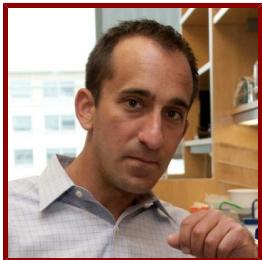


# Stanford

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## Michael Fischbach

Liu (Liao) Family Professor  
Bioengineering

### Bio

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#### 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 Lucille 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 Kelonia and Revolution Medicines, a member of the scientific advisory boards of the Chan Zuckerberg Initiative, NGM Biopharmaceuticals, 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

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#### 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.

## **Teaching**

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### **COURSES**

#### **2023-24**

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

#### **2022-23**

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

#### **2021-22**

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

#### **2020-21**

- 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)**

Kaisha Benjamin, Alex Soohoo

#### **Postdoctoral Faculty Sponsor**

Kate Bauman, Djenet Bousbaine, Gabriel Filsinger, Amina Jbara, Nathan Johns, Martin McLaughlin, Xianfeng Zeng, Aishan Zhao

**Doctoral Dissertation Advisor (AC)**

Sriya Chitti, Elliot Hershberg

**Undergraduate Major Advisor**

Raina Talwar Bhatia, Claudia Zimmerman

**Doctoral (Program)**

Elliot Hershberg, Charlie Jiang, Andrew Setiadi, Yifan Sun, Jerry Yan, Xiaowei Zhang, Kyle Zolkin

## Publications

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### PUBLICATIONS

● **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

2023

● **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. 2023

● **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*

Cheng, A. G., Ho, P., Aranda-Diaz, A., Jain, S., Yu, F. B., Meng, X., Wang, M., Iakiviak, M., Nagashima, K., Zhao, A., Murugkar, P., Patil, A., Atabakhsh, et al 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 2022

● **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., Hugenholz, 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

● **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., Aksенov, 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.  
2020; 577 (7792): S9

● **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*

Nimer, N. n., Choucair, I. n., Wang, Z. n., Nemet, I. n., Li, L. n., Gukasyan, J. n., Weeks, T. L., Alkhouri, N. n., Zein, N. n., Tang, W. H., Fischbach, M. A., Brown, J. M., Allayee, et al  
2020: 154457

● **A Cardiovascular Disease-Linked Gut Microbial Metabolite Acts via Adrenergic Receptors.** *Cell*

Nemet, I. n., Saha, P. P., Gupta, N. n., Zhu, W. n., Romano, K. A., Skye, S. M., Cajka, T. n., Mohan, M. L., Li, L. n., Wu, Y. n., Funabashi, M. n., Ramer-Tait, A. E., Naga Prasad, et al  
2020; 180 (5): 862–77.e22

● **Characterization of Serine Hydrolases Across Clinical Isolates of Commensal Skin Bacteria *Staphylococcus epidermidis* Using Activity-Based Protein Profiling.** *ACS infectious diseases*

Keller, L. J., Lentz, C. S., Chen, Y. E., Metivier, R. J., Weerapana, E. n., Fischbach, M. A., Bogyo, M. n.  
2020

● **Author Correction: Bile acid metabolites control TH17 and Treg cell differentiation.** *Nature*

Hang, S. n., Paik, D. n., Yao, L. n., Kim, E. n., Trinath, J. n., Lu, J. n., Ha, S. n., Nelson, B. N., Kelly, S. P., Wu, L. n., Zheng, Y. n., Longman, R. S., Rastinejad, et al  
2020

● **Expansion of RiPP biosynthetic space through integration of pan-genomics and machine learning uncovers a novel class of lantibiotics.** *PLoS biology*

Kloosterman, A. M., Cimermancic, P. n., Elsayed, S. S., Du, C. n., Hadjithomas, M. n., Donia, M. S., Fischbach, M. A., van Wezel, G. P., Medema, M. H.  
2020; 18 (12): e3001026

● **A metabolic pathway for bile acid dehydroxylation by the gut microbiome.** *Nature*

Funabashi, M. n., Grove, T. L., Wang, M. n., Varma, Y. n., McFadden, M. E., Brown, L. C., Guo, C. n., Higginbottom, S. n., Almo, S. C., Fischbach, M. A.  
2020

● **Depletion of microbiome-derived molecules in the host using Clostridium genetics.** *Science (New York, N.Y.)*

