

---

## BIOGRAPHICAL SKETCH

Provide the following information for the key personnel and other significant contributors.  
Follow this format for each person. **DO NOT EXCEED FOUR PAGES.**

---

NAME Susannah Green Tringe	POSITION TITLE Staff Scientist		
eRA COMMONS USER NAME			
EDUCATION/TRAINING <i>(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)</i>			
INSTITUTION AND LOCATION	DEGREE <i>(if applicable)</i>	YEAR(s)	FIELD OF STUDY
Harvard University, Cambridge, MA	A.B.	1994	Physics
Stanford University, Stanford, CA	Ph.D.	2000	Biophysics
University of New Mexico, Albuquerque, NM	Postdoctoral	2003	Molecular Genetics and Microbiology
DOE Joint Genome Institute, Walnut Creek, CA	Postdoctoral	2006	Genomics

### A. Positions and Honors.

#### Positions and Employment

1994-2000 Graduate student, Radiation Oncology, Stanford University, Stanford, CA  
2000-2003 Postdoctoral fellow (Ruby lab), Molecular Genetics and Microbiology, University of New Mexico Medical School, Albuquerque, NM  
2003-2006 Postdoctoral fellow (Rubin lab), DOE Joint Genome Institute, Walnut Creek, CA  
2006-2010 Research Scientist, DOE Joint Genome Institute, Walnut Creek, CA  
2010-2011 Metagenome Program Deputy Lead, DOE Joint Genome Institute, Walnut Creek, CA  
2010-2013 Career Research Scientist, DOE Joint Genome Institute, Walnut Creek, CA  
2010-2011 Microbial Systems Group Lead, DOE Joint Genome Institute, Walnut Creek, CA  
2011 Visiting Associate Professor, University of California, Berkeley, CA  
2011-2013 Metagenome Program Lead, DOE Joint Genome Institute, Walnut Creek, CA  
2013-2015 Staff Scientist, DOE Joint Genome Institute, Walnut Creek, CA  
2015- Deputy Director, User Programs, DOE Joint Genome Institute, Walnut Creek, CA

#### Other Experience and Professional Memberships

1992 Course assistant, Mathematics 21a: Multivariable Calculus, Harvard University, Cambridge, MA  
1994 Teaching fellow, Applied Math 105b: Vector Calculus and Differential Equations, Harvard University, Cambridge, MA  
1994- Member, American Association for the Advancement of Science  
1996-1998 Teaching assistant, Cancer Biology 263: Apoptosis, Stanford University, Stanford, CA  
2002-2004 Member, International Society for Computational Biology  
2007- Member, American Society for Microbiology  
2009- Member, Society for Industrial Microbiology  
2010- Member, International Society for Microbial Ecology  
2010- Review editor, Frontiers in Microbiology  
2011-2013 Scientific Advisory Board, Hydrocarbon Metagenomics, Genome Alberta  
2014- Scientific Advisory Committee, Plant-Microbial Interfaces SFA, Oak Ridge National Laboratory  
2015- Scientific Advisory Committee, Principles of Microbial Community Design FSFA, Pacific Northwest National Laboratory  
2012- Editorial Board, Microbiome  
2013- Editorial Board, Scientific Data  
2015- Senior editor, mSphere

#### Honors

1993 Phi Beta Kappa  
1994 *summa cum laude*, Harvard College, Physics

1996-1999	Lucille P. Markey Fellowship in Molecular Mechanisms of Disease
1999	AACR-Pharmacia & Upjohn Young Investigator award
2006	First author on publication named "New Hot Paper" by Essential Science Indicators
2011	DOE Early Career Research Program Award
2011	Named one of Popular Science's "Brilliant 10" for 2011
2013	Featured in "Women @ Energy" highlighting female scientists in the DOE

