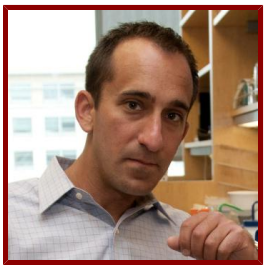
Stanford



Michael Fischbach

Liu (Liao) Family Professor

Bioengineering

Bio

BIO

Michael Fischbach is the Liu (Liao) Family Professor of Bioengineering at Stanford University, an Institute Scholar of Stanford ChEM-H, and the director of the Stanford Microbiome Therapies Initiative. Fischbach is a recipient of the NIH Director's Pioneer and New Innovator Awards, an HHMI-Simons Faculty Scholars Award, a Fellowship for Science and Engineering from the David and Lucile Packard Foundation, a Medical Research Award from the W.M. Keck Foundation, a Burroughs Wellcome Fund Investigators in the Pathogenesis of Infectious Disease award, and the Vannevar Bush Faculty Fellowship. His laboratory studies the mechanisms of microbiome-host interactions. Fischbach received his Ph.D. as a John and Fannie Hertz Foundation Fellow in chemistry from Harvard in 2007, where he studied the role of iron acquisition in bacterial pathogenesis and the biosynthesis of antibiotics. After two years as an independent fellow at Massachusetts General Hospital, Fischbach joined the faculty at UCSF, where he founded his lab before moving to Stanford in 2017. Fischbach is a co-founder of Revolution Medicines and Kelonia, a co-founder and director of Azalea, a member of the scientific advisory boards of the Chan Zuckerberg Initiative, Stand Up to Cancer, and TCG Labs/Soleil Labs, and an innovation partner at The Column Group.

ACADEMIC APPOINTMENTS

- Professor, Bioengineering
- Member, Bio-X
- Member, Wu Tsai Human Performance Alliance
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Stanford Medicine Children’s Health Center for IBD and Celiac Disease
- Institute Scholar, Sarafan ChEM-H
- Director, Microbiome Therapies Initiative (MITI)
- Member, Stanford Cancer Institute

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

The microbiome carries out extraordinary feats of biology: it produces hundreds of molecules, many of which impact host physiology; modulates immune function potently and specifically; self-organizes biogeographically; and exhibits profound stability in the face of perturbations. Our lab studies the mechanisms of microbiome-host interactions. Our approach is based on two technologies we recently developed: a complex (119-member) defined gut community that serves as an analytically manageable but biologically relevant system for experimentation, and new genetic systems for common species from the microbiome. Using these systems, we investigate mechanisms at the community level and the strain level.

1) Community-level mechanisms. A typical gut microbiome consists of 200-250 bacterial species that span >6 orders of magnitude in relative abundance. As a system, these bacteria carry out extraordinary feats of metabolite consumption and production, elicit a variety of specific immune cell populations, self-organize geographically and metabolically, and exhibit profound resilience against a wide range of perturbations. Yet remarkably little is known about how the community functions as a system. We are exploring this by asking two broad questions: How do groups of organisms work together to influence immune function? What are the mechanisms that govern metabolism and ecology at the 100+ strain scale? Our goal is to learn rules that will enable us to design communities that solve specific therapeutic problems.

2) Strain-level mechanisms. Even though gut and skin colonists live in communities, individual strains can have an extraordinary impact on host biology. We focus on two broad (and partially overlapping) categories:

Immune modulation: Can we redirect colonist-specific T cells against an antigen of interest by expressing it on the surface of a bacterium? How do skin colonists induce high levels of Staphylococcus-specific antibodies in mice and humans?

Abundant microbiome-derived molecules: By constructing single-strain/single-gene knockouts in a complex defined community, we will ask: What are the effects of bacterially produced molecules on host metabolism and immunology? Can the molecular output of low-abundance organisms impact host physiology?

3) Cell and gene therapy. We have begun two new efforts in mammalian cell and gene therapies. First, we are developing methods that enable cell-type specific delivery of genome editing payloads in vivo. We are especially interested in delivery vehicles that are customizable and easy to manufacture. Second, we have begun a comprehensive genome mining effort with an emphasis on understudied or entirely novel enzyme systems with utility in mammalian genome editing.

