

Publications during 2022 acknowledging the Roy J Carver Biotechnology Center at the University of Illinois at Urbana-Champaign

Abdel-Hamid, A.M., D'Alessandro-Gabazza, C.N., Yasuma, T., Walden, K.K., Fields, C.J., Gabazza, E.C. and Cann, I., 2022. Complete Genome Sequences of Three *Staphylococcus haemolyticus* Strains Isolated from the Lung of a TGF β 1 Transgenic Mouse with Lung Fibrosis. *Microbiology Resource Announcements*, 11(4), pp.e01176-21.

Aguilar-Lopez, M., Wetzel, C., MacDonald, A., Ho, T.T. and Donovan, S.M., 2022. Metagenomic profile of the fecal microbiome of preterm infants consuming mother's own milk with bovine milk-based fortifier or infant formula: a cross-sectional study. *The American Journal of Clinical Nutrition*, 116(2), pp.435-445.

Alcamán-Arias, M.E., Cifuentes-Anticevic, J., Díez, B., Testa, G., Troncoso, M., Bello, E. and Farías, L., 2022. Surface ammonia-oxidizer abundance during the late summer in the west Antarctic coastal system. *Frontiers in Microbiology*, 13.

Alexander, C., Brauchla, M., Sanoshy, K.D., Blonquist, T.M., Maloney, G.N., Mah, E., Kelley-Garvin, K., Chen, O., Liska, D.J., Shin, J.E. and Boileau, T.W., 2022. Bowel habits, faecal microbiota and faecal bile acid composition of healthy adults consuming fruit pomace fibres: two-arm, randomised, double-blinded, placebo-controlled trials. *British Journal of Nutrition*, pp.1-14.

Anthony-samy, W.J., Dreslik, M.J., Baker, S.J., Davis, M.A., Douglas, M.R., Douglas, M.E. and Phillips, C.A., 2022. Limited gene flow and pronounced population genetic structure of Eastern Massasauga (*Sistrurus catenatus*) in a Midwestern prairie remnant. *PloS one*, 17(3), p.e0265666.

Asangba, A.E., Mugisha, L., Rukundo, J., Lewis, R.J., Halajian, A., Cortés-Ortiz, L., Junge, R.E., Irwin, M.T., Karlson, J., Perkin, A. and Watsa, M., 2022. Large comparative analyses of primate body site microbiomes indicate that the oral microbiome is unique among all body sites and conserved among nonhuman primates. *Microbiology Spectrum*, 10(3), pp.e01643-21.

Assmus, M.A., Lee, M.S., Sivaguru, M., Agarwal, D.K., Large, T., Fouke, B.W. and Krambeck, A.E., 2022. Laser fiber degradation following holmium laser enucleation of the prostate utilizing Moses technology versus regular mode. *World journal of urology*, 40(5), pp.1203-1209.

Avachat, A.V., Leja, A.G., Mahmoud, K.H., Anastasio, M.A., Sivaguru, M. and Di Fulvio, A., 2022. Positron annihilation lifetime spectroscopy of adipose, hepatic, and muscle tissues.

- Ayikpoe, R.S., Shi, C., Battiste, A.J., Eslami, S.M., Ramesh, S., Simon, M.A., Bothwell, I.R., Lee, H., Rice, A.J., Ren, H. and Tian, Q., 2022. A scalable platform to discover antimicrobials of ribosomal origin. *Nature communications*, 13(1), p.6135.
- Bassitta, M., Alemany, I., Pérez-Mellado, V., Pérez-Cembranos, A., Navarro, P., Lluch, J., Jurado-Rivera, J.A., Castro, J.A., Picornell, A. and Ramon, C., 2022. Phylogenetic, Microbiome, and Diet Characterisation of Wall Lizards in the Columbretes Archipelago (Spain): Clues for Their Conservation. *Diversity*, 14(5), p.408.
- Beckman, E.J., Vargas Campos, W., Benham, P.M., Schmitt, C.J., Cheviron, Z.A. and Witt, C.C., 2022. Selection on embryonic haemoglobin in an elevational generalist songbird. *Biology Letters*, 18(10), p.20220105.
- Behnke, G.D., Kim, N., Riggins, C.W., Zabaloy, M.C., Rodriguez-Zas, S.L. and Villamil, M.B., 2022. A longitudinal study of the microbial basis of nitrous oxide emissions within a long-term agricultural experiment. *Frontiers in Agronomy*, 4, p.20.
- Benjamin, R., Giacoletto, C.J., FitzHugh, Z.T., Eames, D., Buczek, L., Wu, X., Newsome, J., Han, M.V., Pearson, T., Wei, Z. and Banerjee, A., 2022. GigaAssay—an adaptable high-throughput saturation mutagenesis assay platform. *Genomics*, 114(4), p.110439.
- Boudreau, M.W., Mulligan, M.P., Shapiro, D.J., Fan, T.M. and Hergenrother, P.J., 2022. Activators of the Anticipatory Unfolded Protein Response with Enhanced Selectivity for Estrogen Receptor Positive Breast Cancer. *Journal of medicinal chemistry*, 65(5), pp.3894-3912.
- Brandenburg, J.T., Clark, L., Botha, G., Panji, S., Baichoo, S., Fields, C. and Hazelhurst, S., 2022. H3AGWAS: a portable workflow for genome wide association studies. *BMC bioinformatics*, 23(1), p.498.
- Breitenbach, A.T., Bowden, R.M. and Paitz, R.T., 2022. Effects of Constant and Fluctuating Temperatures on Gene Expression During Gonadal Development. *Integrative and Comparative Biology*, 62(1), pp.21-29.
- Brown, M.D., Shinn, L.M., Reeser, G., Browning, M., Schwingel, A., Khan, N.A. and Holscher, H.D., 2022. Fecal and soil microbiota composition of gardening and non-gardening families. *Scientific reports*, 12(1), p.1595.
- Burnham, M.B., Simon, S.J., Lee, D., Kent, A.D., DeLucia, E.H. and Yang, W.H., 2022. Intra_ and inter_ annual variability of nitrification in the rhizosphere of field_grown bioenergy sorghum. *GCB Bioenergy*, 14(3), pp.393-410.
- Cerritos Garcia, D.G., Huang, S.Y., Kleczewski, N.M. and Mideros, S., 2022. Virulence, Aggressiveness, and Fungicide Sensitivity of *Phytophthora* spp. Associated with Soybean in Illinois. *Plant Disease*, (ja).

Chen, C.Y., Seward, C.H., Song, Y., Inamdar, M., Leddy, A.M., Zhang, H., Yoo, J., Kao, W.C., Pawlowski, H. and Stubbs, L.J., 2022. Galnt17 loss-of-function leads to developmental delay and abnormal coordination, activity, and social interactions with cerebellar vermis pathology. *Developmental Biology*, 490, pp.155-171.

Chen, M., Conroy, J.L., Geyman, E.C., Sanford, R.A., Chee_Sanford, J.C. and Connor, L.M., 2022. Stable carbon isotope values of syndepositional carbonate spherules and micrite record spatial and temporal changes in photosynthesis intensity. *Geobiology*, 20(5), pp.667-689.

Chiu, K.K., Bashir, S.T., Abdel-Hamid, A.M., Clark, L.V., Laws, M.J., Cann, I., Nowak, R.A. and Flaws, J.A., 2022. Isolation of DiNP-Degrading Microbes from the Mouse Colon and the Influence DiNP Exposure Has on the Microbiota, Intestinal Integrity, and Immune Status of the Colon. *Toxics*, 10(2), p.75.

Cho, Y.B., Boyd, R.A., Ren, Y., Lee, M., Jones, S.I., Ruiz Vera, U.M., McGrath, J.M., Masters, M.D. and Ort, D.R., 2022. Reducing chlorophyll level in seed filling stages results in higher seed nitrogen without impacting canopy carbon assimilation. *bioRxiv*, pp.2022-07.

Clark, L.V., Mays, W., Lipka, A.E. and Sacks, E.J., 2022. A population-level statistic for assessing Mendelian behavior of genotyping-by-sequencing data from highly duplicated genomes. *BMC bioinformatics*, 23(1), p.101.

Costello, E.K., DiGiulio, D.B., Robaczewska, A., Symul, L., Wong, R.J., Shaw, G.M., Stevenson, D.K., Holmes, S.P., Kwon, D.S. and Relman, D.A., 2022. Longitudinal dynamics of the human vaginal ecosystem across the reproductive cycle. *bioRxiv*, pp.2022-11.

Cowell, T.W., Dobria, A. and Han, H.S., 2022. Simplified, Shear Induced Generation of Double Emulsions for Robust Compartmentalization during Single Genome Analysis. *ACS Applied Materials & Interfaces*, 14(18), pp.20528-20537.

Das, S., Song, Z., Han, H., Ge, X., Desert, R., Athavale, D., Komakula, S.S.B., Magdaleno, F., Chen, W., Lantvit, D. and Guzman, G., 2022. Intestinal osteopontin protects from alcohol-induced liver injury by preserving the gut microbiome and the intestinal barrier function. *Cellular and Molecular Gastroenterology and Hepatology*, 14(4), pp.813-839.

