Curriculum Vitae

Wolfgang Florian Fricke, Ph.D.
Professor, Nutrigenomics
Department of Biological Chemistry and Nutrition
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Languages: German (native), English, French, Spanish (fluent), Italian (working knowledge)

Education

1995 - 2000	Studies of biology Georg-August-University Göttingen, Germany
1999 - 2000	**Biology Diploma** Dept. of Plant Biochemistry Albrecht-von-Haller-Institute for Plant Sciences Georg-August-University Göttingen, Germany “Functional analysis of *ENOD40* genes from *Leguminosae* and *Actinorhiza* plants” Advisor: Prof Dr. Hans-Werner Heldt
2003 - 2005	**Ph.D.** Goettingen Genomics Laboratory, Institute for Microbiology and Genetics Georg-August-University Göttingen, Germany Dissertation: “Comparative analysis of the genomes and genome organisations of *Ralstonia eutropha* H16 and *Methanosphaera stadtmanae*” Advisor: Prof. Dr. Gerhard Gottschalk

Post Graduate Education and Training

2005 - 2006	**Post-doctoral Fellow** Goettingen Genomics Laboratory, Institute for Microbiology and Genetics Georg-August-University Göttingen, Germany Mentor: Prof. Dr. Gerhard Gottschalk
2006 - 2007	**Post-doctoral Fellow** The Institute for Genomic Research (TIGR) / J. Craig Venter Institute Rockville, Maryland, USA

	Mentor: Dr. Jacques Ravel
2007 - 2008	**Post-doctoral Fellow** University of Maryland School of Medicine Institute for Genome Sciences Baltimore, Maryland, USA Mentor: Dr. Jacques Ravel

Employment History

1998 - 2003	**Research Assistant** Georg-August-University Göttingen Institute for Microbiology and Genetics Göttingen, Germany
2003 - 2005	**Scientific Assistant** Georg-August-University Institute for Microbiology and Genetics Göttingen, Germany
2009 - 2010	**Research Associate** University of Maryland School of Medicine Dept. of Microbiology & Immunology Institute for Genome Sciences Baltimore, Maryland, USA
2010 - 2013	**Assistant Professor, non-tenure track** University of Maryland School of Medicine Dept. of Microbiology & Immunology Institute for Genome Sciences Baltimore, Maryland, USA
2013 - current	**Assistant Professor, tenure track** University of Maryland School of Medicine Dept. of Microbiology & Immunology Institute for Genome Sciences Baltimore, Maryland, USA

Professional Society Memberships

2006 - present	American Society for Microbiology (ASM)
2012 - present	American Association for Cancer Research (AACR)

Awards

2010	"Tomorrow's PI" by GenomeWeb Genome Technology Journal

Administrative Service

Institutional Service

Since 2010	Jeanette Davies, Ph.D. committee member Ph.D. mentor: Russell Hill, Ph.D.
Since 2010	Lindsay Morningstar, Ph.D. committee member Ph.D. mentor: Thomas Blanchard, Ph.D.
Since 2013	Gloria Serena, Ph.D. committee member Ph.D. mentor: Alessio Fasano, M.D.
Since 2013	Kelly Robinson, Ph.D. committee member

	Ph.D. mentor: Julie Dunning-Hotopp, Ph.D.
Since 2013	Bre-Onna De Laine, Ph.D. committee member Ph.D. mentor: Eileen Barry, Ph.D.
Since 2013	Grant Jones, Ph.D. committee member Ph.D. mentor: Allen Place, Ph.D.

