

## **Publications during 2016 acknowledging the Roy J Carver Biotechnology Center at the University of Illinois at Urbana-Champaign**

Adams, H.A., Sonstegard, T.S., VanRaden, P.M., Null, D.J., Van Tassell, C.P., Larkin, D.M. and Lewin, H.A., 2016. Identification of a nonsense mutation in APAF1 that is likely causal for a decrease in reproductive efficiency in Holstein dairy cattle. *Journal of dairy science*, 99(8), pp.6693-6701.

Amato KR, Ulanov A, Ju K-S, and Garber PA. 2017. Metabolomic data suggest regulation of black howler monkey (*Alouatta pigra*) diet composition at the molecular level. *Am J Primatol.* 2017;79:e22616. <https://doi.org/10.1002/ajp.22616>.

Arnold, W.R., Baylon, J.L., Tajkhorshid, E. and Das, A., 2016. Asymmetric binding and metabolism of polyunsaturated fatty acids (PUFAs) by CYP2J2 epoxygenase. *Biochemistry*, 55(50), pp.6969-6980.

Arruda, M.P., Brown, P., Brown-Guedira, G., Krill, A.M., Thurber, C., Merrill, K.R., Foresman, B.J. and Kolb, F.L., 2016. Genome-Wide Association Mapping of Fusarium Head Blight Resistance in Wheat using Genotyping-by-Sequencing. *The plant genome*, 9(1).

Balasubramanian, D., Rangunathan, P.T., Fei, J. and Vanderpool, C.K., 2016. A prophage-encoded small RNA controls metabolism and cell division in *Escherichia coli*. *mSystems*, 1(1), pp.e00021-15.

Beals, J.W., Sukiennik, R.A., Nallabelli, J., Emmons, R.S., van Vliet, S., Young, J.R., Ulanov, A.V., Li, Z., Paluska, S.A., De Lisio, M. and Burd, N.A., 2016. Anabolic sensitivity of postprandial muscle protein synthesis to the ingestion of a protein-dense food is reduced in overweight and obese young adults. *The American journal of clinical nutrition*, 104(4), pp.1014-1022.

Bi, H., Zhu, L., Jia, J., Zeng, L. and Cronan, J.E., 2016. Unsaturated Fatty Acid Synthesis in the Gastric Pathogen *Helicobacter pylori* Proceeds via a Backtracking Mechanism. *Cell chemical biology*, 23(12), pp.1480-1489.

Blazier, J.C., Jansen, R.K., Mower, J.P., Govindu, M., Zhang, J., Weng, M.L. and Ruhlman, T.A., 2016. Variable presence of the inverted repeat and plastome stability in *Erodium*. *Annals of botany*, 117(7), pp.1209-1220.

Bledsoe, J.W., Peterson, B.C., Swanson, K.S. and Small, B.C., 2016. Ontogenetic characterization of the intestinal microbiota of channel catfish through 16S rRNA gene sequencing reveals insights on temporal shifts and the influence of environmental microbes. *PLoS one*, 11(11), p.e0166379.

Bobrovskyy, M. and Vanderpool, C.K., 2016. Diverse mechanisms of post - transcriptional repression by the small RNA regulator of glucose - phosphate stress. *Molecular microbiology*, 99(2), pp.254-273.

Boyd, B.M., Allen, J.M., Koga, R., Fukatsu, T., Sweet, A.D., Johnson, K.P. and Reed, D.L., 2016. Two bacterial genera, *Sodalis* and *Rickettsia*, associated with the seal louse *Proechinophthirus fluctus* (Phthiraptera: Anoplura). *Applied and environmental microbiology*, 82(11), pp.3185-3197.  
Vancouver

Bradley, I.M., Pinto, A.J. and Guest, J.S., 2016. Design and Evaluation of Illumina MiSeq-Compatible, 18S rRNA Gene-Specific Primers for Improved Characterization of Mixed Phototrophic Communities. *Applied and environmental microbiology*, 82(19), pp.5878-5891.

Bradley, I.M., Pinto, A.J. and Guest, J.S., 2016. Design and Evaluation of Illumina MiSeq Compatible Primers for the 18S rRNA Gene for Improved Characterization of Mixed Microalgal Communities. *Applied and Environmental Microbiology*, pp.AEM-01630.

Brown, S.P., Ferrer, A., Dalling, J.W. and Heath, K.D., 2016. Don't put all your eggs in one basket: a cost - effective and powerful method to optimize primer choice for rRNA environmental community analyses using the Fluidigm Access Array. *Molecular ecology resources*, 16(4), pp.946-956.

Burch, A.Y., Do, P.T., Sbodio, A., Suslow, T.V. and Lindow, S.E., 2016. High-level culturability of epiphytic bacteria and frequency of biosurfactant producers on leaves. *Applied and environmental microbiology*, 82(19), pp.5997-6009.

Busby, R.R., Rodriguez, G., Gebhart, D.L. and Yannarell, A.C., 2016. Native *Lespedeza* species harbor greater non-rhizobial bacterial diversity in root nodules compared to the coexisting invader, *L. cuneata*. *Plant and soil*, 401(1-2), pp.427-436.

Cacioppo, J.A., Koo, Y., Lin, P.C.P., Osmulski, S.A., Ko, C.D. and Ko, C., 2016. Generation of an estrogen receptor beta - iCre knock - in mouse. *genesis*, 54(1), pp.38-52.

Cameron, S.A., Lim, H.C., Lozier, J.D., Duennes, M.A. and Thorp, R., 2016. Test of the invasive pathogen hypothesis of bumble bee decline in North America. *Proceedings of the National Academy of Sciences*, 113(16), pp.4386-4391.

Castro, J.J., Morrison, S.Y., Hosseinni, A., Loor, J.J., Drackley, J.K. and Ipharraguerre, I.R., 2016. Secretion of glucagon-like peptide-2 responds to nutrient intake but not glucose provision in milk-fed calves. *Journal of dairy science*, 99(7), pp.5793-5807.