CLINICAL TRIALS

- Use of A Complex Gut Bacterial Consortium (MITI 001) for the Treatment of Irritable Bowel Syndrome With Diarrhea, Recruiting

Teaching

COURSES

2026-27

- Problem choice and decision trees in science and engineering: BIOE 395 (Spr)
- Systems Physiology and Design: BIOE 103 (Spr)

2025-26

- Problem choice and decision trees in science and engineering: BIOE 395 (Spr)
- Systems Physiology and Design: BIOE 103 (Spr)

2024-25

- Problem choice and decision trees in science and engineering: BIOE 395 (Spr)
- Systems Physiology and Design: BIOE 103 (Spr)

2023-24

- Problem choice and decision trees in science and engineering: BIOE 395 (Spr)
- Systems Physiology and Design: BIOE 103 (Spr)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Kylie Burdsall, Ryan Kong, Colin Raposo

Postdoctoral Faculty Sponsor

Kate Bauman, Amina Jbara, Raj Sajjath, Xianfeng Zeng

Doctoral Dissertation Advisor (AC)

Sriya Chitti, Pranav Lalgudi, David Li

Master's Program Advisor

Mathilde Esteves, Vanessa Garlepp, Renata Hemstreet, Max Kemper, Xuan Liu, Adarsh Nallapa, Daniel Ramos Mejia, Alex Ravel, Siena Rodeschin,

Ariana Rodrigues, Brian Ross, Michelle Simon, Sankalpa Venkatraghavan, Hanwen Yan, Zhenhao Yan, Keyi Yu, Jordan Zhang, Veronica Zhang

Doctoral (Program)

Xiaowei Zhang, Kyle Zolkin

Publications

PUBLICATIONS

- **Antigen-specific activation of gut immune cells drives autoimmune neuroinflammation.** *Gut microbes*
  Siewert, L. K., Berve, K., Pössnecker, E., Dyckow, J., Zulji, A., Baumann, R., Munoz-Blazquez, A., Krishnamoorthy, G., Schreiner, D., Sagan, S., Nelson, C., Sabatino, J. J., Nagashima, et al
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- **Gut microbial composition modulates food-specific CD4+T cells in food allergy**
  Weingarden, A., Dahlberg, F., Broude, C., Meng, X., Jain, S., Weakley, A., Cabrera, A., Dileepan, T., Fischbach, M., Jenkins, M.
  OXFORD UNIV PRESS.2026

- **Gut microbe-derived short-chain fatty acids regulate alphavirus arthritis and macrophage activation in mice.** *The Journal of clinical investigation*
  Zhao, F. R., Kleverov, M., Winkler, E. S., Williams, R. B., Janova, H., Droit, L., Wang, L., Li, T. T., Heath, L., Jung, A., Mack, M., Baldridge, M. T., Stappenbeck, et al
  2026; 136 (14)

- **Gut microbial composition modulates endogenous food-specific CD4+ T cells in food allergy.** *Journal of immunology (Baltimore, Md. : 1950)*
  Weingarden, A. R., Dahlberg, F. S., Broude, C. N., Meng, X., Jain, S., Weakley, A. M., Cabrera, A. V., Dileepan, T., Fischbach, M. A., Jenkins, M. K.
  2026; 215 (7)

- **A single-strain dropout screen reveals mechanistic links between microbial ecology and metabolism.** *bioRxiv : the preprint server for biology*
  Zeng, X., Meng, X., Weakley, A. M., Higginbottom, S., Lopez, E. M., Cabrera, A. V., Gray, I. J., DeFelice, B. C., Terasaki, M., Zhao, A., Hall, K. R., Levia, M., Arreola, et al
  2026

- **Ecology and engineering to modify the bile acid output of a defined microbial community.** *bioRxiv : the preprint server for biology*
  Zeng, X., Meng, X., Weakley, A. M., Jarrett, K. E., Higginbottom, S., Lopez, E. M., Cabrera, A. V., Gray, I. J., DeFelice, B. C., Terasaki, M., Lai, R., Brearley-Sholto, M., Zhao, et al
  2026