Local and National Service

2009	Ad Hoc Grant Reviewer *National Science Foundation (NSF), National Institutes of Health (NIH), UK Medical Research Council (MRC), Irish Health Review Board (HRB)*
2009	Ad Hoc Reviewer *Applied and Environmental Microbiology, BMC Microbiology, BMC Genomics, FEMS Microbiology Ecology, FEMS Pathogens and Disease, Gut Microbes, Journal of Clinical Microbiology, Microbial Drug Resistance*, *Microbiome*, *Plasmid*, *PLoS One*, *Water Research*
2011	Editorial Board Member, *Plasmid*

Teaching Service

1998	Lecturer Plant Physiology Seminar on Introduction to Plant physiology 1st year biology students - 2 hours/week, 5 months/yr Georg-August-University Göttingen, Germany
1998 - 1999	Mentor, supervisor Plant Biochemistry Practical courses in Basics of Plant Biochemistry 30 2nd year biology students - 4 hours/week, 1 month/yr Georg-August-University Göttingen, Germany
2000	Mentor, supervisor Practical courses in Plant Biochemistry 4th year biology students - 40 hours/week, 2 weeks/yr Georg-August-University Göttingen, Germany
2000	Mentor, supervisor Plant Biochemistry Diploma thesis in Plant Biochemistry Diploma student - 20 hours/week, 3 months/yr Georg-August-University Göttingen, Germany
2009 - 2010	Lecturer Graduate Program in Life Sciences GPLS 635 Bacterial Genetics 2nd + 3rd year graduate students - 3 hours/yr
2011	Mentor, supervisor Visiting student from Medical University Graz, Austria Diploma student - 4 weeks
2011, 2013	Lecturer Graduate Program in Life Sciences GPILS 710 Principles of Microbial Pathogenesis 2nd + 3rd year graduate students - 3 hours/yr
Since 2011	Lecturer

	Graduate Program in Life Sciences GPLS 717 Molecular Genetics and Genomics 2nd + 3rd year graduate students - 3 hours/yr
Since 2013	Organizer and lecturer of small group discussion on bacteriotherapy Host Defenses and Infectious Diseases MSPR 520 2nd year medical student, 3 hours/yr
Since 2013	Lecturer Graduate Program in Life Sciences GPLS 692 Current Topics in Genetics and Genomics 2nd + 3rd year graduate students - 3 hours/yr

Grant Support

Pending Grants

10/01/14 - 09/30/19	(co-PI, 10%) PI: Jonathan Bromberg, University of Maryland Microbiota impact on allograft transplant outcome NIH R01 Total direct cost: $1,625,600
06/01/14 - 05/31/19	(co-Investigator, 10%) PI: Aiping Zhao, University of Maryland Role of IL-25 on energy homeostasis NIH R01

Active Grants

04/01/15 - 03/30/17	(co-PI, 10%) PI: Mihai Pop, University of Maryland Algorithms and Software for the Assembly of Metagenomic Data NIH R01 Total direct cost (sub-contract): $197,288
12/01/11 - 11/30/15	(co-Investigator, 10%) PI: O. White, University of Maryland The Open Science Data Framework (OSDF) NIH/NHGRI Total direct cost: $3,129,218
06/01/12 - 05/30/17	(PI, 20%) co-PI: David Rasko, University of Maryland Cloud-enabled genomics resource for automated pathogen diagnostics in the field NIH R21/R33, RFA-AI-11-024 Total direct cost: $1,145,002
06/01/13 - 02/28/14	(project-PI, 15%) PI: C. Fraser, University of Maryland Tool integration for data visualization and editing Supplement: Automated Cloud-enabled Sequence Analysis Pipeline for Comparative Genomics NIAID Genomic Sequencing Center for Infectious Diseases Total direct cost: $47,472

Completed Grants

07/01/11 - 06/30/13	(co-PI, 10%) PI: J. Bromberg, University of Maryland Changes in the human microbiota induced by post-transplant medication American Society of Transplant Surgeons (ASTS) Total direct cost: $100,000