## **B. Peer-reviewed publications (94 total published or in press; in chronological order).**

1. Pargellis, A. N., **Green, S.**, and Yurke, B. Planar XY-model dynamics in a nematic liquid crystal system. *Physical Review E* 49: 4250-4257, 1994.
2. Fried, L. M., Koumenis, C., Peterson, S. R., **Green, S. L.**, Van Zijl, P., Allalunis-Turner, J., Chen, D. J., Fishel, R., Giaccia, A. J., Brown, J. M., and Kirchgessner, C. U. The DNA damage response in DNA-dependent protein kinase-deficient SCID mouse cells: Replication protein A hyperphosphorylation and p53 induction. *Proceedings of the National Academy of Sciences* 93: 13825-13830, 1996.
3. **Green, S. L.**, and Giaccia, A. J. Tumor Hypoxia and the Cell Cycle: Implications for Malignant Progression and Response to Therapy. *The Cancer Journal from Scientific American* 4: 218-223, 1998.
4. Denko, N. C., **Green, S. L.**, Edwards, D., and Giaccia, A. J. p53 checkpoint-defective cells are sensitive to x-rays, but not hypoxia. *Experimental Cell Research* 10: 82-91, 2000.
5. **Green, S. L.**, Freiberg, R. A., and Giaccia, A. J. p21Cip1 and p27Kip1 regulate cell cycle re-entry after hypoxic stress but are not necessary for hypoxia-induced arrest. *Molecular and Cellular Biology* 21: 1196-1206, 2001.
6. Hammond, E.M., **Green, S.L.**, and Giaccia, A.J. Comparison of hypoxia-induced replication arrest with hydroxyurea and aphidicolin-induced arrest. *Mutation Research* 532: 205-213, 2003.
7. **Tringe, S.G.**, Wagner, A. and Ruby, S.W. Enriching for direct regulatory targets in perturbed gene-expression profiles. *Genome Biology* 5: R29, 2004.
8. **Tringe, S.G.**, von Mering, C., Kobayashi, A., Salamov, A.A., Chen, K., Chang, H.W., Podar, M., Short, J.M., Mathur, E.J., Detter, J.C., Bork, P., Hugenholtz, P., and Rubin, E.M. Comparative Metagenomics of Microbial Communities. *Science* 308: 554-557, 2005.
9. **Tringe, S.G.** and Rubin, E.M. Metagenomics: DNA sequencing of environmental samples. *Nature Reviews Genetics* 6: 805-814, 2005
10. **Tringe, S.G.**, Willis, J., Liberatore, K. and Ruby, S.W. The WTM genes in budding yeast amplify expression of the stress-inducible gene RNR3. *Genetics* 174: 1215-1228, 2006.
11. von Mering, C., Hugenholtz, P., Raes, J., **Tringe, S. G.**, Doerks, T., Jensen, L. J., Ward, N., Bork, P. Quantitative Phylogenetic Assessment of Microbial Communities in Diverse Environments. *Science* 315: 1126-1130, 2007.
12. Warnecke, F., Luginbühl, P., Ivanova, N., Ghassemian, M., Richardson, T.H., Stege, J.T., Cayouette, M., McHardy, A.C., Djordjevic, G., Aboushadi, N., Sorek, R., **Tringe, S.G.**, Podar, M., Martin, H.G., Kunin, V., Dalevi, D., Madejska, J., Kirton, E., Platt, D., Szeto, E., Salamov, A., Barry, K., Mikhailova, N., Kyrpides, N.C., Matson, E.G., Ottesen, E.A., Zhang, X., Hernandez, M., Murillo, C., Acosta, L.G., Rigoutsos, I., Tamayo, G., Green, B.D., Chang, C., Rubin, E.M., Mathur, E.J., Robertson, D.E., Hugenholtz, P., Leadbetter, J.R. Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. *Nature* 450: 560-566, 2007.

