Philipp Engel

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/4635415/philipp-engel-publications-by-year.pdf

Version: 2024-04-28

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.

| 53 | 4,189 citations | 31 | 63 |
|-------------------|------------------------|-------------|-----------------|
| papers | | h-index | g-index |
| 63 ext. papers | 5,785 ext. citations | 8.9 avg, IF | 6.24 L-index |

| # | Paper | IF | Citations |
|----|--|------------------|-----------|
| 53 | Home or hospital birth: the neonatal microbiota perspective <i>Lancet Microbe, The</i> , 2022 , 3, e247 | 22.2 | |
| 52 | Mild chronic exposure to pesticides alters physiological markers of honey bee health without perturbing the core gut microbiota <i>Scientific Reports</i> , 2022 , 12, 4281 | 4.9 | 3 |
| 51 | Impact of Chronic Exposure to Sublethal Doses of Glyphosate on Honey Bee Immunity, Gut Microbiota and Infection by Pathogens. <i>Microorganisms</i> , 2021 , 9, | 4.9 | 5 |
| 50 | A prevalent and culturable microbiota links ecological balance to clinical stability of the human lung after transplantation. <i>Nature Communications</i> , 2021 , 12, 2126 | 17.4 | 8 |
| 49 | Niche partitioning facilitates coexistence of closely related honey bee gut bacteria. <i>ELife</i> , 2021 , 10, | 8.9 | 7 |
| 48 | Functional strain redundancy and persistent phage infection in Swiss hard cheese starter cultures. <i>ISME Journal</i> , 2021 , | 11.9 | 2 |
| 47 | Mechanisms underlying gut microbiota-host interactions in insects. <i>Journal of Experimental Biology</i> , 2021 , 224, | 3 | 14 |
| 46 | Suppression of High-Fat Diet-Induced Obesity by Platycodon Grandiflorus in Mice Is Linked to Changes in the Gut Microbiota. <i>Journal of Nutrition</i> , 2020 , 150, 2364-2374 | 4.1 | 7 |
| 45 | Honey bees harbor a diverse gut virome engaging in nested strain-level interactions with the microbiota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 7355-7362 | 11.5 | 14 |
| 44 | The gut microbiota - brain axis of insects. Current Opinion in Insect Science, 2020, 39, 6-13 | 5.1 | 18 |
| 43 | Gut microbiota structure differs between honeybees in winter and summer. ISME Journal, 2020, 14, 801 | -811. 4) | 78 |
| 42 | Vast Differences in Strain-Level Diversity in the Gut Microbiota of Two Closely Related Honey Bee Species. <i>Current Biology</i> , 2020 , 30, 2520-2531.e7 | 6.3 | 28 |
| 41 | Genomic diversity landscape of the honey bee gut microbiota. <i>Nature Communications</i> , 2019 , 10, 446 | 17.4 | 93 |
| 40 | High dietary fat intake induces a microbiota signature that promotes food allergy. <i>Journal of Allergy and Clinical Immunology</i> , 2019 , 144, 157-170.e8 | 11.5 | 49 |
| 39 | Genomic changes underlying host specialization in the bee gut symbiont Lactobacillus Firm5. <i>Molecular Ecology</i> , 2019 , 28, 2224-2237 | 5.7 | 18 |
| 38 | Bacterial communities within caterpillars are shifted following transition from solitary living to social parasitism of ant colonies. <i>Ecology and Evolution</i> , 2019 , 9, 4452-4464 | 2.8 | 8 |
| 37 | Herbivorous turtle ants obtain essential nutrients from a conserved nitrogen-recycling gut microbiome. <i>Nature Communications</i> , 2018 , 9, 964 | 17.4 | 57 |

(2015-2018)