Guo, C., Allen, B. M., Hiam, K. J., Dodd, D., Van Treuren, W., Higginbottom, S., Nagashima, K., Fischer, C. R., Sonnenburg, J. L., Spitzer, M. H., Fischbach, M. A.  
2019; 366 (6471)

● **Quantification of bile acids: A mass spectrometry platform for studying gut microbiome connection to metabolic diseases.** *Journal of lipid research*

Choucair, I., Nemet, I., Li, L., Cole, M. A., Skye, S. M., Kirson, J. D., Fischbach, M., Gogonea, V., Brown, J. M., Tang, W. H., Hazen, S. L.  
2019

● **Bile acid metabolites control TH17 and Treg cell differentiation.** *Nature*

Hang, S. n., Paik, D. n., Yao, L. n., Kim, E. n., Jamma, T. n., Lu, J. n., Ha, S. n., Nelson, B. N., Kelly, S. P., Wu, L. n., Zheng, Y. n., Longman, R. S., Rastinejad, et al

2019

● **MAIT cells are imprinted by the microbiota in early life and promote tissue repair.** *Science (New York, N.Y.)*

Constantinides, M. G., Link, V. M., Tamoutounour, S., Wong, A. C., Perez-Chaparro, P. J., Han, S., Chen, Y. E., Li, K., Farhat, S., Weckel, A., Krishnamurthy, S. R., Vujkovic-Cvijin, I., Linehan, et al  
2019; 366 (6464)

● **Recovery of the Gut Microbiota after Antibiotics Depends on Host Diet, Community Context, and Environmental Reservoirs.** *Cell host & microbe*

Ng, K. M., Aranda-Díaz, A. n., Tropini, C. n., Frankel, M. R., Van Treuren, W. n., O'Laughlin, C. T., Merrill, B. D., Yu, F. B., Pruss, K. M., Oliveira, R. A., Higginbottom, S. K., Neff, N. F., Fischbach, et al  
2019; 26 (5): 650–65.e4

● **Microbial Transplantation With Human Gut Commensals Containing CutC Is Sufficient to Transmit Enhanced Platelet Reactivity and Thrombosis Potential.** *Circulation research*

Skye, S. M., Zhu, W., Romano, K. A., Guo, C., Wang, Z., Jia, X., Kirsop, J., Haag, B., Lang, J. M., DiDonato, J. A., Tang, W. H., Lusis, A. J., Rey, et al  
2018; 123 (10): 1164–76

● **Microbial Transplantation With Human Gut Commensals Containing CutC Is Sufficient to Transmit Enhanced Platelet Reactivity and Thrombosis Potential** *CIRCULATION RESEARCH*

Skye, S. M., Zhu, W., Romano, K. A., Guo, C., Wang, Z., Jia, X., Kirsop, J., Haag, B., Lang, J. M., DiDonato, J. A., Tang, W., Lusis, A. J., Rey, et al  
2018; 123 (10): 1164–76

● **Microbiome: Focus on Causation and Mechanism.** *Cell*

Fischbach, M. A.  
2018; 174 (4): 785–90

● **Microbiome: Focus on Causation and Mechanism** *CELL*

Fischbach, M. A.  
2018; 174 (4): 785–90

● **Mapping the Genetic Landscape of Human Cells** *CELL*

Horlbeck, M. A., Xu, A., Wang, M., Bennett, N. K., Park, C. Y., Bogdanoff, D., Adamson, B., Chow, E. D., Kampmann, M., Peterson, T. R., Nakamura, K., Fischbach, M. A., Weissman, et al  
2018; 174 (4): 953–+

● **Gut Microbiota-Produced Tryptamine Activates an Epithelial G-Protein-Coupled Receptor to Increase Colonic Secretion** *CELL HOST & MICROBE*

Bhattarai, Y., Williams, B. B., Battaglioli, E. J., Whitaker, W. R., Till, L., Grover, M., Linden, D. R., Akiba, Y., Kandimalla, K. K., Zachos, N. C., Kaunitz, J. D., Sonnenburg, J. L., Fischbach, et al  
2018; 23 (6): 775–+

● **Contextual control of skin immunity and inflammation by Corynebacterium.** *The Journal of experimental medicine*

Ridaura, V. K., Boulaudoux, N. n., Claesen, J. n., Chen, Y. E., Byrd, A. L., Constantinides, M. G., Merrill, E. D., Tamoutounour, S. n., Fischbach, M. A., Belkaid, Y. n.  
2018; 215 (3): 785–99

