Tandem Quadruplication is Associated with Ketoconazole Resistance in. <i>Journal of Microbiology and Biotechnology</i> , <b>2018</b> , 28, 1937-1945	3.3	16
40	Differential expression and role of two dithiol glutaredoxins Grx1 and Grx2 in <i>Schizosaccharomyces pombe</i> . <i>Biochemical and Biophysical Research Communications</i> , <b>2004</b> , 321, 922-9	3.4	15
39	The <i>Salmonella</i> virulence protein MgtC promotes phosphate uptake inside macrophages. <i>Nature Communications</i> , <b>2019</b> , 10, 3326	17.4	13
38	Complete genome sequence of <i>Pseudomonas antarctica</i> PAMC 27494, a bacteriocin-producing psychrophile isolated from Antarctica. <i>Journal of Biotechnology</i> , <b>2017</b> , 259, 15-18	3.7	13
37	Genome sequence of <i>Lactobacillus salivarius</i> GJ-24, a probiotic strain isolated from healthy adult intestine. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 5021-2	3.5	12
36	Comparative genomics of <i>Neisseria weaveri</i> clarifies the taxonomy of this species and identifies genetic determinants that may be associated with virulence. <i>FEMS Microbiology Letters</i> , <b>2012</b> , 328, 100-5 <sup>2.9</sup>		11
35	Transcriptomic analysis of genes modulated by cyclo(L-phenylalanine-L-proline) in <i>Vibrio vulnificus</i> . <i>Journal of Microbiology and Biotechnology</i> , <b>2013</b> , 23, 1791-801	3.3	10
34	Complete genome sequence of <i>Hymenobacter swuensis</i> , an ionizing-radiation resistant bacterium isolated from mountain soil. <i>Journal of Biotechnology</i> , <b>2014</b> , 178, 65-6	3.7	9
33	Microbial Diversity in Moonmilk of Baeg-nyong Cave, Korean CZO. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 613	5.7	7
32	Reclassification of <i>Serpens flexibilis</i> Hespell 1977 as <i>Pseudomonas flexibilis</i> comb. nov., with <i>Pseudomonas tuomuerensis</i> Xin et al. 2009 as a later heterotypic synonym. <i>Systematic and Applied Microbiology</i> , <b>2015</b> , 38, 563-6	4.2	7
31	<i>Fretibacter rubidus</i> gen. nov., sp. nov., isolated from seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2013</b> , 63, 4633-4638	2.2	7
30	Genome sequence of the chromate-resistant bacterium <i>Leucobacter salsicius</i> type strain M1-8(T). <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 495-504		7
29	Genome sequence of <i>Escherichia coli</i> AA86, isolated from cow feces. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 3681	3.5	7
28	Resequencing the Genome of Strain KCTC 27527. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	6
27	Genome sequence of the moderately halophilic bacterium <i>Salinicoccus carniancri</i> type strain Crm(T) (= DSM 23852(T)). <i>Standards in Genomic Sciences</i> , <b>2013</b> , 8, 255-63		6
26	sp. nov., isolated from stream water. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2017</b> , 67, 153-157	2.2	6

25	The latitudinal gradient in rock-inhabiting bacterial community compositions in Victoria Land, Antarctica. <i>Science of the Total Environment</i> , <b>2019</b> , 657, 731-738	10.2	6
24	Methane production in the oxygenated water column of a perennially ice-covered Antarctic lake. <i>Limnology and Oceanography</i> , <b>2020</b> , 65, 143-156	4.8	6
23	Genomic Multiplication and Drug Efflux Influence Ketoconazole Resistance in. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2020</b> , 10, 191	5.9	5
22	Antifungal Mechanism of Action of Lauryl Betaine Against Skin-Associated Fungus. <i>Mycobiology</i> , <b>2019</b> , 47, 242-249	1.7	5
21	Non-contiguous finished genome sequence and description of the gliding bacterium <i>Flavobacterium seoulense</i> sp. nov. <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 34		5