- **Identification and characterization of dietary antigens in oral tolerance.** *Science immunology*
  Blum, J. E., Kong, R., Schulman, E. A., Chen, F. M., Upadhyay, R., Romero-Meza, G., Littman, D. R., Fischbach, M. A., Nagashima, K., Sattely, E. S.
  2026; 11 (117): eaeb4684

- **Gut microbiota gate host exposure to cholinesterase inhibitors from dietary Solanums.** *bioRxiv : the preprint server for biology*
  Liou, C. S., Louwies, T., Iakiviak, M., Rajniak, J., Murugkar, P. P., Higginbottom, S. K., Weakley, A., Meng, X., Htet, P., Cabrera, A. V., Jasper, M., Dimas, A., Schulman, et al

2025

- **gutSMASH 2.0: extended identification of primary metabolic gene clusters from the human gut microbiota.** *Journal of molecular biology*
  Zhu, Y., Augustijn, H. E., Andreu, V. P., Draisma, A., van Wezel, G. P., Dodd, D., Fischbach, M. A., Medema, M. H.
  2025: 169567
- **A shift in gut microbial community alters antigen-specific regulatory T cells and disease phenotype in a model of food allergy**
  Weingarden, A., Dahlberg, F., Broude, C., Fischbach, M.
  OXFORD UNIV PRESS.2025
- **Systematic identification and characterization of regulators of aryl hydrocarbon receptor signaling.** *bioRxiv : the preprint server for biology*
  Verma, M., Desai, K., Ding, Y., Wang, X., Bae, M., Rakoff-Nahoum, S., Balskus, E. P., Fischbach, M. A., Jost, M.
  2025
- **Microbiota and kidney disease: the road ahead.** *Nature reviews. Nephrology*
  Bloom, P. P., Garrett, W. S., Penniston, K. L., Winkler, M. H., Hazen, S. L., Agudelo, J., Suryavanshi, M., Babiker, A., Dodd, D., Fischbach, M. A., Huang, K. C., Huttenhower, C., Joe, et al
  2025
- **Publisher Correction: Skin autonomous antibody production regulates host-microbiota interactions.** *Nature*
  Gribonika, I., Band, V. I., Chi, L., Perez-Chaparro, P. J., Link, V. M., Ansaldo, E., Oguz, C., Bousbaine, D., Fischbach, M. A., Belkaid, Y.
  2025
- **A gut pathobiont regulates circulating glycine and host metabolism in a twin study comparing vegan and omnivorous diets.** *medRxiv : the preprint server for health sciences*
  Carter, M. M., Zeng, X., Ward, C. P., Landry, M., Perelman, D., Hennings, T., Meng, X., Weakley, A. M., Cabrera, A. V., Robinson, J. L., Nguyen, T., Higginbottom, S., Maecker, et al
  2025
- **Discovery and engineering of the antibody response to a prominent skin commensal.** *Nature*
  Bousbaine, D., Bauman, K. D., Chen, Y. E., Lalgudi, P. V., Nguyen, T. T., Swenson, J. M., Yu, V. K., Tsang, E., Conlan, S., Li, D. B., Jbara, A., Zhao, A., Naziripour, et al
  2024
- **Skin autonomous antibody production regulates host-microbiota interactions.** *Nature*
  Gribonika, I., Band, V. I., Chi, L., Perez-Chaparro, P. J., Link, V. M., Ansaldo, E., Oguz, C., Bousbaine, D., Fischbach, M. A., Belkaid, Y.
  2024
- **PTER is a N-acetyltaurine hydrolase that regulates feeding and obesity.** *Nature*
  Wei, W., Lyu, X., Markhard, A. L., Fu, S., Mardjuki, R. E., Cavanagh, P. E., Zeng, X., Rajniak, J., Lu, N., Xiao, S., Zhao, M., Moya-Garzon, M. D., Truong, et al
  2024
- **Gut microbe-generated phenylacetylglutamine is an endogenous allosteric modulator of β2-adrenergic receptors.** *Nature communications*
  Saha, P. P., Gogonea, V., Sweet, W., Mohan, M. L., Singh, K. D., Anderson, J. T., Mallela, D., Witherow, C., Kar, N., Stenson, K., Harford, T., Fischbach, M. A., Brown, et al
  2024; 15 (1): 6696
- **Discovery and characterization of dietary antigens in oral tolerance.** *bioRxiv : the preprint server for biology*
  Blum, J. E., Kong, R., Schulman, E. A., Chen, F. M., Upadhyay, R., Romero-Meza, G., Littman, D. R., Fischbach, M. A., Nagashima, K., Sattely, E. S.
  2024
- **Production of deoxycholic acid by low-abundant microbial species is associated with impaired glucose metabolism.** *Nature communications*
  Wahlström, A., Brumbaugh, A., Sjöland, W., Olsson, L., Wu, H., Henricsson, M., Lundqvist, A., Makki, K., Hazen, S. L., Bergström, G., Marschall, H. U., Fischbach, M. A., Bäckhed, et al
  2024; 15 (1): 4276
- **Comprehensive clinical and genetic analyses of circulating bile acids and their associations with diabetes and its indices.** *Diabetes*
  Choucair, I., Mallela, D. P., Hilser, J. R., Hartiala, J. A., Nemet, I., Gogonea, V., Li, L., Lusis, A. J., Fischbach, M. A., Tang, W. H., Allayee, H., Hazen, S. L.