● **A Pressure Test to Make 10 Molecules in 90 Days: External Evaluation of Methods to Engineer Biology.** *Journal of the American Chemical Society*

Casini, A. n., Chang, F. Y., Eluere, R. n., King, A. M., Young, E. M., Dudley, Q. M., Karim, A. n., Pratt, K. n., Bristol, C. n., Forget, A. n., Ghodasara, A. n., Warden-Rothman, R. n., Gan, et al  
2018

● **The Biosynthesis of Lipooligosaccharide from Bacteroides thetaiotaomicron.** *mBio*

Jacobson, A. N., Choudhury, B. P., Fischbach, M. A.  
2018; 9 (2)

● **Skin microbiota-host interactions.** *Nature*

Chen, Y. E., Fischbach, M. A., Belkaid, Y. n.  
2018; 553 (7689): 427–36

● **Discovery of Reactive Microbiota-Derived Metabolites that Inhibit Host Proteases** *CELL*

Guo, C., Chang, F., Wyche, T. P., Backus, K. M., Acker, T. M., Funabashi, M., Taketani, M., Donia, M. S., Nayfach, S., Pollard, K. S., Craik, C. S., Cravatt, B. F., Clardy, et al

2017; 168 (3): 517-?

● **A gut bacterial pathway metabolizes aromatic amino acids into nine circulating metabolites.** *Nature*

Dodd, D. n., Spitzer, M. H., Van Treuren, W. n., Merrill, B. D., Hryckowian, A. J., Higginbottom, S. K., Le, A. n., Cowan, T. M., Nolan, G. P., Fischbach, M. A., Sonnenburg, J. L.

2017; 551 (7682): 648-52

● **Modulation of a Circulating Uremic Solute via Rational Genetic Manipulation of the Gut Microbiota** *CELL HOST & MICROBE*

Devlin, A. S., Marcabal, A., Dodd, D., Nayfach, S., Plummer, N., Meyer, T., Pollard, K. S., Sonnenburg, J. L., Fischbach, M. A.

2016; 20 (6): 709-715

● **Signaling in Host-Associated Microbial Communities** *CELL*

Fischbach, M. A., Segre, J. A.

2016; 164 (6): 1288-1300

● **Synthetic biology to access and expand nature's chemical diversity** *NATURE REVIEWS MICROBIOLOGY*

Smanski, M. J., Zhou, H., Claesen, J., Shen, B., Fischbach, M. A., Voigt, C. A.

2016; 14 (3): 135-149

● **A Wave of Regulatory T Cells into Neonatal Skin Mediates Tolerance to Commensal Microbes** *IMMUNITY*

Scharschmidt, T. C., Vasquez, K. S., Truong, H., Gearty, S. V., Pauli, M. L., Nosbaum, A., Gratz, I. K., Otto, M., Moon, J. J., Liese, J., Abbas, A. K., Fischbach, M. A., Rosenblum, et al

2015; 43 (5): 1011-1021

● **MetaQuery: a web server for rapid annotation and quantitative analysis of specific genes in the human gut microbiome** *BIOINFORMATICS*

Nayfach, S., Fischbach, M. A., Pollard, K. S.

2015; 31 (20): 3368-3370

● **Mammalian Lipopolysaccharide Receptors Incorporated into the Retroviral Envelope Augment Virus Transmission** *CELL HOST & MICROBE*

Wilks, J., Lien, E., Jacobson, A. N., Fischbach, M. A., Qureshi, N., Chervonsky, A. V., Golovkina, T. V.

2015; 18 (4): 456-462

● **Genome-Directed Lead Discovery: Biosynthesis, Structure Elucidation, and Biological Evaluation of Two Families of Polyene Macrolactams against Trypanosoma brucei** *ACS CHEMICAL BIOLOGY*

Schulze, C. J., Donia, M. S., Siqueira-Neto, J. L., Ray, D., Raskatov, J. A., Green, R. E., McKerrow, J. H., Fischbach, M. A., Linington, R. G.

2015; 10 (10): 2373-2381

● **Computational approaches to natural product discovery** *NATURE CHEMICAL BIOLOGY*

Medema, M. H., Fischbach, M. A.

2015; 11 (9): 639-648

● **A biosynthetic pathway for a prominent class of microbiota-derived bile acids** *NATURE CHEMICAL BIOLOGY*

Devlin, A. S., Fischbach, M. A.

2015; 11 (9): 685-?

