

DAFTAR PUSTAKA

- Abo-Zed, A., Yassin, M., & Phan, T. (2020). *Acinetobacter junii* as a rare pathogen of urinary tract infection. *Urology Case Reports*, 32, 101209. <https://doi.org/10.1016/j.eucr.2020.101209>
- Adebayo, A. S., Ackermann, G., Bowyer, R. C. E., Wells, P. M., Humphreys, G., Knight, R., Spector, T. D., & Steves, C. J. (2020). The Urinary Tract Microbiome in Older Women Exhibits Host Genetic and Environmental Influences. *Cell Host and Microbe*, 28(2), 298-305.e3. <https://doi.org/10.1016/j.chom.2020.06.022>
- Agosti, M., Tandoi, F., Morlacchi, L., & Bossi, A. (2017). Nutritional and metabolic programming during the first thousand days of life. *La Pediatria Medica e Chirurgica: Medical and Surgical Pediatrics*, 39(2), 157. <https://doi.org/10.4081/pmc.2017.157>
- Akter, M., Jannat, R., & Nova, T. T. (2018). *Lactobacillus* species As a Cause of Urinary Tract Infection. *Journal of Dhaka Medical College*, 27(2), 215–217. <https://doi.org/10.3329/jdmc.v27i2.45837>
- Al-Azawi, I. H., & Abbas, M. H. (2020). Determination *Enterococcus faecalis* in asymptomatic urinary tract infection associated with diabetes type 2 patients in Suwayrah general hospital-Iraq. *Medico-Legal Update*, 20(1), 661–666. <https://doi.org/10.37506/v20/il/2020/mlu/194399>
- Al-Kashif, M. M. L. (2019). Urinary tract infection among pregnant women and its associated risk factors: A cross-sectional study. *Biomedical and Pharmacology Journal*, 12(4), 2003–2010. <https://doi.org/10.13005/bpj/1832>
- Alauzet, C., Lozniewski, A., & Marchandin, H. (2019). Metronidazole resistance and *nim* genes in anaerobes: A review. *Anaerobe*, 55, 40–53. <https://doi.org/10.1016/j.anaerobe.2018.10.004>
- Ambite, I., Lutay, N., Stork, C., Dobrindt, U., Wullt, B., & Svanborg, C. (2016). Bacterial Suppression of RNA Polymerase II-Dependent Host Gene Expression. *Pathogens (Basel, Switzerland)*, 5(3), 1–11. <https://doi.org/10.3390/pathogens5030049>
- Ammitzbøll, N., Bau, B. P. J., Bundgaard-Nielsen, C., Villadsen, A. B., Jensen, A. M., Leutscher, P. D. C., Glavind, K., Hagstrøm, S., Arenholt, L. T. S., & Sørensen, S. (2021). Pre- and postmenopausal women have different core urinary microbiota. *Scientific Reports*, 11(1), 1–10. <https://doi.org/10.1038/s41598-021-81790-8>
- Andersen, S., Nawrocki, A., Johansen, A. E., Herrero-Fresno, A., Menéndez, V. G., Møller-Jensen, J., & Olsen, J. E. (2022). Proteomes of Uropathogenic *Escherichia coli* Growing in Human Urine and in J82 Urinary Bladder Cells. *Proteomes*, 10(2), 1–20. <https://doi.org/10.3390/proteomes10020015>
- Appanna, V. D. (2018). The Human Microbiome: The Origin in: Human Microbes - The Power Within. In *Springer Nature Singapore*. Springer Nature Singapore Pte Ltd. <https://doi.org/10.1097/01.NAJ.0000524523.42427.40>
- Bajic, P., Van Kuiken, M. E., Burge, B. K., Kirshenbaum, E. J., Joyce, C. J., Wolfe, A.

- J., Branch, J. D., Bresler, L., & Farooq, A. V. (2018). Male bladder microbiome relates to lower urinary tract symptoms. *European Urology Focus*, 6(2), 1–7. <https://doi.org/10.1016/j.euf.2018.08.001>
- Bi, H., Tian, Y., Song, C., Li, J., Liu, T., Chen, Z., Chen, C., Huang, Y., & Zhang, Y. (2019). Urinary microbiota - a potential biomarker and therapeutic target for bladder cancer. *Journal of Medical Microbiology*, 68(10), 1471–1478. <https://doi.org/10.1099/jmm.0.001058>
- Boiten, K. E., Jean-Pierre, H., & Veloo, A. C. M. (2018). Assessing the clinical relevance of *Fenollaria massiliensis* in human infections, using MALDI-TOF MS. *Anaerobe*, 54, 240–245. <https://doi.org/10.1016/j.anaerobe.2018.03.008>
- Boyanova, L., Marteva-Proevska, Y., Gergova, R., & Markovska, R. (2021). *Gardnerella vaginalis* in urinary tract infections, are men spared? *Anaerobe*, 72, 102438. <https://doi.org/10.1016/j.anaerobe.2021.102438>
- Brahimi, S., Cadoret, F., Founier, P. E., Moal, V., & Raoult, D. (2017). ‘*Peptoniphilus urinimassiliensis*’ sp. nov., a new bacterial species isolated from a human urine sample after de novo kidney transplantation. *New Microbes and New Infections*, 16(February), 49–50. <https://doi.org/10.1016/j.nmni.2017.01.001>
- Brannon, J. R., Dunigan, T. L., Beebout, C. J., Reynolds, W. S., Hadjifrangiskou, M., Ross, T., & Wiebe, M. A. (2020). Invasion of vaginal epithelial cells by uropathogenic *Escherichia coli*. *Nature Communications*, 11(2803), 1–11. <https://doi.org/10.1038/s41467-020-16627-5>
- Brook, I. (2004). Urinary tract and genito-urinary suppurative infections due to anaerobic bacteria. *International Journal of Urology*, 11(3), 133–141. <https://doi.org/10.1111/j.1442-2042.2003.00756.x>
- Brown, R. G., Al-Memar, M., Marchesi, J. R., Lee, Y. S., Smith, A., Chan, D., Lewis, H., Kindinger, L., Terzidou, V., Bourne, T., Bennett, P. R., & MacIntyre, D. A. (2019). Establishment of vaginal microbiota composition in early pregnancy and its association with subsequent preterm prelabor rupture of the fetal membranes. *Translational Research*, 207, 30–43. <https://doi.org/10.1016/j.trsl.2018.12.005>
- Brown, S. P., Cornforth, D. M., & Mideo, N. (2012). Evolution of virulence in opportunistic pathogens: Generalism, plasticity, and control. *Trends in Microbiology*, 20(7), 336–342. <https://doi.org/10.1016/j.tim.2012.04.005>
- Brubaker, L., Putonti, C., Dong, Q., & Wolfe, A. J. (2021). The human urobiome. *Mammalian Genome*, 32(4), 232–238. <https://doi.org/10.1007/s00335-021-09862-8>
- Brubaker, Linda, & Wolfe, A. J. (2017). The female urinary microbiota, urinary health and common urinary disorders. *Annals of Translational Medicine*, 5(2), 34–34. <https://doi.org/10.21037/atm.2016.11.62>
- Bryce, A., Hay, A. D., Lane, I. F., Thornton, H. V., Wootton, M., & Costelloe, C. (2016). Global prevalence of antibiotic resistance in paediatric urinary tract infections caused by *Escherichia coli* and association with routine use of antibiotics in primary care: systematic review and meta-analysis. *Bmj*, i939. <https://doi.org/10.1136/bmj.i939>

- Bush, K., & Bradford, P. A. (2016). β -Lactams and β -Lactamase Inhibitors: An Overview. *Cold Spring Harbor Laboratory Press*, 6(a025247).
- Cappelli, E. A., Barros, R. R., Camello, T. C. F., Teixeira, L. M., & Merquior, V. L. C. (1999). *Leuconostoc pseudomesenteroides* as a cause of nosocomial urinary tract infections. *Journal of Clinical Microbiology*, 37(12), 4124–4126. <https://doi.org/10.1128/jcm.37.12.4124-4126.1999>
- Castro, J., Machado, D., & Cerca, N. (2019). Unveiling the role of *Gardnerella vaginalis* in polymicrobial Bacterial Vaginosis biofilms: the impact of other vaginal pathogens living as neighbors. *The ISME Journal*, 13, 1306–1317. <https://doi.org/10.1038/s41396-018-0337-0>
- Castro, J., Machado, D., Cerca, N., & Salazar, A. (2016). *Escherichia coli* and *Enterococcus faecalis* are able to incorporate and enhance a pre-formed *Gardnerella vaginalis* biofilm. *Pathogens and Disease*, January, 1–4. <https://doi.org/10.1093/femspd/ftw007>
- Ceccarani, C., Foschi, C., Parolin, C., D’Antuono, A., Gaspari, V., Consolandi, C., Laghi, L., Camboni, T., Vitali, B., Severgnini, M., & Marangoni, A. (2019). Diversity of vaginal microbiome and metabolome during genital infections. *Scientific Reports*, 9(1), 1–12. <https://doi.org/10.1038/s41598-019-50410-x>
- Cegelski, L., Marshall, G. R., Eldridge, G. R., & Hultgren, S. J. (2008). The biology and future prospects of antivirulence therapies. *Nature Reviews Microbiology*, 6(1), 17–27. <https://doi.org/10.1038/nrmicro1818>
- Chagneau, C. V., Massip, C., Bossuet-Greif, N., Fremez, C., Motta, J.-P., Shima, A., Besson, C., Faouder, P. Le, Cénac, N., Roth, M.-P., Coppin, H., Fontanié, M., Martin, P., Nougayrède, J.-P., & Oswald, E. (2020). Uropathogenic *E. coli* induces DNA damage in the bladder. *BioRxiv*, 1–22. <https://doi.org/https://doi.org/10.1101/2020.05.07.080291>
- Chagneau, C. V., Massip, C., Bossuet-Greif, N., Fremez, C., Motta, J. P., Shima, A., Besson, C., Le Faouder, P., Cénac, N., Roth, M. P., Coppin, H., Fontanié, M., Martin, P., Nougayrède, J. P., & Oswald, E. (2021). Uropathogenic *E. coli* induces DNA damage in the bladder. *PLoS Pathogens*, 17(2), 1–18. <https://doi.org/10.1371/JOURNAL.PPAT.1009310>
- Chang, D. H., Shin, J., Rhee, M. S., Park, K. R., Cho, B. K., Lee, S. K., & Kim, B. C. (2020). Vaginal microbiota profiles of native Korean women and associations with high-risk pregnancy. *Journal of Microbiology and Biotechnology*, 30(2), 248–258. <https://doi.org/10.4014/jmb.1908.08016>
- Chee, W. J. Y., Chew, S. Y., & Than, L. T. L. (2020). Vaginal microbiota and the potential of *Lactobacillus* derivatives in maintaining vaginal health. *Microbial Cell Factories*, 19(1), 1–24. <https://doi.org/10.1186/s12934-020-01464-4>
- Chen, X., Lu, Y., Chen, T., & Li, R. (2021). The Female Vaginal Microbiome in Health and Bacterial Vaginosis. *Frontiers in Cellular and Infection Microbiology*, 11(April), 1–15. <https://doi.org/10.3389/fcimb.2021.631972>
- Chesca, A., Abdulina, G., Medetova, A., Kabduova, A., Beysembayeva, G., Moraru, D., & Sandle, T. (2022). Opportunistic Pathogens in Patients with Urinary Tract

