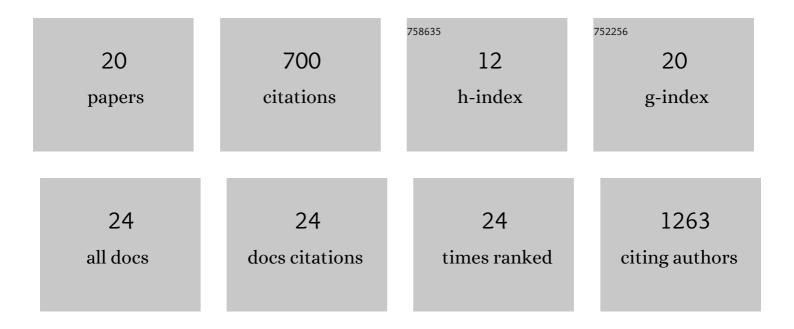
## Wei Zhou

List of Publications by Year in descending order

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Μει Ζησι

| #  | Article  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | A commensal strain of <i>Staphylococcus epidermidis</i> protects against skin neoplasia. Science<br>Advances, 2018, 4, eaao4502.   | 4.7  | 183       |
| 2  | Host-Specific Evolutionary and Transmission Dynamics Shape the Functional Diversification of Staphylococcus epidermidis in Human Skin. Cell, 2020, 180, 454-470.e18.                                       | 13.5 | 102       |
| 3  | Tuning of human MAIT cell activation by commensal bacteria species and MR1-dependent T-cell presentation. Mucosal Immunology, 2018, 11, 1591-1605.   | 2.7  | 91        |
| 4  | Functional Cloning and Characterization of Antibiotic Resistance Genes from the Chicken Gut<br>Microbiome. Applied and Environmental Microbiology, 2012, 78, 3028-3032.                                    | 1.4  | 40        |
| 5  | Selective colonization ability of human fecal microbes in different mouse gut environments. ISME<br>Journal, 2019, 13, 805-823.  | 4.4  | 39        |
| 6  | Thanatomicrobiome composition profiling as a tool for forensic investigation. Forensic Sciences Research, 2018, 3, 105-110.  | 0.9  | 34        |
| 7  | Distribution of cp32 Prophages among Lyme Disease-Causing Spirochetes and Natural Diversity of Their<br>Lipoprotein-Encoding <i>erp</i> Loci. Applied and Environmental Microbiology, 2013, 79, 4115-4128. | 1.4  | 32        |
| 8  | Analysis of genetic admixture in Uyghur using the 26 Y-STR loci system. Scientific Reports, 2016, 6,<br>19998.   | 1.6  | 30        |
| 9  | Population genetics study using 26 Y-chromosomal STR loci in the Hui ethnic group in China. Forensic<br>Science International: Genetics, 2017, 28, e26-e27.  | 1.6  | 26        |
| 10 | Evolution and population genomics of the Lyme borreliosis pathogen, Borrelia burgdorferi. Trends in<br>Genetics, 2015, 31, 201-207.  | 2.9  | 23        |
| 11 | ReprDB and panDB: minimalist databases with maximal microbial representation. Microbiome, 2018, 6, 15.   | 4.9  | 21        |
| 12 | Metagenomic growth rate inferences of strains in situ. Science Advances, 2020, 6, eaaz2299.  | 4.7  | 19        |
| 13 | Skin Microbiome Variation with CancerÂProgression in Human Cutaneous Squamous Cell Carcinoma.<br>Journal of Investigative Dermatology, 2022, 142, 2773-2782.e16.   | 0.3  | 16        |
| 14 | Development and validation of a novel 29-plex Y-STR typing system for forensic application. Forensic<br>Science International: Genetics, 2020, 44, 102169.   | 1.6  | 12        |
| 15 | High-Dose siRNAs Upregulate Mouse Eri-1 at both Transcription and Posttranscription Levels. PLoS<br>ONE, 2011, 6, e26466.  | 1.1  | 11        |
| 16 | Potentially conflicting selective forces that shape the vls antigenic variation system in Borrelia burgdorferi. Infection, Genetics and Evolution, 2014, 27, 559-565.                                      | 1.0  | 6         |
| 17 | Mutation rates of 13 RM Y-STRs in a Han population from Shandong province, China. Forensic Science<br>International: Genetics Supplement Series, 2017, 6, e346-e348.                                       | 0.1  | 6         |
| 18 | Interactions between host immune response and antigenic variation that control Borrelia<br>burgdorferi population dynamics. Microbiology (United Kingdom), 2017, 163, 1179-1188.                           | 0.7  | 5         |

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|----|---|-----|-----------|
| 19 | A study of the genetic diversity in the Heze Han population using a novel genotyping system based on 24 Y-chromosomal STR loci. Forensic Science International: Genetics Supplement Series, 2017, 6, e86-e88. | 0.1 | 2         |
| 20 | Correlation between antigenicity and variability in the vls antigenic variation system of Borrelia burgdorferi. Microbes and Infection, 2017, 19, 267-276.  | 1.0 | 1         |