● **A Phase-Variable Surface Layer from the Gut Symbiont Bacteroides thetaiotaomicron** *MBIO*

Taketani, M., Donia, M. S., Jacobson, A. N., Lambris, J. D., Fischbach, M. A.

2015; 6 (5)

● **Minimum Information about a Biosynthetic Gene cluster** *NATURE CHEMICAL BIOLOGY*

Medema, M. H., Kottmann, R., Yilmaz, P., Cummings, M., Biggins, J. B., Blin, K., de Bruijn, I., Chooi, Y. H., Claesen, J., Coates, R. C., Cruz-Morales, P., Duddela, S., Duesterhus, et al

2015; 11 (9): 625-631

● **HUMAN MICROBIOTA. Small molecules from the human microbiota.** *Science*

Donia, M. S., Fischbach, M. A.

2015; 349 (6246)

● **IMG-ABC: A Knowledge Base To Fuel Discovery of Biosynthetic Gene Clusters and Novel Secondary Metabolites** *MBIO*

Hadjithomas, M., Chen, I. A., Chu, K., Ratner, A., Palaniappan, K., Szeto, E., Huang, J., Reddy, T. B., Cimermancic, P., Fischbach, M. A., Ivanova, N. N., Markowitz, V. M., Kyripies, et al

2015; 6 (4)

● **antiSMASH 3.0-a comprehensive resource for the genome mining of biosynthetic gene clusters** *NUCLEIC ACIDS RESEARCH*

Weber, T., Blin, K., Duddela, S., Krug, D., Kim, H. U., Brucolieri, R., Lee, S. Y., Fischbach, M. A., Mueller, R., Wohlleben, W., Breitling, R., Takano, E., Medema, et al  
2015; 43 (W1): W237-W243

● **Synthetic Microbes As Drug Delivery Systems** *ACS SYNTHETIC BIOLOGY*

Claesen, J., Fischbach, M. A.  
2015; 4 (4): 358-364

● **A Systematic Computational Analysis of Biosynthetic Gene Cluster Evolution: Lessons for Engineering Biosynthesis** *PLOS COMPUTATIONAL BIOLOGY*

Medema, M. H., Cimermancic, P., Sali, A., Takano, E., Fischbach, M. A.  
2014; 10 (12)

● **Discovery and Characterization of Gut Microbiota Decarboxylases that Can Produce the Neurotransmitter Tryptamine** *CELL HOST & MICROBE*

Williams, B. B., Van Benschoten, A. H., Cimermancic, P., Donia, M. S., Zimmermann, M., Taketani, M., Ishihara, A., Kashyap, P. C., Fraser, J. S., Fischbach, M. A.  
2014; 16 (4): 495-503

● **A Systematic Analysis of Biosynthetic Gene Clusters in the Human Microbiome Reveals a Common Family of Antibiotics** *CELL*

Donia, M. S., Cimermancic, P., Schulze, C. J., Brown, L. C., Martin, J., Mitreva, M., Clardy, J., Linington, R. G., Fischbach, M. A.  
2014; 158 (6): 1402-1414

● **Insights into secondary metabolism from a global analysis of prokaryotic biosynthetic gene clusters.** *Cell*

Cimermancic, P., Medema, M. H., Claesen, J., Kurita, K., Wieland Brown, L. C., Mavrommatis, K., Pati, A., Godfrey, P. A., Koehrsen, M., Clardy, J., Birren, B. W., Takano, E., Sali, et al  
2014; 158 (2): 412-421

● **Propionibacterium-Produced Coproporphyrin III Induces Staphylococcus aureus Aggregation and Biofilm Formation** *MBIO*

Wollenberg, M. S., Claesen, J., Escapa, I. F., Aldridge, K. L., Fischbach, M. A., Lemon, K. P.  
2014; 5 (4)

● **Key applications of plant metabolic engineering.** *PLoS biology*

Lau, W., Fischbach, M. A., Osbourn, A., Sattely, E. S.  
2014; 12 (6): e1001879

● **Key applications of plant metabolic engineering.** *PLoS biology*

Lau, W., Fischbach, M. A., Osbourn, A., Sattely, E. S.  
2014; 12 (6)

● **The Prevalence of Species and Strains in the Human Microbiome: A Resource for Experimental Efforts** *PLOS ONE*

Kraal, L., Abubucker, S., Kota, K., Fischbach, M. A., Mitreva, M.  
2014; 9 (5)

● **Diet rapidly and reproducibly alters the human gut microbiome** *NATURE*

David, L. A., Maurice, C. F., Carmody, R. N., Gootenberg, D. B., Button, J. E., Wolfe, B. E., Ling, A. V., Devlin, A. S., Varma, Y., Fischbach, M. A., Biddinger, S. B., Dutton, R. J., Turnbaugh, et al  
2014; 505 (7484): 559-?