- Infection Department of Biomedicine , Karaganda Medical University , Kazakhstan Karaganda Clinical Microbiology Laboratory MediTEC-NS , Kazakhstan Karaganda Regional multidisciplinary clinical hospita. *Preprints.Org*, December 2018, 1–15. <https://doi.org/10.20944/preprints202201.0473.v1>
- Cho, I., & Blaser, M. J. (2012). The human microbiome: at the interface of health and disease. *Nature Publishing Group*, 13(4), 260–270. <https://doi.org/10.1038/nrg3182>
- Choe, H. S., Lee, S. J., Cho, Y. H., Çek, M., Tandoğdu, Z., Wagenlehner, F., Bjerklund-Johansen, T. E., Naber, K., & Investigators, the G. A. (2018). Aspects of urinary tract infections and antimicrobial resistance in hospitalized urology patients in Asia: 10-Year results of the Global Prevalence Study of Infections in Urology (GPIU). *Journal of Infection and Chemotherapy*, 24(4), 278–283. <https://doi.org/10.1016/j.jiac.2017.11.013>
- Christine, G., Budiarti, S., & Astuti, R. I. (2018). Diversity of urinary tract infection bacteria in children in Indonesia based on metagenomic approach. *Biodiversitas*, 19(4), 1375–1381. <https://doi.org/10.13057/biodiv/d190425>
- Chu, C. M., & Lowder, J. L. (2018). Diagnosis and treatment of urinary tract infections across age groups. *American Journal of Obstetrics and Gynecology*, 1–12. <https://doi.org/10.1016/j.ajog.2017.12.231>
- Clokie, M. R. J., Millard, A. D., Letarov, A. V., & Heaphy, S. (2011). Phages in nature. *Bacteriophage*, 1(1), 31–45. <https://doi.org/10.4161/bact.1.1.14942>
- Colas, L., Mongodin, E. F., Montassier, E., Chesneau, M., Guerif, P., Hittle, L., Giral, M., Bromberg, J. S., Brouard, S., & Consortium, D. (2020). Unique and specific Proteobacteria diversity in urinary microbiota of tolerant kidney transplanted recipients. *American Journal of Transplantation*, 20(1), 145–158. <https://doi.org/10.1111/ajt.15549>
- Colodner, R., Rock, W., Chazan, B., Keller, N., Guy, N., Sakran, W., & Raz, R. (2004). Risk factors for the development of extended-spectrum beta-lactamase- producing bacteria in nonhospitalized patients. *European Journal of Clinical Microbiology and Infectious Diseases*, 23(3), 163–167. <https://doi.org/10.1007/s10096-003-1084-2>
- Comerlato, C. B., Ritter, A. C., Miyamoto, K. N., & Brandelli, A. (2020). Proteomic study of *Enterococcus durans* LAB18S growing on prebiotic oligosaccharides. *Food Microbiology*, 89(January), 103430. <https://doi.org/10.1016/j.fm.2020.103430>
- Cotter, P. D., Ross, R. P., & Hill, C. (2013). Bacteriocins-a viable alternative to antibiotics? *Nature Reviews Microbiology*, 11(2), 95–105. <https://doi.org/10.1038/nrmicro2937>
- Czajkowski, K., Broś-Konopielko, M., & Teliga-Czajkowska, J. (2021). Urinary tract infection in women. *Przegląd Menopauzalny*, 20(1), 40–47. <https://doi.org/10.5114/pm.2021.105382>
- Dason, S., Dason, J. T., & Kapoor, A. (2011). Guidelines for the diagnosis and

- management of recurrent urinary tract infection in women. *Journal of the Canadian Urological Association*, 5(5), 316–322. <https://doi.org/10.5489/cuaj.11214>
- Day, M., Doumith, M., Jenkins, C., Dallman, T. J., Hopkins, K. L., Elson, R., Godbole, G., & Woodford, N. (2017). Antimicrobial resistance in Shiga toxin-producing *Escherichia coli* serogroups O157 and O26 isolated from human cases of diarrhoeal disease in England, 2015. *Journal of Antimicrobial Chemotherapy*, 72(1), 145–152. <https://doi.org/10.1093/jac/dkw371>
- Deng, Z.-L., Gottschick, C., Bhuj, S., Masur, C., Abels, C., & Wagner-Döbler, I. (2018). Metatranscriptome Analysis of the Vaginal Microbiota Reveals Potential Mechanisms for Protection against Metronidazole in Bacterial Vaginosis. *MSphere*, 3(3), 1–16. <https://doi.org/10.1128/mspheredirect.00262-18>
- Deurenberg, R. H., Bathoorn, E., Chlebowicz, M. A., Couto, N., Ferdous, M., García-Cobos, S., Kooistra-Smid, A. M. D., Raangs, E. C., Rosema, S., Veloo, A. C. M., Zhou, K., Friedrich, A. W., & Rossen, J. W. A. (2017). Application of next generation sequencing in clinical microbiology and infection prevention. *Journal of Biotechnology*, 243, 16–24. <https://doi.org/10.1016/j.jbiotec.2016.12.022>
- Dhingra, S., Rahman, N. A. A., Peile, E., Rahman, M., Sartelli, M., Hassali, M. A., Islam, T., Islam, S., & Haque, M. (2020). Microbial Resistance Movements: An Overview of Global Public Health Threats Posed by Antimicrobial Resistance, and How Best to Counter. *Frontiers in Public Health*, 8(November), 1–22. <https://doi.org/10.3389/fpubh.2020.535668>
- Dirar, M. H., Bilal, N. E., Ibrahim, M. E., & Hamid, M. E. (2020). Prevalence of extended-spectrum β -lactamase (Esbl) and molecular detection of blatem, blashv and blactx-m genotypes among enterobacteriaceae isolates from patients in khartoum, sudan. *Pan African Medical Journal*, 37(213), 1–11. <https://doi.org/10.11604/pamj.2020.37.213.24988>
- Dixon, M., Stefil, M., McDonald, M., Bjerklund-Johansen, T. E., Naber, K., Wagenlehner, F., & Mouraviev, V. (2020). Metagenomics in diagnosis and improved targeted treatment of UTI. *World Journal of Urology*, 38(1), 35–43. <https://doi.org/10.1007/s00345-019-02731-9>
- Dominguez-Bello, M. G., Costello, E. K., Contreras, M., Magris, M., Hidalgo, G., Fierer, N., & Knight, R. (2010). Delivery mode shapes the acquisition and structure of the initial microbiota across multiple body habitats in newborns. *Proceedings of the National Academy of Sciences of the United States of America*, 107(26), 11971–11975. <https://doi.org/10.1073/pnas.1002601107>
- Dong, Q., Nelson, D. E., Toh, E., Diao, L., Gao, X., Fortenberry, J. D., & van Der Pol, B. (2011). The microbial communities in male first catch urine are highly similar to those in paired urethral swab specimens. *PLoS ONE*, 6(5), 1–5. <https://doi.org/10.1371/journal.pone.0019709>
- Du, M., Song, L., Wang, Y., Suo, J., Bai, Y., Xing, Y., Xie, L., Liu, B., Li, L., Luo, Y., & Liu, Y. (2021). Investigation and control of an outbreak of urinary tract infections caused by *Burkholderia cepacia*-contaminated anesthetic gel.

- Antimicrobial Resistance and Infection Control*, 10(1), 1–7.
<https://doi.org/10.1186/s13756-020-00855-x>
- Dune, T. J., Price, T. K., Hilt, E. E., Krystal J. Thomas-White, S. K. C. B., Brubaker, L., Schreckenberger, P., Wolfe, A. J., & Mueller, E. R. (2018). Urinary symptoms and their associations with urinary tract infections in urogynecologic patients. *Obstet Gynecol*, 130(4), 718–725.
<https://doi.org/10.1097/AOG.0000000000002239>.Urinary
- Duployez, C., Le Guern, R., Faure, E., Wallet, F., & Loïez, C. (2020). Sneathia amnii, an unusual pathogen in spondylitis: A case report. *Anaerobe*, 66, 1–3.
<https://doi.org/10.1016/j.anaerobe.2020.102277>
- Eltai, N. O., Al Thani, A. A., Al-Ansari, K., Deshmukh, A. S., Wehedy, E., Al-Hadidi, S. H., & Yassine, H. M. (2018). Molecular characterization of extended spectrum β -lactamases enterobacteriaceae causing lower urinary tract infection among pediatric population. *Antimicrobial Resistance and Infection Control*, 7(1), 1–9.
<https://doi.org/10.1186/s13756-018-0381-6>
- Fagan, M., Lindbæk, M., Grude, N., Reiso, H., Romøren, M., Skaare, D., & Berild, D. (2015). Antibiotic resistance patterns of bacteria causing urinary tract infections in the elderly living in nursing homes versus the elderly living at home: an observational study. *BMC Geriatrics*, 15(1), 98. <https://doi.org/10.1186/s12877-015-0097-x>
- Farkas, A., Tarco, E., & Butiuc-Keul, A. (2019). Antibiotic resistance profiling of pathogenic enterobacteriaceae from cluj- napoca, Romania. *Germs*, 9(1), 17–27.
<https://doi.org/10.18683/germs.2019.1153>
- Ferretti, P., Pasolli, E., Tett, A., Asnicar, F., Gorfer, V., Fedi, S., Armanini, F., Truong, D. T., Manara, S., Zolfo, M., Beghini, F., Bertorelli, R., De Sanctis, V., Bariletti, I., Canto, R., Clementi, R., Cologna, M., Crifò, T., Cusumano, G., ... Segata, N. (2018). Mother-to-Infant Microbial Transmission from Different Body Sites Shapes the Developing Infant Gut Microbiome. *Cell Host and Microbe*, 24(1), 133-145.e5. <https://doi.org/10.1016/j.chom.2018.06.005>
- Flores-Meireles, A., Walker, J., Caparon, M., & Hultgren, S. (2015). Urinary tract infections: epidemiology, mechanisms of infection and treatment options. *Nature Reviews Microbiology*, 13(5), 269–284.
<https://doi.org/10.1038/nrmicro3432>.Urinary
- Fok, C. S., Gao, X., Huaiying, L., Thomas-White, K. J., Mueller, E. R., Wolfe, A. J., Dong, Q., & Brubaker, L. (2019). Urinary symptoms are associated with certain urinary microbes in urogynecologic surgical patients. *Physiology & Behavior*, 176(3), 139–148. <https://doi.org/10.1007/s00192-018-3732-1>
- Foxman, B. (2014). Urinary tract infection syndromes. Occurrence, recurrence, bacteriology, risk factors, and disease burden. *Infectious Disease Clinics of North America*, 28(1), 1–13. <https://doi.org/10.1016/j.idc.2013.09.003>
- France, M. T., Rutt, L., Narina, S., Arbaugh, S., McComb, E., Humphrys, M. S., Ma, B., Hayward, M. R., Costello, E. K., Relman, D. A., Kwon, D. S., & Ravel, J. (2020). Complete Genome Sequences of Six Lactobacillus iners Strains Isolated