10/01/09 - 09/01/12	(PI, 20%) co-PI: O. White, University of Maryland Automated and portable sequence analysis using virtual machines and cloud computing National Science Foundation USDA-CSREES-AFRI-001967 Total direct cost: $313,850
10/01/09 - 09/30/11	(PI, 30%) co-PI: O. White, University of Maryland Virtual machines and Cloud Computing for automated and portable sequence analysis NIH/NHGRI ARRA RFA-OD-09-004 Total direct cost: $910,307
02/01/11 - 01/31/13	(project-PI, 30%) PI: C. Fraser, University of Maryland Comparative sequence analysis of *H. pylori* isolates from subjects with distinct gastric pathologies NIAID Genomic Sequencing Center for Infectious Diseases Total direct cost: $822,341
04/01/12 - 03/31/13	(project-PI, 10%) PI: C. Fraser, University of Maryland Automated Cloud-enabled Sequence Analysis Pipeline for Comparative Genomics. NIAID Genomic Sequencing Center for Infectious Diseases Total direct cost: $131,820

Patents, Inventions and Copyrights

10/13	"Method for Identification of Microbial Community Signatures as Diagnostic Markers for Inflammatory Bowel Diseases" (Patent pending)

Publications

Peer-reviewed Journal Articles

1. Bruggemann H, Baumer S, **Fricke WF,** Wiezer A, Liesegang H, Decker I, Herzberg C, Martinez-Arias R, Merkl R, Henne A, and Gottschalk G, (2003). The genome sequence of *Clostridium tetani*, the causative agent of tetanus disease. Proc Natl Acad Sci U S A, 100(3): p. 1316-21.
2. Potter M, Muller H, Reinecke F, Wieczorek R, **Fricke WF,** Bowien B, Friedrich B, and Steinbuchel A, (2004). The complex structure of polyhydroxybutyrate (PHB) granules: four orthologous and paralogous phasins occur in *Ralstonia eutropha.* Microbiology, 150(Pt 7): p. 2301-11.
3. Prust C, Hoffmeister M, Liesegang H, Wiezer A, **Fricke WF,** Ehrenreich A, Gottschalk G, and Deppenmeier U, (2005) Complete genome sequence of the acetic acid bacterium *Gluconobacter oxydans.* Nat Biotechnol, 23(2): p. 195-200.
4. **Fricke WF,** Seedorf H, Henne A, Kruer M, Liesegang H, Hedderich R, Gottschalk G, and Thauer RK, (2006). The genome sequence of *Methanosphaera stadtmanae* reveals why this human intestinal archaeon is restricted to methanol and H2 for methane formation and ATP synthesis. J Bacteriol, 188(2): p. 642-58.
5. Waack S, Keller O, Asper R, Brodag T, Damm C, **Fricke WF,** Surovcik K, Meinicke P, and Merkl R, (2006). Score-based prediction of genomic islands in prokaryotic genomes using hidden Markov models. BMC Bioinformatics, 7: p. 142.
6. Meinicke P, Brodag T, **Fricke WF,** and Waack S, (2006). P-value based visualization

of codon usage data. Algorithms Mol Biol, 1(1): p. 10.