● **What Lives On Our Skin: Ecology, Genomics and Therapeutic Opportunities Of the Skin Microbiome.** *Drug discovery today. Disease mechanisms*

Schärschmidt, T. C., Fischbach, M. A.  
2013; 10 (3-4)

● **A metabolomic view of how the human gut microbiota impacts the host metabolome using humanized and gnotobiotic mice.** *ISME journal*

Marcabal, A., Kashyap, P. C., Nelson, T. A., Aronov, P. A., Donia, M. S., Spormann, A., Fischbach, M. A., Sonnenburg, J. L.  
2013; 7 (10): 1933-1943

● **Production of alpha-Galactosylceramide by a Prominent Member of the Human Gut Microbiota** *PLOS BIOLOGY*

Brown, L. C., Penaranda, C., Kashyap, P. C., Williams, B. B., Clardy, J., Kronenberg, M., Sonnenburg, J. L., Comstock, L. E., Bluestone, J. A., Fischbach, M. A.  
2013; 11 (7)

- **antiSMASH 2.0--a versatile platform for genome mining of secondary metabolite producers.** *Nucleic acids research*  
Blin, K., Medema, M. H., Kazempour, D., Fischbach, M. A., Breitling, R., Takano, E., Weber, T.  
2013; 41 (Web Server issue): W204-12
- **Production of a-galactosylceramide by a prominent member of the human gut microbiota.** *PLoS biology*  
Wieland Brown, L. C., Penaranda, C., Kashyap, P. C., Williams, B. B., Clardy, J., Kronenberg, M., Sonnenburg, J. L., Comstock, L. E., Bluestone, J. A., Fischbach, M. A.  
2013; 11 (7)
- **Cell-Based Therapeutics: The Next Pillar of Medicine** *SCIENCE TRANSLATIONAL MEDICINE*  
Fischbach, M. A., Bluestone, J. A., Lim, W. A.  
2013; 5 (179)
- **Trehalose Biosynthesis Promotes *Pseudomonas aeruginosa* Pathogenicity in Plants** *PLOS PATHOGENS*  
Djonovic, S., Urbach, J. M., Drenkard, E., Bush, J., Feinbaum, R., Ausubel, J. L., Traficante, D., Risech, M., Kocks, C., Fischbach, M. A., Priebe, G. P., Ausubel, F. M.  
2013; 9 (3)
- **Dyeing to Learn More about the Gut Microbiota** *CELL HOST & MICROBE*  
Donia, M. S., Fischbach, M. A.  
2013; 13 (2): 119-120
- **Ribosomally synthesized and post-translationally modified peptide natural products: overview and recommendations for a universal nomenclature.** *Natural product reports*  
Arnison, P. G., Bibb, M. J., Bierbaum, G., Bowers, A. A., Bugni, T. S., Bulaj, G., Camarero, J. A., Campopiano, D. J., Challis, G. L., Clardy, J., Cotter, P. D., Craik, D. J., Dawson, et al  
2013; 30 (1): 108-160
- **Molecular Analysis of Model Gut Microbiotas by Imaging Mass Spectrometry and Nanodesorption Electrospray Ionization Reveals Dietary Metabolite Transformations** *ANALYTICAL CHEMISTRY*  
Rath, C. M., Alexandrov, T., Higginbottom, S. K., Song, J., Milla, M. E., Fischbach, M. A., Sonnenburg, J. L., Dorrestein, P. C.  
2012; 84 (21): 9259-9267
- **Molecular Insights into the Biosynthesis of Guadinomine: A Type III Secretion System Inhibitor** *JOURNAL OF THE AMERICAN CHEMICAL SOCIETY*  
Holmes, T. C., May, A. E., Zaleta-Riyera, K., Ruby, J. G., Skewes-Cox, P., Fischbach, M. A., DeRisi, J. L., Iwatsuki, M., Omura, S., Khosla, C.  
2012; 134 (42): 17797-17806
- **Microbiota-Targeted Therapies: An Ecological Perspective** *SCIENCE TRANSLATIONAL MEDICINE*  
Lemon, K. P., Armitage, G. C., Relman, D. A., Fischbach, M. A.  
2012; 4 (137)
- **Production of an NKT cell stimulatory glycosphingolipid by a prominent member of the human gut microbiota**  
Penaranda, C., Brown, L., Kashyap, P., Clardy, J., Kronenberg, M., Sonnenburg, J., Comstock, L., Bluestone, J., Fischbach, M.  
AMER ASSOC IMMUNOLOGISTS.2012
- **A mass spectrometry-guided genome mining approach for natural product peptidogenomics** *NATURE CHEMICAL BIOLOGY*  
Kersten, R. D., Yang, Y., Xu, Y., Cimermancic, P., Nam, S., Fenical, W., Fischbach, M. A., Moore, B. S., Dorrestein, P. C.  
2011; 7 (11): 794-802
- **Eating For Two: How Metabolism Establishes Interspecies Interactions in the Gut** *CELL HOST & MICROBE*  
Fischbach, M. A., Sonnenburg, J. L.  
2011; 10 (4): 336-347
- **Combination therapies for combating antimicrobial resistance** *CURRENT OPINION IN MICROBIOLOGY*  
Fischbach, M. A.  
2011; 14 (5): 519-523
- **antiSMASH: rapid identification, annotation and analysis of secondary metabolite biosynthesis gene clusters in bacterial and fungal genome sequences** *NUCLEIC ACIDS RESEARCH*  
Medema, M. H., Blin, K., Cimermancic, P., de Jager, V., Zakrzewski, P., Fischbach, M. A., Weber, T., Takano, E., Breitling, R.