- from the Human Vagina. *Microbiology Resource Announcements*, 9(20), 17–19.
<https://doi.org/10.1128/mra.00234-20>
- Frimodt-Møller, N. (2019). The urine microbiome – Contamination or a novel paradigm? *EBioMedicine*, 44, 20–21.
<https://doi.org/10.1016/j.ebiom.2019.05.016>
- Gajdács, M., Ábrók, M., Lázár, A., & Burián, K. (2021). Urinary tract infections in elderly patients: A 10-year study on their epidemiology and antibiotic resistance based on the who access, watch, reserve (aware) classification. *Antibiotics*, 10(9).
<https://doi.org/10.3390/antibiotics10091098>
- Gharajalar, N. (2018). Molecular characterisation of multidrug resistant lactobacillus isolated from dental plaque of dogs using a multiplex pcr assay. *Bulgarian Journal of Veterinary Medicine*, 21(4), 436–444. <https://doi.org/10.15547/bjvm.2000>
- Gilbert, J. A., Blaser, M. J., Caporaso, J. G., Jansson, J. K., Lynch, S. V., & Knight, R. (2018). Current understanding of the human microbiome. *Nature Medicine*, 24(4), 392–400. <https://doi.org/10.1038/nm.4517>
- Girard, R., Gaujard, S., Pergay, V., Pornon, P., Martin-Gaujard, G., & Bourguignon, L. (2017). Risk factors for urinary tract infections in geriatric hospitals. *Journal of Hospital Infection*, 97(1), 74–78. <https://doi.org/10.1016/j.jhin.2017.05.007>
- Godaly, G., Ambite, I., Puthia, M., Nadeem, A., Ho, J., Nagy, K., Huang, Y., Rydström, G., & Svanborg, C. (2016). Urinary Tract Infection Molecular Mechanisms and Clinical Translation. *Pathogens*, 5(1), 24.
<https://doi.org/10.3390/pathogens5010024>
- González, M. J., Cunda, P. Da, Notejane, M., Zuninoa, P., Scavone, P., & Robinoc, L. (2019). Fosfomycin tromethamine activity on biofilm and intracellular bacterial communities produced by uropathogenic E. coli isolated from patients with urinary tract infection. Maria José González. *Pathog Dis*, 77(3), 1–25.
- Goodrich, J., Waters, J., Poole, A., Sutter, J., Koren, O., Blekhman, R., Beaumont, M., Van Treuren, W., Knight, R., Bell, J., Spector, T., Clark, A., & Ley, R. E. (2014). Human genetics shape the gut microbiome . PubMed Commons. *Cell*, 159(4), 789–799. <https://doi.org/10.1016/j.cell.2014.09.053>. Human
- Gottschick, C., Deng, Z. L., Vital, M., Masur, C., Abels, C., Pieper, D. H., & Wagner-Döbler, I. (2017). The urinary microbiota of men and women and its changes in women during bacterial vaginosis and antibiotic treatment. *Microbiome*, 5(1), 99.
<https://doi.org/10.1186/s40168-017-0305-3>
- Govender, K. N., Street, T. L., Sanderson, N. D., & Eyre, D. W. (2020). Metagenomic sequencing as a clinical diagnostic tool for infectious diseases: a systematic review and meta-analysis. *MedRxiv*.
<https://doi.org/10.1017/CBO9781107415324.004>
- Govender, Y., Gabriel, I., Minassian, V., & Fichorova, R. (2019). The current evidence on the association between the urinary microbiome and urinary incontinence in women. *Frontiers in Cellular and Infection Microbiology*, 9(MAY), 1–10.
<https://doi.org/10.3389/fcimb.2019.00133>
- Greenbaum, S., Greenbaum, G., Moran-Gilad, J., & Weintraub, A. Y. (2019).

- Ecological dynamics of the vaginal microbiome in relation to health and disease. *American Journal of Obstetrics and Gynecology*, 220(4), 324–335. <https://doi.org/10.1016/j.ajog.2018.11.1089>
- Güler, E., Güvenir, M., Süer, K., Oygur, D. D., Kılıç, S., & Çakır, N. (2021). A Rare Urinary Tract Infection Agent in a Dialysis Patient: *Brevundimonas diminuta*. *Flora the Journal of Infectious Diseases and Clinical Microbiology*, 26(1), 216–219. <https://doi.org/10.5578/flora.20219923>
- Gündoğdu, A., Long, Y. B., Vollmerhausen, T. L., & Katouli, M. (2011). Antimicrobial resistance and distribution of sul genes and integron-associated int genes among uropathogenic *Escherichia coli* in Queensland, Australia. *Journal of Medical Microbiology*, 60(11), 1633–1642. <https://doi.org/10.1099/jmm.0.034140-0>
- Gupta, P., Singh, M. P., & Goyal, K. (2020). Diversity of Vaginal Microbiome in Pregnancy: Deciphering the Obscurity. *Frontiers in Public Health*, 8(July), 1–12. <https://doi.org/10.3389/fpubh.2020.00326>
- Hardy, L., Jespers, V., Abdellati, S., De Baetselier, I., Mwambarangwe, L., Musengamana, V., Van De Wijgert, J., Vaneechoutte, M., & Crucitti, T. (2016). A fruitful alliance: The synergy between *Atopobium vaginae* and *Gardnerella vaginalis* in bacterial vaginosis-associated biofilm. *Sexually Transmitted Infections*, 92(7), 487–491. <https://doi.org/10.1136/sextrans-2015-052475>
- Hasman, H., Saputra, D., Sicheritz-Ponten, T., Lund, O., Svendsen, C. A., Frimodt-Møller, N., & Aarestrup, F. M. (2014). Rapid whole-genome sequencing for detection and characterization of microorganisms directly from clinical samples. *Journal of Clinical Microbiology*, 52(1), 139–146. <https://doi.org/10.1128/JCM.02452-13>
- Heilbronner, S., Krismer, B., Brötz-Oesterhelt, H., & Peschel, A. (2021). The microbiome-shaping roles of bacteriocins. In *Nature Reviews Microbiology* (Vol. 19, Issue 11, pp. 726–739). <https://doi.org/10.1038/s41579-021-00569-w>
- Hiergeist, A., & Gessner, A. (2017). Clinical implications of the microbiome in urinary tract diseases. *Current Opinion in Urology*, 27(2), 93–98. <https://doi.org/10.1097/MOU.0000000000000367>
- Hill, M. O. (1973). Diversity and Evenness: A Unifying Notation and Its Consequences. *Ecology*, 54(2), 427–432.
- Hilty, M., Betsch, B. Y., Bögli-Stuber, K., Heiniger, N., Stadler, M., Küffer, M., Kronenberg, A., Rohrer, C., Aebi, S., Endimiani, A., Droz, S., & Mühlemann, K. (2012). Transmission dynamics of extended-spectrum β -lactamase-producing enterobacteriaceae in the tertiary care hospital and the household setting. *Clinical Infectious Diseases*, 55(7), 967–975. <https://doi.org/10.1093/cid/cis581>
- Horsley, H., Malone-Lee, J., Holland, D., Tuz, M., Hibbert, A., Kelsey, M., Kupelian, A., & Rohn, J. L. (2013). *Enterococcus faecalis* subverts and invades the host urothelium in patients with chronic urinary tract infection. *PLoS ONE*, 8(12), 1–13. <https://doi.org/10.1371/journal.pone.0083637>
- Horwitz, D., McCue, T., Mapesa, A. C., Ajam, N. J., Petrosino, J. F., Ramig, R. F.,

- & Trautner, B. W. (2016). Decreased microbiota diversity associated with urinary tract infection in a trial of bacterial interference. *Physiology & Behavior*, 176(1), 139–148. <https://doi.org/10.1016/j.physbeh.2017.03.040>
- Hrbacek, J., Morais, D., Cermak, P., Hanacek, V., & Zachoval, R. (2021). Alpha-diversity and microbial community structure of the male urinary microbiota depend on urine sampling method. *Scientific Reports*, 11(1). <https://doi.org/10.1038/s41598-021-03292-x>
- Huang, L., Li, X., Zheng, B., Li, P., Wei, D., Huang, C., Sun, L., & Li, H. (2022). Differential Urinary Microbiota Composition Between Women With and Without Recurrent Urinary Tract Infection. *Frontiers in Microbiology*, 13(May), 1–12. <https://doi.org/10.3389/fmicb.2022.888681>
- Hugenholtz, F., van der Veer, C., Terpstra, M. L., Borgdorff, H., van Houdt, R., Bruisten, S., Geerlings, S. E., & van de Wijgert, J. H. H. M. (2022). Urine and vaginal microbiota compositions of postmenopausal and premenopausal women differ regardless of recurrent urinary tract infection and renal transplant status. *Scientific Reports*, 12(1), 1–11. <https://doi.org/10.1038/s41598-022-06646-1>
- Hur, J., Lee, A., Hong, J., Jo, W. Y., Cho, O. H., Kim, S., & Bae, I. G. (2016). *Staphylococcus saprophyticus* bacteremia originating from urinary tract infections: A case report and literature review. *Infection and Chemotherapy*, 48(2), 136–139. <https://doi.org/10.3947/ic.2016.48.2.136>
- Hussain, H. I., Aqib, A. I., Seleem, M. N., Shabbir, M. A., Hao, H., Iqbal, Z., Kulyar, M. F. e. A., Zaheer, T., & Li, K. (2021). Genetic basis of molecular mechanisms in β -lactam resistant gram-negative bacteria. *Microbial Pathogenesis*, 158. <https://doi.org/10.1016/j.micpath.2021.105040>
- iHMP. (2019). The Integrative Human Microbiome Project. *Nature*, 569(7758), 641–648. <https://doi.org/10.1038/s41586-019-1238-8>
- Jacoby, G. A., Zeil, C., Widmann, M., Fademrecht, S., Vogel, C., & Network, P. J. (2016). The Curious Case of TEM-116. *Antimicrobial Agents and Chemotherapy*, 1119(82), 90015. <https://doi.org/10.1128/AAC.01777-16.Address>
- Janssen, D. A. W. (2019). The Microbiome: Another Dimension in the Pathophysiology of Urogenital Disease. *European Urology*, 75(4), 647–648. <https://doi.org/10.1016/j.eururo.2019.01.014>
- Jašarević, E., Hill, E. M., Kane, P. J., Rutt, L., Gyles, T., Folts, L., Rock, K. D., Howard, C. D., Morrison, K. E., Ravel, J., & Bale, T. L. (2021). The composition of human vaginal microbiota transferred at birth affects offspring health in a mouse model. In *Nature Communications* (Vol. 12, Issue 1). <https://doi.org/10.1038/s41467-021-26634-9>
- Jeong, S. H., Bae, I. K., Lee, J. H., Sohn, S. G., Kang, G. H., Jeon, G. J., Kim, Y. H., Jeong, B. C., & Lee, S. H. (2004). Molecular characterization of extended-spectrum beta-lactamases produced by clinical isolates of *Klebsiella pneumoniae* and *Escherichia coli* from a Korean nationwide survey. *Journal of Clinical Microbiology*, 42(7), 2902–2906. <https://doi.org/10.1128/JCM.42.7.2902-2906.2004>