7. Pohlmann A*, **Fricke WF*,** Reinecke F*, Kusian B, Liesegang H, Cramm R, Eitinger T, Ewering C, Potter M, Schwartz E, Strittmatter A, Voss I, Gottschalk G, Steinbuchel A, Friedrich B, and Bowien B, (2006). Genome sequence of the bioplastic-producing "Knallgas" bacterium *Ralstonia eutropha* H16. Nat Biotechnol, 24(10): p. 1257-62. *contributed equally.
8. Welch TJ, **Fricke WF,** McDermott PF, White DG, Rosso ML, Rasko DA, Mammel MK, Eppinger M, Rosovitz MJ, Wagner D, Rahalison L, Leclerc JE, Hinshaw JM, Lindler LE, Cebula TA, Carniel E, and Ravel J, (2007). Multiple antimicrobial resistance in plague: an emerging public health risk. PLoS ONE, 2(3): p. e309.
9. Eppinger M, Rosovitz MJ, **Fricke WF,** Rasko DA, Kokorina G, Fayolle C, Lindler LE, Carniel E, and Ravel J, (2007). The complete genome sequence of *Yersinia pseudotuberculosis* IP31758, the causative agent of Far East scarlet-like fever. PLoS Genet, 3(8): p. e142.
10. Seedorf H, **Fricke WF,** Veith B, Bruggemann H, Liesegang H, Strittmatter A, Miethke M, Buckel W, Hinderberger J, Li F, Hagemeier C, Thauer RK, and Gottschalk G, (2008). The genome of *Clostridium kluyveri*, a strict anaerobe with unique metabolic features. Proc Natl Acad Sci U S A, 105(6): p. 2128-33.
11. Raberg M, Reinecke F, Reichelt R, Malkus U, Konig S, Potter M, **Fricke WF,** Pohlmann A, Voigt B, Hecker M, Friedrich B, Bowien B, and Steinbuchel A, (2008). *Ralstonia eutropha* H16 flagellation changes according to nutrient supply and state of poly(3-hydroxybutyrate) accumulation. Appl Environ Microbiol, 74(14): p. 4477-90.
12. Rasko DA, Rosovitz MJ, Myers GS, Mongodin EF, **Fricke WF,** Gajer P, Crabtree J, Sebaihia M, Thomson NR, Chaudhuri R, Henderson IR, Sperandio V, and Ravel J, (2008). The pangenome structure of *Escherichia coli*: comparative genomic analysis of *E. coli* commensal and pathogenic isolates. J Bacteriol, 190(20): p. 6881-93.
13. **Fricke,WF,** Wright MS, Lindell AH, Harkins DM, Baker-Austin C, Ravel J, and Stepanauskas R, (2008). Insights into the environmental resistance gene pool from the genome sequence of the multidrug-resistant environmental isolate *Escherichia coli* SMS-3-5. J Bacteriol, 190(20): p. 6779-94.
14. **Fricke WF,** Kusian B, and Bowien B (2009). The genome organization of *Ralstonia eutropha* strain H16 and related species of the *Burkholderiaceae.* J Mol Microbiol Biotechnol, 16(1-2): p. 124-35.
15. Strittmatter AW, Liesegang H, Rabus R, Decker I, Amann J, Andres S, Henne A, **Fricke WF,** Martinez-Arias R, Bartels D, Goesmann A, Krause L, Puhler A, Klenk HP, Richter M, Schuler M, Glockner FO, Meyerdierks A, Gottschalk G, and Amann R, (2009). Genome sequence of *Desulfobacterium autotrophicum* HRM2, a marine sulfate reducer oxidizing organic carbon completely to carbon dioxide. Environ Microbiol, 11(5): p. 1038-55.
16. **Fricke WF,** Welch TJ, McDermott PF, Mammel MK, LeClerc JE, White DG, Cebula TA, and Ravel J, (2009). Comparative genomics of the IncA/C multidrug resistance plasmid family. J Bacteriol, 191(15): p. 4750-7.
17. **Fricke WF,** McDermott PF, Mammel MK, Zhao S, Johnson TJ, Rasko DA, Fedorka-Cray PJ, Pedroso A, Whichard J, LeClerc JE, White DG, Cebula TA, and Ravel J, (2009). Antimicrobial resistance-encoding APEC plasmids in *Salmonella enterica* serovar Kentucky from poultry. Appl Environ Microbiol, 75(18): p. 5963-71.
18. **Fricke WF,** Rasko DA, and Ravel J (2009). The role of genomics in the identification, prediction and prevention of biological threats. PLoS Biol, 7(10):e1000217.
19. Wagner DM, Runberg J, Vogler AJ, Lee J, Driebe E, Price LB, Engelthaler DM, **Fricke WF**, Ravel J, and Keim P (2010). No resistance plasmid in *Yersinia pestis*, North America. Emerg Infect Dis, 16(5):885-87.
20. Johnson TJ, Thorsness JL, Anderson CP, Lynne AM, Foley SL, Han J, **Fricke WF**, McDermott PF, White DG, Khatri M, Stell AL, Flores C, and Singer RS (2010).