13. **Tringe, S.G.**, Zhang, T., Liu, X., Yu, Y., Lee, W.H., Yap, J., Yao, F., Suan, S.T., Ing, S.K., Haynes, M., Rohwer, F., Wei, C.L., Tan, P., Bristow, J., Rubin, E.M. and Ruan, Y. The airborne metagenome in an urban environment. *PLoS One* 3: e1862, 2008.
14. Kalyuzhnaya M.G., Lapidus A., Ivanova N., Copeland A.C., McHardy A.C., Szeto E., Salamov A., Grigoriev I.V., Suciú D., Levine S.R., Markowitz V.M., Rigoutsos I., **Tringe S.G.**, Bruce D.C., Richardson P.M., Lidstrom M.E., Chistoserdova L. High-resolution metagenomics targets specific functional types in complex microbial communities. *Nature Biotechnology* 26: 1029-1034, 2008.
15. **Tringe, S.G.**, Hugenholtz, P. A renaissance for the pioneering 16S rRNA gene. *Current Opinion in Microbiology* 11: 442-446, 2008.
16. Walsh, D.A., Zaikova, E., Howes, C.G., Song, Y.C., **Tringe, S.G.**, Tortell, P.D., Hallam, S.J. Metagenome of a Versatile Chemolithoautotroph from Expanding Oceanic Dead Zones. *Science* 326:578-582, 2009.
17. Duncan, K.E., Gieg, L.M., Parisi, V.A., Tanner, R.S., **Tringe, S.G.**, Bristow, J., Suflita, J.M. Biocorrosive Thermophilic Microbial Communities in Alaskan North Slope Oil Facilities. *Environmental Science & Technology* 43: 7977-7984, 2009.
18. Hemme, C.L., Deng, Y., Gentry, T.J., Fields, M.W., Wu, L., Barua, S., Barry, K., **Tringe, S.G.**, Watson, D.B., He, Z., Hazen, T.C., Tiedje, J.M., Rubin, E.M., Zhou, J. Metagenomic Insights into Evolution of a Heavy Metal-Contaminated Groundwater Microbial Community. *ISME Journal* 4: 660-672, 2010.
19. Ivanova, N., **Tringe, S.G.**, Liolios, K., Liu, W.T., Morrison, N., Hugenholtz, P., Kyrpides, N.C. A call for standardized classification of metagenome projects. *Environmental Microbiology* 12: 1803-1805, 2010.
20. Pope, P.B., Denman, S.E., Jones, M., **Tringe, S.G.**, Barry, K., Malfatti, S.A., McHardy, A.C., Cheng, J.-F., Hugenholtz, P., McSweeney, C.S., Morrison, M. Adaptation to herbivory by the Tammar wallaby includes bacterial and glycoside hydrolase profiles different from other herbivores. *Proceedings of the National Academy of Sciences* 107: 14793-14798, 2010.