Davis, E.C., Wang, M. and Donovan, S.M., 2022. Microbial Interrelationships across sites of breastfeeding mothers and infants at 6 weeks postpartum. *Microorganisms*, 10(6), p.1155.

de Flamingh, A., Ishida, Y., Pecnerova, P., Vilchis, S., Siegismund, H., van Aarde, R., Malhi, R. and Roca, A., 2022. Non-invasive fecal DNA yields whole genome and metagenomic data for species conservation. *bioRxiv*, pp.2022-08.

de Moya, R.S., 2022. Illumina whole genome sequencing indicates ploidy level differences within the *Valenzuela flavidus* (Psocodea: Psocomorpha: Caeciliusidae) species complex. *Systematic Entomology*, 47(1), pp.202-212.

de Moya, R.S., 2022. Phylogenomics and host-switching patterns of Philopterae (Psocodea: Phthiraptera) feather lice. *International Journal for Parasitology*, 52(8), pp.525-537.

Dean, C.A., Easley, J., Katz, A.D., Berlocher, S.H. and Berenbaum, M.R., 2022. Genetic Structure and Colonization of North America by *Depressaria depressana* (Fabricius 1775)(Lepidoptera: Depressariidae) over 15 Years; Contrasts with Westward Expansion of *Depressaria radiella* (Goeze, 1783) over 160 Years. *Insects*, 13(9), p.789.

Dean, J.V., Willis, M. and Shaban, L., 2022. Transport of acylated anthocyanins by the *Arabidopsis* ATP_binding cassette transporters AtABCC1, AtABCC2, and AtABCC14. *Physiologia Plantarum*, 174(5), p.e13780.

DeBiasse, M.B., Stubler, A.D. and Kelly, M.W., 2022. Comparative transcriptomics reveals altered species interaction between the bioeroding sponge *Cliona varians* and the coral *Porites furcata* under ocean acidification. *Molecular ecology*, 31(10), pp.3002-3017.

Delgado, G., Miller, A.N., Hashimoto, A., Iida, T., Ohkuma, M. and Okada, G., 2022. A phylogenetic assessment of *Endocalyx* (Cainiaceae, Xylariales) with *E. grossus* comb. et stat. nov. *Mycological Progress*, 21(1), pp.221-242.

Devotta, D.A., Kent, A.D., Nelson, D.M., Walsh, P.B., Fraterrigo, J.M. and Hu, F.S., 2022. Effects of alder-and salmon-derived nutrients on aquatic bacterial community structure and microbial community metabolism in subarctic lakes. *Oecologia*, 199(3), pp.711-724.

DeWerff, S.J., Zhang, C., Schneider, J. and Whitaker, R.J., 2022. Intraspecific antagonism through viral toxin encoded by chronic *Sulfolobus* spindle-shaped virus. *Philosophical Transactions of the Royal Society B*, 377(1842), p.20200476.

Dey, P., Wang, A., Ziegler, Y., Kumar, S., Yan, S., Kim, S.H., Katzenellenbogen, J.A. and Katzenellenbogen, B.S., 2022. Estrogen Receptor Beta 1: A Potential Therapeutic Target for Female Triple Negative Breast Cancer. *Endocrinology*, 163(12), p.bqac172.

Dias, N.P., Hu, R., Hensley, D.D., Hansen, Z.R., Domier, L.L. and Hajimorad, M.R., 2022. A Survey for Viruses and Viroids of Peach in Tennessee Orchards by RNA Sequencing. *Plant Health Progress*, 23(3), pp.265-268.

Domínguez-Estrada, A., Galindo-Sánchez, C.E., Ventura-López, C., Rosas, C. and Juárez, O.E., 2022. Response of optic gland pathways to thermal stress in the reproductive phase of female *Octopus maya*. *Journal of Molluscan Studies*, 88(3), p.eyac018.

Doña, J. and Johnson, K.P., 2022. Host body size, not host population size, predicts genome-wide effective population size of parasites. *bioRxiv*, pp.2022-10.

Dong, M. and Feng, H., 2022. Microbial community analysis and food safety practice survey-based hazard identification and risk assessment for controlled environment hydroponic/aquaponic farming systems. *Frontiers in Microbiology*, 13.

Dudek, N.K., Switzer, A.D., Costello, E.K., Murray, M.J., Tomoleoni, J.A., Staedler, M.M., Tinker, M.T. and Relman, D.A., 2022. Characterizing the oral and distal gut microbiota of the threatened southern sea otter (*Enhydra lutris nereis*) to enhance conservation practice. *Conservation science and practice*, 4(4), p.e12640.

Edwards, J.D., Yang, W.H. and Yannarell, A.C., 2022. Soil microbial communities are not altered by garlic mustard in recently invaded central Illinois forests. *Ecosphere*, 13(4), p.e3967.

Egenriether, S., Sanford, R., Yang, W.H. and Kent, A.D., 2022. Nitrogen Cycling Microbial Diversity and Operational Taxonomic Unit Clustering: When to Prioritize Accuracy Over Speed. *Frontiers in Microbiology*, 13, p.730340.

Eliason, C.M., Hains, T., McCullough, J., Andersen, M.J. and Hackett, S.J., 2022. Genomic novelty within a great speciator revealed by a high-quality reference genome of the collared kingfisher (*Todiramphus chloris collaris*). *G3*, 12(11), p.jkac260.

Ellis, J.L., Wang, M., Fu, X., Fields, C.J., Donovan, S.M. and Booth, S.L., 2022. Feeding Practice and Delivery Mode Are Determinants of Vitamin K in the Infant Gut: An Exploratory Analysis. *Current developments in nutrition*, 6(3), p.nzac019.

Eshel, G., Duppen, N., Wang, G., Oh, D.H., Kazachkova, Y., Herzyk, P., Amtmann, A., Gordon, M., Chalifa_Caspi, V., Oscar, M.A. and Bar_David, S., 2022. Positive selection and heat_response transcriptomes reveal adaptive features of the Brassicaceae desert model, *Anastatica hierochuntica*. *New Phytologist*, 236(3), pp.1006-1026.

Falcão, L.L., Silva-Werneck, J.O., Albuquerque, P.S.B., Alves, R.M., Grynberg, P., Togawa, R.C., Costa, M.M.D.C., Brigido, M.M. and Marcellino, L.H., 2022. Comparative transcriptomics of cupuassu (*Theobroma grandiflorum*) offers insights into the early defense mechanism to *Moniliophthora perniciosa*, the causal agent of witches' broom disease. *Journal of Plant Interactions*, 17(1), pp.991-1005.

Farjo, M., Koelle, K., Martin, M.A., Gibson, L.L., Walden, K.K., Rendon, G., Fields, C.J., Alnaji, F.G., Gallagher, N., Luo, C.H. and Mostafa, H.H., 2022. Within-host evolutionary dynamics and tissue compartmentalization during acute SARS-CoV-2 infection. *bioRxiv*, pp.2022-06.

Favela, A., Bohn, M. and Kent, A., 2022. N-cycling microbiome recruitment differences between modern and wild *Zea mays*. *Phytobiomes Journal*, 6(2), pp.151-160.

Ferrer, A., Heath, K.D., Mosquera, S.L., Suárez, Y. and Dalling, J.W., 2022. Assembly of wood-inhabiting archaeal, bacterial and fungal communities along a salinity gradient: common taxa are broadly distributed but locally abundant in preferred habitats. *FEMS microbiology ecology*, 98(5), p.fiac040.

Finet, S., He, F., Clark, L.V. and De Godoy, M.R.C., 2022. Functional properties of miscanthus fiber and prebiotic blends in extruded canine diets. *Journal of animal science*, 100(4), p.skac078.

Fliege, C.E., Ward, R.A., Vogel, P., Nguyen, H., Quach, T., Guo, M., Viana, J.P.G., Dos Santos, L.B., Specht, J.E., Clemente, T.E. and Hudson, M.E., 2022. Fine mapping and cloning of the major seed protein quantitative trait loci on soybean chromosome 20. *The Plant Journal*, 110(1), pp.114-128.

Flinn, M., Alvarez-Argote, S., Knas, M.C., Alencar, V., Paddock, S.J., Zhou, X., Buddell, T., Jamal, A., Liu, P., Drnevich, J. and Patterson, M., 2022. Myofibroblast *Ccn3* is regulated by *Yap* and *Wwtr1* and contributes to adverse cardiac outcomes. *bioRxiv*, pp.2022-12.

Fouke, B.W., Bhattacharjee, A.S., Fried, G.A., Sivaguru, M., Sanford, R.A., Zhou, L., Alcalde, R.E., Wunch, K., Stephenson, A., Ferrar, J.A. and Hernandez, A.G., 2022. Sulfate-reducing bacteria streamers and iron sulfides abruptly occlude porosity and increase hydraulic resistance in proppant-filled shale fractures. *AAPG Bulletin*, 106(1), pp.179-208.

Fournier, E., Denis, S., Dominicis, A., Van de Wiele, T., Alric, M., Mercier-Bonin, M., Etienne-Mesmin, L. and Blanquet-Diot, S., 2022. A child is not an adult: development of a new in vitro model of the toddler colon. *Applied Microbiology and Biotechnology*, 106(21), pp.7315-7336.