2024

- **Problem choice and decision trees in science and engineering.** *Cell*
  Fischbach, M. A.
  2024; 187 (8): 1828-1833

- **A PTER-dependent pathway of taurine metabolism linked to energy balance.** *bioRxiv : the preprint server for biology*
  Wei, W., Lyu, X., Markhard, A. L., Fu, S., Mardjuki, R. E., Cavanagh, P. E., Zeng, X., Rajniak, J., Lu, N., Xiao, S., Zhao, M., Moya-Garzon, M. D., Truong, et al
  2024

- **Prognostic Value of Gut Microbe-Generated Metabolite Phenylacetylglutamine in Patients with Heart Failure.** *European journal of heart failure*
  Tang, W. H., Nemet, I., Li, X. S., Wu, Y., Haghikia, A., Witkowski, M., Koeth, R. A., Demuth, I., König, M., Steinhagen-Thiessen, E., Bäckhed, F., Fischbach, M. A., Deb, et al
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- **Microbe-derived uremic solutes enhance thrombosis potential in the host.** *mBio*
  Nemet, I., Funabashi, M., Li, X. S., Dwidar, M., Sangwan, N., Skye, S. M., Romano, K. A., Cajka, T., Needham, B. D., Mazmanian, S. K., Hajjar, A. M., Rey, F. E., Fiehn, et al
  2023: e0133123

- **Microbial triggering of myelin-specific immune cells in the gut drives central nervous system inflammation**
  Siewert, L., Poessnecker, E., Dyckow, J., Baumann, R., Zulji, A., Schreiner, D., Sagan, S., Bosch, F., Wettig, A., Kogl, E., Modabber, M., Dhungel, B., Sabatino, et al
  SAGE PUBLICATIONS LTD.2023: 819-820

- **Identification of human skin microbiome odorants that manipulate mosquito landing behavior.** *bioRxiv : the preprint server for biology*
  Coutinho-Abreu, I. V., Jamshidi, O., Raban, R., Atabakhsh, K., Merriman, J. A., Fischbach, M. A., Akbari, O. S.
  2023

- **Mapping the T cell repertoire to a complex gut bacterial community.** *Nature*
  Nagashima, K., Zhao, A., Atabakhsh, K., Bae, M., Blum, J. E., Weakley, A., Jain, S., Meng, X., Cheng, A. G., Wang, M., Higginbottom, S., Dimas, A., Murugkar, et al
  2023