21. Cuvelier, M.L., Allen, A.E., Monier, A., McCrow, J.P., Messie, M., **Tringe, S.G.**, Woyke, T., Welsh, R.M., Ishoey, T., Lee, J.-H., Binder, B.J., Latasa, M., Guigand, C., Buck, K.R., DuPont, C.L., Hilton, J.A., Thiagarajan, M., Caler, E., Lasken, R., Chavez, F.P., Worden, A.Z. Targeted metagenomics and ecology of globally important uncultured eukaryotic phytoplankton. *Proceedings of the National Academy of Sciences* 107: 14679-14684, 2010.
22. Hollister, E.B., Forrest, A.K., Wilkinson, H.H., Ebbole, D.J., Malfatti, S.A., **Tringe, S.G.**, Holtzapple, M.T., Gentry, T.J. Structure and dynamics of the microbial communities underlying the carboxylate platform for biofuel production. *Applied Microbiology and Biotechnology* 88: 389-99, 2010.
23. He, S., Wurtzel, O., Singh, K., Froula, J.L., Yilmaz, S., **Tringe, S.G.**, Wang, Z., Chen, F., Lindquist, E.A., Sorek, R., Hugenholtz, P. Validation of two ribosomal RNA removal methods for microbial metatranscriptomics. *Nature Methods* 7: 807-12, 2010.
24. Suen, G., Scott, J.J., Aylward, F.O., Adams, S.M., **Tringe, S.G.**, Pinto-Tomás, A.A., Foster, C.E., Pauly, M., Weimer, P.J., Barry, K.W., Goodwin, L.A., Bouffard, P., Li, L., Osterberger, J., Harkins, T.T., Slater, S.C., Donahue, T.J., Currie, C.R. An insect herbivore microbiome with high plant biomass-degrading capacity. *PLoS Genetics* 6: e1001129, 2010.
25. Lykidis, A., Chen, C.-L., **Tringe, S.G.**, McHardy, A., Copeland, A., Kyrpides, N.C., Hugenholtz, P., Macarie, H., Olmos, A., Monroy, O. and Liu, W.-T. Multiple syntrophic interactions in a terephthalate-degrading methanogenic consortium. *ISME Journal* 5: 122-30, 2011.
26. Hess, M., Sczyrba, A., Egan, R., Kim, T.-W., Chokhawala, H., Schroth, G., Luo, S., Clark, D.S., Chen, F., Zhang, T., Mackie, R.I., Pennacchio, L.A., **Tringe, S.G.**, Visel, A., Woyke, T., Wang, Z., Rubin, E.M.