- Johnson, J. S., Spakowicz, D. J., Hong, B. Y., Petersen, L. M., Demkowicz, P., Chen, L., Leopold, S. R., Hanson, B. M., Agresta, H. O., Gerstein, M., Sodergren, E., & Weinstock, G. M. (2019). Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis. *Nature Communications*, 10(1), 1–11. <https://doi.org/10.1038/s41467-019-13036-1>
- Juda, M., Korona-Glowniak, I., Prystupa, A., & Malm, A. (2018). Streptococcus pneumoniae as an agent of urinary tract infection. *Journal of Pre-Clinical and Clinical Research*, 12(3), 87–88. <https://doi.org/10.26444/jpccr/94205>
- Jung, C., & Brubaker, L. (2019). The Etiology and Management of Recurrent Urinary Tract Infections in Postmenopausal Women. *Climateric*, 22(3), 242–249. <https://doi.org/10.1080/13697137.2018.1551871>.The
- Kakoullis, L., Papachristodoulou, E., Chra, P., & Panos, G. (2021). Mechanisms of Antibiotic Resistance in Campylobacter. *Antibiotics*, 10(415), 263–276. <https://doi.org/10.1128/9781555815554.ch14>
- Kamińska, D., & Gajecka, M. (2017). Is the role of human female reproductive tract microbiota underestimated? *Beneficial Microbes*, 8(3), 327–343. <https://doi.org/10.3920/BM2015.0174>
- Karstens, L., Asquith, M., Caruso, V., Rosenbaum, J. T., Braun, J., Gregory, T., Nardos, R., Mcweeney, S., Biology, C., Health, O., Health, O., Health, O., Health, O., Health, O., Health, O., Health, O., & Angeles, L. (2019). Community profiling of the urinary microbiota: Methodological considerations for low microbial biomass biological samples. *Nat Rev Urol.*, 15(12), 735–749. <https://doi.org/10.1038/s41585-018-0104-z>
- Karstens, L., Asquith, M., Davin, S., Stauffer, P., Fair, D., Gregory, W. T., Rosenbaum, J. T., McWeeney, S. K., & Nardos, R. (2016). Does the Urinary Microbiome Play a Role in Urgency Urinary Incontinence and Its Severity? *Frontiers in Cellular and Infection Microbiology*, 6(July), 1–13. <https://doi.org/10.3389/fcimb.2016.00078>
- Khawcharoenporn, T., Vasoo, S., & Singh, K. (2013). Urinary Tract Infections due to Multidrug-Resistant Enterobacteriaceae: Prevalence and Risk Factors in a Chicago Emergency Department. *Emergency Medicine International*, 2013, 1–7. <https://doi.org/10.1155/2013/258517>
- Kim, H., Kim, T., Kang, J., Kim, Y., & Kim, H. (2020). Is lactobacillus gram-positive? A case study of lactobacillus iners. *Microorganisms*, 8(7), 1–8. <https://doi.org/10.3390/microorganisms8070969>
- Kim, J.-M., & Park, Y.-J. (2018). Lactobacillus and urine microbiome in association with urinary tract infections and bacterial vaginosis. *Urogenital Tract Infection*, 13(1), 7. <https://doi.org/10.14777/uti.2018.13.1.7>
- Kim, Y. S., Unno, T., Kim, B. Y., & Park, M. S. (2020). Sex differences in gut microbiota. *World Journal of Men's Health*, 38(1), 48–60. <https://doi.org/10.5534/wjmh.190009>
- Klein, R. D., & Hultgren, S. J. (2020). Urinary tract infections: microbial pathogenesis, host–pathogen interactions and new treatment strategies. *Nature Reviews*

- Microbiology*, 18, 211–226. <https://doi.org/10.1038/s41579-020-0324-0>
- Koedooder, R., Mackens, S., Budding, A., Fares, D., Blockeel, C., Laven, J., & Schoenmakers, S. (2019). Identification and evaluation of the microbiome in the female and male reproductive tracts. *Human Reproduction Update*, 25(3), 298–325. <https://doi.org/10.1093/humupd/dmy048>
- Komesu, Y. M., Dinwiddie, D. L., Richter, H. E., Lukacz, E. S., Sung, V. W., Siddiqui, N. Y., Zyczynski, H. M., Ridgeway, B., Rogers, R. G., Arya, L. A., Mazloomdoost, D., Levy, J., Carper, B., Gantz, M. G., & Network, N. P. F. D. (2020). Defining the relationship between vaginal and urinary microbiomes. *Am J Obstet Gynecol.*, 222(2), 139–148. <https://doi.org/10.1016/j.physbeh.2017.03.040>
- Komesu, Y. M., Richter, H. E., Carper, B., Dinwiddie, D. L., Lukacz, E. S., Siddiqui, N. Y., Sung, V. W., Zyczynski, H. M., Ridgeway, B., Rogers, R. G., Arya, L. A., Mazloomdoost, D., & Gantz, M. G. (2018). The urinary microbiome in women with mixed urinary incontinence compared to similarly aged controls. *International Urogynecology Journal*, 29(12), 1785–1795. <https://doi.org/10.1007/s00192-018-3683-6>
- Kumar, M. S., & Das, A. P. (2016). Molecular identification of multi drug resistant bacteria from urinary tract infected urine samples. *Microbial Pathogenesis*, 98, 37–44. <https://doi.org/10.1016/j.micpath.2016.06.029>
- Kunze, A. N., & Larsen, B. (2019). Current concepts of Gardnerella vaginalis biofilm: significance in bacterial vaginosis. *Open Journal of Obstetrics and Gynecology*, 09(12), 1569–1585. <https://doi.org/10.4236/ojog.2019.912153>
- Kuroda, M., Yamashita, A., Hirakawa, H., Kumano, M., Morikawa, K., Higashide, M., Maruyama, A., Inose, Y., Matoba, K., Toh, H., Kuhara, S., Hattori, M., & Ohta, T. (2005). Whole genome sequence of Staphylococcus saprophyticus reveals the pathogenesis of uncomplicated urinary tract infection. *Proceedings of the National Academy of Sciences of the United States of America*, 102(37), 13272–13277. <https://doi.org/10.1073/pnas.0502950102>
- Lafon, T., Hernandez Padilla, A. C., Baisse, A., Lavaud, L., Goudelin, M., Barraud, O., Daix, T., Francois, B., & Vignon, P. (2019). Community-acquired Staphylococcus aureus bacteriuria: A warning microbiological marker for infective endocarditis? *BMC Infectious Diseases*, 19(1), 1–5. <https://doi.org/10.1186/s12879-019-4106-0>
- Lahlaoui, H., Dahmen, S., Moussa, M. B., & Omrane, B. (2011). First detection of TEM-116 extended-spectrum β -lactamase in a Providencia stuartii isolate from a Tunisian hospital. *Indian Journal of Medical Microbiology*, 29(3), 258–261. <https://doi.org/10.4103/0255-0857.83909>
- Lakshminarayanan, B., Stanton, C., O'Toole, P. W., & Ross, R. P. (2014). Compositional dynamics of the human intestinal microbiota with aging: Implications for health. *Journal of Nutrition, Health and Aging*, 18(9), 773–786. <https://doi.org/10.1007/s12603-014-0549-6>
- Langille, M. G. I., Zaneveld, J., Caporaso, J. G., McDonald, D., Knights, D., Reyes, J.

- A., Clemente, J. C., Burkepille, D. E., Vega Thurber, R. L., Knight, R., Beiko, R. G., & Huttenhower, C. (2013). Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. *Nature Biotechnology*, 31(9), 814–821. <https://doi.org/10.1038/nbt.2676>
- Lee, K. W., Song, H. Y., & Kim, Y. H. (2020). The microbiome in urological diseases. *Investigative and Clinical Urology*, 61(4), 338–348. <https://doi.org/10.4111/icu.2020.61.4.338>
- Lee, S., Oh, K. Y., Hong, H., Jin, C. H., Shim, E., Kim, S. H., & Kim, B. Y. (2020). Community State Types of Vaginal Microbiota and Four Types of Abnormal Vaginal Microbiota in Pregnant Korean Women. *Frontiers in Public Health*, 8(October), 1–11. <https://doi.org/10.3389/fpubh.2020.507024>
- Lewis, A. L., & Gilbert, N. M. (2020). Roles of the vagina and the vaginal microbiota in urinary tract infection: evidence from clinical correlations and experimental models. *GMS Infectious Diseases*, 8, Doc02. <https://doi.org/10.3205/id000046>
- Lewis, D. A., Brown, R., Williams, J., White, P., Jacobson, S. K., Marchesi, J. R., & Drake, M. J. (2013). The human urinary microbiome; bacterial DNA in voided urine of asymptomatic adults. *Frontiers in Cellular and Infection Microbiology*, 3(August), 1–14. <https://doi.org/10.3389/fcimb.2013.00041>
- Li, M., Yang, F., Lu, Y., & Huang, W. (2020). Identification of *Enterococcus faecalis* in a patient with urinary-tract infection based on metagenomic next-generation sequencing: A case report. *BMC Infectious Diseases*, 20(1), 1–7. <https://doi.org/10.1186/s12879-020-05179-0>
- Ling, Z., Kong, J., Liu, F., Zhu, H., Chen, X., Wang, Y., Li, L., Nelson, K. E., Xia, Y., & Xiang, C. (2010a). Molecular analysis of the diversity of vaginal microbiota associated with bacterial vaginosis. *BMC Genomics*, 11(488), 1–16.
- Ling, Z., Kong, J., Liu, F., Zhu, H., Chen, X., Wang, Y., Li, L., Nelson, K. E., Xia, Y., & Xiang, C. (2010b). Molecular analysis of the diversity of vaginal microbiota associated with bacterial vaginosis. *BMC Genomics*, 11(1). <https://doi.org/10.1186/1471-2164-11-488>
- LiPuma, J. J. (2005). Update on the *Burkholderia cepacia* complex. *Current Opinion in Pulmonary Medicine*, 11(6), 528–533. <https://doi.org/10.1097/01.mcp.0000181475.85187.ed>
- Liu, L., Qin, L., Hao, S., Lan, R., Xu, B., Guo, Y., Jiang, R., Sun, H., Chen, X., Lv, X., Xu, J., & Zhao, C. (2020). Lineage, antimicrobial resistance and virulence of *Citrobacter* spp. *Pathogens*, 9(3), 1–21. <https://doi.org/10.3390/pathogens9030195>
- Livermore, D. M., & Woodford, N. (2006). The β -lactamase threat in *Enterobacteriaceae*, *Pseudomonas* and *Acinetobacter*. *Trends in Microbiology*, 14(9), 413–420. <https://doi.org/10.1016/j.tim.2006.07.008>
- Lu, H., Du, Y., Pan, T., Lou, Z., Li, H., Liao, Y., & Wang, L. (2022). *Gardnerella vaginalis* purulent meningitis in an adolescent male: a case report. *BMC Neurology*, 22(1), 1–4. <https://doi.org/10.1186/s12883-022-02733-y>
- Lubarsky, D. (2019). *Streptococcus pneumoniae* urinary tract infection in 3-year-old

