

# Wei Zhou

## List of Publications by Year in Descending Order

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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.

19  
papers

400  
citations

11  
h-index

20  
g-index

24  
ext. papers

575  
ext. citations

8.8  
avg, IF

3.69  
L-index

#	Paper	IF	Citations
19	Host-Specific Evolutionary and Transmission Dynamics Shape the Functional Diversification of <i>Staphylococcus epidermidis</i> in Human Skin. <i>Cell</i> , <b>2020</b> , 180, 454-470.e18	56.2	38
18	Metagenomic growth rate inferences of strains in situ. <i>Science Advances</i> , <b>2020</b> , 6, eaaz2299	14.3	5
17	Development and validation of a novel 29-plex Y-STR typing system for forensic application. <i>Forensic Science International: Genetics</i> , <b>2020</b> , 44, 102169	4.3	7
16	Selective colonization ability of human fecal microbes in different mouse gut environments. <i>ISME Journal</i> , <b>2019</b> , 13, 805-823	11.9	23
15	A commensal strain of protects against skin neoplasia. <i>Science Advances</i> , <b>2018</b> , 4, eaao4502	14.3	106
14	ReprDB and panDB: minimalist databases with maximal microbial representation. <i>Microbiome</i> , <b>2018</b> , 6, 15	16.6	12
13	Tuning of human MAIT cell activation by commensal bacteria species and MR1-dependent T-cell presentation. <i>Mucosal Immunology</i> , <b>2018</b> , 11, 1591-1605	9.2	57
12	Thanatobiome composition profiling as a tool for forensic investigation. <i>Forensic Sciences Research</i> , <b>2018</b> , 3, 105-110	3.6	12
11	Correlation between antigenicity and variability in the vls antigenic variation system of <i>Borrelia burgdorferi</i> . <i>Microbes and Infection</i> , <b>2017</b> , 19, 267-276	9.3	1
10	Population genetics study using 26 Y-chromosomal STR loci in the Hui ethnic group in China. <i>Forensic Science International: Genetics</i> , <b>2017</b> , 28, e26-e27	4.3	17
9	A study of the genetic diversity in the Heze Han population using a novel genotyping system based on 24 Y-chromosomal STR loci. <i>Forensic Science International: Genetics Supplement Series</i> , <b>2017</b> , 6, e86-e88	0.5	1
8	Mutation rates of 13 RM Y-STRs in a Han population from Shandong province, China. <i>Forensic Science International: Genetics Supplement Series</i> , <b>2017</b> , 6, e346-e348	0.5	4
7	Interactions between host immune response and antigenic variation that control <i>Borrelia burgdorferi</i> population dynamics. <i>Microbiology (United Kingdom)</i> , <b>2017</b> , 163, 1179-1188	2.9	3
6	Analysis of genetic admixture in Uyghur using the 26 Y-STR loci system. <i>Scientific Reports</i> , <b>2016</b> , 6, 19998	4.9	27
5	Evolution and population genomics of the Lyme borreliosis pathogen, <i>Borrelia burgdorferi</i> . <i>Trends in Genetics</i> , <b>2015</b> , 31, 201-7	8.5	17
4	Potentially conflicting selective forces that shape the vls antigenic variation system in <i>Borrelia burgdorferi</i> . <i>Infection, Genetics and Evolution</i> , <b>2014</b> , 27, 559-65	4.5	6
3	Distribution of cp32 prophages among Lyme disease-causing spirochetes and natural diversity of their lipoprotein-encoding erp loci. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 4115-28	4.8	21

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|---|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|----|
| 2 | Functional cloning and characterization of antibiotic resistance genes from the chicken gut microbiome. <i>Applied and Environmental Microbiology</i> , <b>2012</b> , 78, 3028-32 | 4.8 | 32 |
| 1 | High-dose siRNAs upregulate mouse Eri-1 at both transcription and posttranscription levels. <i>PLoS ONE</i> , <b>2011</b> , 6, e26466                                             | 3.7 | 10 |