Horizontal gene transfer of a ColV plasmid has resulted in a dominant avian clonal type of *Salmonella enterica s*erovar Kentucky. PLoS One, 5(12):e15524.

21. Donia MS, **Fricke WF**, Ravel J, and Schmidt EW (2011). Variation in tropical reef symbiont metagenomes defined by secondary metabolism. PLoS One. 22;6(3):e17897.
22. **Fricke WF,** Mammel MK, McDermott PF, Tartera C, White DG, LeClerc JE, Ravel J, and Cebula TA (2011). Comparative genomics of 17 non-typhoidal *Salmonella enterica* isolates: CRISPR-mediated adaptive sublineage evolution via gene acquisition and loss? J Bacteriol. 193(14):3556-68
23. Zan J, **Fricke WF**, Fuqua C, Ravel J, Hill RT (2011) Genome sequence of *Ruegeria* sp. strain KLH11, an N-acylhomoserine lactone-producing bacterium isolated from the marine sponge *Mycale laxissima*. J Bacteriol. 193(18):5011-2.
24. Angiuoli SV, Matalka M, Gussman A, Galens K, Vangala M, Riley D, Arze C, White JR, White O, and **Fricke WF** (2011). CloVR: A virtual machine for automated and portable sequence analysis from the desktop using cloud computing. BMC Bioinformatics, 12(1):356.
25. Angiuoli SV, White, JR, Matalka M, White, O and **Fricke WF** (2011). Resources and costs for microbial sequence analysis evaluated using virtual machines and cloud computing. PLoS One, 6(10):e26624
26. Donia MS, **Fricke WF**, Partensky F, Cox J, Elshahawi SI, White JR, Phillippy AM, Schatz MC, Piel J, Haygood MG, Ravel J, and Schmidt EW (2011). Complex microbiome underlying secondary and primary metabolism in the tunicate-Prochloron symbiosis. Proc Natl Acad Sci U S A. 108(51):E1423-32.
27. Schmidt EW, Donia MS, McIntosh JA, **Fricke WF**, and Ravel J (2012). Origin and Variation of Tunicate Secondary Metabolites. J Nat Prod, 75(2):295-304
28. Sellitto M, Bai G, Serena G, **Fricke WF**, Sturgeon C, Gajer P, White JR, Koenig SS, Sakamoto J, Boothe D, Gicquelais R, Kryszak D, Puppa E, Catassi C, Ravel J, and Fasano A (2012). Proof of concept of microbiome-metabolome analysis and delayed gluten exposure on celiac disease autoimmunity in genetically at-risk infants. PLoS One. 2012;7(3):e33387
29. Earl AM, Eppinger M, **Fricke WF**, Rosovitz MJ, Rasko DA, Daugherty S, Losick R, Kolter R, and Ravel J (2012). Whole-Genome Sequences of *Bacillus subtilis* and Close Relatives. J Bacteriol. 194(9):2378-9.
30. Domingues S, Harms K, **Fricke WF**, Johnsen PJ, da Silva GJ, and Nielsen KM (2012). Natural Transformation Facilitates Transfer of Transposons, Integrons and Gene Cassettes between Bacterial Species. PLoS Pathog. 8(8):e1002837.
31. White JR, Maddox C, White O, Angiuoli SF, and **Fricke WF** (2013) CloVR-ITS: Automated internal transcribed spacer amplicon sequence analysis pipeline for the characterization of fungal microbiota. Microbiome 1(1):1-11.
32. von Rosenvinge EC, White JR, Maddox C, Blanchard T, and **Fricke WF** (2013) Immune status and antibiotic medication are associated with reduced diversity and altered gastric fluid microbiota. ISME. 7(7):1354-66. doi: 10.1038/ismej.2013.33
33. Blanchard TG, Czinn SJ, Correa P, Nakazawa T, Keelan M, Morningstar L, Santana-Cruz I, Maroo A, McCracken C, Shefchek K, Daugherty S, Song Y, Fraser CM and **Fricke WF** (2013) Genome sequences of 65 *Helicobacter pylori* strains isolated from asymptomatic individuals and patients with gastric cancer, peptic ulcer disease, or gastritis. Pathog Dis. 68(2):39-43. doi: 10.1111/2049-632X.12045.
34. Deng X, Salazar JK, Frezet S, Maccannell D, Ribot EM, Fields PI, **Fricke WF**, Zhang W. (2013) Genome Sequence of *Salmonella enterica* Serotype Tennessee Strain CDC07-0191, Implicated in the 2006-2007 Multistate Food-Borne Outbreak Linked to Peanut Butter in the United States. Genome Announc. 1(3). doi:pii: e00260-13
35. Davis J, **Fricke WF**, Hamann M, Esquenazi E, Dorrestein P and Hill R (2013) Characterization of the bacterial community of the chemically defended Hawaiian