Frostegård, Å., Vick, S.H., Lim, N.Y., Bakken, L.R. and Shapleigh, J.P., 2022. Linking meta-omics to the kinetics of denitrification intermediates reveals pH-dependent causes of N₂O emissions and nitrite accumulation in soil. *The ISME journal*, 16(1), pp.26-37.

Gal, A., Fries, R., Kadotani, S., Ulanov, A.V., Li, Z., Scott-Moncrieff, J.C., Burchell, R.K., Lopez-Villalobos, N. and Petreanu, Y., 2022. Canine urinary lactate and cortisol metabolites in hypercortisolism, nonadrenal disease, congestive heart failure, and health. *Journal of Veterinary Diagnostic Investigation*, 34(4), pp.622-630.

Geary, E.L., Oba, P.M., Applegate, C.C., Clark, L.V., Fields, C.J. and Swanson, K.S., 2022. Effects of a mildly cooked human-grade dog diet on gene expression, skin and coat health measures, and fecal microbiota of healthy adult dogs. *Journal of animal science*, 100(10), p.skac265.

Gordon, E., Dirikolu, L., Liu, C.C., Ulanov, A.V., Li, Z., Welborn, M., Armstrong, C., Vallotton, D., Keeton, S., Camlic, S. and Scully, C.M., 2022. Pharmacokinetic profiles of three dose rates of morphine sulfate following single intravenous, intramuscular, and subcutaneous administration in the goat. *Journal of veterinary pharmacology and therapeutics*, 45(1), pp.107-116.

Gramajo, M.E., Lake, R.J., Lu, Y. and Peinetti, A.S., 2022. In vitro Selection of Aptamers to Differentiate Infectious from Non-Infectious Viruses. *JoVE (Journal of Visualized Experiments)*, (187), p.e64127.

Grunwald, D.J., Zapotocny, R.W., Ozer, S., Diers, B.W. and Bent, A.F., 2022. Detection of rare nematode resistance Rhg1 haplotypes in Glycine soja and a novel Rhg1 __SNAP. *The Plant Genome*, 15(1), p.e20152.

Gupta, S.K., Pfeltz, R.F., Wilkinson, B.J. and Gustafson, J.E., 2022. Transcriptomic and Metabolomic Analysis of a Fusidic Acid-Selected fusA Mutant of *Staphylococcus aureus*. *Antibiotics*, 11(8), p.1051.

Haber, M., Roth Rosenberg, D., Lalzar, M., Burgsdorf, I., Saurav, K., Lionheart, R., Lehahn, Y., Aharonovich, D., Gomez-Consarnau, L., Sher, D. and Krom, M.D., 2022. Spatiotemporal variation of microbial communities in the ultra-oligotrophic Eastern Mediterranean Sea. *Frontiers in Microbiology*, 13, p.1129.

Hagadorn, M.A., Hunter, F.K., DeLory, T., Johnson, M.M., Pitts-Singer, T.L. and Kapheim, K.M., 2022. Maternal body condition and season influence RNA deposition in the oocytes of alfalfa leafcutting bees (*Megachile rotundata*). *bioRxiv*, pp.2022-10.

Harder, A.M., Walden, K.K., Marra, N.J. and Willoughby, J.R., 2022. High-quality reference genome for an arid-adapted mammal, the banner-tailed kangaroo rat (*Dipodomys spectabilis*). *Genome Biology and Evolution*, 14(1), p.evac005.

Hernández_Leal, M.S., Suárez_Atilano, M., Nicasio_Arzeta, S., Piñero, D. and González_Rodríguez, A., 2022. Landscape genetics of the tropical willow *Salix humboldtiana*: influence of climate, salinity, and orography in an altitudinal gradient. *American Journal of Botany*, 109(3), pp.456-469.

Hoang, K.N.L., Wheeler, K.E. and Murphy, C.J., 2022. Isolation methods influence the protein corona composition on gold-coated iron oxide nanoparticles. *Analytical Chemistry*, 94(11), pp.4737-4746.

Hu, W.Y., Lu, R., Hu, D.P., Imir, O.B., Zuo, Q., Moline, D., Afradiasbagharani, P., Liu, L., Lowe, S., Birch, L. and Vander Griend, D.J., 2022. Per-and polyfluoroalkyl substances target and alter human prostate stem-progenitor cells. *Biochemical Pharmacology*, 197, p.114902.

Hussain, J., Ousley, C.G., Krauklis, S.A., Dray, E.L., Drnevich, J., Justyna, K., Distefano, M.D. and McKim, D.B., 2022. Mevalonate metabolites contribute to granulocyte chemotaxis and mortality in murine endotoxemia. *bioRxiv*, pp.2022-09.

Hwang, H., Yun, S., Arcanjo, R.B., Chen, S., Mei, W., Nowak, R.A., Kwon, T. and Yang, J., 2022. Regulation of RNA localization during oocyte maturation by dynamic RNA-ER association and remodeling of the ER. *Cell reports*, 41(11), p.111802.

Ikeda-Ohtsubo, W., Summers, K.L. and Sjöling, Å., 2022. Raphaële Gresse^{1, 2}, Frédérique Chaucheyras-Durand^{1, 2}, Juan J. Garrido³, Sylvain Denis¹, Angeles Jiménez-Marín³, Martin Beaumont⁴, Tom Van de Wiele⁵, Evelyne Forano¹ and Stéphanie Blanquet-Diot¹. Beyond Conventional Models: Expanding Experimental Systems for Animal-Microbiome Interaction Research.

Inskeep, K.A., Doellman, M.M., Powell, T.H., Berlocher, S.H., Seifert, N.R., Hood, G.R., Ragland, G.J., Meyers, P.J. and Feder, J.L., 2022. Divergent diapause life history timing drives both allochronic speciation and reticulate hybridization in an adaptive radiation of *Rhagoletis* flies. *Molecular Ecology*, 31(15), pp.4031-4049.

Singh, P., Huang, S.Y., Hernandez, A.G., Adhikari, P., Jamann, T.M. and Mideros, S.X., 2022. Genomic regions associated with virulence in *Setosphaeria turcica* identified by linkage mapping in a biparental population. *Fungal Genetics and Biology*, 159, p.103655.

James, J.J., Bach, E.M., Baker, K., Barber, N.A., Buck, R., Shahrtash, M. and Brown, S.P., 2022. Herbicide control of the invasive Amur honeysuckle (*Lonicera maackii*) does not alter soil microbial communities or activity. *Ecological Solutions and Evidence*, 3(3), p.e12157.

Johnson, K.P., Matthee, C. and Doña, J., 2022. Phylogenomics reveals the origin of mammal lice out of Afrotheria. *Nature Ecology & Evolution*, 6(8), pp.1205-1210.

Katuuramu, D.N., Branham, S.E., Levi, A. and Wechter, W.P., 2022. Genome-wide association analysis of resistance to *Pseudoperonospora cubensis* in citron watermelon. *Plant Disease*, 106(7), pp.1952-1958.

Ke, R., Martinez, P.P., Smith, R.L., Gibson, L.L., Achenbach, C.J., McFall, S., Qi, C., Jacob, J., Dembele, E., Bundy, C. and Simons, L.M., 2022, July. Longitudinal analysis of SARS-CoV-2 vaccine breakthrough infections reveals limited infectious virus shedding and restricted tissue distribution. In *Open forum infectious diseases* (Vol. 9, No. 7, p. ofac192). Oxford University Press.

Ke, R., Martinez, P.P., Smith, R.L., Gibson, L.L., Mirza, A., Conte, M., Gallagher, N., Luo, C.H., Jarrett, J., Zhou, R. and Conte, A., 2022. Daily longitudinal sampling of SARS-CoV-2 infection reveals substantial heterogeneity in infectiousness. *Nature Microbiology*, 7(5), pp.640-652.

Keenan-Jones, D., Motta, D., Garcia, M.H., Sivaguru, M., Perillo, M., Shosted, R.K. and Fouke, B.W., 2022. Travertine crystal growth ripples record the hydraulic history of ancient Rome's Anio Novus aqueduct. *Scientific reports*, 12(1), p.1239.

Kelley, D.P., Chaichi, A., Duplooy, A., Singh, D., Gartia, M.R. and Francis, J., 2022. Label-free mapping and profiling of altered lipid homeostasis in the rat hippocampus after traumatic stress: Role of oxidative homeostasis. *Neurobiology of stress*, 20, p.100476.

Kelly, A.M., Berry, M.R., Tasker, S.Z., McKee, S.A., Fan, T.M. and Hergenrother, P.J., 2022. Target-Agnostic P-Glycoprotein Assessment Yields Strategies to Evade Efflux, Leading to a BRAF Inhibitor with Intracranial Efficacy. *Journal of the American Chemical Society*, 144(27), pp.12367-12380.

Khan, S.R. and Kuzminov, A., 2022. Thymine_starvation_induced chromosomal fragmentation is not required for thymineless death in *Escherichia coli*. *Molecular Microbiology*, 117(5), pp.1138-1155.

Khan, U.W. and Newmark, P.A., 2022. Somatic regulation of female germ cell regeneration and development in planarians. *Cell reports*, 38(11), p.110525.