Caetano-Anollés, K., Rhodes, J.S., Garland Jr, T., Perez, S.D., Hernandez, A.G., Southey, B.R. and Rodriguez-Zas, S.L., 2016. Cerebellum transcriptome of mice bred for high voluntary activity offers insights into locomotor control and reward-dependent behaviors. *PloS one*, 11(11), p.e0167095.

Cassano, J.A., Choi, S.K., McDonald, W., Szundi, I., Villa Gawboy, T.R., Gennis, R.B. and Einarsdóttir, Ó., 2016. The CO Photodissociation and Recombination Dynamics of the W172Y/F282T Ligand Channel Mutant of *Rhodobacter sphaeroides* aa3 Cytochrome c Oxidase. *Photochemistry and photobiology*, 92(3), pp.410-419.

Chang, H.X., Domier, L.L., Radwan, O., Yendrek, C.R., Hudson, M.E. and Hartman, G.L., 2016. Identification of multiple phytotoxins produced by *Fusarium virguliforme* including a phytotoxic effector (FvNIS1) associated with sudden death syndrome foliar symptoms. *Molecular Plant-Microbe Interactions*, 29(2), pp.96-108.

Chen, C., Dienhart, J.A. and Bolton, E.C., 2016. Androgen-Sensitized Apoptosis of HPr-1AR Human Prostate Epithelial Cells. *PloS one*, 11(5), p.e0156145.

Chen, W.T., Tang, L., Qian, W., Scheppe, K., Nair, K., Wu, Z., Gai, C., Zhang, P. and Zhang, Y., 2016. Extract nitrogen-containing compounds in biocrude oil converted from wet biowaste via hydrothermal liquefaction. *ACS Sustainable Chemistry & Engineering*, 4(4), pp.2182-2190.

Choe, E., Drnevich, J. and Williams II, M.M., 2016. Identification of Crowding Stress Tolerance Co-Expression Networks Involved in Sweet Corn Yield. *PloS one*, 11(1), p.e0147418.

Coates, B.S., Alves, A.P., Wang, H., Zhou, X., Nowatzki, T., Chen, H., Rangasamy, M., Robertson, H.M., Whitfield, C.W., Walden, K.K. and Kachman, S.D., 2016. Quantitative trait locus mapping and functional genomics of an organophosphate resistance trait in the western corn rootworm, *Diabrotica virgifera virgifera*. *Insect molecular biology*, 25(1), pp.1-15.

Collins, S.P., Labelle, A.L., Dirikolu, L., Li, Z., Mitchell, M.A. and Hamor, R.E., 2016. Tear film concentrations of doxycycline following oral administration in ophthalmologically normal dogs. *Journal of the American Veterinary Medical Association*, 249(5), pp.508-514.

Collins III, J.J., Wendt, G.R., Iyer, H. and Newmark, P.A., 2016. Stem cell progeny contribute to the schistosome host-parasite interface. *Elife*, 5, p.e12473.

de Almeida, D.A.C., Gusmão, L.F.P. and Miller, A.N., 2016. Taxonomy and molecular phylogeny of Diatrypaceae (Ascomycota, Xylariales) species from the Brazilian semi-arid region, including four new species. *Mycological progress*, 15(6), p.53.

Davidson, J.H. and Balakrishnan, C.N., 2016. Gene regulatory evolution during speciation in a songbird. *G3: Genes, Genomes, Genetics*, 6(5), pp.1357-1364.

Davyd, WC, A Pruzinska, S Hortensteiner, DR Ort. 2006. The role of pheophorbide a oxygenase expression and activity in the canola green seed problem. *Plant Phys* 142:88-97.

Despres, J., Forano, E., Lepercq, P., Comtet-Marre, S., Jubelin, G., Yeoman, C.J., Miller, M.E.B., Fields, C.J., Terrapon, N., Bourvellec, C. and Renard, C.M., 2016. Unraveling the pectinolytic function of *Bacteroides xylanisolvens* using a RNA-seq approach and mutagenesis. *BMC genomics*, 17(1), p.147.

Despres, J., Forano, E., Lepercq, P., Comtet-Marre, S., Jubelin, G., Chambon, C., Yeoman, C.J., Miller, M.E.B., Fields, C.J., Martens, E. and Terrapon, N., 2016. Xylan degradation by the human gut *Bacteroides xylanisolvens* XB1A T involves two distinct gene clusters that are linked at the transcriptional level. *BMC genomics*, 17(1), p.326.

Devendran, S., Abdel-Hamid, A.M., Evans, A.F., Iakiviak, M., Kwon, I.H., Mackie, R.I. and Cann, I., 2016. Multiple cellobiohydrolases and cellobiose phosphorylases cooperate in the ruminal bacterium *Ruminococcus albus* 8 to degrade cellooligosaccharides. *Scientific reports*, 6, p.35342.

Dhoble, A.S., Bekal, S., Dolatowski, W., Yanz, C., Lambert, K.N. and Bhalerao, K.D., 2016. A novel high-throughput multi-parameter flow cytometry based method for monitoring and rapid characterization of microbiome dynamics in anaerobic systems. *Bioresource technology*, 220, pp.566-571.  
Vancouver

Ding, W., Liu, W.Q., Jia, Y., Li, Y., van der Donk, W.A. and Zhang, Q., 2016. Biosynthetic investigation of phomopsins reveals a widespread pathway for ribosomal natural products in Ascomycetes. *Proceedings of the National Academy of Sciences*, 113(13), pp.3521-3526.

Divilov, K. and Walker, D.R., 2016. Reaction of *Diaporthe longicolla* to a strain of *Sarocladium kiliense*. *Biocontrol Science and Technology*, 26(7), pp.938-950.

Dong, Y., Chang, Y.J., Sanford, R.A. and Fouke, B.W., 2016. Draft genome sequence of *Tepidibacillus decaturensis* strain Z9, an anaerobic, moderately thermophilic, and heterotrophic bacterium from the deep subsurface of the Illinois Basin, USA. *Genome announcements*, 4(2), pp.e00190-16.