- girl. *UTJMS*, 6.
- Lüthje, P., Brauner, H., Ramos, N. L., Övregaard, A., Gläser, R., Hirschberg, A. L., Aspenström, P., & Brauner, A. (2013). Estrogen supports urothelial defense mechanisms. *Science Translational Medicine*, 5(190), 1–10. <https://doi.org/10.1126/scitranslmed.3005574>
- Ma, Z. S. (2022). Microbiome Transmission During Sexual Intercourse Appears Stochastic and Supports the Red Queen Hypothesis. *Frontiers in Microbiology*, 12(March), 1–14. <https://doi.org/10.3389/fmicb.2021.789983>
- Machado, D., Castro, J., Palmeira-de-Oliveira, A., Martinez-de-Oliveira, J., & Cerca, N. (2016). Bacterial vaginosis biofilms: Challenges to current therapies and emerging solutions. *Frontiers in Microbiology*, 6(JAN). <https://doi.org/10.3389/fmicb.2015.01528>
- MacIntyre, D. A., Sykes, L., & Bennett, P. R. (2017). The human female urogenital microbiome: Complexity in normality. *Emerging Topics in Life Sciences*, 1(4), 363–372. <https://doi.org/10.1042/ETLS20170042>
- Macklaim, J. M., Gloor, G. B., Anukam, K. C., Cribby, S., & Reid, G. (2011). At the crossroads of vaginal health and disease, the genome sequence of *Lactobacillus iners* AB-1. *Proceedings of the National Academy of Sciences of the United States of America*, 108(SUPPL. 1), 4688–4695. <https://doi.org/10.1073/pnas.1000086107>
- Magistro, G., & Stief, C. G. (2019). The urinary tract microbiome: The answer to all our open questions? *European Urology Focus*, 5(1), 36–38. <https://doi.org/10.1016/j.euf.2018.06.011>
- Magruder, M., Sholi, A. N., Gong, C., Zhang, L., Edusei, E., Huang, J., Albakry, S., Satlin, M. J., Westblade, L. F., Crawford, C., Dadhania, D. M., Lubetzky, M., Taur, Y., Littman, E., Ling, L., Burnham, P., De Vlaminc, I., Pamer, E., Suthanthiran, M., & Lee, J. R. (2019). Gut uropathogen abundance is a risk factor for development of bacteriuria and urinary tract infection. *Nature Communications*, 10(1), 1–9. <https://doi.org/10.1038/s41467-019-13467-w>
- Magurran, A. (2004). Measuring Biological Diversity - Chapter 2. In *Measuring biological diversity*.
- Malki, K., Shapiro, J. W., Price, T. K., Hilt, E. E., Thomas-white, K., Sircar, T., Rosenfeld, A. B., Kuffel, G., Zilliox, M. J., Wolfe, A. J., & Putonti, C. (2016). Genomes of *Gardnerella* Strains Reveal an Abundance of Prophages within the Bladder Microbiome. *PLOS ONE*, 1–16. <https://doi.org/10.1371/journal.pone.0166757>
- Maravić, A., Skočibušić, M., Fredotović, Ž., Šamanić, I., Cvjetan, S., Knezović, M., & Puizina, J. (2016). Urban riverine environment is a source of multidrug-resistant and ESBL-producing clinically important *Acinetobacter* spp. *Environmental Science and Pollution Research*, 23(4), 3525–3535. <https://doi.org/10.1007/s11356-015-5586-0>
- Marshall, C. W., Kurs-Lasky, M., McElheny, C. L., Bridwell, S., Liu, H., & Shaikh, N. (2021). Performance of Conventional Urine Culture Compared to 16S rRNA

- Gene Amplicon Sequencing in Children with Suspected Urinary Tract Infection. *Microbiology Spectrum*, 9(3), 1–10. <https://doi.org/10.1128/spectrum.01861-21>
- McKloud, E., Sherry, L., Kean, R., Delaney, C., Williams, S., Metcalfe, R., Thomas, R., Williams, C., & Ramage, G. (2021). Recurrent Vulvovaginal Candidiasis; a dynamic interkingdom biofilm disease of *Candida* and *Lactobacillus*. *BioRxiv*, 1–41. <https://www.biorxiv.org/content/10.1101/2021.02.12.430906v1.abstract>
- Mendes, M. D., Cavallo, R. R., Carvalhães, C. H. V. F. G., & Ferrarini, M. A. G. (2016). Septic arthritis by *Sphingobacterium multivorum* in immunocompromised pediatric patient. *Revista Paulista de Pediatria (English Edition)*, 34(3), 379–383. <https://doi.org/10.1016/j.rppede.2016.03.014>
- Meštrović, T., Matijašić, M., Perić, M., Čipčić Paljetak, H., Barešić, A., & Verbanac, D. (2020). The role of gut, vaginal, and urinary microbiome in urinary tract infections: From bench to bedside. *Diagnostics*, 11(1), 7. <https://doi.org/10.3390/diagnostics11010007>
- Milani, C., Duranti, S., Bottacini, F., Casey, E., Turrone, F., Mahony, J., Belzer, C., Delgado Palacio, S., Arbolea Montes, S., Mancabelli, L., Lugli, G. A., Rodriguez, J. M., Bode, L., de Vos, W., Gueimonde, M., Margolles, A., van Sinderen, D., & Ventura, M. (2017). The First Microbial Colonizers of the Human Gut: Composition, Activities, and Health Implications of the Infant Gut Microbiota. *Microbiology and Molecular Biology Reviews*, 81(4). <https://doi.org/10.1128/mmb.00036-17>
- Miller, S., Miller-Ensminger, T., Voukadinova, A., Wolfe, A. J., & Putonti, C. (2020). Draft Genome Sequence of *Streptococcus anginosus* UMB7768, Isolated from a Woman with Recurrent UTI Symptoms. *Microbiology Resource Announcements*, 9(21), 13–14. <https://doi.org/10.1128/mra.00418-20>
- Mitsuhashi, S., Kryukov, K., Nakagawa, S., Takeuchi, J. S., Shiraishi, Y., Asano, K., & Imanishi, T. (2017). A portable system for rapid bacterial composition analysis using a nanopore-based sequencer and laptop computer. *Scientific Reports*, 7(1), 1–9. <https://doi.org/10.1038/s41598-017-05772-5>
- Mobley, H. (2016). Measuring *Escherichia coli* Gene Expression during Human Urinary Tract Infections. *Pathogens*, 5(1), 1–9. <https://doi.org/10.3390/pathogens5010007>
- Morrill, S., Gilbert, N. M., & Lewis, A. L. (2020). *Gardnerella vaginalis* as a cause of bacterial vaginosis: Appraisal of the evidence from in vivo models. *Frontiers in Cellular and Infection Microbiology*, 10(April). <https://doi.org/10.3389/fcimb.2020.00168>
- Mortensen, M. S., Rasmussen, M. A., Stokholm, J., Brejnrod, A. D., Balle, C., Thorsen, J., Krogfelt, K. A., Bisgaard, H., & Sørensen, S. J. (2021). Modeling transfer of vaginal microbiota from mother to infant in early life. *ELife*, 10, 1–19. <https://doi.org/10.7554/ELIFE.57051>
- Moustafa, A., Li, W., Singh, H., Moncera, K. J., Torralba, M. G., Yu, Y., Manuel, O., Biggs, W., Venter, J. C., Nelson, K. E., Pieper, R., & Telenti, A. (2018). Microbial metagenome of urinary tract infection. *Scientific Reports*, 8(1), 1–12.