Kim, H.W., Kim, N.K., Phillips, A.P., Parker, D.A., Liu, P., Whitaker, R.J., Rao, C.V. and Mackie, R.I., 2022. Genome sequence of a thermoacidophilic methanotroph belonging to the verrucomicrobiota phylum from geothermal hot springs in Yellowstone National Park: a metagenomic assembly and reconstruction. *Microorganisms*, 10(1), p.142.

- Kim, J., Oh, S.H., Rodriguez-Bobadilla, R., Vuong, V.M., Hubka, V., Zhao, X. and Hoyer, L.L., 2022. Peering Into Candida albicans Pir Protein Function and Comparative Genomics of the Pir Family. *Frontiers in Cellular and Infection Microbiology*, p.211.
- Kim, J.S., Arango, A.S., Shah, S., Arnold, W.R., Tajkhorshid, E. and Das, A., 2022. Anthracycline derivatives inhibit cardiac CYP2J2. *Journal of Inorganic Biochemistry*, 229, p.111722.
- Kim, N., Riggins, C.W., Zabaloy, M.C., Allegrini, M., Rodriguez-Zas, S.L. and Villamil, M.B., 2022. High-Resolution Indicators of Soil Microbial Responses to N Fertilization and Cover Cropping in Corn Monocultures. *Agronomy*, 12(4), p.954.
- Kim, N., Riggins, C.W., Zabaloy, M.C., Rodriguez-Zas, S.L. and Villamil, M.B., 2022. Limited Impacts of Cover Cropping on Soil N-Cycling Microbial Communities of Long-Term Corn Monocultures. *Frontiers in Microbiology*, 13.
- Kong, X., Kapustka, A., Sullivan, B., Schwarz, G.J. and Leckband, D.E., 2022. Extracellular matrix regulates force transduction at VE-cadherin junctions. *Molecular biology of the cell*, 33(11), p.ar95.
- Krishnan, H.R., Zhang, H., Chen, Y., Bohnsack, J.P., Shieh, A.W., Kusumo, H., Drnevich, J., Liu, C., Grayson, D.R., Maienschein-Cline, M. and Pandey, S.C., 2022. Unraveling the epigenomic and transcriptomic interplay during alcohol-induced anxiolysis. *Molecular Psychiatry*, pp.1-9.
- Laia, N.L., Barko, P.C., Sullivan, D.R., McMichael, M.A., Williams, D.A. and Reinhart, J.M., 2022. Longitudinal analysis of the rectal microbiome in dogs with diabetes mellitus after initiation of insulin therapy. *Plos one*, 17(9), p.e0273792.
- Lata, D., Coates, B.S., Walden, K.K., Robertson, H.M. and Miller, N.J., 2022. Genome size evolution in the beetle genus *Diabrotica*. *G3*, 12(4), p.jkac052.
- Lee, A.H., Lin, C.Y., Do, S., Oba, P.M., Belchik, S.E., Steelman, A.J., Schauwecker, A. and Swanson, K.S., 2022. Dietary supplementation with fiber,biotics, and spray-dried plasma affects apparent total tract macronutrient digestibility and the fecal characteristics, fecal microbiota, and immune function of adult dogs. *Journal of animal science*, 100(3), p.skac048.
- Lehtinen, M.J., Kumar, R., Zabel, B., Mäkelä, S.M., Nedveck, D., Tang, P., Latvala, S., Guery, S. and Budinoff, C.R., 2022. The effect of the probiotic consortia on SARS-CoV-2 infection in ferrets and on human immune cell response in vitro. *Iscience*, 25(6), p.104445.

Lei, R., Tan, T.J., Hernandez Garcia, A., Wang, Y., Diefenbacher, M., Teo, C., Gopan, G., Tavakoli Dargani, Z., Teo, Q.W., Graham, C.S. and Brooke, C.B., 2022. Prevalence and mechanisms of evolutionary contingency in human influenza H3N2 neuraminidase. *Nature communications*, 13(1), p.6443.

Li, S., Moller, C.A., Mitchell, N.G., Martin, D.G., Sacks, E.J., Saikia, S., Labonte, N.R., Baldwin, B.S., Morrison, J.I., Ferguson, J.N. and Leakey, A.D., 2022. The leaf economics spectrum of triploid and tetraploid C4 grass *Miscanthus x giganteus*. *Plant, Cell & Environment*, 45(12), pp.3462-3475.

Lim, C.K., McCallister, T.X., Saporito-Magriña, C., McPheron, G.D., Krishnan, R., Powell, J.E., Clark, L.V., Perez-Pinera, P. and Gaj, T., 2022. CRISPR base editing of cis-regulatory elements enables the perturbation of neurodegeneration-linked genes. *Molecular Therapy*, 30(12), pp.3619-3631.

Lim, C.K., McCallister, T.X., Saporito-Magrina, C., McPheron, G.D., Krishnan, R., Zeballos, M.A., Powell, J.E., Clark, L.V., Perez-Pinera, P. and Gaj, T., 2022. CRISPR base editing of cis-regulatory elements enables target gene perturbations. *bioRxiv*, pp.2022-05.

Lin, C.Y., Jha, A.R., Oba, P.M., Yotis, S.M., Shmalberg, J., Honaker, R.W. and Swanson, K.S., 2022. Longitudinal fecal microbiome and metabolite data demonstrate rapid shifts and subsequent stabilization after an abrupt dietary change in healthy adult dogs. *Animal Microbiome*, 4(1), pp.1-21.

Lin, H.A. and Mideros, S.X., 2022. The effect of *Septoria glycines* and fungicide application on the soybean phyllosphere mycobiome. *Phytobiomes Journal*, pp.PBIOMES-12.

London, E.W., Roca, A.L., Novakofski, J.E. and Mateus-Pinilla, N.E., 2022. A de novo chromosome-level genome assembly of the white-tailed deer, *Odocoileus virginianus*. *Journal of Heredity*, 113(4), pp.479-489.

Lopez-Ortiz, C., Edwards, M., Natarajan, P., Pacheco-Valenciana, A., Nimmakayala, P., Adjeroh, D.A., Sirbu, C. and Reddy, U.K., 2022. Peppers in Diet: Genome-Wide Transcriptome and Metabolome Changes in *Drosophila melanogaster*. *International Journal of Molecular Sciences*, 23(17), p.9924.

Louie, A.Y., Tingling, J., Dray, E., Hussain, J., McKim, D.B., Swanson, K.S. and Steelman, A.J., 2022. Dietary cholesterol causes inflammatory imbalance and exacerbates morbidity in mice infected with influenza A virus. *The Journal of Immunology*, 208(11), pp.2523-2539.

Lucadamo, E.E., Holmes, A.A., Wortman, S.E. and Yannarell, A.C., 2022. Post-termination Effects of Cover Crop Monocultures and Mixtures on Soil Inorganic Nitrogen and Microbial Communities on Two Organic Farms in Illinois. *Frontiers in Soil Science*, 2, p.2.

Lumibao, J.C., Haak, P., Kolossov, V.L., Chen, J.W.E., Stutchman, J., Ruiz, A., Sivaguru, M., Sarkaria, J.N., Harley, B.C., Steelman, A.J. and Gaskins, R., 2022. CHCHD2 mediates glioblastoma cell proliferation, mitochondrial metabolism, hypoxia-induced invasion, and therapeutic resistance. *bioRxiv*, pp.2022-07.

Lundregan, S.L., Mäkinen, H., Buer, A., Holand, H., Jensen, H. and Husby, A., 2022. Infection by a helminth parasite is associated with changes in DNA methylation in the house sparrow. *Ecology and Evolution*, 12(11), p.e9539.

Lundstrom, C.C., Hervig, R., Fischer, T.P., Sivaguru, M., Yin, L., Zhou, Z., Lin, X. and Grossi-Diniz, R., 2022. Insight into differentiation in alkalic systems: Nephelinite-carbonate-water experiments aimed at Ol Doinyo Lengai carbonatite genesis. *Frontiers in Earth Science*, 10.

Ma, Q., Beal, J.R., Bhurke, A., Kannan, A., Yu, J., Taylor, R.N., Bagchi, I.C. and Bagchi, M.K., 2022. Extracellular vesicles secreted by human uterine stromal cells regulate decidualization, angiogenesis, and trophoblast differentiation. *Proceedings of the National Academy of Sciences*, 119(38), p.e2200252119.

Ma, Q., Beal, J.R., Song, X., Bhurke, A., Bagchi, I.C. and Bagchi, M.K., 2022. Extracellular Vesicles Secreted by Mouse Decidual Cells Carry Critical Information for the Establishment of Pregnancy. *Endocrinology*, 163(12), p.bqac165.

Mackay, A.J., Cara, C., Kim, C.H. and Stone, C.M., 2022. Update on the distribution of *Culiseta melanura* in regions of Illinois with prior eastern equine encephalitis virus activity. *Journal of Vector Ecology*, 47(2), pp.230-234.

Mallott, E.K., Skovmand, L.H., Garber, P.A. and Amato, K.R., 2022. The faecal metabolome of black howler monkeys (*Alouatta pigra*) varies in response to seasonal dietary changes. *Molecular Ecology*, 31(15), pp.4146-4161.