Dong, Y., Sanford, R.A., Chang, Y.J., McInerney, M.J. and Fouke, B.W., 2016. Hematite Reduction Buffers Acid Generation and Enhances Nutrient Uptake by a Fermentative Iron Reducing Bacterium, *Orenia metallireducens* Strain Z6. *Environmental science & technology*, 51(1), pp.232-242.

Dor, L., Shirak, A., Rosenfeld, H., Ashkenazi, I.M., Band, M.R., Korol, A., Ronin, Y., Seroussi, E., Weller, J.I. and Ron, M., 2016. Identification of the sex - determining region in flathead grey mullet (*Mugil cephalus*). *Animal genetics*, 47(6), pp.698-707.

Dündar, E., 2016. Physiological and Molecular Analysis of a Valine Resistant Mutant in *Arabidopsis thaliana*. *Balıkesir Üniversitesi Fen Bilimleri Enstitüsü Dergisi*, 6(1), pp.4-15.  
Vancouver

Eckstrum, K.S., Weis, K.E., Baur, N.G., Yoshihara, Y. and Raetzman, L.T., 2016. Icam5 expression exhibits sex differences in the neonatal pituitary and is regulated by estradiol and bisphenol A. *Endocrinology*, 157(4), pp.1408-1420.

Emmons, R., Niemi, G.M., Owolabi, O. and De Lisio, M., 2016. Acute exercise mobilizes hematopoietic stem and progenitor cells and alters the mesenchymal stromal cell secretome. *Journal of Applied Physiology*, 120(6), pp.624-632.

Eerkens, J.W., Carlson, T., Malhi, R.S., Blake, J., Bartelink, E.J., Barfod, G.H., Estes, A., Garibay, R., Glessner, J., Greenwald, A.M. and Lentz, K., 2016. Isotopic and genetic analyses of a mass grave in central California: Implications for precontact hunter - gatherer warfare. *American journal of physical anthropology*, 159(1), pp.116-125.

Escalante, G.C., Sweet, A.D., McCracken, K.G., Gustafsson, D.R., Wilson, R.E. and Johnson, K.P., 2016. Patterns of cryptic host specificity in duck lice based on molecular data. *Medical and veterinary entomology*, 30(2), pp.200-208.

Falagan-Lotsch, P., Grzincic, E.M. and Murphy, C.J., 2016. One low-dose exposure of gold nanoparticles induces long-term changes in human cells. *Proceedings of the National Academy of Sciences*, 113(47), pp.13318-13323.

Fang, J., Wood, A., Chen, R. and Ming, R., 2016. Molecular basis of off-type microsatellite markers in papaya. *Euphytica*, 209(2), pp.323-339.

Freestone, T.S. and Zhao, H., 2016. Combinatorial pathway engineering for optimized production of the anti - malarial FR900098. *Biotechnology and bioengineering*, 113(2), pp.384-392.

Gardinassi, L.G., Garcia, G.R., Costa, C.H.N., Silva, V.C. and de Miranda Santos, I.K.F., 2016. Blood transcriptional profiling reveals immunological signatures of distinct states of infection of humans with *Leishmania infantum*. *PLoS neglected tropical diseases*, 10(11), p.e0005123.

Gonzalez-Pena, D., Nixon, S.E., O'Connor, J.C., Southey, B.R., Lawson, M.A., McCusker, R.H., Borrás, T., Machuca, D., Hernandez, A.G., Dantzer, R. and Kelley, K.W., 2016. Microglia transcriptome changes in a model of depressive behavior after immune challenge. *PloS one*, 11(3), p.e0150858.

Gonzalez-Pena, D., Nixon, S.E., Southey, B.R., Lawson, M.A., McCusker, R.H., Hernandez, A.G., Dantzer, R., Kelley, K.W. and Rodriguez-Zas, S.L., 2016. Differential transcriptome networks between IDO1-knockout and wild-type mice in brain microglia and macrophages. *PloS one*, 11(6), p.e0157727.

Gordon, B.R., Klinger, C.R., Weese, D.J., Lau, J.A., Burke, P.V., Dentinger, B. and Heath, K.D., 2016. Decoupled genomic elements and the evolution of partner quality in nitrogen - fixing rhizobia. *Ecology and evolution*, 6(5), pp.1317-1327.

Graves, H., Rayburn, A.L., Kim, S. and Lee, D.K., 2016. Chloroplast DNA variation within prairie cordgrass (*Spartina pectinata* Link) populations in the US. *Journal of systematics and evolution*, 54(2), pp.104-112.

Grillo, M.A., Mita, S., Burke, P.V., Solórzano - Lowell, K.L. and Heath, K.D., 2016. Intrapopulation genomics in a model mutualist: Population structure and candidate symbiosis genes under selection in *Medicago truncatula*. *Evolution*, 70(12), pp.2704-2717.

Han, J., Domier, L., Cassone, B. and Qu, F., 2016. Assessment of Common Soybean-Infecting Viruses in Ohio, USA, Through Multi-site Sampling and High-Throughput Sequencing. *Plant Health Progress*, 17(2), p.133.

Haney, S.L., Upchurch, G.M., Opavska, J., Klinkebiel, D., Appiah, A.K., Smith, L.M., Heavican, T.B., Iqbal, J., Joshi, S. and Opavsky, R., 2016. Loss of Dnmt3a induces CLL and PTCL with distinct methylomes and transcriptomes in mice. *Scientific reports*, 6, p.34222.

Haney, S.L., Upchurch, G.M., Opavska, J., Klinkebiel, D., Hlady, R.A., Roy, S., Dutta, S., Datta, K. and Opavsky, R., 2016. Dnmt3a Is a Haploinsufficient Tumor Suppressor in CD8+ Peripheral T Cell Lymphoma. *PLoS genetics*, 12(9), p.e1006334.