- Metagenomic Discovery of Biomass-Degrading Genes and Genomes from Cow Rumen. *Science* 331: 463-467, 2011.
27. Pope, P.B., Smith, W., Denman, S.E., **Tringe, S.G.**, Barry, K., Hugenholtz, P., McSweeney, C.S., McHardy, A.C., Morrison, M. Isolation of Succinivibrionaceae Implicated in Low Methane Emissions from Tamar Wallabies. *Science* 333: 646-648, 2011.
28. Li, L.L., Taghavi, S., McCorkle, S.M., Zhang, Y.B., Blewitt, M.G., Brunecky, R., Adney, W.S., Himmel, M.E., Brumm P., Drinkwater C., Mead, D.A., **Tringe, S.G.**, van der Lelie, D. Bioprospecting metagenomics of decaying wood: mining for new glycosyl hydrolases. *Biotechnology for Biofuels* 4: 23, 2011.
29. Gori, F., **Tringe, S.G.**, Kartal, B., Marchiori, E., Jetten, M. The metagenomic basis of anammox metabolism in *Candidatus "Brocadia fulgida."* *Biochemical Society Transactions* 39: 1799-1804, 2011.
30. Godoy-Vitorino, F., Goldfarb, K.C., Karaoz, U., Leal, S., Garcia-Amado, M.A., Hugenholtz, P., **Tringe, S.G.**, Brodie, E.L., Dominguez-Bello, M.G. Comparative analyses of foregut and hindgut bacterial communities in hoatzins and cows. *ISME Journal* 6: 531-41, 2012.
31. Berg Miller, M.E., Yeoman, C.J., Chia, N., **Tringe, S.G.**, Angly, F.E., Edwards, R.A., Flint, H.J., Lamed, R., Bayer, E.A., White, B.A. Phage-bacteria relationships and CRISPR elements revealed by a metagenomic survey of the rumen microbiome. *Environmental Microbiology* 14: 207-227, 2012.
32. Harhangi, H.R., Le Roy, M., van Alen, T., Hu, B.L., Groen, J., Kartal, B., **Tringe, S.G.**, Quan, Z.X., Jetten, M.S., Op den Camp, H.J. Hydrazine synthase, a unique phylomarker to study the presence and biodiversity of anammox bacteria. *Applied and Environmental Microbiology* 78: 752-758, 2012.
33. Aylward, F.O., Burnum, K.E., Scott, J.J., Suen, G., **Tringe, S.G.**, Adams, S.M., Barry, K.W., Nicora, C.D., Piehowski, P.D., Purvine, S.O., Starrett, G.J., Goodwin, L.A., Smith, R.D., Lipton, M.S., Currie, C.R. Metagenomic and metaproteomic insights into bacterial communities in leaf-cutter ant fungus gardens. *ISME Journal* 6: 1688-1701, 2012.
34. Brisson, V.L., West, K.A., Lee, P.K.H., **Tringe, S.G.**, Brodie, E.L., Alvarez-Cohen, L. Metagenomic Analysis of a Stable Trichloroethene-Degrading Microbial Community. *ISME Journal* 6: 1702-1714, 2012.
35. Mason, O.U., Hazen, T.C., Borglin, S., Chain, P.S.G., Dubinsky, E.A., Fortney, J.L., Han, J., Holman, H.Y.N., Hultman, J., Lamendella, R., Mackelprang, R., Malfatti, S., Tom, L.M., **Tringe, S.G.**, Woyke, T., Zhou, J., Rubin, E.M., Jansson, J.K. Metagenome, metatranscriptome and single-cell sequencing reveal microbial response to Deepwater Horizon oil spill. *ISME Journal* 6: 1715-1727, 2012.
36. Kozubal, M.A., Macur, R.E., Jay, Z.J., Beam, J.P., Malfatti, S.A., **Tringe, S.G.**, Kocar, B.D., Borch, T., Inskeep, W.P. Microbial iron cycling in acidic geothermal springs of Yellowstone National Park: Integrating molecular surveys, geochemical processes and isolation of novel Fe-active microorganisms. *Frontiers in Microbiology* 3: 109, 2012.
37. van de Vossenberg, J., Woebken, D., Maalcke, W.J., Wessels, H.J.C.T., Dutilh, B.E., Kartal, B., Janssen-Megens, E.M., Roeselers, G., Yan, J., Speth, D., Gloerich, J., Geerts, W., van der Biezen, E., Pluk, W., Francoijs, K.J., Russ, L., Lam, P., Malfatti, S.A., **Tringe, S.G.**, Haaijer, S.C.M., Op den Camp, H., Stunnenberg, H.G., Amann, R., Kuypers, M.M.M., Jetten, M.S.M. The metagenome of the marine anammox bacterium "*Candidatus Scalindua profunda*" illustrates the versatility of this globally important nitrogen cycle bacterium. *Environmental Microbiology*, 2012 (epub ahead of print).
38. van der Lelie, D., Taghavi, S., McCorkle, S.M., Li, L.-L., Malfatti, S.A., Monteleone, D., Donohoe, B.S., Ding, S.-Y., Adney, W.S., Himmel, M.E., **Tringe, S.G.** The metagenome of an anaerobic microbial community decomposing poplar wood chips. *PLoS One* 7: e36740, 2012.