Mancini, S.L., Early, P.J., Slater, B.M., Olby, N.J., Mariani, C.L., Munana, K.R., Woelfel, C.W., Schacher, J.A., Zhong, L. and Messenger, K.M., 2022. Novel subcutaneous cytarabine infusion with the Omnipod system in dogs with meningoencephalomyelitis of unknown etiology. *American Journal of Veterinary Research*, 83(9).

Martins, A.C.Q., Mota, A.P.Z., Carvalho, P.A.S.V., Passos, M.A.S., Gimenes, M.A., Guimaraes, P.M. and Brasileiro, A.C.M., 2022. Transcriptome Responses of Wild *Arachis* to UV-C Exposure Reveal Genes Involved in General Plant Defense and Priming. *Plants*, 11(3), p.408.

- McEntire, M.S., Reinhart, J.M., Cox, S.K. and Keller, K.A., 2022. Single-dose pharmacokinetics of orally administered terbinafine in bearded dragons (*Pogona vitticeps*) and the antifungal susceptibility patterns of *Nannizziopsis guarroi*. *American journal of veterinary research*, 83(3), pp.256-263.
- McKee, R.K., Buhlmann, K.A., Moore, C.T., Allender, M.C., Stacy, N.I. and Tuberville, T.D., 2022. Island of misfit tortoises: waif gopher tortoise health assessment following translocation. *Conservation Physiology*, 10(1), p.coac051.
- McKenna, C.F., Salvador, A.F., Keeble, A.R., Khan, N.A., De Lisio, M., Konopka, A.R., Paluska, S.A. and Burd, N.A., 2022. Muscle strength after resistance training correlates to mediators of muscle mass and mitochondrial respiration in middle-aged adults. *Journal of Applied Physiology*.
- McLaughlin, M.I., Yu, Y. and Van Der Donk, W.A., 2022. Substrate recognition by the peptidyl-(S)-2-mercaptoglycine synthase TglHI during 3-thiaglutamate biosynthesis. *ACS chemical biology*, 17(4), pp.930-940.
- Mei, R. and Liu, W.T., 2022. Meta-Omics-Supervised Characterization of Respiration Activities Associated with Microbial Immigrants in Anaerobic Sludge Digesters. *Environmental Science & Technology*, 56(10), pp.6689-6698.
- Menshaw, M.N., Abdel-Hamid, A.M., Mohamed, S.K. and Mo'men, H., 2022. Isolation and molecular identification of cellulose/hemicellulose degrading bacteria from agricultural compost and determination of their hydrolytic potential. *South African Journal of Botany*, 149, pp.617-621.
- Miller, A.N., Dirks, A.C., Filippova, N., Popov, E. and Methven, A.S., 2022. Studies in *Gyromitra* II: cryptic speciation in the *Gyromitra gigas* species complex; rediscovery of *G. ussuriensis* and *G. americanigigas* sp. nov. *Mycological Progress*, 21(9), p.81.
- Miller, A.N., Karakehian, J. and Raudabaugh, D.B., 2022. Next-Generation Sequencing of Ancient and Recent Fungarium Specimens. *Journal of Fungi*, 8(9), p.932.
- Miller, J.C. and Schuler, M.A., 2022. Single mutations toggle the substrate selectivity of multifunctional *Camptotheca* secologanic acid synthases. *Journal of Biological Chemistry*, 298(9).
- Monteiro, H.F., Zhou, Z., Gomes, M.S., Peixoto, P.M., Bonsaglia, E.C., Canisso, I.F., Weimer, B.C. and Lima, F.S., 2022. Rumen and lower gut microbiomes relationship with feed efficiency and production traits throughout the lactation of Holstein dairy cows. *Scientific reports*, 12(1), p.4904.

- Morales, M.E., Allegrini, M., Iocoli, G.A., Basualdo, J., Villamil, M.B. and Zabaloy, M.C., 2022. Rhizospheric Microbiome Responses to Cover Crop Suppression Methods. *Agronomy*, 12(10), p.2246.
- Moss, W.E., Harper, L.R., Davis, M.A., Goldberg, C.S., Smith, M.M. and Johnson, P.T., 2022. Navigating the trade_offs between environmental DNA and conventional field surveys for improved amphibian monitoring. *Ecosphere*, 13(2), p.e3941.
- Mouton, J.C., Duckworth, R.A., Paitz, R.T. and Martin, T.E., 2022. Nest predation risk and deposition of yolk steroids in a cavity-nesting songbird: an experimental test. *Journal of Experimental Biology*, 225(7), p.jeb243047.
- Nelczyk, A.T., Ma, L., Gupta, A.D., Gamage, H.E.V., McHenry, M.T., Henn, M.A., Kadiri, M., Wang, Y., Krawczynska, N., Bendre, S. and He, S., 2022. The nuclear receptor TLX (NR2E1) inhibits growth and progression of triple-negative breast cancer. *Biochimica et Biophysica Acta (BBA)-Molecular Basis of Disease*, 1868(11), p.166515.
- Nell, L.A., Einarsson, Á., Ives, A.R., Phillips, J.S., Botsch, J.C., Book, K.R., Weng, Y.M. and Schoville, S.D., Genome assembly and annotation of the non-biting midge *Tanytarsus gracilentus* and a phylogenomic tree of the family Chironomidae. *Interactions between ecological and evolutionary processes in experimental, theoretical, and wild populations*, p.72.
- Nunes, J.J., Raiyemo, D.A., Arneson, N.J., Rosa, A.T., Tranel, P.J. and Werle, R., 2022. Target site resistance to acetolactate synthase inhibitors in a fall panicum (*Panicum dichotomiflorum* Michx.) accession from Wisconsin and its response to alternative herbicides. *Weed Technology*, 36(1), pp.48-55.
- Oh, C., Chowdhury, R., Samineni, L., Shisler, J.L., Kumar, M. and Nguyen, T.H., 2022. Inactivation mechanism and efficacy of grape seed extract for Human Norovirus surrogate. *Applied and environmental microbiology*, 88(9), pp.e02247-21.
- Oh, S.H., Coleman, D.A., Zhao, X. and Hoyer, L.L., 2022. Development and validation of monoclonal antibodies specific for *Candida albicans* Als2, Als9-1, and Als9-2. *Plos one*, 17(7), p.e0269681.
- Oh, S.H., Martin-Yken, H., Coleman, D.A., Dague, E. and Hoyer, L.L., 2022. Development and Use of a Monoclonal Antibody Specific for the *Candida albicans* Cell-Surface Protein Hwp1. *Frontiers in Cellular and Infection Microbiology*, p.792.
- Ostadi Moghaddam, A., Arshee, M., Lin, Z., Sivaguru, M., Phillips, H., McFarlin, B., Toussaint, K. and Wagoner Johnson, A., An Indentation-Based Framework for Probing the Glycosaminoglycan-Mediated Interactions of Collagen Fibrils. Available at SSRN 4279323.

Ouyang, W.O., Tan, T.J., Lei, R., Song, G., Kieffer, C., Andrabi, R., Matreyek, K.A. and Wu, N.C., 2022. Probing the biophysical constraints of SARS-CoV-2 spike N-terminal domain using deep mutational scanning. *Science Advances*, 8(47), p.eadd7221.

Pacyga, D.C., Chiang, C., Li, Z., Strakovsky, R.S. and Ziv-Gal, A., 2022. Parabens and Menopause-Related Health Outcomes in Midlife Women: A Pilot Study. *Journal of Women's Health*, 31(11), pp.1645-1654.

Pacyga, D.C., Ryva, B.A., Nowak, R.A., Bulun, S.E., Yin, P., Li, Z., Flaws, J.A. and Strakovsky, R.S., 2022. Midlife urinary phthalate metabolite concentrations and prior uterine fibroid diagnosis. *International journal of environmental research and public health*, 19(5), p.2741.

Paitz, R.T. and Dugas, M.B., 2022. Steroid levels in frog eggs: Manipulations, developmental changes, and implications for maternal steroid effects. *Journal of Experimental Zoology Part A: Ecological and Integrative Physiology*, 337(4), pp.293-302.

Pan, C., Tabatabaei, S.K., Tabatabaei Yazdi, S.H., Hernandez, A.G., Schroeder, C.M. and Milenkovic, O., 2022. Rewritable two-dimensional DNA-based data storage with machine learning reconstruction. *Nature communications*, 13(1), p.2984.

Pan, M., Morovic, W., Hidalgo-Cantabrana, C., Roberts, A., Walden, K.K., Goh, Y.J. and Barrangou, R., 2022. Genomic and epigenetic landscapes drive CRISPR-based genome editing in *Bifidobacterium*. *Proceedings of the National Academy of Sciences*, 119(30), p.e2205068119.

Parker, E.N., Cain, B.N., Hajian, B., Ulrich, R.J., Geddes, E.J., Barkho, S., Lee, H.Y., Williams, J.D., Raynor, M., Caridha, D. and Zaino, A., 2022. An iterative approach guides discovery of the FabI inhibitor fabimycin, a late-stage antibiotic candidate with in vivo efficacy against drug-resistant gram-negative infections. *ACS Central Science*, 8(8), pp.1145-1158.