2011; 39: W339-W346

- **Community Health Care: Therapeutic Opportunities in the Human Microbiome** *SCIENCE TRANSLATIONAL MEDICINE*  
Sonnenburg, J. L., Fischbach, M. A.  
2011; 3 (78)
- **Draft Genome Sequence of *Streptomyces clavuligerus* NRRL 3585, a Producer of Diverse Secondary Metabolites** *JOURNAL OF BACTERIOLOGY*  
Song, J. Y., Jeong, H., Yu, D. S., Fischbach, M. A., Park, H., Kim, J. J., Seo, J., Jensen, S. E., Oh, T. K., Lee, K. J., Kim, J. F.  
2010; 192 (23): 6317-6318
- **A Family of Pyrazinone Natural Products from a Conserved Nonribosomal Peptide Synthetase in *Staphylococcus aureus*** *CHEMISTRY & BIOLOGY*  
Zimmermann, M., Fischbach, M. A.  
2010; 17 (9): 925-930
- **A Chromatin-Mediated Reversible Drug-Tolerant State in Cancer Cell Subpopulations** *CELL*  
Sharma, S. V., Lee, D. Y., Li, B., Quinlan, M. P., Takahashi, F., Maheswaran, S., McDermott, U., Azizian, N., Zou, L., Fischbach, M. A., Wong, K., Brandstetter, K., Witner, et al  
2010; 141 (1): 69-80
- **Natural Products Version 2.0: Connecting Genes to Molecules** *JOURNAL OF THE AMERICAN CHEMICAL SOCIETY*  
Walsh, C. T., Fischbach, M. A.  
2010; 132 (8): 2469-2493
- **Dapdiamides, Tripeptide Antibiotics Formed by Unconventional Amide Ligases** *JOURNAL OF NATURAL PRODUCTS*  
Dawlaty, J., Zhang, X., Fischbach, M. A., Clardy, J.  
2010; 73 (3): 441-446
- **The next frontier of systems biology: higher-order and interspecies interactions** *GENOME BIOLOGY*  
Fischbach, M. A., Krogan, N. J.  
2010; 11 (5)
- **Antibiotics from microbes: converging to kill** *CURRENT OPINION IN MICROBIOLOGY*  
Fischbach, M. A.  
2009; 12 (5): 520-527
- **Genome sequence and analysis of the Irish potato famine pathogen *Phytophthora infestans*** *NATURE*  
Haas, B. J., Kamoun, S., Zody, M. C., Jiang, R. H., Handsaker, R. E., Cano, L. M., Grabherr, M., Kodira, C. D., Raffaele, S., Torto-Alalibo, T., Bozkurt, T. O., Ah-Fong, A. M., Alvarado, et al  
2009; 461 (7262): 393-398
- **Antibiotics for Emerging Pathogens** *SCIENCE*  
Fischbach, M. A., Walsh, C. T.  
2009; 325 (5944): 1089-1093
- **New Ways to Squash Superbugs** *SCIENTIFIC AMERICAN*  
Walsh, C. T., Fischbach, M. A.  
2009; 301 (1): 44-51
- **The natural history of antibiotics** *CURRENT BIOLOGY*  
Clardy, J., Fischbach, M. A., Currie, C. R.  
2009; 19 (11): R437-R441
- **Thirteen posttranslational modifications convert a 14-residue peptide into the antibiotic thiocillin** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Brown, L. C., Acker, M. G., Clardy, J., Walsh, C. T., Fischbach, M. A.  
2009; 106 (8): 2549-2553
- **Repurposing libraries of eukaryotic protein kinase inhibitors for antibiotic discovery** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Walsh, C. T., Fischbach, M. A.  
2009; 106 (6): 1689-1690