39. Baelum, J., Borglin, S., Chakraborty, R., Fortney, J.L., Lamendella, R., Mason, O.U., Auer, M., Zemla, M., Bill, M., Conrad, M.E., Malfatti, S.A., **Tringe, S.G.**, Holman, H.Y., Hazen, T.C., Jansson, J.K. Deep-sea bacteria enriched by oil and dispersant from the Deepwater Horizon spill. *Environmental Microbiology* 14: 2405-2416, 2012.
40. Hollister, E.B., Forrest, A.K., Wilkinson, H.H., Ebbole, D.J., **Tringe, S.G.**, Malfatti, S.A., Holtzapple, M.T., Gentry, T.J. Mesophilic and Thermophilic Conditions Select for Unique but Highly Parallel Microbial Communities to Perform Carboxylate Platform Biomass Conversion. *PLoS ONE* 7: e39689, 2012.
41. Lundberg, D.S., Lebeis, S.L., Herrera Paredes, S., Yourstone, S., Gehring, J., Malfatti, S., Tremblay, J., Engelbrekton, A., Kunin, V., Glavina del Rio, T., Eickhorst, T., Ley, R.E., Hugenholtz, P., **Tringe, S.G.**, Dangl, J.L. Defining the core *Arabidopsis thaliana* root microbiome. *Nature* 488: 86-90, 2012.
42. Gilbert, J., Li, L.L., Taghavi, S., McCorkle, S.M., **Tringe, S.**, van der Lelie, D. Bioprospecting metagenomics for new glycoside hydrolases. *Methods in Molecular Biology* 908: 141-151, 2012.
43. Worden, A.Z., Janouskovec, J., McRose, D., Engman, A., Welsh, R.M., Malfatti, S., **Tringe, S.G.**, Keeling, P.J. Global distribution of a wild alga revealed by targeted metagenomics. *Current Biology* 22: R675-577, 2012.
44. Kozubal, M.A., Romine, M., Jennings, R.D., Jay, Z.J., **Tringe, S.G.**, Rusch, D.B., Beam, J.P., McCue, L.A., Inskeep, W.P. Geoarchaeota: a new candidate phylum in the Archaea from high-temperature acidic iron mats in Yellowstone National Park. *ISME Journal* 7: 622-634, 2013.
45. Hunt, D.E., Lin, Y., Church, M.J., Karl, D.M., **Tringe, S.G.**, Izzo, L.K., Johnson, Z.I. The relationship between abundance and specific activity of bacterioplankton in open ocean surface waters. *Applied and Environmental Microbiology* 79: 177-84, 2013.
46. Burow, L.C., Woebken, D., Marshall, I. P.G., Lindquist, E.A., Bebout, B.M., Prufert-Bebout, L., Hoehler, T.M., **Tringe, S.G.**, Pett-Ridge, J., Weber, P.K., Spormann, A.M., Singer, S.W. Anoxic carbon flux in photosynthetic microbial mats as revealed by metatranscriptomics. *ISME Journal* 7: 817-829, 2013.
47. Gori, F., **Tringe, S.G.**, Folino, G., van Hijum, S.A.F.T., Op den Camp, H.J.M, Jetten, M.S.M., Marchiori, E. Differences in sequencing technologies improve the retrieval of anammox bacterial genome from metagenomes. *BMC Genomics* 14:7, 2013.
48. Sentchilo, V., Mayer, A.P., Guy, L., Miyazaki, R., **Tringe, S.G.**, Barry, K., Malfatti, S., Goessman, A., Robinson-Rechavi, M., van der Meer, J.R. Community-Wide Plasmid Gene Mobilization and Selection. *ISME Journal* 7: 1173-1186, 2013.
49. Beck, D.A., Kalyuzhnaya, M.G., Malfatti, S.A., **Tringe, S.G.**, Glavina del Rio, T., Ivanova, N., Lidstrom, M.E., Chistoserdova, L. A metagenomic insight into freshwater methane-utilizing communities and evidence for cooperation between the *Methylococcaceae* and the *Methylophilaceae*. *PeerJ* 1: e23, 2013.
50. DeAngelis, K.M., D'Haeseleer, P.D., Chivian, D., Simmons, B., Arkin, A.P., Mavromatis, K., Malfatti, S., **Tringe, S.**, Hazen, T.C. Metagenomes of tropical soil-derived anaerobic switchgrass-adapted consortia with and without iron. *Standards in Genomic Sciences* 7:382-398, 2013.
51. Peiffer, J.A., Spor, A., Koren, O., Jin, Z., **Tringe, S.G.**, Dangl, J.L., Buckler, E.S., Ley, R.E. Diversity and heritability of the maize rhizosphere microbiome under field conditions. *Proceedings of the National Academy of Sciences* 110: 6548-6553, 2013.
52. He, S., Ivanova, N., Kirton, E., Allgaier, M., Bergin, C., Scheffrahn, R.H., Kyrpides, N.C., Warnecke, F., **Tringe, S.G.**, Hugenholtz, P. Comparative metagenomic and metatranscriptomic analysis of hindgut paunch