Haney, S.L., Upchurch, G.M., Opavska, J., Klinkebiel, D., Hlady, R.A., Suresh, A., Pirruccello, S.J., Shukla, V., Lu, R., Costinean, S. and Rizzino, A., 2016. Promoter hypomethylation and expression is conserved in mouse chronic lymphocytic leukemia induced by decreased or inactivated Dnmt3a. *Cell reports*, 15(6), pp.1190-1201.

Harris, N.L., Cock, P.J., Chapman, B.A., Goecks, J., Hotz, H.R. and Lapp, H., 2014. The Bioinformatics Open Source Conference (BOSC) 2013.

Hirsch, C., Hirsch, C.D., Brohammer, A.B., Bowman, M.J., Soifer, I., Barad, O., Shem-Tov, D., Baruch, K., Lu, F., Hernandez, A.G. and Fields, C.J., 2016. Draft assembly of elite inbred line PH207 provides insights into genomic and transcriptome diversity in maize. *The Plant Cell Online*, pp.tpc-00353.

Hladilek, M.D., Gaines, K.F., Novak, J.M., Collard, D.A., Johnson, D.B. and Canam, T., 2016. Microbial community structure of a freshwater system receiving wastewater effluent. *Environmental monitoring and assessment*, 188(11), p.626.

Huang, X.F., Chaparro, J.M., Reardon, K.F., Judd, T.M. and Vivanco, J.M., 2016. Supplementing Blends of Sugars, Amino Acids, and Secondary Metabolites to the Diet of Termites (*Reticulitermes flavipes*) Drive Distinct Gut Bacterial Communities. *Microbial ecology*, 72(3), pp.497-502.

Huber, S.C., Li, K., Nelson, R., Ulanov, A., DeMuro, C.M. and Baxter, I., 2016. Canopy position has a profound effect on soybean seed composition. *PeerJ*, 4, p.e2452.

Itkin, M., Davidovich-Rikanati, R., Cohen, S., Portnoy, V., Doron-Faigenboim, A., Oren, E., Freilich, S., Tzuri, G., Baranes, N., Shen, S. and Petreikov, M., 2016. The biosynthetic pathway of the nonsugar, high-intensity sweetener mogroside V from *Siraitia grosvenorii*. *Proceedings of the National Academy of Sciences*, 113(47), pp.E7619-E7628.

Jeraldo, P., Hernandez, A., Nielsen, H.B., Chen, X., White, B.A., Goldenfeld, N., Nelson, H., Alhquist, D., Boardman, L. and Chia, N., 2016. Capturing one of the human gut microbiome's most wanted: reconstructing the genome of a novel butyrate-producing, clostridial scavenger from metagenomic sequence data. *Frontiers in microbiology*, 7.

Jiang, S., Li, X., Hess, N.J., Guan, Y. and Tapping, R.I., 2016. TLR10 is a negative regulator of both MyD88-dependent and-independent TLR signaling. *The Journal of Immunology*, 196(9), pp.3834-3841.

Jiang, T., Chen, Y., Mao, L., Marshall, A.G. and Xu, W., 2016. Extracting biomolecule collision cross sections from the high-resolution FT-ICR mass spectral linewidths. *Physical Chemistry Chemical Physics*, 18(2), pp.713-717

Johnson, B.R., Hymes, J., Sanozky-Dawes, R., Henriksen, E.D., Barrangou, R. and Klaenhammer, T.R., 2016. Conserved S-layer-associated proteins revealed by exoproteomic survey of S-layer-forming lactobacilli. *Applied and environmental microbiology*, 82(1), pp.134-145.

Kashiwagi, T., Kingsland, K.M., Pratt, T.C., Pratt, H.L. and Heist, E.J., 2016. Complete mitochondrial genome of the nurse shark *Ginglymostoma cirratum*. *Mitochondrial DNA Part B*, 1(1), pp.464-465.

Kaya Okur, H.S., Das, A., Taylor, R.N., Bagchi, I.C. and Bagchi, M.K., 2016. Roles of estrogen receptor- $\alpha$  and the coactivator MED1 during human endometrial decidualization. *Molecular Endocrinology*, 30(3), pp.302-313.

Kaylan, K.B., Ermilova, V., Yada, R.C. and Underhill, G.H., 2016. Combinatorial microenvironmental regulation of liver progenitor differentiation by Notch ligands, TGF $\beta$ , and extracellular matrix. *Scientific reports*, 6, p.23490.

Kelly, M.W., DeBiasse, M.B., Villela, V.A., Roberts, H.L. and Cecola, C.F., 2016. Adaptation to climate change: trade - offs among responses to multiple stressors in an intertidal crustacean. *Evolutionary applications*, 9(9), pp.1147-1155.

Khan, S.J., Abidi, S.N.F., Tian, Y., Skinner, A. and Smith-Bolton, R.K., 2016. A rapid, gentle and scalable method for dissociation and fluorescent sorting of imaginal disc cells for mRNA sequencing. *Fly*, 10(2), pp.73-80.

Khan, S.R., Mahaseth, T., Kouzminova, E.A., Cronan, G.E. and Kuzminov, A., 2016. Static and dynamic factors limit chromosomal replication complexity in *Escherichia coli*, avoiding dangers of runaway overreplication. *Genetics*, 202(3), pp.945-960.

Kim, D.H., Kwon, S., Byun, S., Xiao, Z., Park, S., Wu, S.Y., Chiang, C.M., Kemper, B. and Kemper, J.K., 2016. Critical role of RanBP2-mediated SUMOylation of Small Heterodimer Partner in maintaining bile acid homeostasis. *Nature communications*, 7, Vancouver

Kim, N.K., Oh, S. and Liu, W.T., 2016. Enrichment and characterization of microbial consortia degrading soluble microbial products discharged from anaerobic methanogenic bioreactors. *Water research*, 90, pp.395-404.