- **Strain dropouts reveal interactions that govern the metabolic output of the gut microbiome.** *Cell*
  Wang, M., Osborn, L. J., Jain, S., Meng, X., Weakley, A., Yan, J., Massey, W. J., Varadharajan, V., Horak, A., Banerjee, R., Allende, D. S., Chan, E. R., Hajjar, et al
  2023; 186 (13): 2839-2852.e21

- **Atlas of gut microbe-derived products from aromatic amino acids and risk of cardiovascular morbidity and mortality.** *European heart journal*
  Nemet, I., Li, X. S., Haghikia, A., Li, L., Wilcox, J., Romano, K. A., Buffa, J. A., Witkowski, M., Demuth, I., König, M., Steinhagen-Thiessen, E., Bäckhed, F., Fischbach, et al
  2023

- **Deciphering the crosstalk between skin commensals and the immune system.**
  Bouladoux, N., Chen, Y., Fischbach, M. A., Belkaid, Y.
  AMER ASSOC IMMUNOLOGISTS.2023

- **Mapping the T cell repertoire to a complex defined gut bacterial community**
  Nagashima, K., Fischbach, M. A.
  AMER ASSOC IMMUNOLOGISTS.2023

- **Engineered skin bacteria induce antitumor T cell responses against melanoma.** *Science (New York, N.Y.)*
  Chen, Y. E., Bousbaine, D., Veinbachs, A., Atabakhsh, K., Dimas, A., Yu, V. K., Zhao, A., Enright, N. J., Nagashima, K., Belkaid, Y., Fischbach, M. A.
  2023; 380 (6641): 203-210

- **gutSMASH predicts specialized primary metabolic pathways from the human gut microbiota.** *Nature biotechnology*
  Pascal Andreu, V., Augustijn, H. E., Chen, L., Zhernakova, A., Fu, J., Fischbach, M. A., Dodd, D., Medema, M. H.
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- **Host-microbe co-metabolism via MCAD generates circulating metabolites including hippuric acid.** *Nature communications*
  Pruss, K. M., Chen, H., Liu, Y., Van Treuren, W., Higginbottom, S. K., Jarman, J. B., Fischer, C. R., Mak, J., Wong, B., Cowan, T. M., Fischbach, M. A., Sonnenburg, J. L., Dodd, et al
  2023; 14 (1): 512

- **Retroviral Infection and Commensal Bacteria Dependently Alter the Metabolomic Profile in a Sterile Organ.** *Viruses*
  Spring, J., Beilinson, V., DeFelice, B. C., Sanchez, J. M., Fischbach, M., Chervonsky, A., Golovkina, T.
  2023; 15 (2)

- **A Limited Effect of Chronic Renal Insufficiency on the Colon Microbiome.** *Journal of the American Society of Nephrology : JASN*
  Guthrie, L., Sonnenburg, J. L., Fischbach, M. A., Meyer, T. W.
  2023

- **Two distinct gut microbial pathways contribute to meta-organismal production of phenylacetylglutamine with links to cardiovascular disease.** *Cell host & microbe*
  Zhu, Y., Dwidar, M., Nemet, I., Buffa, J. A., Sangwan, N., Li, X. S., Anderson, J. T., Romano, K. A., Fu, X., Funabashi, M., Wang, Z., Keranahalli, P., Battle, et al
  2022

- **Bacteroides thetaiotaomicron rough-type lipopolysaccharide: The chemical structure and the immunological activity** *CARBOHYDRATE POLYMERS*
  Pither, M., Illiano, A., Pagliuca, C., Jacobson, A., Mantova, G., Stornaiuolo, A., Colicchio, R., Vitiello, M., Pinto, G., Silipo, A., Fischbach, M. A., Salvatore, P., Amoresano, et al
  2022; 297: 120040

- **Gut commensal bacteria enhance pathogenesis of a tumorigenic murine retrovirus.** *Cell reports*
  Spring, J., Khan, A. A., Lara, S., O'Grady, K., Wilks, J., Gurbuxani, S., Erickson, S., Fischbach, M., Jacobson, A., Chervonsky, A., Golovkina, T.
  2022; 40 (11): 111341