microbiota in wood-feeding and dung-residing higher termite species (*Nasutitermes corniger* and *Amitermes wheeleri*). PLOS One 8: e61126, 2013.

53. Dodsworth, J.A., Blainey, P.C., Murugapiran, S.K., Swingley, W.D., Ross, C.A., **Tringe, S.G.**, Chain, P.S.G., Raymond, J., Quake, S.R., Hedlund, B.P. Single-cell genomics and metagenomics suggest a fermentative, saccharolytic lifestyle for members of the OP9 lineage. Nature Communications 4: 1854, 2013.

54. Aylward, F.O., Burnum-Johnson, K.E., **Tringe, S.G.**, Teiling, C., Tremmel, D.M., Moeller, J.A., Scott, J.J., Barry, K.W., Piehowski, P.D., Nicora, C.D., Malfatti, S.A., Monroe, M.E., Purvine, S.O., Goodwin, L.A., Smith, R.D., Weinstock, G.M., Gerardo, N.M., Suen, G., Lipton, M.S., Currie, C.R. *Leucoagaricus gongylophorus* produces diverse enzymes for the degradation of recalcitrant plant polymers in leaf-cutter ant fungus gardens. Applied and Environmental Microbiology 79: 3770-3778, 2013.

55. Inskeep, W.P., Jay, Z.J., **Tringe, S.G.**, Herrgard, M., Rusch, D.B., YNP Metagenome Project Steering Committee and Working Group Members. The YNP Metagenome Project: Environmental Parameters Responsible for Microbial Distribution in the Yellowstone Geothermal Ecosystem. Frontiers in Microbiology 4: 67, 2013. (*co-corresponding author*)

56. Takacs-Vesbach, C., Inskeep, W.P., Jay, Z.J., Herrgard, M., Rusch, D.B., **Tringe, S.G.**, Kozubal, M.A., Hamamura, N., Macur, R.E., Fouke, B.W., Reysenbach, A.L., McDermott, T.R., Jennings, R., Hengartner, N.W., Xie, G. Metagenome Sequence Analysis of Filamentous Microbial Communities Obtained from Geochemically Distinct Geothermal Channels Reveals Specialization of Three Aquificales Lineages. Frontiers in Microbiology 4: 84, 2013.

57. Inskeep, W.P., Jay, Z.J., Herrgard, M., Kozubal, M.A., Rusch, D.B., **Tringe, S.G.**, Macur, R.E., Jennings, R., Boyd, E.S., Spear, J.R., Roberto, F., Young, M.J. Phylogenetic and functional analysis of metagenome sequence from high-temperature archaeal habitats demonstrate linkages between metabolic potential and geochemistry. Frontiers in Microbiology 4: 95, 2013.

58. Klatt, C.G., Inskeep, W.P., Herrgard, M., Jay, Z.J., Rusch, D.B., **Tringe, S.G.**, Parenteau, M.N., Ward, D.M., Boomer, S.M., Bryant, D.A., Miller, S.R. Community Structure and Function of High-temperature Chlorophototrophic Microbial Mats Inhabiting Diverse Geothermal Environments. Frontiers in Microbiology 4: 106, 2013.

59. Flowers, J.J., He, S., Malfatti, S., Glavina del Rio, T., **Tringe, S.G.**, Hugenholtz, P., McMahon, K.D. Comparative genomics of two "*Candidatus Accumulibacter*" clades performing biological phosphorus removal. ISME Journal 7: 2301-2314, 2013.

60. D'haeseleer, P., Gladden, J.M., Allgaier, M., Chain, P.S.G., **Tringe, S.G.**, Malfatti, S.A., Aldrich, J.T., Nicora, C.D., Robinson, E.W., Pasa-Tolic, L., Hugenholtz, P., Simmons, B.A., Singer, S.W. Proteogenomic Analysis of a Thermophilic Bacterial Consortium Adapted to Deconstruct Switchgrass. PLoSOne 8: e68465, 2013.

61. Rivers, A.R., Sharma, S., **Tringe, S.G.**, Martin, J., Joye, S., Moran, M.A. Transcriptional response of bathypelagic marine bacterioplankton to the Deepwater Horizon Oil Spill. ISME Journal 7: 2315-2329, 2013.