Klinger, C.R., Lau, J.A. and Heath, K.D., 2016, March. Ecological genomics of mutualism decline in nitrogen-fixing bacteria. In *Proc. R. Soc. B* (Vol. 283, No. 1826, p. 20152563). The Royal Society. Vancouver

Koirala, S., Wang, X. and Rao, C.V., 2016. Reciprocal regulation of l-arabinose and d-xylose metabolism in *Escherichia coli*. *Journal of bacteriology*, 198(3), pp.386-393.

Kuroda, K., Nobu, M.K., Mei, R., Narihiro, T., Bocher, B.T., Yamaguchi, T. and Liu, W.T., 2016. A Single-Granule-Level Approach Reveals Ecological Heterogeneity in an Upflow Anaerobic Sludge Blanket Reactor. *PloS one*, 11(12), p.e0167788.

Lagos-Kutz, D., Favret, C., Giordano, R. and Voegtlin, D.J., 2016. The status of the members of the *Aphis asclepiadis* species group (Hemiptera: Aphididae) in the United States of America. *Annals of the Entomological Society of America*, 109(4), pp.585-594.



- Iakiviak, M., Devendran, S., Skorupski, A., Moon, Y.H., Mackie, R.I. and Cann, I., 2016. Functional and modular analyses of diverse endoglucanases from *Ruminococcus albus* 8, a specialist plant cell wall degrading bacterium. *Scientific reports*, 6.
- Itkin, M., Davidovich-Rikanati, R., Cohen, S., Portnoy, V., Doron-Faigenboim, A., Oren, E., Freilich, S., Tzuri, G., Baranes, N., Hernandez, A.G., Shen, S. and Petreikov, M., 2016. The biosynthetic pathway of the nonsugar, high-intensity sweetener mogroside V from *Siraitia grosvenorii*. *Proceedings of the National Academy of Sciences*, 113(47), pp.E7619-E7628.
- Jordana, R., 2016. New diagnosis for species of *Plutomurus Yosii* (Collembola, Tomoceridae), with descriptions of two new species from Georgian caves. *Zootaxa*, 4126(1), pp.077-096.
- Lago, D.C., Humann, F.C., Barchuk, A.R., Abraham, K.J. and Hartfelder, K., 2016. Differential gene expression underlying ovarian phenotype determination in honey bee, *Apis mellifera* L., caste development. *Insect biochemistry and molecular biology*, 79, pp.1-12.
- Lambert, B., Dassanayake, M., Oh, D.H., Garrett, S.B., Lee, S.Y. and Pettis, G.S., 2016. A novel phase variant of the cholera pathogen shows stress-adaptive cryptic transcriptomic signatures. *BMC genomics*, 17(1), p.914.
- Lee, J., Abdeen, A.A., Wycislo, K.L., Fan, T.M. and Kilian, K.A., 2016. Interfacial geometry dictates cancer cell tumorigenicity. *Nature materials*, 15(8), pp.856-862.  
Vancouver
- Lee, T.G., Diers, B.W. and Hudson, M.E., 2016. An efficient method for measuring copy number variation applied to improvement of nematode resistance in soybean. *The Plant Journal*, 88(1), pp.143-153.
- Lee, M.S., Rayburn, A.L. and Lee, D.K., 2016. Genesis and Identification of Octoploids Generated from Tetraploid Prairie Cordgrass. *Crop Science*, 56(6), pp.2973-2982.
- Lesser, M.P., Fiore, C., Slattery, M. and Zaneveld, J., 2016. Climate change stressors destabilize the microbiome of the Caribbean barrel sponge, *Xestospongia muta*. *Journal of Experimental Marine Biology and Ecology*, 475, pp.11-18.
- Levine, B.A., Smith, C.F., Douglas, M.R., Davis, M.A., Schuett, G.W., Beaupre, S.J. and Douglas, M.E., 2016. Population genetics of the Copperhead at its most northeastern distribution. *Copeia*, 104(2), pp.448-457.
- Li, D., Voigt, T.B. and Kent, A.D., 2016. Plant and soil effects on bacterial communities associated with *Miscanthus × giganteus* rhizosphere and rhizomes. *Gcb Bioenergy*, 8(1), pp.183-193.

Li, P., Meng, J., Liu, W., Smith, G.W., Yao, J. and Lyu, L., 2016. Transcriptome analysis of bovine ovarian follicles at predeviation and onset of deviation stages of a follicular wave. *International journal of genomics*, 2016.

Li, Y., Lin, Q., Wang, S., Li, X., Liu, W., Luo, C., Zhang, Z., Zhu, X., Jiang, L. and Li, X., 2016. Soil bacterial community responses to warming and grazing in a Tibetan alpine meadow. *FEMS microbiology ecology*, 92(1).

Lim, N.Y., Roco, C.A. and Frostegård, Å., 2016. Transparent DNA/RNA co-extraction workflow protocol suitable for inhibitor-rich environmental samples that focuses on complete DNA removal for transcriptomic analyses. *Frontiers in microbiology*, 7.

Ling, F., Hwang, C., LeChevallier, M.W., Andersen, G.L. and Liu, W.T., 2016. Core-satellite populations and seasonality of water meter biofilms in a metropolitan drinking water distribution system. *The ISME journal*, 10(3), pp.582-595.

Liu, G., Ling, F.Q., Van der Mark, E.J., Zhang, X.D., Knezev, A., Verberk, J.Q.J.C., Van der Meer, W.G.J., Medema, G.J., Liu, W.T. and Van Dijk, J.C., 2016. Comparison of particle-associated bacteria from a drinking water treatment plant and distribution reservoirs with different water sources. *Scientific reports*, 6, p.20367.

Liu, S., Clark, L.V., Swaminathan, K., Gifford, J.M., Juvik, J.A. and Sacks, E.J., 2016. High - density genetic map of *Miscanthus sinensis* reveals inheritance of zebra stripe. *Gcb Bioenergy*, 8(3), pp.616-630.