- <https://doi.org/10.1038/s41598-018-22660-8>
- Muhammad, I., Golparian, D., Dillon, J. A. R., Johansson, Å., Ohnishi, M., Sethi, S., Chen, S. chun, Nakayama, S. ichi, Sundqvist, M., Bala, M., & Unemo, M. (2014). Characterisation of bla TEM genes and types of β -lactamase plasmids in *Neisseria gonorrhoeae* - the prevalent and conserved bla TEM-135 has not recently evolved and existed in the Toronto plasmid from the origin. *BMC Infectious Diseases*, 14(1), 1–7. <https://doi.org/10.1186/1471-2334-14-454>
- Muhleisen, A. L., & Herbst-Kralovetz, M. M. (2016). Menopause and the vaginal microbiome. *Maturitas*, 91, 42–50. <https://doi.org/10.1016/j.maturitas.2016.05.015>
- Mundangalam, N. (2018). Urinary Tract Infection in Tertiary Care Hospital in Kerala and Burkholderia Cepacia in Uncomplicated Uti. *Journal of Evidence Based Medicine and Healthcare*, 5(23), 1751–1754. <https://doi.org/10.18410/jebmh/2018/367>
- Nelson, D. E., van der Pol, B., Dong, Q., Revanna, K. V., Fan, B., Easwaran, S., Sodergren, E., Weinstock, G. M., Diao, L., & Fortenberry, D. J. (2010). Characteristic male urine microbiomes associate with asymptomatic sexually transmitted infection. *PLoS ONE*, 5(11), 1–7. <https://doi.org/10.1371/journal.pone.0014116>
- Neugent, M. L., Hulyalkar, N. V., Nguyen, V. H., Zimmern, P. E., & De Nisco, N. J. (2020). Advances in understanding the human urinary microbiome and its potential role in urinary tract infection. *MBio*, 11(2), 1–15. <https://doi.org/10.1128/mBio.00218-20>
- Neugent, M. L., Kumar, A., Hulyalkar, N. V., Lutz, K. C., Nguyen, V. H., Fuentes, J. L., Zhang, C., Nguyen, A., Sharon, B. M., Kuprasertkul, A., Arute, A. P., Ebrahimzadeh, T., Natesan, N., Li, Q., Xing, C., Zimmern, P. E., Palmer, K. L., Nisco, N. J. De, & Sciences, D. (2022). Recurrent urinary tract infection and estrogen shape the taxonomic ecology and functional potential of the postmenopausal urobiome. *BioRxiv*. <https://doi.org/https://doi.org/10.1101/2021.11.06.467345>
- O'Brien, V. P., Lewis, A. L., & Gilbert, N. M. (2021). Bladder Exposure to *Gardnerella* Activates Host Pathways Necessary for *Escherichia coli* Recurrent UTI. *Frontiers in Cellular and Infection Microbiology*, 11(December), 1–13. <https://doi.org/10.3389/fcimb.2021.788229>
- Ohland, C. L., & MacNaughton, W. K. (2010). Probiotic bacteria and intestinal epithelial barrier function. *American Journal of Physiology - Gastrointestinal and Liver Physiology*, 298(6). <https://doi.org/10.1152/ajpgi.00243.2009>
- Orsini, J., Tam, E., Hauser, N., & Rajayer, S. (2014). Polymicrobial bacteremia involving *comamonas testosteroni*. *Case Reports in Medicine*, 2014, 15–18. <https://doi.org/10.1155/2014/578127>
- Oulas, A., Pavludi, C., Polymenakou, P., Pavlopoulos, G. A., Papanikolaou, N., Kotoulas, G., Arvanitidis, C., & Iliopoulos, I. (2015). Metagenomics: Tools and insights for analyzing next-generation sequencing data derived from biodiversity

- studies. *Bioinformatics and Biology Insights*, 9, 75–88. <https://doi.org/10.4137/BBI.S12462>
- Pagan, L., Ederveen, R. A. M., Huisman, B. W., Schoones, J. W., Zwittink, R. D., Schuren, F. H. J., Rissmann, R., Piek, J. M. J., & van Poelgeest, M. I. E. (2021). The human vulvar microbiome: A systematic review. *Microorganisms*, 9(12), 1–16. <https://doi.org/10.3390/microorganisms9122568>
- Pagnier, I., Croce, O., Robert, C., Raoult, D., & La Scola, B. (2015). Non-contiguous finished genome sequence and description of *Fenollaria massiliensis* gen. nov., sp. nov., a new genus of anaerobic bacterium. *Standards in Genomic Sciences*, 9(3), 704–717. <https://doi.org/10.4056/sigs.3957647>
- Park, J. J., Seo, Y. Bin, & Lee, J. (2017). Antimicrobial susceptibilities of Enterobacteriaceae in community-acquired urinary tract infections during a 5-year period: A single hospital study in Korea. *Infection and Chemotherapy*, 49(3), 184–193. <https://doi.org/10.3947/ic.2017.49.3.184>
- Park, S. H., Choi, S. M., Lee, D. G., Cho, S. Y., Lee, H. J., Choi, J. K., Choi, J. H., & Yoo, J. H. (2015). Impact of extended-spectrum β -lactamase production on treatment outcomes of acute pyelonephritis caused by *Escherichia coli* in patients without health care-associated risk factors. *Antimicrobial Agents and Chemotherapy*, 59(4), 1962–1968. <https://doi.org/10.1128/AAC.04821-14>
- Pearce, M. M., Hilt, E. E., & Rosenfeld, A. B. (2014). The Female Urinary Microbiome: a Comparison of Women with and without Urgency Urinary Incontinence. *MBio*, 5(4), 1–12. <https://doi.org/10.1128/mBio.01283-14>
- Pekmezovic, M., Mogavero, S., Naglik, J. R., & Hube, B. (2019). Host–Pathogen Interactions during Female Genital Tract Infections. *Trends in Microbiology*, 27(12), 982–996. <https://doi.org/10.1016/j.tim.2019.07.006>
- Perez-Carrasco, V., Soriano-Lerma, A., Soriano, M., Gutiérrez-Fernández, J., & Garcia-Salcedo, J. A. (2021). Urinary Microbiome: Yin and Yang of the Urinary Tract. *Frontiers in Cellular and Infection Microbiology*, 11(May), 1–17. <https://doi.org/10.3389/fcimb.2021.617002>
- Petrova, M. I., Lievens, E., Malik, S., Imholz, N., & Lebeer, S. (2015). *Lactobacillus* species as biomarkers and agents that can promote various aspects of vaginal health. *Frontiers in Physiology*, 6(MAR), 1–18. <https://doi.org/10.3389/fphys.2015.00081>
- Petrova, M. I., Reid, G., Vaneechoutte, M., & Lebeer, S. (2017). *Lactobacillus iners*: Friend or Foe? *Trends in Microbiology*, 25(3), 182–191. <https://doi.org/10.1016/j.tim.2016.11.007>
- Petti, C. A. (2007). Detection and Identification of Microorganisms by Gene Amplification and Sequencing. *Clinical Infectious Diseases*, 44(8), 1108–1114. <https://doi.org/10.1086/512818>
- Pohl, H. G., Groah, S. L., Pérez-Losada, M., Ljungberg, I., Sprague, B. M., Chandal, N., Caldovic, L., & Hsieh, M. (2020). The urine microbiome of healthy men and women differs by urine collection method. *International Neurourology Journal*, 24(1), 41–51. <https://doi.org/10.5213/inj.1938244.122>

- Popović, B. V., Šitum, M., Chow, C. E. T., Chan, L. S., Roje, B., & Terzić, J. (2018). The urinary microbiome associated with bladder cancer. *Scientific Reports*, 8(1), 1–8. <https://doi.org/10.1038/s41598-018-29054-w>
- Price, T K, Hilt, E. E., Thomas-white, K., Mueller, E. R., & Wolfe, A. J. (2019). The urobiome of continent adult women : a cross-sectional study. *BJOG*, 1–9. <https://doi.org/10.1111/1471-0528.15920>
- Price, Travis K., Wolff, B., Halverson, T., Limeira, R., Brubaker, L., Dong, Q., Mueller, E. R., & Wolfe, A. J. (2020). Temporal Dynamics of the Adult Female Lower Urinary Tract Microbiota. *MBio*, 11(2), 1–14. <https://doi.org/10.1128/mBio.00475-20>
- Price, Travis K, Hilt, E. E., Dune, T. J., Mueller, E. R., Wolfe, A. J., & Brubaker, L. (2018). Urine trouble : should we think differently about UTI ? *Int Urogynecol J.*, 29, 205–210.
- Price, Travis K, Hilt, E. E., Thomas-White, K., Mueller, E. R., Wolfe, A. J., & Brubaker, L. (2020). The urobiome of continent adult women: a cross-sectional study. *BJOG*, 127(2), 193–201. <https://doi.org/10.1111/1471-0528.15920>
- Qin, J., Shi, X., Xu, J., Yuan, S., Zheng, B., Zhang, E., Huang, G., Li, G., Jiang, G., Gao, S., Tian, C., Guo, R., Fu, Z., Huang, Q., Yang, R., Zhang, W., Li, S., & Wu, S. (2021). Characterization of the Genitourinary Microbiome of 1,165 Middle-Aged and Elderly Healthy Individuals. *Frontiers in Microbiology*, 12(August), 1–14. <https://doi.org/10.3389/fmicb.2021.673969>
- Ragaliauskas, T., Plečkaitytė, M., Jankunec, M., Labanauskas, L., Baranauskienė, L., & Valincius, G. (2019). Inerolysin and vaginolysin, the cytolysins implicated in vaginal dysbiosis, differently impair molecular integrity of phospholipid membranes. *Scientific Reports*, 9(1), 1–11. <https://doi.org/10.1038/s41598-019-47043-5>
- Ramasethu, J. (2017). Prevention and treatment of neonatal nosocomial infections. *Maternal Health, Neonatology and Perinatology*, 3(1), 1–11. <https://doi.org/10.1186/s40748-017-0043-3>
- Ramos, S., Silva, V., Dapkevicius, M. de L. E., Igrejas, G., & Poeta, P. (2020). Enterococci, from harmless bacteria to a pathogen. *Microorganisms*, 8(8), 1–12. <https://doi.org/10.3390/microorganisms8081118>
- Robertson, R. C., Manges, A. R., Finlay, B. B., & Prendergast, A. J. (2019). The Human Microbiome and Child Growth – First 1000 Days and Beyond. *Trends in Microbiology*, 27(2), 131–147. <https://doi.org/10.1016/j.tim.2018.09.008>
- Rodino-Janeiro, B. K., Vicario, M., Alonso-Cotner, C., Pascua-García, R., & Santos, J. (2018). A Review of Microbiota and Irritable Bowel Syndrome: Future in Therapies. *Adv Ther*, 35, 289–310.
- Rodrigues, W. F., Miguel, C. B., Nogueira, A. P. O., Ueira-Vieira, C., Paulino, T. D. P., Soares, S. D. C., De Resende, E. A. M. R., Lazo-Chica, J. E., Araújo, M. C., & Oliveira, C. J. (2016). Antibiotic resistance of bacteria involved in urinary infections in Brazil: A cross-sectional and retrospective study. *International Journal of Environmental Research and Public Health*, 13(9).