Passante, E.K., Dechant, L.E., Paradis, C.J. and McLellan, S.L., 2022. Halophilic bacteria in a Lake Michigan drainage basin as potential biological indicators of chloride-impacted freshwaters. *Science of The Total Environment*, 846, p.157458.

Pastrana-Otero, I., Majumdar, S., Gilchrist, A.E., Harley, B.A. and Kraft, M.L., 2022. Identification of the Differentiation Stages of Living Cells from the Six Most Immature Murine Hematopoietic Cell Populations by Multivariate Analysis of Single-Cell Raman Spectra. *Analytical Chemistry*, 94(35), pp.11999-12007.

Paudel, B., Pedersen, C., Yen, Y. and Marzano, S.Y.L., 2022. *Fusarium graminearum* virus-1 strain fgv1-sd4 infection eliminates mycotoxin deoxynivalenol synthesis by *Fusarium graminearum* in FHB. *Microorganisms*, 10(8), p.1484.

Paula, D.P., Barros, S.K.A., Pitta, R.M., Barreto, M.R., Togawa, R.C. and Andow, D.A., 2022. Metabarcoding versus mapping unassembled shotgun reads for identification of prey consumed by arthropod epigeal predators. *GigaScience*, 11.

Paull, R.E., Zepa_Catanho, D., Chen, N.J., Uruu, G., Wai, C.M.J. and Kantar, M., 2022. Taro raphide-associated proteins: Allergens and crystal growth. *Plant Direct*, 6(9), p.e443.

Pease, J.B., Driver, R.J., de la Cerda, D.A., Day, L.B., Lindsay, W.R., Schlinger, B.A., Schuppe, E.R., Balakrishnan, C.N. and Fuxjager, M.J., 2022. Layered evolution of gene expression in superfast muscles for courtship. *Proceedings of the National Academy of Sciences*, 119(14), p.e2119671119.

Pei, S., Liu, P., Parker, D.A., Mackie, R.I. and Rao, C.V., 2022. Systems analysis of the effect of hydrogen sulfide on the growth of *Methylococcus capsulatus* Bath. *Applied Microbiology and Biotechnology*, pp.1-12.

Pei, Z.F., Zhu, L., Sarkisian, R., Van Der Donk, W.A. and Nair, S.K., 2022. Class V Lanthipeptide Cyclase Directs the Biosynthesis of a Stapled Peptide Natural Product. *Journal of the American Chemical Society*, 144(38), pp.17549-17557.

Perrin-Stowe, T.I., Ishida, Y., Reed, D.M., Terrill, E.E., Ryder, O.A., Novakofski, J.E., Mateus-Pinilla, N.E., Pukazhenthi, B.S. and Roca, A.L., 2022. Extrapolating the susceptibility of Eld's deer (*Rucervus eldii* thamin) to chronic wasting disease from prion protein gene (PRNP) polymorphisms. *Frontiers in Conservation Science*, p.107.

Perrin-Stowe, T.I., Ishida, Y., Terrill, E.E., Beetem, D., Ryder, O.A., Novakofski, J.E., Mateus-Pinilla, N.E. and Roca, A.L., 2022. Variation in the PRNP gene of Pere David's deer (*Elaphurus davidianus*) may impact genetic vulnerability to chronic wasting disease. *Conservation Genetics*, 23(2), pp.313-323.

Phungviwatnikul, T., Lee, A.H., Belchik, S.E., Suchodolski, J.S. and Swanson, K.S., 2022. Weight loss and high-protein, high-fiber diet consumption impact blood metabolite profiles, body composition, voluntary physical activity, fecal microbiota, and fecal metabolites of adult dogs. *Journal of animal science*, 100(2), p.skab379.

Pikus, E. and Minias, P., 2022. Using de novo genome assembly and high-throughput sequencing to characterize the MHC region in a non-model bird, the Eurasian coot. *Scientific Reports*, 12(1), p.7031.

Powell, J.E., Lim, C.K., Krishnan, R., McCallister, T.X., Saporito-Magriña, C., Zeballos, M.A., McPheron, G.D. and Gaj, T., 2022. Targeted gene silencing in the nervous system with CRISPR-Cas13. *Science advances*, 8(3), p.eabk2485.

Prabhakara, K.H. and Kuehn, S., 2022. Algae drive convergent bacterial community assembly when nutrients are scarce. *bioRxiv*, pp.2022-06.

Qian, H., Counihan, M.J., Doan, H.A., Ibrahim, N.A., Danis, A.S., Setwipatanachai, W., Purwanto, N.S., Rodríguez-López, J., Assary, R.S. and Moore, J.S., 2022. Mesolytic cleavage of homobenzylic ethers for programmable end-of-life function in redoxmers. *Journal of Materials Chemistry A*, 10(14), pp.7739-7753.

Raglin, S.S., Kent, A.D. and Ngumbi, E.N., 2022. Herbivory protection via volatile organic compounds is influenced by maize genotype, not *Bacillus altitudinis*-enriched bacterial communities. *Frontiers in Microbiology*, p.475.

Raglin, S.S., Soman, C., Ma, Y. and Kent, A.D., 2022. Long Term Influence of Fertility and Rotation on Soil Nitrification Potential and Nitrifier Communities. *Frontiers in Soil Science*, 2, p.10.

Ramayo-Caldas, Y., Crespo-Piazuelo, D., Morata, J., Gonzalez-Rodriguez, O., Sebastia, C., Castello, A., Dalmau, A., Ramos-Onsins, S.E., Alexiou, K., Folch, J.M. and Quintanilla, R., 2022. Copy number variation on ABCC2-DNMBP loci impacts the diversity and composition of the gut microbiota in pigs. *bioRxiv*, pp.2022-10.

Raudabaugh, D.B., Ishida, Y., Haley, N.J., Brown, W.M., Novakofski, J., Roca, A.L. and Mateus-Pinilla, N.E., 2022. County-wide assessments of Illinois white-tailed deer (*Odocoileus virginianus*) prion protein gene variation using improved primers and potential implications for management. *Plos one*, 17(11), p.e0274640.

Rayamajhi, N., Cheng, C.H.C. and Catchen, J.M., 2022. Evaluating Illumina-, Nanopore-, and PacBio-based genome assembly strategies with the bald notothen, *Trematomus borchgrevinki*. *G3*, 12(11), p.jkac192.

Reed, A.D., Fletcher, J.R., Huang, Y.Y., Thanissery, R., Rivera, A.J., Parsons, R.J., Stewart, A.K., Kountz, D.J., Shen, A., Balskus, E.P. and Theriot, C.M., 2022. The Stickland reaction precursor trans-4-hydroxy-L-proline differentially impacts the metabolism of *Clostridioides difficile* and commensal clostridia. *Mosphere*, 7(2), pp.e00926-21.

Reilly, L.M., Hu, Y., von Schaumburg, P.C., de Oliveira, M.R., He, F., Rodriguez-Zas, S.L., Southey, B.R., Parsons, C.M., Utterback, P., Lambrakis, L. and da Costa, D.V., 2022. Chemical composition of selected insect meals and their effect on apparent total tract digestibility, fecal metabolites, and microbiota of adult cats fed insect-based retorted diets. *Journal of animal science*, 100(2), p.skac024.

Riley, A.B., Grillo, M.A., Epstein, B., Tiffin, P. and Heath, K.D., 2022. Discordant population structure among rhizobium divided genomes and their legume hosts. *Molecular ecology*.

Rivera-Colón, A.G. and Catchen, J., 2022. Population genomics analysis with RAD, reprised: Stacks 2. In *Marine Genomics: Methods and Protocols* (pp. 99-149). New York, NY: Springer US.

Roach, S.N., Fiege, J.K., Shepherd, F.K., Wiggen, T.D., Hunter, R.C. and Langlois, R.A., 2022. Respiratory influenza virus infection causes dynamic tuft cell and innate lymphoid cell changes in the small intestine. *Journal of virology*, 96(9), pp.e00352-22.

Rogers, M.B., Simon, D., Firek, B., Silfies, L., Fabio, A., Bell, M.J., Yeh, A., Azar, J., Cheek, R., Kochanek, P.M. and Peddada, S.D., 2022. Temporal and spatial changes in the microbiome following pediatric severe traumatic brain injury. *Pediatric critical care medicine*.

Ross, B.T., Zidack, N., McDonald, R. and Flenniken, M.L., 2022. Transcriptome and small RNA profiling of potato virus Y infected potato cultivars, including systemically infected russet Burbank. *Viruses*, 14(3), p.523.

Rucker, H.R. and Parker, M.R., 2022. Decreased attractivity in female garter snakes treated with an aromatase inhibitor. *Journal of Experimental Zoology Part A: Ecological and Integrative Physiology*, 337(2), pp.171-180.

Ryva, B.A., Haggerty, D.K., Pacyga, D.C., James-Todd, T., Li, Z., Flaws, J.A. and Strakovsky, R.S., 2022. Determinants of urinary phthalate biomarker concentrations in pre-and perimenopausal women with consideration of race. *Environmental Research*, 214, p.114056.