Liu, T.W., Cephas, K.D., Holscher, H.D., Kerr, K.R., Mangian, H.F., Tappenden, K.A. and Swanson, K.S., 2016. Nondigestible fructans alter gastrointestinal barrier function, gene expression, histomorphology, and the microbiota profiles of diet-induced obese C57BL/6J mice. *The Journal of nutrition*, 146(5), pp.949-956.

Lu, H., Ulanov, A.V., Nobu, M. and Liu, W.T., 2016. Global metabolomic responses of *Nitrosomonas europaea* 19718 to cold stress and altered ammonia feeding patterns. *Applied microbiology and biotechnology*, 100(4), pp.1843-1852.

Lu, H., Xue, Z., Saikaly, P., Nunes, S.P., Bluver, T.R. and Liu, W.T., 2016. Membrane biofouling in a wastewater nitrification reactor: Microbial succession from autotrophic colonization to heterotrophic domination. *Water research*, 88, pp.337-345.

Ma, L., Liu, T.W., Wallig, M.A., Dobrucki, I.T., Dobrucki, L.W., Nelson, E.R., Swanson, K.S. and Smith, A.M., 2016. Efficient targeting of adipose tissue macrophages in obesity with polysaccharide nanocarriers. *ACS nano*, 10(7), pp.6952-6962.

- Ma, B., Zhao, S., Wu, B., Wang, D., Peng, Q., Owiti, A., Fang, T., Liao, L., Ogutu, C., Korban, S.S. and Li, S., 2016. Construction of a high density linkage map and its application in the identification of QTLs for soluble sugar and organic acid components in apple. *Tree genetics & genomes*, 12(1), p.1.
- Marcelino, J.A., Giordano, R., Borges, P.A., Garcia, P.V., Soto-Adames, F.N. and Soares, A.O., 2016. Distribution and genetic variability of Staphylinidae across a gradient of anthropogenically influenced insular landscapes. *Bulletin of Insectology*, 69(1), pp.117-126.
- Marsboom, G., Zhang, G.F., Pohl-Avila, N., Zhang, Y., Yuan, Y., Kang, H., Hao, B., Brunengraber, H., Malik, A.B. and Rehman, J., 2016. Glutamine metabolism regulates the pluripotency transcription factor OCT4. *Cell reports*, 16(2), pp.323-332.
- Matsumura, H., Chakraborty, S., Reed, J., Lu, Y. and Moënne-Loccoz, P., 2016. Effect of Outer-Sphere Side Chain Substitutions on the Fate of the trans Iron–Nitrosyl Dimer in Heme/Nonheme Engineered Myoglobins (FeBMbs): Insights into the Mechanism of Denitrifying NO Reductases. *Biochemistry*, 55(14), pp.2091-2099.
- Mei, R., Narihiro, T., Nobu, M.K., Kuroda, K. and Liu, W.T., 2016. Evaluating digestion efficiency in full-scale anaerobic digesters by identifying active microbial populations through the lens of microbial activity. *Scientific reports*, 6.
- Mirshafiee, V., Kim, R., Park, S., Mahmoudi, M. and Kraft, M.L., 2016. Impact of protein pre-coating on the protein corona composition and nanoparticle cellular uptake. *Biomaterials*, 75, pp.295-304.
- Mirshafiee, V., Kim, R., Mahmoudi, M. and Kraft, M.L., 2016. The importance of selecting a proper biological milieu for protein corona analysis in vitro: Human plasma versus human serum. *The international journal of biochemistry & cell biology*, 75, pp.188-195.
- Molloy, E.M., Tietz, J.I., Blair, P.M. and Mitchell, D.A., 2016. Biological characterization of the hygrobafilomycin antibiotic JBIR-100 and bioinformatic insights into the hygrolide family of natural products. *Bioorganic & medicinal chemistry*, 24(24), pp.6276-6290.
- Morales, P., Fujio, S., Navarrete, P., Ugalde, J.A., Magne, F., Carrasco-Pozo, C., Tralma, K., Quezada, M., Hurtado, C., Covarrubias, N. and Brignardello, J., 2016. Impact of dietary lipids on colonic function and microbiota: an experimental approach involving orlistat-induced fat malabsorption in human volunteers. *Clinical and translational gastroenterology*, 7(4), p.e161.
- Morrow, K.M., Fiore, C.L. and Lesser, M.P., 2016. Environmental drivers of microbial community shifts in the giant barrel sponge, *Xestospongia muta*, over a shallow to mesophotic depth gradient. *Environmental microbiology*, 18(6), pp.2025-2038.

Mudd, A.T., Alexander, L.S., Berding, K., Waworuntu, R.V., Berg, B.M., Donovan, S.M. and Dilger, R.N., 2016. Dietary prebiotics, milk fat globule membrane, and lactoferrin affects structural neurodevelopment in the young piglet. *Frontiers in pediatrics*, 4.

Munroe, M.R., Garg, K., Jensen, T. and Boppart, M.D., 2016. Diet-induced obesity regulates adipose-resident stromal cell quantity and extracellular matrix gene expression. *Stem Cell Research* 17:181-190.

Muturi, E.J., Bara, J.J., Rooney, A.P. and Hansen, A.K., 2016. Midgut fungal and bacterial microbiota of *Aedes triseriatus* and *Aedes japonicus* shift in response to La Crosse virus infection. *Molecular ecology*, 25(16), pp.4075-4090.

Muturi, E.J., Kim, C.H., Bara, J., Bach, E.M. and Siddappaji, M.H., 2016. *Culex pipiens* and *Culex restuans* mosquitoes harbor distinct microbiota dominated by few bacterial taxa. *Parasites & vectors*, 9(1), p.18.

Naeger, N.L. and Robinson, G.E., 2016. Transcriptomic analysis of instinctive and learned reward-related behaviors in honey bees. *Journal of Experimental Biology*, 219(22), pp.3554-3561.

Nah, G., Lee, M., Kim, D.S., Rayburn, A.L., Voigt, T. and Lee, D.K., 2016. Transcriptome analysis of *Spartina pectinata* in response to freezing stress. *PloS one*, 11(3), p.e0152294.