- <https://doi.org/10.3390/ijerph13090918>
- Rodríguez-Bano, J., Navarro, M. D., Romero, L., Martínez-martínez, L., Muniain, M. A., Perea, E. J., & Pascual, A. (2004). Epidemiology and Clinical Features of Infections Caused by Extended-Spectrum Beta-Lactamase-Producing *Escherichia coli* in Nonhospitalized Patients. In *Journal of clinical microbiology* (Vol. 42, Issue 3, pp. 1089–1094).
- Rossi, F., Amadoro, C., & Colavita, G. (2019). Members of the lactobacillus genus complex (LGC) as opportunistic pathogens: A review. *Microorganisms*, 7(5), 1–15. <https://doi.org/10.3390/microorganisms7050126>
- Ryan, M. P., & Pembroke, J. T. (2018). *Brevundimonas* spp: Emerging global opportunistic pathogens. *Virulence*, 9(1), 480–493. <https://doi.org/10.1080/21505594.2017.1419116>
- Sabat, A. J., Van Zanten, E., Akkerboom, V., Wisselink, G., Van Slochteren, K., De Boer, R. F., Hendrix, R., Friedrich, A. W., Rossen, J. W. A., & Kooistra-Smid, A. M. D. M. (2017). Targeted next-generation sequencing of the 16S-23S rRNA region for culture-independent bacterial identification-increased discrimination of closely related species. *Scientific Reports*, 7(1), 1–12. <https://doi.org/10.1038/s41598-017-03458-6>
- Salverda, M. L. M., de Visser, J. A. G. M., & Barlow, M. (2010). Natural evolution of TEM-1 β -lactamase: Experimental reconstruction and clinical relevance. *FEMS Microbiology Reviews*, 34(6), 1015–1036. <https://doi.org/10.1111/j.1574-6976.2010.00222.x>
- Sammoni, A., Abdalah, A., & Al-Aissami, M. (2022). *Comamonas testosteroni* bacteremia: A rare unusual pathogen detected in a burned patient: Case report and literature review. *Annals of Medicine and Surgery*, 75(February), 103371. <https://doi.org/10.1016/j.amsu.2022.103371>
- Sarshar, S., Mirnejad, R., & Babapour, E. (2021). Frequency of blaCTX-M and blaTEM Virulence Genes and Antibiotic Resistance Profiles among *Klebsiella pneumoniae* Isolates in Urinary Tract Infection (UTI) Samples from Hashtgerd, Iran. *Reports of Biochemistry and Molecular Biology*, 10(3), 412–419. <https://doi.org/10.52547/rbmb.10.3.412>
- Schneeweiss, J., Koch, M., & Umek, W. (2016). The human urinary microbiome and how it relates to urogynecology. *International Urogynecology Journal*, 27(9), 1307–1312. <https://doi.org/10.1007/s00192-016-2944-5>
- Scott, V. C. S., Haake, D. A., Churchill, B. M., Justice, S. S., & Kim, J. H. (2015). Intracellular Bacterial Communities: A Potential Etiology for Chronic Lower Urinary Tract Symptoms. *Urology*, 86(3), 425–431. <https://doi.org/10.1016/j.urology.2015.04.002>
- Selma-royo, M., Tarrazó, M., García-mantrana, I., Gómez-gallego, C., Salminen, S., & Collado, M. C. (2019). Shaping Microbiota During the First 1000 Days of Life. In *Advances in Experimental Medicine and Biology* (pp. 3–24).
- Shahzad, N., Aslam, B., Hussain, I., Ijaz, M., Rasool, M. H., Tasneem, F., Hamid, T., Tayyeb, A., & Hussain, T. (2016). Distribution and phylogenetic analysis of

- bacterial isolates from Urinary Tract Infection patients of Pakistan. *Pakistan Journal of Zoology*, 48(6), 1925–1930.
- Shaikh, S., Fatima, J., Shakil, S., Rizvi, S. M. D., & Kamal, M. A. (2015). Antibiotic resistance and extended spectrum beta-lactamases: Types, epidemiology and treatment. *Saudi Journal of Biological Sciences*, 22(1), 90–101. <https://doi.org/10.1016/j.sjbs.2014.08.002>
- Sharma, N., Gupta, A., Walia, G., & Bakhshi, R. (2016). Pattern of Antimicrobial Resistance of Escherichia coli Isolates from Urinary Tract Infection Patients: A Three Year Retrospective Study. *Journal of Applied Pharmaceutical Science*, 6(01), 62–65. <https://doi.org/10.7324/JAPS.2016.600110>
- Sheppard, S. K. (2022). Strain wars and the evolution of opportunistic pathogens. *Current Opinion in Microbiology*, 67, 102138. <https://doi.org/10.1016/j.mib.2022.01.009>
- Shobha, K., Ramachandra, L., Gowrish, S., & Nagalakshmi, N. (2013). Brevundimonas Diminuta Causing Urinary Tract Infection. *Webmedcentral*, June, 4–8. https://www.webmedcentral.com/article_view/4411
- Simons, A., Alhanout, K., & Duval, R. E. (2020). Bacteriocins, antimicrobial peptides from bacterial origin: Overview of their biology and their impact against multidrug-resistant bacteria. *Microorganisms*, 8(5). <https://doi.org/10.3390/microorganisms8050639>
- Singhal, L., Gupta, V., Gupta, M., Goel, P., & Chander, J. (2020). Identification and Sensitivity of Vaginal and Probiotic Lactobacillus species to Urinary Antibiotics. *J Lab Physician*, 12(2), 111–114. <https://doi.org/https://doi.org/10.1055/s-0040-1716604>
- Smelov, V., Naber, K., & Bjerklund Johansen, T. E. (2016). Letter to the Editor: Diagnostic Criteria in Urological Diseases do not Always Match with Findings by Extended Culture Techniques and Metagenomic Sequencing of 16S rDNA. *The Open Microbiology Journal*, 10(1), 23–26. <https://doi.org/10.2174/1874285801610010023>
- Spaulding, C., & Hultgren, S. (2016). Adhesive Pili in UTI Pathogenesis and Drug Development. *Pathogens*, 5(1), 30. <https://doi.org/10.3390/pathogens5010030>
- Srinivasan, S., Morgan, M. T., Fiedler, T. L., Djukovic, D., Hoffman, N. G., Raftery, D., Marrazzo, J. M., & Fredricks, D. N. (2015). Metabolic signatures of bacterial vaginosis. *MBio*, 6(2). <https://doi.org/10.1128/mBio.00204-15>
- Stinson, L. F., Payne, M. S., & Keelan, J. A. (2018). A critical review of the bacterial baptism hypothesis and the impact of cesarean delivery on the infant microbiome. *Frontiers in Medicine*, 5(MAY). <https://doi.org/10.3389/fmed.2018.00135>
- Stout, M. J., Wylie, T. N., Gula, H., Miller, A., & Wylie, K. M. (2020). The microbiome of the human female reproductive tract. *Current Opinion in Physiology*, 13, 87–93. <https://doi.org/10.1016/j.cophys.2019.10.011>
- Sugianli, A. K., Ginting, F., Kusumawati, R. L., Pranggono, E. H., Pasaribu, A. P., Gronthoud, F., Geerlings, S., Parwati, I., De Jong, M. D., Van Leth, F., & Schultz, C. (2017). Antimicrobial resistance in uropathogens and appropriateness

- of empirical treatment: A population-based surveillance study in Indonesia. *Journal of Antimicrobial Chemotherapy*, 72(5), 1469–1477. <https://doi.org/10.1093/jac/dkw578>
- Szabados, F., Kleine, B., Anders, A., Kaase, M., Sakinç, T., Schmitz, I., & Gatermann, S. (2008). *Staphylococcus saprophyticus* ATCC 15305 is internalized into human urinary bladder carcinoma cell line 5637. *FEMS Microbiology Letters*, 285(2), 163–169. <https://doi.org/10.1111/j.1574-6968.2008.01218.x>
- Takahashi, Y., Funaki, T., Ishiguro, A., & Miyairi, I. (2022). Urinary Tract Infection Caused By Bacterial Pathogens of The Respiratory Tract In Children. *Research Square*, 1–9. <https://doi.org/https://doi.org/10.21203/rs.3.rs-1216166/v1> License:
- Tamburini, S., Shen, N., Wu, H. C., & Clemente, J. C. (2016). The microbiome in early life: Implications for health outcomes. *Nature Medicine*, 22(7), 713–722. <https://doi.org/10.1038/nm.4142>
- Tan, C. W., & Chlebicki, M. P. (2016). Urinary tract infections in adults. *Singapore Medical Journal*, 57(9), 485–490. <https://doi.org/10.11622/smedj.2016153>
- Tang, S. S., Apisarnthanarak, A., & Hsu, L. Y. (2014). Mechanisms of β -lactam antimicrobial resistance and epidemiology of major community- and healthcare-associated multidrug-resistant bacteria. *Advanced Drug Delivery Reviews*, 78, 3–13. <https://doi.org/10.1016/j.addr.2014.08.003>
- Tariq, E. F., Irshad, Y., Khalil, H. B., Khakwani, A. S., & Khan, U. A. (2020). Urinary Tract Infection Caused by the Novel Pathogen, *Lactococcus Garvieae*: A Case Report. *Cureus*, 12(7), 10–13. <https://doi.org/10.7759/cureus.9462>
- Tayh, G., Al Laham, N., Ben Yahia, H., Ben Sallem, R., Elottol, A. E., & Ben Slama, K. (2019). Extended-spectrum β -lactamases among Enterobacteriaceae isolated from urinary tract infections in Gaza Strip, Palestine. *BioMed Research International*, 2019. <https://doi.org/10.1155/2019/4041801>
- Terlizzi, M. E., Gribaudo, G., & Maffei, M. E. (2017). UroPathogenic *Escherichia coli* (UPEC) infections: Virulence factors, bladder responses, antibiotic, and non-antibiotic antimicrobial strategies. *Frontiers in Microbiology*, 8(AUG). <https://doi.org/10.3389/fmicb.2017.01566>
- Tett, A., Pasolli, E., Masetti, G., Ercolini, D., & Segata, N. (2021). Prevotella diversity, niches and interactions with the human host. *Nature Reviews Microbiology*, 19(9), 585–599. <https://doi.org/10.1038/s41579-021-00559-y>
- The Human Microbiome Project Consortium. (2012). Structure, function and diversity of the healthy human microbiome. *Nature*, 486(7402), 207–214. <https://doi.org/10.1038/nature11234>
- Thomas-White, K., Forster, S. C., Kumar, N., Van Kuiken, M., Putonti, C., Stares, M. D., Hilt, E. E., Price, T. K., Wolfe, A. J., & Lawley, T. D. (2018). Culturing of female bladder bacteria reveals an interconnected urogenital microbiota. *Nature Communications*, 9(1), 1–7. <https://doi.org/10.1038/s41467-018-03968-5>
- Tomasek, K., Leithner, A., Glatzova, I., Lukesch, M. S., Guet, C. C., & Sixt, M. (2022). Type 1 pilated uropathogenic *Escherichia coli* hijack the host immune response by binding to CD14. *ELife*, 11, 1–35.