- **Design, construction, and invivo augmentation of a complex gut microbiome.** *Cell*
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  2022

- **Gut Microbe-derived Short-Chain Fatty Acids Regulate Arthritis and Myositis During Chikungunya Virus Infection**
  Zhao, F. R., Winkler, E., Guo, C., Williams, R. B., Wang, L., Jung, A., Droit, L., Heath, L., Li, T., Mack, M., Baldridge, M. T., Stappenbeck, T. S., Thackray, et al
  WILEY.2022: 4325-4326

- **Impact of a 7-day homogeneous diet on interpersonal variation in human gut microbiomes and metabolomes.** *Cell host & microbe*
  Guthrie, L., Spencer, S. P., Perelman, D., Van Treuren, W., Han, S., Yu, F. B., Sonnenburg, E. D., Fischbach, M. A., Meyer, T. W., Sonnenburg, J. L.
  2022

- **A gut-derived metabolite alters brain activity and anxiety behaviour in mice.** *Nature*
  Needham, B. D., Funabashi, M., Adame, M. D., Wang, Z., Boktor, J. C., Haney, J., Wu, W., Rabut, C., Ladinsky, M. S., Hwang, S., Guo, Y., Zhu, Q., Griffiths, et al
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- **Novel bile acid biosynthetic pathways are enriched in the microbiome of centenarians.** *Nature*
  Sato, Y., Atarashi, K., Plichta, D. R., Arai, Y., Sasajima, S., Kearney, S. M., Suda, W., Takeshita, K., Sasaki, T., Okamoto, S., Skelly, A. N., Okamura, Y., Vlamakis, et al
  2021

- **Metagenomic compendium of 189,680 DNA viruses from the human gut microbiome.** *Nature microbiology*
  Nayfach, S., Paez-Espino, D., Call, L., Low, S. J., Sberro, H., Ivanova, N. N., Proal, A. D., Fischbach, M. A., Bhatt, A. S., Hugenholtz, P., Kyrpides, N. C.
  2021

- **Gut microbes impact stroke severity via the trimethylamine N-oxide pathway.** *Cell host & microbe*
  Zhu, W., Romano, K. A., Li, L., Buffa, J. A., Sangwan, N., Prakash, P., Tittle, A. N., Li, X. S., Fu, X., Androjna, C., DiDonato, A. J., Brinson, K., Trapp, et al