Nardi, J.B., Bee, C.M., Miller, L.A., Imai, B.S. and Yau, P.M., 2016. Segmental pairs of giant insect cells discharge presumptive immune proteins at each larval molt. *Developmental biology*, 413(2), pp.199-206.

McNeill, M.S., Kapheim, K.M., Brockmann, A., McGill, T.A.W. and Robinson, G.E., 2016. Brain regions and molecular pathways responding to food reward type and value in honey bees. *Genes, Brain and Behavior*, 15(3), pp.305-317.

Niemiro, G.M., Raine, L.B., Khan, N.A., Emmons, R., Little, J., Kramer, A.F., Hillman, C.H. and De Lisio, M., 2016. Circulating progenitor cells are positively associated with cognitive function among overweight/obese children. *Brain, behavior, and immunity*, 57, pp.47-52.

O'Flaherty, S. and Klaenhammer, T.R., 2016. Multivalent Chromosomal Expression of the *Clostridium botulinum* Serotype A Neurotoxin Heavy-Chain Antigen and the *Bacillus anthracis* Protective Antigen in *Lactobacillus acidophilus*. *Applied and environmental microbiology*, 82(20), pp.6091-6101.

Vancouver

Oakley, O.R., Kim, K.J., Lin, P.C., Barakat, R., Cacioppo, J.A., Li, Z., Whitaker, A., Chung, K.C., Mei, W. and Ko, C., 2016. Estradiol synthesis in gut-associated lymphoid tissue: leukocyte regulation by a sexually monomorphic system. *Endocrinology*, 157(12), pp.4579-4587.

Oh, E.J., Skerker, J.M., Kim, S.R., Wei, N., Turner, T.L., Maurer, M.J., Arkin, A.P. and Jin, Y.S., 2016. Gene amplification on demand accelerates cellobiose utilization in engineered *Saccharomyces cerevisiae*. *Applied and environmental microbiology*, 82(12), pp.3631-3639.

Oh, S., Zhang, R., Wu, Q.L. and Liu, W.T., 2016. Evolution and adaptation of SAR11 and *Cyanobium* in a saline Tibetan lake. *Environmental microbiology reports*, 8(5), pp.595-604.

Ojo, J.A., Valero, M.C., Sun, W., Coates, B.S., Omoloye, A.A. and Pittendrigh, B.R., 2016. Comparison of full mitochondrial genomes for the rice weevil, *Sitophilus oryzae* and the maize weevil, *Sitophilus zeamais* (Coleoptera: Curculionidae). *Agri Gene*, 2, pp.29-37.

Oosterkamp, M.J., Méndez-García, C., Kim, C.H., Bauer, S., Ibáñez, A.B., Zimmerman, S., Hong, P.Y., Cann, I.K. and Mackie, R.I., 2016. Lignocellulose-derived thin stillage composition and efficient biological treatment with a high-rate hybrid anaerobic bioreactor system. *Biotechnology for biofuels*, 9(1), p.120.

Ottesen, A., Telias, A., White, J.R., Newell, M.J., Pahl, D., Brown, E.W., Musser, S. and Walsh, C., 2016. Bacteria of tomatoes managed with well water and pond water: Impact of agricultural water sources on carposphere microbiota. *Intl J. Env & Agri Res* 2:7-14.

Page, A.F., Cseke, L.J., Minocha, R., Turlapati, S.A., Podila, G.K., Ulanov, A., Li, Z. and Minocha, S.C., 2016. Genetic manipulation of putrescine biosynthesis reprograms the cellular transcriptome and the metabolome. *BMC plant biology*, 16(1), p.113.

Paitz, R.T., Bukhari, S.A. and Bell, A.M., 2016, March. Stickleback embryos use ATP-binding cassette transporters as a buffer against exposure to maternally derived cortisol. In *Proc. R. Soc. B* (Vol. 283, No. 1826, p. 20152838). The Royal Society.

Peterson, J.R., Thor, S., Kohler, L., Kohler, P.R., Metcalf, W.W. and Luthey-Schulten, Z., 2016. Genome-wide gene expression and RNA half-life measurements allow predictions of regulation and metabolic behavior in *Methanosarcina acetivorans*. *BMC genomics*, 17(1), p.924.

Pincu, Y., Huntsman, H.D., Zou, K., De Lisio, M., Mahmassani, Z.S., Munroe, M.R., Garg, K., Jensen, T. and Boppart, M.D., 2016. Diet-induced obesity regulates adipose-resident stromal cell quantity and extracellular matrix gene expression. *Stem cell research*, 17(1), pp.181-190.

Prather, G.R., MacLean, J.A., Shi, M., Boadu, D.K., Paquet, M. and Hayashi, K., 2016. Niclosamide as a potential nonsteroidal therapy for endometriosis that preserves reproductive function in an experimental mouse model. *Biology of reproduction*, 95(4), pp.74-1.

Quarterman, J., Skerker, J.M., Feng, X., Liu, I.Y., Zhao, H., Arkin, A.P. and Jin, Y.S., 2016. Rapid and efficient galactose fermentation by engineered *Saccharomyces cerevisiae*. *Journal of biotechnology*, 229, pp.13-21.

Randrianandrasana, M., Berlocher, S.H., Rougerie, R. and Berenbaum, M.R., 2016. Intraspecific Variation in *Antherina suraka* (Lepidoptera: Saturniidae), an Endemic Resident of Endangered Forests in Madagascar. *Annals of the Entomological Society of America*, 109(3), pp.384-395.

Roberts-Galbraith, R.H., Brubacher, J.L. and Newmark, P.A., 2016. A functional genomics screen in planarians reveals regulators of whole-brain regeneration. *eLife*, 5.

Roy, A., Dutta, D., Iqbal, J., Pisano, G., Gjyshi, O., Ansari, M.A., Kumar, B. and Chandran, B., 2016. Nuclear innate immune DNA sensor IFI16 is degraded during lytic reactivation of Kaposi's sarcoma-associated herpesvirus (KSHV): role of IFI16 in maintenance of KSHV latency. *Journal of virology*, 90(19), pp.8822-8841.