Saenz Manchola, O.F., Samacá Sáenz, E., Virrueta Herrera, S., D'Alessio, L.M., García Aldrete, A.N. and Johnson, K.P., 2022. Mining Ultraconserved elements from transcriptome and genome data to explore the Phylogenomics of the free-living lice suborder Psocomorpha (Insecta: Psocodea). *Insect Systematics and Diversity*, 6(4), p.1.

Sakkour, A., Mascher, M., Himmelbach, A., Haberer, G., Lux, T., Spannagl, M., Stein, N., Kawamoto, S. and Sato, K., 2022. Chromosome-scale assembly of barley cv.'Haruna Nijo' as a resource for barley genetics. *DNA Research*, 29(1), p.dsac001.

Salem, M., Al-Tobasei, R., Ali, A. and Kenney, B., 2022. Integrated analyses of DNA methylation and gene expression of rainbow trout muscle under variable ploidy and muscle atrophy conditions. *Genes*, 13(7), p.1151.

Salgado, O., Guajardo-Leiva, S., Moya-Beltrán, A., Barbosa, C., Ridley, C., Tamayo-Leiva, J., Quatrini, R., Mojica, F.J. and Díez, B., 2022. Global phylogenomic novelty of the Cas1 gene from hot spring microbial communities.

Samaradivakara, S.P., Chen, H., Lu, Y.J., Li, P., Kim, Y., Tsuda, K., Mine, A. and Day, B., 2022. Overexpression of NDR1 leads to pathogen resistance at elevated temperatures. *New Phytologist*, 235(3), pp.1146-1162.

Sarksian, R. and van der Donk, W.A., 2022. Divergent Evolution of Lanthipeptide Stereochemistry. *ACS Chemical Biology*, 17(9), pp.2551-2558.

Sarksian, R., Hegemann, J.D., Simon, M.A., Acedo, J.Z. and Van Der Donk, W.A., 2022. Unexpected methyllanthionine stereochemistry in the morphogenetic lanthipeptide SapT. *Journal of the American Chemical Society*, 144(14), pp.6373-6382.

Seok, S., Kim, Y.C., Zhang, Y., Kong, B., Guo, G., Ma, J., Kemper, B. and Kemper, J.K., 2022. Feeding activates FGF15_SHP_TFEB-mediated lipophagy in the gut. *The EMBO Journal*, 41(17), p.e109997.

Seward, C.H., Saul, M.C., Troy, J.M., Dibaeinia, P., Zhang, H., Sinha, S. and Stubbs, L.J., 2022. An epigenomic shift in amygdala marks the transition to maternal behaviors in alloparenting virgin female mice. *Plos one*, 17(2), p.e0263632.

Seyfried, G.S., Corrales, A., Kent, A.D., Dalling, J.W. and Yang, W.H., 2022. Watershed-scale Variation in Potential Fungal Community Contributions to Ectomycorrhizal Biogeochemical Syndromes. *Ecosystems*, pp.1-16.

Sheldon, E., Zimmer, C., Hanson, H., Koussayer, B., Schrey, A., Reece, D., Wigley, P., Wedley, A. and Martin, L., 2022. House sparrows with high epigenetic potential in the Toll-like receptor 4 promoter are better able to resist a pathogenic *Salmonella enterica* infection. *Authorea Preprints*.

Shinn, L.M., Mansharamani, A., Baer, D.J., Novotny, J.A., Charron, C.S., Khan, N.A., Zhu, R. and Holscher, H.D., 2022. Fecal metabolites as biomarkers for predicting food intake by healthy adults. *The Journal of nutrition*, 152(12), pp.2956-2965.

Singh, P., Huang, S.Y., Hernandez, A.G., Adhikari, P., Jamann, T.M. and Mideros, S.X., 2022. Genomic regions associated with virulence in *Setosphaeria turcica* identified by linkage mapping in a biparental population. *Fungal Genetics and Biology*, 159, p.103655.

Singh, R., Fazal, Z., Bikorimana, E., Boyd, R.I., Yerby, C., Tomlin, M., Baldwin, H., Shokry, D., Corbet, A.K., Shahid, K. and Hattab, A., 2022. Reciprocal epigenetic remodeling controls testicular cancer hypersensitivity to hypomethylating agents and chemotherapy. *Molecular Oncology*, 16(3), pp.683-698.

Sivaguru, M. and Fouke, B.W., 2022. Renal Macrophages and Multinucleated Giant Cells: Ferrymen of the River Styx?. *Kidney360*, 3(9), pp.1616-1619.

Sivaguru, M., Fouke, K.W., Keenan-Jones, D., Motta, D., Garcia, M.H. and Fouke, B.W., 2022. Depositional and diagenetic history of travertine deposited within the Anio Novus aqueduct of ancient Rome. From the Guajira Desert to the Apennines, and from the Sardinia/Corsica Microplate to the Killer Asteroid: Honoring the Career of Walter Alvarez.

Sonam, S., Bangru, S., Perry, K.J., Chembazhi, U.V., Kalsotra, A. and Henry, J.J., 2022. Cellular and molecular profiles of larval and adult *Xenopus* corneal epithelia resolved at the single-cell level. *Developmental Biology*, 491, pp.13-30.

Song, Y., Perlman, K. and Gyarmati, P., 2022. Microbial and host factors contribute to bloodstream infection in a pediatric acute lymphocytic leukemia mouse model. *Heliyon*, 8(11), p.e11340.

Svec, R.L., McKee, S.A., Berry, M.R., Kelly, A.M., Fan, T.M. and Hergenrother, P.J., 2022. Novel imidazotetrazine evades known resistance mechanisms and is effective against temozolomide-resistant brain cancer in cell culture. *ACS chemical biology*, 17(2), pp.299-313.

Tabatabaei, S.K., Pham, B., Pan, C., Liu, J., Chandak, S., Shorkey, S.A., Hernandez, A.G., Aksimentiev, A., Chen, M., Schroeder, C.M. and Milenkovic, O., 2022. Expanding the molecular alphabet of DNA-based data storage systems with neural network nanopore readout processing. *Nano letters*, 22(5), pp.1905-1914.

Tan, L.R., Liu, J.J., Deewan, A., Lee, J.W., Xia, P.F., Rao, C.V., Jin, Y.S. and Wang, S.G., 2022. Genome-wide transcriptional regulation in *Saccharomyces cerevisiae* in response to carbon dioxide. *FEMS yeast research*, 22(1), p.foac032.

Todorov, L.G., Sivaguru, M., Krambeck, A.E., Lee, M.S., Lieske, J.C. and Fouke, B.W., 2022. GeoBioMed perspectives on kidney stone recurrence from the reactive surface area of SWL-derived particles. *Scientific reports*, 12(1), p.18371.

Todorov, L.G., Sivaguru, M., Krambeck, A.E., Lee, M.S., Lieske, J.C. and Fouke, B.W., 2022. Size Frequency Distributions, Fracture Patterns, and Reactive Surface Area of Shock Wave Lithotripsy-Derived Particles: A GeoBioMed Perspective on Kidney Stone Recurrence.

Tonero, M.E., Li, Z. and Reinhart, J.M., 2022. Cytochrome P450 reaction phenotyping of itraconazole hydroxylation in the dog. *Journal of Veterinary Pharmacology and Therapeutics*, 45(3), pp.255-264.

Traniello, I.M., Bukhari, S.A., Dibaeinia, P., Serrano, G., Avalos, A., Ahmed, A.C., Sankey, A., Hernaez, M., Sinha, S., Zhao, S.D. and Catchen, J., 2022. Evolution of decreased aggression in honey bees targeted brain cell gene regulatory networks.

Traniello, I.M., Bukhari, S.A., Dibaeinia, P., Serrano, G., Avalos, A., Ahmed, A.C., Sankey, A.L., Hernaez, M., Sinha, S., Zhao, S.D. and Catchen, J., 2022. Single-cell dissection of a collective behaviour in honeybees. *bioRxiv*, pp.2022-03.

Trivellone, V., Cao, Y. and Dietrich, C.H., 2022. Comparison of Traditional and Next-Generation Approaches for Uncovering Phytoplasma Diversity, with Discovery of New Groups, Subgroups and Potential Vectors. *Biology*, 11(7), p.977.

Trivellone, V., Cao, Y., Blackshear, M., Kim, C.H. and Stone, C., 2022. Landscape Composition Affects Elements of Metacommunity Structure for Culicidae Across South-Eastern Illinois. *Frontiers in Public Health*, 10.

Vailati-Riboni, M., Rund, L., Caetano-Silva, M.E., Hutchinson, N.T., Wang, S.S., Soto-Díaz, K., Woods, J.A., Steelman, A.J. and Johnson, R.W., 2022. Dietary fiber as a counterbalance to age-related microglial cell dysfunction. *Frontiers in Nutrition*, 9.

Van Dam, A.R., Covas Orizondo, J.O., Lam, A.W., McKenna, D.D. and Van Dam, M.H., 2022. Metagenomic clustering reveals microbial contamination as an essential consideration in ultraconserved element design for phylogenomics with insect museum specimens. *Ecology and evolution*, 12(3), p.e8625.