- Structurally diverse natural products that cause potassium leakage trigger multicellularity in *Bacillus subtilis* *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Lopez, D., Fischbach, M. A., Chu, F., Losick, R., Kolter, R.  
2009; 106 (1): 280-285
- Total biosynthesis: in vitro reconstitution of polyketide and nonribosomal peptide pathways *NATURAL PRODUCT REPORTS*  
Sattely, E. S., Fischbach, M. A., Walsh, C. T.  
2008; 25 (4): 757-793
- Insights from the complete genome sequence of *Mycobacterium marinum* on the evolution of *Mycobacterium tuberculosis* *GENOME RESEARCH*  
Stinear, T. P., Seemann, T., Harrison, P. F., Jenkin, G. A., Davies, J. K., Johnson, P. D., Abdellah, Z., Arrowsmith, C., Chillingworth, T., Churcher, C., Clarke, K., Cronin, A., Davis, et al  
2008; 18 (5): 729-741
- The evolution of gene collectives: How natural selection drives chemical innovation *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Fischbach, M. A., Walsh, C. T., Clardy, J.  
2008; 105 (12): 4601-4608
- Inhibitors of sterol biosynthesis as *Staphylococcus aureus* antibiotics *ANGEWANDTE CHEMIE-INTERNATIONAL EDITION*  
Walsh, C. T., Fischbach, M. A.  
2008; 47 (31): 5700-5702
- Biosynthetic tailoring of microcin e492m: Post-translational modification affords an antibacterial siderophore-peptide conjugate *JOURNAL OF THE AMERICAN CHEMICAL SOCIETY*  
Nolan, E. M., Fischbach, M. A., Koglin, A., Walsh, C. T.  
2007; 129 (46): 14336-14347
- Directed evolution can rapidly improve the activity of chimeric assembly-line enzymes *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Fischbach, M. A., Lai, J. R., Roche, E. D., Walsh, C. T., Liu, D. R.  
2007; 104 (29): 11951-11956
- One pathway, many products *NATURE CHEMICAL BIOLOGY*  
Fischbach, M. A., Clardy, J.  
2007; 3 (7): 353-355
- The identification of bacillaene, the product of the PksX megacomplex in *Bacillus subtilis* *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Butcher, R. A., Schroeder, F. C., Fischbach, M. A., Straightt, P. D., Kolter, R., Walsh, C. T., Clardy, J.  
2007; 104 (5): 1506-1509
- A singular enzymatic megacomplex from *Bacillus subtilis* *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Straight, P. D., Fischbach, M. A., Walsh, C. T., Rudner, D. Z., Kolter, R.  
2007; 104 (1): 305-310
- New antibiotics from bacterial natural products *NATURE BIOTECHNOLOGY*  
Clardy, J., Fischbach, M. A., Walsh, C. T.  
2006; 24 (12): 1541-1550
- The pathogen-associated iroA gene cluster mediates bacterial evasion of lipocalin 2 *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Fischbach, M. A., Lin, H., Zhou, L., Yu, Y., Abergel, R. J., Liu, D. R., Raymond, K. N., Wanner, B. L., Strong, R. K., Walsh, C. T., Aderem, A., Smith, K. D.  
2006; 103 (44): 16502-16507
- Biochemistry - Directing biosynthesis *SCIENCE*  
Fischbach, M. A., Walsh, C. T.  
2006; 314 (5799): 603-605