Schroeder, A.L., Metzger, K.J., Miller, A. and Rhen, T., 2016. A novel candidate gene for temperature-dependent sex determination in the common snapping turtle. *Genetics*, 203(1), pp.557-571.

Stewart, J.L., Shipley, C.F., Katich, A.S., Po, E., Ellerbrock, R.E., Lima, F.S. and Canisso, I.F., 2016. Cryopreservation of white-tailed deer (*Odocoileus virginianus*) semen using soybean-, liposome-, and egg yolk-based extenders. *Animal reproduction science*, 171, pp.7-16.

Stumpf, R.M., Gomez, A., Amato, K.R., Yeoman, C.J., Polk, J.D., Wilson, B.A., Nelson, K.E., White, B.A. and Leigh, S.R., 2016. Microbiomes, metagenomics, and primate conservation: New strategies, tools, and applications. *Biological Conservation*, 199, pp.56-66.

Sun, Y., Zhang, H., Kazemian, M., Troy, J.M., Seward, C., Lu, X. and Stubbs, L., 2016. ZSCAN5B and primate-specific paralogs bind RNA polymerase III genes and extra-TFIIC (ETC) sites to modulate mitotic progression. *Oncotarget*, 7(45), p.72571.

Sweet, A.D. and Johnson, K.P., 2016. Cophylogenetic analysis of New World ground-doves (Aves: Columbidae) and their parasitic wing lice (Insecta: Phthiraptera: Columbicola). *Molecular phylogenetics and evolution*, 103, pp.122-132.

Thibodeaux, C.J., Wagoner, J., Yu, Y. and van der Donk, W.A., 2016. Leader peptide establishes dehydration order, promotes efficiency, and ensures fidelity during lactacin 481 biosynthesis. *J. Am. Chem. Soc.*, 138(20), pp.6436-6444.  
Vancouver

- Vallejo, R.L., Leeds, T.D., Fragomeni, B.O., Gao, G., Hernandez, A.G., Misztal, I., Welch, T.J., Wiens, G.D. and Palti, Y., 2016. Evaluation of genome-enabled selection for bacterial cold water disease resistance using progeny performance data in rainbow trout: insights on genotyping methods and genomic prediction models. *Frontiers in genetics*, 7.
- Vallejo, R., Tilley, D.M., Cedeño, D.L., Kelley, C.A., DeMaegd, M. and Benyamin, R., 2016. Genomics of the effect of spinal cord stimulation on an animal model of neuropathic pain. *Neuromodulation: Technology at the Neural Interface*, 19(6), pp.576-586.
- van Vliet, S., Beals, J.W., Parel, J.T., Hanna, C.D., Utterback, P.L., Dilger, A.C., Ulanov, A.V., Li, Z., Paluska, S.A., Moore, D.R. and Parsons, C.M., 2016. Development of Intrinsically Labeled Eggs and Poultry Meat for Use in Human Metabolic Research. *The Journal of nutrition*, 146(7), pp.1428-1433.  
Vancouver
- Vlčková, K., Gomez, A., Petrželková, K.J., Whittier, C.A., Todd, A.F., Yeoman, C.J., Nelson, K.E., Wilson, B.A., Stumpf, R.M., Modrý, D. and White, B.A., 2016. Effect of Antibiotic Treatment on the Gastrointestinal Microbiome of Free-Ranging Western Lowland Gorillas (*Gorilla g. gorilla*). *Microbial ecology*, 72(4), pp.943-954.
- Wang, J., Fu, L., Koganti, P.P., Wang, L., Hand, J.M., Ma, H. and Yao, J., 2016. Identification and functional prediction of large intergenic noncoding RNAs (lincRNAs) in rainbow trout (*Oncorhynchus mykiss*). *Marine biotechnology*, 18(2), pp.271-282.
- Welly, R.J., Liu, T.W., Zidon, T.M., Rowles III, J.L., Park, Y.M., Smith, T.N., Swanson, K.S., Padilla, J. and Vieira-Potter, V.J., 2016. Comparison of diet versus exercise on metabolic function and gut microbiota in obese rats. *Medicine and science in sports and exercise*, 48(9), pp.1688-1698.
- Wooten, J., Liu, X. and Miller, M.J., 2016. Draft genome sequence of *Lactobacillus crispatus* JCM5810, which can reduce *Campylobacter jejuni* colonization in chicken intestine. *Genome announcements*, 4(2), pp.e00255-16.
- Wysocki, W.P., Ruiz-Sanchez, E., Yin, Y. and Duvall, M.R., 2016. The floral transcriptomes of four bamboo species (Bambusoideae; Poaceae): support for common ancestry among woody bamboos. *BMC genomics*, 17(1), p.384.
- Yang, C.Y., Yu, K., Wang, Y., Chen, S.A., Liu, D.D., Wang, Z.Y., Su, Y.N., Yang, S.Z., Chen, T.T., Livnat, I. and Vilim, F.S., 2016. *Aplysia* Locomotion: Network and Behavioral Actions of GdFFD, a D-Amino Acid-Containing Neuropeptide. *PloS one*, 11(1), p.e0147335.

Zeng, F. and Jin, H., 2016. Peptide release promoted by methylated RF2 and ArfA in nonstop translation is achieved by an induced-fit mechanism. *Rna*, 22(1), pp.49-60.

Zhen-Yuan Wang, G.W.S., Esau, B.D., Portis Jr, A.R. and Ogren, W.L., Species-Dependent Variation in the Interaction of Substrate-Bound Ribulose-1, 5-Bisphosphate Carboxylase/Oxygenase.

Zhou, J., Wu, K. and Rao, C.V., 2016. Evolutionary engineering of *Geobacillus thermoglucosidasius* for improved ethanol production. *Biotechnology and bioengineering*, 113(10), pp.2156-2167.