sacoglossan *Elysia rufescens*. Appl Environ Microbiol. 79(22):7073-81. doi: 10.1128/AEM.01568-13

36. Song Y, Garg S, Girotra M, Maddox C, von Rosenvinge EC, Dutta A, Dutta S, and **Fricke WF** (2013) Microbiota Dynamics in Patients Treated with Fecal Microbiota Transplantation for Recurrent *Clostridium difficile* Infection. PLoS One. 8(11):e81330. doi: 10.1371/journal.pone.0081330
37. Crits-Christoph A, Robinson CK, Barnum T, **Fricke WF**, Davila AF, Jedynak B, McKay CP, Diruggiero J (2013) Colonization patterns of soil microbial communities in the Atacama Desert. Microbiome. 1(1):28. doi: 10.1186/2049-2618-1-28.
38. **Fricke WF**, Maddox C, Song Y and Bromberg JS (2014) Human Microbiota Characterization in the Course of Renal Transplantation. Am J Transplant. 14(2):416-27. doi: 10.1111/ajt.12588. Epub 2013 Dec 26.
39. **Fricke WF**, and Rasko DA (2014) Bacterial genome sequencing in the clinic: bioinformatic challenges and solutions. Nat Rev Genet. 15(1):49-55. doi: 10.1038/nrg3624
40. Dutta SK, Girotra M, Garg S, Dutta A, von Rosenvinge EC, Maddox C, Song Y, Bartlett JG, Vinayek R, **Fricke WF** (2014) Efficacy of Simultaneous Jejunal and Colonic administration of Fecal Microbiota Transplantation for Recurrent Clostridium difficile Infection with Molecular Characterization data. Clin Gastroenterol Hepatol. pii: S1542-3565(14)00048-2. doi: 10.1016/j.cgh.2013.12.032.

Non-peer-reviewed Journal Articles

1. White JR, Matalka M, **Fricke WF**, and Angiuoli SV (2011). Cunningham: a BLAST Runtime Estimator. Nat Preced, doi:10.1038/npre.2011.5593.1
2. White JR, Arze C, Matalka M, the CloVR team, Angiuoli SV, and **Fricke WF** (2011). CloVR-Metagenomics: Functional and taxonomic microbial community characterization from metagenomic whole-genome shotgun (WGS) sequences – standard operating procedure, version 1.0. Nature Preced, doi:10.1038/npre.2011.5886.1
3. White JR, Arze C, Matalka M, the CloVR team, Angiuoli SV, and **Fricke, WF** (2011). CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing – standard operating procedure, version 1.1. Nature Preced, doi:10.1038/npre.2011.6287.1
4. Galens K, White JR, Arze C, Matalka M, Gwinn Giglio M, the CloVR Team, White O, Angiuoli SV, and **Fricke WF** (2011). CloVR-Microbe: Assembly, gene finding and functional annotation of raw sequence data from single microbial genome projects – standard operating procedure, version 1.0. Nature Preced, doi:10.1038/npre.2011.5887.2