- **Localized protein interaction surfaces on the EntB carrier protein revealed by combinatorial mutagenesis and selection** *JOURNAL OF THE AMERICAN CHEMICAL SOCIETY*  
Lai, J. R., Fischbach, M. A., Liu, D. R., Walsh, C. T.  
2006; 128 (34): 11002-11003
- **Structural characterization of enterobactin hydrolase IroE** *BIOCHEMISTRY*  
Larsen, N. A., Lin, H., Wei, R., Fischbach, M. A., Walsh, C. T.  
2006; 45 (34): 10184-10190
- **A biosynthetic gene cluster for the acetyl-CoA carboxylase inhibitor andrimid** *JOURNAL OF THE AMERICAN CHEMICAL SOCIETY*  
Jin, M., Fischbach, M. A., Clardy, J.  
2006; 128 (33): 10660-10661
- **Assembly-line enzymology for polyketide and nonribosomal peptide antibiotics: Logic, machinery, and mechanisms** *CHEMICAL REVIEWS*  
Fischbach, M. A., Walsh, C. T.  
2006; 106 (8): 3468-3496
- **Bromoenterobactins as potent inhibitors of a pathogen-associated, siderophore-modifying C-glycosyltransferase** *JOURNAL OF THE AMERICAN CHEMICAL SOCIETY*  
Lin, H., Fischbach, M. A., Gatto, G. J., Liu, D. R., Walsh, C. T.  
2006; 128 (29): 9324-9325
- **"Oncogenic shock": Explaining oncogene addiction through differential signal attenuation** *CLINICAL CANCER RESEARCH*  
Sharma, S. V., Fischbach, M. A., Haber, D. A., Settleman, J.  
2006; 12 (14): 4392S-4395S
- **A protein interaction surface in nonribosomal peptide synthesis mapped by combinatorial mutagenesis and selection** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Lai, J. R., Fischbach, M. A., Liu, D. R., Walsh, C. T.  
2006; 103 (14): 5314-5319
- **How pathogenic bacteria evade mammalian sabotage in the battle for iron** *NATURE CHEMICAL BIOLOGY*  
Fischbach, M. A., Lin, H. N., Liu, D. R., Walsh, C. T.  
2006; 2 (3): 132-138
- **Activity screening of carrier domains within nonribosomal peptide synthetases using complex substrate mixtures and large molecule mass spectrometry** *BIOCHEMISTRY*  
Dorrestein, P. C., Blackhall, J., Straight, P. D., Fischbach, M. A., Garneau-Tsodikova, S., Edwards, D. J., McLaughlin, S., Lin, M., Gerwick, W. H., Kolter, R., Walsh, C. T., Kelleher, N. L.  
2006; 45 (6): 1537-1546
- **Mixing with bubbles: a practical technology for use with portable microfluidic devices** *LAB ON A CHIP*  
Garstecki, P., Fuerstman, M. J., Fischbach, M. A., Sia, S. K., Whitesides, G. M.  
2006; 6 (2): 207-212
- **Enzymatic tailoring of enterobactin alters membrane partitioning and iron acquisition** *ACS CHEMICAL BIOLOGY*  
Luo, M., Lin, H., Fischbach, M. A., Liu, D. R., Walsh, C. T., Groves, J. T.  
2006; 1 (1): 29-32
- **Regulation of the nucleotide state of oncogenic Ras proteins by nucleoside diphosphate kinase** *REGULATORS AND EFFECTORS OF SMALL GTPASES: RAS FAMILY*  
Fischbach, M. A., Settleman, J.  
2006; 407: 33-45
- **In vitro characterization of salmochelin and enterobactin trilactone hydrolases IroD, IroE, and Fes** *JOURNAL OF THE AMERICAN CHEMICAL SOCIETY*  
Lin, H., Fischbach, M. A., Liu, D. R., Walsh, C. T.  
2005; 127 (31): 11075-11084
- **In vitro characterization of IroB, a pathogen-associated C-glycosyltransferase** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Fischbach, M. A., Lin, H. N., Liu, D. R., Walsh, C. T.

2005; 102 (3): 571-576

- **Dynamic control of liquid-core/liquid-cladding optical waveguides** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*

Wolfe, D. B., Conroy, R. S., Garstecki, P., Mayers, B. T., Fischbach, M. A., Paul, K. E., Prentiss, M., Whitesides, G. M.  
2004; 101 (34): 12434-12438

- **Specific biochemical inactivation of oncogenic Ras proteins by nucleoside diphosphate kinase** *CANCER RESEARCH*

Fischbach, M. A., Settleman, J.  
2003; 63 (14): 4089-4094