Vergara-Barros, P., Alcorta, J., Casanova-Katny, A., Nürnberg, D.J. and Díez, B., 2022. Compensatory Transcriptional Response of *Fischerella thermalis* to Thermal Damage of the Photosynthetic Electron Transfer Chain. *Molecules*, 27(23), p.8515.

Vilardi, K.J., Cotto, I., Sevillano, M., Dai, Z., Anderson, C.L. and Pinto, A., 2022. Comammox *Nitrospira* bacteria outnumber canonical nitrifiers irrespective of electron donor mode and availability in biofiltration systems. *FEMS Microbiology Ecology*, 98(4), p.fiac032.

Virrueta Herrera, S., Johnson, K.P., Sweet, A.D., Ylinen, E., Kunnasranta, M. and Nyman, T., 2022. High levels of inbreeding with spatial and host-associated structure in lice of an endangered freshwater seal. *Molecular ecology*, 31(18), pp.4593-4606.

Vocking, O. and Famulski, J., 2022. Temporal single cell transcriptome atlas of zebrafish anterior segment development reveals high degree of conservation between the trabecular meshwork and the annular ligament. *bioRxiv*, pp.2022-10.

Vroman, R., Hunter, R., Wood, M.J., Davis, O.C., Malfait, Z., George, D.S., Ren, D., Tavares-Ferreira, D., Price, T.J., Malfait, A.M. and Malfait, F., 2022. The matrisome of the murine and human dorsal root ganglion: a transcriptomal approach. *bioRxiv*, pp.2022-10.

Wei, W., Wu, X., Blahut-Beatty, L., Simmonds, D.H. and Clough, S.J., 2022. Transcriptome Profiling Reveals Molecular Players in Early Soybean–*Sclerotinia sclerotiorum* Interaction. *Phytopathology*®, 112(8), pp.1739-1752.

Welden, J.R., Margvelani, G., Arizaca Maquera, K.A., Gudlavalleti, B., Miranda Sardón, S.C., Campos, A.R., Robil, N., Lee, D.C., Hernandez, A.G., Wang, W.X. and Di, J., 2022. RNA editing of microtubule-associated protein tau circular RNAs promotes their translation and tau tangle formation. *Nucleic Acids Research*, 50(22), pp.12979-12996.

Wen, Y., Rashid, F., Fazal, Z., Singh, R., Spinella, M.J. and Irudayaraj, J., 2022. Nephrotoxicity of perfluorooctane sulfonate (PFOS)—effect on transcription and epigenetic factors. *Environmental Epigenetics*, 8(1), p.dvac010.

Wijesinghege, C., Tran, K.N. and Dassanayake, M., 2022. Alternative splicing preferentially increases transcript diversity associated with stress responses in the extremophyte *Schrenkiella parvula*. *bioRxiv*, pp.2022-10.

Willis, N.B., Munoz, C.X., Mysonhimer, A.R., Edwards, C.G., Wolf, P.G., Hillman, C.H., Burd, N.A., Holscher, H.D. and Khan, N.A., 2022. Hydration Biomarkers Are Related to the Differential Abundance of Fecal Microbiota and Plasma Lipopolysaccharide-Binding Protein in Adults. *Annals of Nutrition and Metabolism*, 77(Suppl. 4), pp.37-45.

Wu, Y.F., De La Toba, E.A., Dvoretzkiy, S., Jung, R., Kim, N., Daniels, L., Romanova, E.V., Drnevich, J., Sweedler, J.V. and Boppart, M.D., 2022. Development of a cell_free strategy to recover aged skeletal muscle after disuse. *The Journal of physiology*.

Wu, Z., Aharonovich, D., Roth-Rosenberg, D., Weissberg, O., Luzzatto-Knaan, T., Vogts, A., Zoccarato, L., Eigemann, F., Grossart, H.P., Voss, M. and Follows, M.J., 2022. Significant organic carbon acquisition by *Prochlorococcus* in the oceans. *bioRxiv*, pp.2022-01.

Wu, Z., Aharonovich, D., Roth-Rosenberg, D., Weissberg, O., Luzzatto-Knaan, T., Vogts, A., Zoccarato, L., Eigemann, F., Grossart, H.P., Voss, M. and Follows, M.J., 2022. Single-cell measurements and modelling reveal substantial organic carbon acquisition by *Prochlorococcus*. *Nature Microbiology*, pp.1-10.

Yanckello, L., Chang, Y., Sun, M., Chlipala, G., Green, S., Lei, Z., Ericsson, A., Xing, X., Hammond, T., Bachstetter, A. and Lin, A., 2022. Inulin supplementation prior to mild traumatic brain injury mitigates gut dysbiosis, and brain vascular and white matter deficits in mice. *Frontiers in Microbiomes*, 1.

Yanckello, L.M., Hoffman, J.D., Chang, Y.H., Lin, P., Nehra, G., Chlipala, G., McCulloch, S.D., Hammond, T.C., Yackzan, A.T., Lane, A.N. and Green, S.J., 2022. Apolipoprotein E genotype-dependent nutrigenetic effects to prebiotic inulin for modulating systemic metabolism and neuroprotection in mice via gut-brain axis. *Nutritional Neuroscience*, 25(8), pp.1669-1679.

Yang, S., Bi, J., Drnevich, J., Li, K. and Nowak, R.A., 2022. Basigin is necessary for normal decidualization of human uterine stromal cells. *Human Reproduction*, 37(12), pp.2885-2898.

Yi, Z., Su, X., Asangba, A.E., Abdel-Hamid, A.M., Chakraborty, S., Dodd, D., Stroot, P.G., Mackie, R.I. and Cann, I., 2022. Xylan Deconstruction by Thermophilic *Thermoanaerobacterium bryantii* Hemicellulases Is Stimulated by Two Oxidoreductases. *Catalysts*, 12(2), p.182.

Yuan, F., Sharma, J., Nanjappa, S.G., Gaulke, C.A. and Fang, Y., 2022. Effect of Killed PRRSV Vaccine on Gut Microbiota Diversity in Pigs. *Viruses*, 14(5), p.1081.

Zerpa-Catanho, D., Clough, S.J. and Ming, R., 2022. Characterization and analysis of the promoter region of monodehydroascorbate reductase 4 (CpMDAR4) in papaya. *Plant Reproduction*, 35(4), pp.233-264.

Zhang, L., Chen, Y. and Belmont, A.S., 2022. Measuring Cytological Proximity of Chromosomal Loci to Defined Nuclear Compartments with TSA-seq. In *Spatial Genome Organization: Methods and Protocols* (pp. 145-186). New York, NY: Springer US.

Zhang, L., Narayanan, K.K., Cooper, L., Chan, K.K., Skeeters, S.S., Devlin, C.A., Aguhob, A., Shirley, K., Rong, L., Rehman, J. and Malik, A.B., 2022. An ACE2 decoy can be administered by inhalation and potently targets omicron variants of SARS_CoV_2. *EMBO Molecular Medicine*, 14(11), p.e16109.

Zhao, L., Shao, H., Zhang, L., Panno, S.V., Kelly, W.R., Lin, T.Y., Liu, W.T., Flynn, T.M. and Berger, P., 2022. Impact of salinity origin on microbial communities in saline springs within the Illinois Basin, USA. *Environmental Microbiology*, 24(12), pp.6112-6127.

Zhao, X., McHugh, C., Coffey, S.R., Jimenez, D.A., Adams, E., Carroll, J.B. and Usdin, K., 2022. Stool is a sensitive and noninvasive source of DNA for monitoring expansion in repeat expansion disease mouse models. *Disease Models & Mechanisms*, 15(5), p.dmm049453.

Zhao, X., Oh, S.H., Coleman, D.A. and Hoyer, L.L., 2022. ALS1 Deletion Increases the Proportion of Small Cells in a *Candida albicans* Culture Population: Hypothesizing a Novel Role for Als1. *Frontiers in Cellular and Infection Microbiology*, p.516.

Zheng, Y., Ongpipattanakul, C. and Nair, S.K., 2022. Bioconjugate Platform for Iterative Backbone N-Methylation of Peptides. *ACS Catalysis*, 12(22), pp.14006-14014.

Zhu, C., Box, M.S., Thiruppathi, D., Hu, H., Yu, Y., Martin, C., Doust, A.N., McSteen, P. and Kellogg, E.A., 2022. Pleiotropic and nonredundant effects of an auxin importer in *Setaria* and maize. *Plant Physiology*, 189(2), pp.715-734.

Zhu, H., Zhao, S.D., Ray, A., Zhang, Y. and Li, X., 2022. A comprehensive temporal patterning gene network in *Drosophila* medulla neuroblasts revealed by single-cell RNA sequencing. *Nature communications*, 13(1), p.1247.

Zuo, Q., Mogol, A.N., Liu, Y.J., Santaliz Casiano, A., Chien, C., Drnevich, J., Imir, O.B., Kulkoyluoglu-Cotul, E., Park, N.H., Shapiro, D.J. and Park, B.H., 2022. Targeting metabolic adaptations in the breast cancer–liver metastatic niche using dietary approaches to improve endocrine therapy efficacy. *Molecular Cancer Research*, 20(6), pp.923-937.