Book Chapters

1. Cebula TA, **Fricke WF**, and Ravel J (2010) Food-Borne Outbreaks: What's New, What's Not, and Where Do We Go From Here? In Eds. Budwole B, Schutzer SE, Breeze RG, Keim PS, and Morse SA. Microbial Forensics, 2nd Edition pp.29-42. San Diego: Elsevier.
2. **Fricke WF**, Cebula TA, and Ravel J (2010). Genomics. In Eds. Budwole B, Schutzer SE, Breeze RG, Keim PS, and Morse SA. Microbial Forensics, 2nd Edition pp. 479-92. San Diego: Elsevier.
3. White JR and **Fricke WF** (2012). Microbial Genomics. In Eds. Foley S., Nayak R., Johnson T., and Shukla S. Molecular Typing Methods for Tracking Foodborne Microorganisms, Hauppauge: Nova Science.

Major Invited Speeches

Local

1. **Fricke, WF**, Comparative analysis of two microbial genomes: *Ralstonia eutropha* H16 and *Methanosphaera stadtmanae*, The Institute for Genomic Research (TIGR), Rockville, MD, 2006.
2. **Fricke, WF**, *Salmonella enterica* genomics and CloVR - automated sequence analysis from your desktop, Institute of Marine and Environmental Technology (IMET), Baltimore, MD, 2011.
3. **Fricke, WF**, CloVR: DIY bioinformatic sequence analysis and the human microbiome, University of Maryland, Baltimore, MD, 2013

National

1. **Fricke, WF**, The Increasing Availability of Antimicrobial Resistance Determinants: Implications for Pathogen Evolution and Biopreparedness, ASM Biodefense Meeting, Baltimore, MD, 2009.
2. **Fricke, WF**, Virtual Machines and Cloud Computer for Automated and Portable Sequence Analysis, NHGRI Cloud Computing Workshop, Bethesda, MD, 2010.
3. **Fricke, WF**, Virtual Machines and Cloud Computing for Automated and Portable Sequence Analysis, Beyond the Genome Meeting, Cloud Computing in Genomics and Bioinformatics Workshop, Boston, MA, 2010.
4. **Fricke, WF**, Comparative genomics of 17 non-typhoidal *Salmonella enterica* isolates: CRISPR-mediated adaptive sublineage evolution via gene acquisition and loss, University of Pennsylvania, Philadelphia, PA, 2011.
5. **Fricke, WF**, CloVR platform and protocols for automated, portable and Cloud computing-enabled sequence analysis, Keystone Symposium "Microbial Communities as Drivers of Ecosystem Complexity, Breckenridge, CO, 2011.
6. **Fricke, WF**, CloVR - Automated, Portable and Cloud-enabled Sequence Analysis, Next-generation Sequencing: Enabling Transformative Technology for Biodiversity Science Meeting, Washington DC, 2011.
7. **Fricke, WF**, CloVR: Automated Sequence Analysis on the Cloud, Wadsworth Center, Albany, NY, 2011.
8. **Fricke, WF**, CloVR: Automated Sequence Analysis on the Cloud, Centers for Disease Control and Prevention (CDC), Atlanta, GA, 2012.
9. **Fricke, WF**, CloVR-supported comparative genome analysis: Mechanisms of *Salmonella enterica* evolution, 2012 Poultry Science Association Annual Meeting, Athens, GA, 2012.
10. **Fricke, WF**, Do-it-yourself Microbial Genome Sequence Analysis, ASM 2013 General Meeting Workshop, Denver, CO, 2013.
11. **Fricke, WF**, Recurrent *Clostridium difficile* infection: A Longitudinal study of alterations in fecal microbiome in patients-donor pairs before and after Fecal Microbiota Therapy. Digestive Disease Week 2013, Orlando, FL, 2013.
12. **Fricke, WF**, CloVR: Do-it-yourself microbial sequence analysis on the cloud, Mid-Atlantic Directors and Staff of Scientific Cores Meeting, Frederick, MD, 2013.
13. **Fricke, WF**, Cloud-enabled Genomic Resource for Automated Pathogen Diagnostics in the Field, 11th Annual Emerging Infectious Diseases & Biodefense Meeting, Technical Symposium, Washington, DC, 2013.
14. **Fricke, WF**, CloVR: Do-it-yourself microbial sequence analysis on the cloud, Food and Drug Administration, Laurel, MD, 2013.
15. **Fricke, WF**, Cloud-enabled Genomic Resource for Automated Pathogen Diagnostics Molecular Dx for Infectious Disease Conference, Washington, DC, 2013.