| 36 | Functional roles and metabolic niches in the honey bee gut microbiota. <i>Current Opinion in Microbiology</i> , 2018 , 43, 69-76 | 7.9 | 62 |
|----|--|-------------------|-----|
| 35 | Origin and Evolution of the Bartonella Gene Transfer Agent. <i>Molecular Biology and Evolution</i> , 2018 , 35, 451-464 | 8.3 | 9 |
| 34 | Gut microbiota composition is associated with environmental landscape in honey bees. <i>Ecology and Evolution</i> , 2018 , 8, 441-451 | 2.8 | 59 |
| 33 | New Reference Genome Sequences for 17 Bacterial Strains of the Honey Bee Gut Microbiota. <i>Microbiology Resource Announcements</i> , 2018 , 7, | 1.3 | 6 |
| 32 | The gut microbiome is associated with behavioural task in honey bees. <i>Insectes Sociaux</i> , 2018 , 65, 419-4 | 29 .5 | 44 |
| 31 | Immune system stimulation by the gut symbiont Frischella perrara in the honey bee (Apis mellifera). <i>Molecular Ecology</i> , 2017 , 26, 2576-2590 | 5.7 | 80 |
| 30 | Genomic changes associated with the evolutionary transition of an insect gut symbiont into a blood-borne pathogen. <i>ISME Journal</i> , 2017 , 11, 1232-1244 | 11.9 | 53 |
| 29 | A bacterial toxin-antitoxin module is the origin of inter-bacterial and inter-kingdom effectors of Bartonella. <i>PLoS Genetics</i> , 2017 , 13, e1007077 | 6 | 32 |
| 28 | Evolutionary Dynamics of Pathoadaptation Revealed by Three Independent Acquisitions of the VirB/D4 Type IV Secretion System in Bartonella. <i>Genome Biology and Evolution</i> , 2017 , 9, 761-776 | 3.9 | 29 |
| 27 | Disentangling metabolic functions of bacteria in the honey bee gut. <i>PLoS Biology</i> , 2017 , 15, e2003467 | 9.7 | 149 |
| 26 | Metabolism of Toxic Sugars by Strains of the Bee Gut Symbiont Gilliamella apicola. MBio, 2016, 7, | 7.8 | 122 |
| 25 | Genome-wide screen identifies host colonization determinants in a bacterial gut symbiont. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 13887-1389 | 2 ^{11.5} | 70 |
| 24 | Bartonella apis sp. nov., a honey bee gut symbiont of the class Alphaproteobacteria. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016 , 66, 414-421 | 2.2 | 65 |
| 23 | Beyond 16S rRNA Community Profiling: Intra-Species Diversity in the Gut Microbiota. <i>Frontiers in Microbiology</i> , 2016 , 7, 1475 | 5.7 | 68 |
| 22 | The Bee Microbiome: Impact on Bee Health and Model for Evolution and Ecology of Host-Microbe Interactions. <i>MBio</i> , 2016 , 7, e02164-15 | 7.8 | 145 |
| 21 | Probiotic Treatment with a Gut Symbiont Leads to Parasite Susceptibility in Honey Bees. <i>Trends in Parasitology</i> , 2016 , 32, 914-916 | 6.4 | 12 |
| 20 | The Bacterium Frischella perrara Causes Scab Formation in the Gut of its Honeybee Host. <i>MBio</i> , 2015 , 6, e00193-15 | 7.8 | 62 |
| 19 | Gut symbionts from distinct hosts exhibit genotoxic activity via divergent colibactin biosynthesis pathways. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 1502-12 | 4.8 | 50 |

| 18 | Genomics and host specialization of honey bee and bumble bee gut symbionts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 11509-14 | 11.5 | 204 |
|----|--|------|------|
| 17 | Comparative metabolomics and structural characterizations illuminate colibactin pathway-dependent small molecules. <i>Journal of the American Chemical Society</i> , 2014 , 136, 9244-7 | 16.4 | 91 |
| 16 | Hidden diversity in honey bee gut symbionts detected by single-cell genomics. <i>PLoS Genetics</i> , 2014 , 10, e1004596 | 6 | 102 |
| 15 | Frischella perrara gen. nov., sp. nov., a gammaproteobacterium isolated from the gut of the honeybee, Apis mellifera. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013 , 63, 3646-3651 | 2.2 | 73 |
| 14 | Disentangling associated genomes. <i>Methods in Enzymology</i> , 2013 , 531, 445-64 | 1.7 | 7 |
| 13 | Functional and evolutionary insights into the simple yet specific gut microbiota of the honey bee from metagenomic analysis. <i>Gut Microbes</i> , 2013 , 4, 60-5 | 8.8 | 70 |
| 12 | The gut microbiota of insects - diversity in structure and function. <i>FEMS Microbiology Reviews</i> , 2013 , 37, 699-735 | 15.1 | 1124 |
| 11 | Standard methods for research on Apis mellifera gut symbionts. <i>Journal of Apicultural Research</i> , 2013 , 52, 1-24 | 2 | 62 |
| 10 | Functional diversity within the simple gut microbiota of the honey bee. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 11002-7 | 11.5 | 470 |
| 9 | Adenylylation control by intra- or intermolecular active-site obstruction in Fic proteins. <i>Nature</i> , 2012 , 482, 107-10 | 50.4 | 114 |
| 8 | Parallel evolution of a type IV secretion system in radiating lineages of the host-restricted bacterial pathogen Bartonella. <i>PLoS Genetics</i> , 2011 , 7, e1001296 | 6 | 75 |
| 7 | The BatR/BatS two-component regulatory system controls the adaptive response of Bartonella henselae during human endothelial cell infection. <i>Journal of Bacteriology</i> , 2010 , 192, 3352-67 | 3.5 | 47 |
| 6 | The Trw type IV secretion system of Bartonella mediates host-specific adhesion to erythrocytes. <i>PLoS Pathogens</i> , 2010 , 6, e1000946 | 7.6 | 84 |
| 5 | Genomics of host-restricted pathogens of the genus bartonella. <i>Genome Dynamics</i> , 2009 , 6, 158-169 | | 19 |
| 4 | Genomic analysis of Bartonella identifies type IV secretion systems as host adaptability factors. <i>Nature Genetics</i> , 2007 , 39, 1469-76 | 36.3 | 111 |
| 3 | Disentangling metabolic functions of bacteria in the honey bee gut | | 4 |
| 2 | Vast differences in strain-level diversity in the gut microbiota of two closely related honey bee species | | 2 |
| 1 | Gut microbiota structure differs between honey bees in winter and summer | | 2 |