- <https://doi.org/https://doi.org/10.7554/eLife.78995>
- Trautner, B. W., Kaye, K. S., Gupta, V., Mulgirigama, A., Mitrani-gold, F. S., Scangarella-oman, N. E., Yu, K., Ye, G., & Joshi, A. V. (2022). Risk Factors Associated With Antimicrobial Resistance and Adverse Short-Term Health Outcomes Among Adult and Adolescent Female Outpatients With Uncomplicated Urinary Tract Infection. *Open Forum Infectious Diseases*, 9(12), 1–8. <https://doi.org/10.1093/ofid/ofac623>
- Trivedi, P. C., Pandey, S., & Bhadauria, S. (2010). Text Book of Microbiology. In *Aavishkar Publishers, Distributors*.
- Valeri, F., & Endres, K. (2021). How biological sex of the host shapes its gut microbiota. *Frontiers in Neuroendocrinology*, 61, 100912. <https://doi.org/10.1016/j.yfrne.2021.100912>
- Van Houdt, R., Ma, B., Bruisten, S. M., Speksnijder, A. G. C. L., Ravel, J., & De Vries, H. J. C. (2018). Lactobacillus iners-dominated vaginal microbiota is associated with increased susceptibility to Chlamydia trachomatis infection in Dutch women: A case-control study. *Sexually Transmitted Infections*, 94(2), 117–123. <https://doi.org/10.1136/sextrans-2017-053133>
- van Teijlingen, N. H., Helgers, L. C., Zijlstra - Willems, E. M., van Hamme, J. L., Ribeiro, C. M. S., Strijbis, K., & Geijtenbeek, T. B. H. (2020). Vaginal dysbiosis associated-bacteria Megasphaera elsdenii and Prevotella timonensis induce immune activation via dendritic cells. *Journal of Reproductive Immunology*, 138(January), 103085. <https://doi.org/10.1016/j.jri.2020.103085>
- Vaneechoutte, M. (2017). Lactobacillus iners, the unusual suspect. *Research in Microbiology*, 168(9–10), 826–836. <https://doi.org/10.1016/j.resmic.2017.09.003>
- Veloo, A. C. M., Chlebowicz, M., Winter, H. L. J., Bathoorn, D., & Rossen, J. W. A. (2018). Three metronidazole-resistant prevotella bivia strains harbour a mobile element, encoding a novel nim gene, nimk, and an efflux small MDR transporter. *Journal of Antimicrobial Chemotherapy*, 73(10), 2687–2690. <https://doi.org/10.1093/jac/dky236>
- Vitali, B., Cruciani, F., Picone, G., Parolin, C., Donders, G., & Laghi, L. (2015). Vaginal microbiome and metabolome highlight specific signatures of bacterial vaginosis. *European Journal of Clinical Microbiology and Infectious Diseases*, 34(12), 2367–2376. <https://doi.org/10.1007/s10096-015-2490-y>
- Vitali, Beatrice, Pugliese, C., Biagi, E., Candela, M., Turroni, S., Bellen, G., Donders, G. G. G., & Brigidi, P. (2007). Dynamics of vaginal bacterial communities in women developing bacterial vaginosis, candidiasis, or no infection, analyzed by PCR-denaturing gradient gel electrophoresis and real-time PCR. *Applied and Environmental Microbiology*, 73(18), 5731–5741. <https://doi.org/10.1128/AEM.01251-07>
- Vlasic-Matas, J., Raos, H., Vuckovic, M., Radic, S., & Capkun, V. (2019). Prevalence of Ureaplasma urealyticum, Mycoplasma hominis and Chlamydia trachomatis in patients with uncomplicated recurrent urinary tract infections. *Nephrology and Renal Diseases*, 4(1), 1–4. <https://doi.org/10.15761/nrd.1000150>

- Vyawahare, M., & Jadhal, G. (2019). Clinical and Laboratory Profile of Urinary Tract Infection in diabetic patients. *International Journal of Biomedical and Advance Research*, 10(9), 1–7. <https://doi.org/10.7439/ijbar.v10i9.5279>
- Wallner, A., King, E., Ngonkeu, E. L. M., Moulin, L., & Béna, G. (2019). Genomic analyses of *Burkholderia cenocepacia* reveal multiple species with differential host-Adaptation to plants and humans. *BMC Genomics*, 20(1), 1–15. <https://doi.org/10.1186/s12864-019-6186-z>
- Walsh, C., & Collyns, T. (2017). The pathophysiology of urinary tract infections. *Surgery (United Kingdom)*, 35(6), 293–298. <https://doi.org/10.1016/j.mpsur.2017.03.007>
- Wang, Y., & Xie, Z. (2022). Exploring the role of gut microbiome in male reproduction. *Andrology*, 10(3), 441–450. <https://doi.org/10.1111/andr.13143>
- Whiteside, S. A., Razvi, H., Dave, S., Reid, G., & Burton, J. P. (2015). The microbiome of the urinary tract - A role beyond infection. *Nature Reviews Urology*, 12(2), 81–90. <https://doi.org/10.1038/nrurol.2014.361>
- Wiles, T. J., Kulesus, R. R., & Mulvey, M. A. (2008). Origins and virulence mechanisms of uropathogenic *Escherichia coli*. *Experimental and Molecular Pathology*, 85(1), 11–19. <https://doi.org/10.1016/j.yexmp.2008.03.007>
- Willner, D., Low, S., Steen, J. A., Willner, D., Low, S., Steen, J. A., George, N., Nimmo, G. R., & Schembri, M. A. (2014). Single Clinical Isolates from Acute Uncomplicated Urinary Tract Infections Are Representative of Dominant In Situ Populations. *MBio*, 5(2), 1–10. <https://doi.org/10.1128/mBio.01064-13>
- Winand, R., Bogaerts, B., Hoffman, S., Lefevre, L., Delvoye, M., Van Braekel, J., Fu, Q., Roosens, N. H. C., De Keersmaecker, S. C. J., & Vanneste, K. (2020). Targeting the 16s rRNA gene for bacterial identification in complex mixed samples: Comparative evaluation of second (illumina) and third (oxford nanopore technologies) generation sequencing technologies. *International Journal of Molecular Sciences*, 21(1), 1–22. <https://doi.org/10.3390/ijms21010298>
- Witkin, S. S., Moron, A. F., Linhares, I. M., & Forney, L. J. (2021). Influence of *Lactobacillus crispatus*, *Lactobacillus iners* and *Gardnerella vaginalis* on bacterial vaginal composition in pregnant women. *Archives of Gynecology and Obstetrics*, 304(2), 395–400. <https://doi.org/10.1007/s00404-021-05978-z>
- Wolfe, A. J., & Brubaker, L. (2019). Urobiome updates: advances in urinary microbiome research. *Nature Reviews Urology*, 16(2), 73–74. <https://doi.org/10.1038/s41585-018-0127-5>
- Wolfe, A. J., Toh, E., Shibata, N., Rong, R., Kenton, K., Fitzgerald, M., Mueller, E. R., Schreckenberger, P., Dong, Q., Nelson, D. E., & Brubaker, L. (2012). Evidence of uncultivated bacteria in the adult female bladder. *Journal of Clinical Microbiology*, 50(4), 1376–1383. <https://doi.org/10.1128/JCM.05852-11>
- Wu, L., Xie, X., Li, Y., Liang, T., Zhong, H., Ma, J., Yang, L., Yang, J., Li, L., Xi, Y., Li, H., Zhang, J., Chen, X., Ding, Y., & Wu, Q. (2021). Metagenomics-based analysis of the age-related cumulative effect of antibiotic resistance genes in gut microbiota. *Antibiotics*, 10(8), 1–16. <https://doi.org/10.3390/antibiotics10081006>

- Wu, P., Chen, Y., Zhao, J., Zhang, G., Chen, J., Wang, J., & Zhang, H. (2017). Urinary microbiome and psychological factors in women with Overactive bladder. *Frontiers in Cellular and Infection Microbiology*, 7(November), 1–11. <https://doi.org/10.3389/fcimb.2017.00488>
- Wu, Y., Wang, C., Wan, J., Yao, H., & Yuan, C.-S. (2021). Dissecting the Interplay Mechanism between Epigenetics and Gut Microbiota: Health Maintenance and Disease Prevention. *International Journal of M*, 22(6933).
- Yao, Y., Cai, X., Ye, Y., Wang, F., Chen, F., & Zheng, C. (2021). The Role of Microbiota in Infant Health: From Early Life to Adulthood. *Frontiers in Immunology*, 12(October), 1–21. <https://doi.org/10.3389/fimmu.2021.708472>
- Yıldırım, S., Shoskes, D., Kulkarni, S., & Laguna, P. (2020). Urinary microbiome in uncomplicated and interstitial cystitis: is there any similarity? *World Journal of Urology*, 38(11), 2721–2731. <https://doi.org/10.1007/s00345-020-03099-x>
- Yoo, J. J., Song, J. S., Kim, W. Bin, Yun, J., Shin, H. B., Jang, M. A., Ryu, C. B., Kim, S. S., Chung, J. C., Kuk, J. C., Shin, E. J., Song, H. Y., Yu, B. C., Lee, E. S., Ryu, S., Kim, J. H., Jung, S. S., & Kim, Y. H. (2022). Gardnerella vaginalis in Recurrent Urinary Tract Infection Is Associated with Dysbiosis of the Bladder Microbiome. *Journal of Clinical Medicine*, 11(9). <https://doi.org/10.3390/jcm11092295>
- Yoshimura, K., Ogawa, M., & Saito, M. (2020). In vitro characteristics of intravaginal Lactobacilli; why is L. iners detected in abnormal vaginal microbial flora? *Archives of Gynecology and Obstetrics*, 302(3), 671–677. <https://doi.org/10.1007/s00404-020-05634-y>
- Zacchè, M. M., & Giarenis, I. (2016). Therapies in early development for the treatment of urinary tract inflammation. *Expert Opinion on Investigational Drugs*, 25(5), 531–540. <https://doi.org/10.1517/13543784.2016.1161024>
- Zeil, C., Widmann, M., Fademrecht, S., Vogel, C., & Pleiss, J. (2016). Network analysis of sequence-function relationships and exploration of sequence space of TEM β -lactamases. *Antimicrobial Agents and Chemotherapy*, 60(5), 2709–2717. <https://doi.org/10.1128/AAC.02930-15>
- Zeng, Z., Zhan, J., Zhang, K., Chen, H., & Cheng, S. (2022). Global, regional, and national burden of urinary tract infections from 1990 to 2019: an analysis of the global burden of disease study 2019. *World Journal of Urology*, 40(3), 755–763. <https://doi.org/10.1007/s00345-021-03913-0>
- Zheng, N., Guo, R., Wang, J., Zhou, W., & Ling, Z. (2021). Contribution of Lactobacillus iners to Vaginal Health and Diseases: A Systematic Review. *Frontiers in Cellular and Infection Microbiology*, 11(November). <https://doi.org/10.3389/fcimb.2021.792787>
- Zheng, N., Guo, R., Yao, Y., Jin, M., Cheng, Y., & Ling, Z. (2019). Lactobacillus iners Is Associated with Vaginal Dysbiosis in Healthy Pregnant Women: A Preliminary Study. *BioMed Research International*, 2019. <https://doi.org/10.1155/2019/6079734>
- Zozaya, M., Ferris, M. J., Siren, J. D., Lillis, R., Myers, L., Nsuami, M. J., Eren, A. M.,



Brown, J., Taylor, C. M., & Martin, D. H. (2016). Bacterial communities in penile skin, male urethra, and vaginas of heterosexual couples with and without bacterial vaginosis. *Microbiome*, 4, 1–10. <https://doi.org/10.1186/s40168-016-0161-6>