20	Draft Genome Sequence of <i>Kitasatospora cheerisanensis</i> KCTC 2395, Which Produces Plecomacrolide against Phytopathogenic Fungi. <i>Genome Announcements</i> , <b>2014</b> , 2,		5
19	Genome sequence of <i>Lactobacillus ruminis</i> SPM0211, isolated from a fecal sample from a healthy Korean. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 5034	3.5	5
18	The role of Rsv1 in the transcriptional regulation of genes involved in sugar metabolism for long-term survival. <i>FEBS Journal</i> , <b>2020</b> , 287, 878-896	5.7	5
17	A Novel Virus Alters Gene Expression and Vacuolar Morphology in Cells and Induces a TLR3-Mediated Inflammatory Immune Response. <i>MBio</i> , <b>2020</b> , 11,	7.8	5
16	Genome sequence of the haloarchaeon <i>Haloterrigena jeotgali</i> type strain A29(T) isolated from salt-fermented food. <i>Standards in Genomic Sciences</i> , <b>2015</b> , 10, 49		4
15	Draft genome sequence of <i>Escherichia coli</i> W26, an enteric strain isolated from cow feces. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 5149-50	3.5	4
14	A Transcriptional Regulatory Map of Iron Homeostasis Reveals a New Control Circuit for Capsule Formation in. <i>Genetics</i> , <b>2020</b> , 215, 1171-1189	4	3
13	Draft genome sequence of the extremely halophilic archaeon <i>Haladaptatus cibarius</i> type strain D43(T) isolated from fermented seafood. <i>Standards in Genomic Sciences</i> , <b>2015</b> , 10, 53		3
12	Draft genome sequence of <i>Shewanella</i> sp. strain HN-41, which produces arsenic-sulfide nanotubes. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 5039-40	3.5	3
11	Functional dissection of the phosphotransferase system provides insight into the prevalence of <i>Faecalibacterium prausnitzii</i> in the host intestinal environment. <i>Environmental Microbiology</i> , <b>2021</b> , 23, 4726-4740	5.2	3
10	gen. nov., sp. nov., a member of the family isolated from an Antarctic lichen. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2020</b> , 70, 5918-5925	2.2	2
9	A novel virus alters gene expression and vacuolar morphology in <i>Malassezia</i> cells and induces a TLR3-mediated inflammatory immune response		2
8	Draft Genome Sequence of <i>Arthrobacter oryzae</i> TNBS02, a Bacterium Containing Heavy Metal Resistance Genes, Isolated from Soil of Antarctica. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	1

7	Draft genome sequence of <i>Pseudomonas</i> sp. strain G5, isolated from a traditional indigo fermentation dye vat <b>2013</b> , 56, 339-341		1
6	Draft Genome sequence of <i>Escherichia coli</i> AI27, a porcine isolate belonging to phylogenetic group B1. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 6640-1	3.5	1
5	Microbial diversity of Baeg-nyong cave and characterization of the antibiotics extracted from <i>Streptomyces exfoliatus</i> . <i>FASEB Journal</i> , <b>2019</b> , 33, 637.4	0.9	1
4	Synonymy of and and Emended Description of. <i>Journal of Microbiology and Biotechnology</i> , <b>2017</b> , 27, 149-154	3.54	1
3	A large-scale metagenomic study for enzyme profiles using the focused identification of the NGS-based definitive enzyme research (FINDER) strategy. <i>Biotechnology and Bioengineering</i> , <b>2021</b> , 118, 4360-4374	4.9	1
2	Regulation of iron homeostasis by peroxide-sensitive CatR, a Fur-family regulator in <i>Streptomyces coelicolor</i> . <i>Journal of Microbiology</i> , <b>2021</b> , 59, 1083-1091	3	
1	Draft Genome Sequence of the Chitin-Degrading Psychrotolerant Bacterium <i>Pedobacter jejuensis</i> TN23, Isolated from Antarctic Soil. <i>Microbiology Resource Announcements</i> , <b>2021</b> , 10, e0052321	1.3	