2021

- **The gutSMASH web server:automated identification of primary metabolic gene clusters from the gut microbiota.** *Nucleic acids research*
  Pascal Andreu, V., Roel-Touris, J., Dodd, D., Fischbach, M. A., Medema, M. H.
  2021
- **CRISPR-based functional genomics in human dendritic cells.** *eLife*
  Jost, M., Jacobson, A. N., Hussmann, J. A., Cirolia, G., Fischbach, M. A., Weissman, J. S.
  2021; 10
- **A method for detection of SARS-CoV-2 RNA in healthy human stool: a validation study.** *The Lancet. Microbe*
  Coryell, M. P., Iakiviak, M., Pereira, N., Murugkar, P. P., Rippe, J., Williams, D. B., Heald-Sargent, T., Sanchez-Pinto, L. N., Chavez, J., Hastie, J. L., Sava, R. L., Lien, C. Z., Wang, et al
  2021
- **Role of dietary fiber in the recovery of the human gut microbiome and its metabolome.** *Cell host & microbe*
  Tanes, C., Bittinger, K., Gao, Y., Friedman, E. S., Nessel, L., Paladhi, U. R., Chau, L., Panfen, E., Fischbach, M. A., Braun, J., Xavier, R. J., Clish, C. B., Li, et al
  2021
- **A metabolomics pipeline for the mechanistic interrogation of the gut microbiome.** *Nature*
  Han, S., Van Treuren, W., Fischer, C. R., Merrill, B. D., DeFelice, B. C., Sanchez, J. M., Higginbottom, S. K., Guthrie, L., Fall, L. A., Dodd, D., Fischbach, M. A., Sonnenburg, J. L.
  2021; 595 (7867): 415-420
- **Endogenous retroviruses promote homeostatic and inflammatory responses to the microbiota.** *Cell*
  Lima-Junior, D. S., Krishnamurthy, S. R., Bouladoux, N., Collins, N., Han, S. J., Chen, E. Y., Constantinides, M. G., Link, V. M., Lim, A. I., Enamorado, M., Cataisson, C., Gil, L., Rao, et al
  2021
- **BiG-MAP: an Automated Pipeline To Profile Metabolic Gene Cluster Abundance and Expression in Microbiomes.** *mSystems*
  Pascal Andreu, V., Augustijn, H. E., van den Berg, K., van der Hooft, J. J., Fischbach, M. A., Medema, M. H.
  2021: e0093721
- **Bacterially Derived Tryptamine Increases Mucus Release by Activating a Host Receptor in a Mouse Model of Inflammatory Bowel Disease.** *iScience*
  Bhattarai, Y., Jie, S., Linden, D. R., Ghatak, S., Mars, R. A., Williams, B. B., Pu, M., Sonnenburg, J. L., Fischbach, M. A., Farrugia, G., Sha, L., Kashyap, P. C.
  2020; 23 (12): 101798
- **A Cutibacterium acnes antibiotic modulates human skin microbiota composition in hair follicles.** *Science translational medicine*
  Claesen, J., Spagnolo, J. B., Ramos, S. F., Kurita, K. L., Byrd, A. L., Aksenov, A. A., Melnik, A. V., Wong, W. R., Wang, S., Hernandez, R. D., Donia, M. S., Dorrestein, P. C., Kong, et al
  2020; 12 (570)
- **Bifidobacterium alters the gut microbiota and modulates the functional metabolism of T regulatory cells in the context of immune checkpoint blockade.** *Proceedings of the National Academy of Sciences of the United States of America*
  Sun, S., Luo, L., Liang, W., Yin, Q., Guo, J., Rush, A. M., Lv, Z., Liang, Q., Fischbach, M. A., Sonnenburg, J. L., Dodd, D., Davis, M. M., Wang, et al
  2020
- **Computational genomic discovery of diverse gene clusters harbouring Fe-S flavoenzymes in anaerobic gut microbiota.** *Microbial genomics*
  Pascal Andreu, V., Fischbach, M. A., Medema, M. H.
  2020
- **MAIT cells are imprinted by the microbiota in early life and promote tissue repair**
  Constantinides, M. G., Link, V. M., Tamoutounour, S., Wong, A. C., Perez-Chaparro, P., Han, S., Chen, Y., Li, K., Farhat, S., Weckel, A., Krishnamurthy, S. R., Vujkovic-Cvijin, I., Linehan, et al
  AMER ASSOC IMMUNOLOGISTS.2020
- **Bile acid metabolites control Th17 and Treg cell differentiation**
  Hang, S., Paik, D., Yao, L., Jamma, T., Lu, J., Ha, S., Nelson, B. N., Kelly, S. P., Wu, L., Zheng, Y., Longman, R. S., Rastinejad, F., Devlin, et al

AMER ASSOC IMMUNOLOGISTS.2020

- **Dysbiosis-Induced Secondary Bile Acid Deficiency Promotes Intestinal Inflammation.** *Cell host & microbe*
  Sinha, S. R., Haileselassie, Y., Nguyen, L. P., Tropini, C., Wang, M., Becker, L. S., Sim, D., Jarr, K., Spear, E. T., Singh, G., Namkoong, H., Bittinger, K., Fischbach, et al
  2020
- **Michael Fischbach: Homing in on the molecules from microbes** *NATURE*
  Scott, A., Fischbach, M.
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- **Michael Fischbach: Homing in on the molecules from microbes** *NATURE*
  Scott, A., Fischbach, M.
  2020; 577 (7792): S9
- **Bile acids profile, histopathological indices and genetic variants for non-alcoholic fatty liver disease progression.** *Metabolism: clinical and experimental*
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