International

1. **Fricke, WF**, Analysis of the genome of *Ralstonia eutropha* H16 for the development of hydrogen-based production strains, Prokagen Conference on Prokaryotic Genomes, Göttingen, Germany, 2005
2. **Fricke, WF**, Antimicrobial resistance-encoding APEC virulence plasmids in *S. enterica* Kentucky, ASM Conference on Antimicrobial Resistance in Zoonotic Bacteria and Foodborne Pathogens, Copenhagen, Denmark, 2008.
3. **Fricke, WF**, Half Microbe, half Cloud: *Salmonella enterica* genomics and Automated Pipelines for Sequence Analysis, University of Tromsø, Norway, 2010.
4. **Fricke, WF**, *Salmonella enterica* genomics and Bioinformatics Tools for Automated Sequence Analysis in the Cloud, Medical University of Graz, Austria, 2010.
5. **Fricke, WF**, Microbes and Clouds: Comparative Genomics of *Salmonella enterica* and Automated Pipelines for Sequence Analysis, University of Erlangen/Nürnberg, Germany, 2011.
6. **Fricke, WF**, Facets of the Human Microbiome and how to study them on the Cloud: CloVR, bacterial and fungal microbiota, body site-specific DNA fingerprints, Medical University of Graz, Austria, 2011.
7. **Fricke, WF**, Developing and applying genomic and bioinformatic tools to study host-microbe systems, Justus-Liebig-University, Giessen, Germany, 2012.
8. **Fricke, WF**, CloVR-supported comparative genome analysis: Mechanisms of *Salmonella enterica* evolution, UK Next Gen Sequencing Meeting, Nottingham, UK, 2012.
9. **Fricke, WF**, Do-it-yourself Bioinformatics with CloVR: Automated Sequence Analysis on the Cloud, Rapid NGS for Public Health Microbiology Meeting, Münster, Germany, 2013.

Poster Presentations

1. **WF Fricke,** B. Kusian, A. Pohlmann, H. Liesegang, F. Reinecke, M. Pötter, B. Friedrich, B. Bowien, A. Steinbuchel and H. Heumann, H. (2004). Genome analysis of *Ralstonia eutropha* H16. Vereinigung für Allgemeine und Angewandte Mikrobiologie (*VAAM*), Jahrestagung 2004, Braunschweig, Germany: March 28-31, 2004.
2. **WF Fricke,** H. Seedorf, A. Henne, M. Kruer, R. Hedderich, G. Gottschalk and R.K. Thauer. (2005). Complete genome sequence of the human commensal *Methanosphaera stadtmanae*. 2nd European Conference on Prokaryotic Genomes - *PROKAGEN 2005*, Goettingen, Germany: September 23-26, 2005.
3. **WF Fricke,** T.J. Welch, D.R. Rasko, M.K. Mammel, M. Eppinger, MJ Rosovitz, D.G. White, P.F. McDermott, L. Rahalison, J.E. LeClerc, J.M. Hinshaw, L.E. Lindler, T.A. Cebula, E. Carniel and J. Ravel (2007). Plasmid-mediated multi-drug resistance in plague: an emerging risk. 107th General Meeting of the American Society for Microbiology, *ASM2007*, Toronto, Canada: May 21-25, 2007.
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