62. Castelle, C.J., Hug, L.A., Wrighton, K.C., Thomas, B.C., Williams, K.H., Wu, D., **Tringe, S.G.**, Singer, S., Eisen, J., Banfield, J.F. Extraordinary phylogenetic diversity and metabolic versatility in aquifer sediment. Nature Communications 4:2120, 2013.

63. Scully, E.D., Geib, S.M., Hoover, K., Tien, M., **Tringe, S.G.**, Barry, K.W., Glavina del Rio, T., Chovatia, M., Herr, J.R., Carlson, J.E. Metagenomic profiling reveals lignocellulose degrading systems in a microbial community associated with a wood-feeding beetle. PLoS One 8: e73827, 2013.

64. DeMaere, M.Z., Williams, T.J., Allen, M.A., Brown, M.V., Gibson, J.A.E., Rich, J., Lauro, F.M., Dyll-Smith, M., Davenport, K.M., Woyke, T., Kyrpides, N.C., **Tringe, S.G.**, Cavicchioli, R. High level of intergenera gene

exchange shapes the evolution of haloarchaea in an isolated Antarctic lake. *Proceedings of the National Academy of Sciences* 110: 16939-16944, 2013.

65. Markowitz, V.M., Chen, I.M., Chu, K., Szeto, E., Palaniappan, K., Pillay, M., Ratner, A., Huang, J., Pagani, I., **Tringe, S.**, Huntemann, M., Billis, K., Varghese, N., Tennesen, K., Mavromatis, K., Pati, A., Ivanova, N.N., Kyrpides, N.C. IMG/M 4 version of the integrated metagenome comparative analysis system. *Nucleic Acids Research* 42: D568-573, 2014.
66. Jay, Z.J., Rusch, D.B., **Tringe, S.G.**, Bailey, C., deM Jennings, R., Inskeep, W.P. Predominant Acidilobus-like populations from geothermal environments in Yellowstone National Park exhibit similar metabolic potential in different hypoxic microbial communities. *Applied Environmental Microbiology* 80: 294-305, 2014.
67. Hug, L.A., Castelle, C.J., Wrighton, K.C., Thomas, B.C., Sharon, I., Frischkorn, K.R., Williams, K.H., **Tringe, S.G.**, Banfield, J.F. Community genomic analyses constrain the distribution of metabolic traits across the Chloroflexi phylum and indicate roles in sediment carbon cycling. *Microbiome* 1: 22, 2013.
68. Lindemann, S.R., Moran, J.J., Stegen, J.C., Renslow, R.S., Hutchinson, J.R., Cole, J.K., Dohnalkova, A.C., Tremblay, J., Singh, K., Malfatti, S.A., Chen, F., **Tringe, S.G.**, Beyenal, H., Fredrickson, J.K. The Epsomitic Phototrophic Microbial Mat of Hot Lake, Washington: Community Structural Responses to Seasonal Cycling. *Frontiers in Microbiology* 4: 323, 2013.
69. Williams, T.J., Allen, M.A., DeMaere, M.Z., Kyrpides, N.C., **Tringe, S.G.**, Woyke, T., Cavicchioli, R. Microbial ecology of an Antarctic hypersaline lake: genomic assessment of ecophysiology among dominant haloarchaea. *ISME Journal*, 2014.
70. Howe, A.C., Jansson, J.K., Malfatti, S.A., **Tringe, S.G.**, Tiedje, J.M., Brown, C.T. Tackling soil diversity with the assembly of large, complex metagenomes. *Proceedings of the National Academy of Sciences* 111: 4904-4909, 2014.
71. Wagner, M.R., Lundberg, D.S., Coleman-Derr, D., **Tringe, S.G.**, Dangl, J.L., Mitchell-Olds, T. Natural soil microbes alter flowering phenology and the intensity of selection on flowering time in a wild Arabidopsis relative. *Ecology Letters* 17:717-726, 2014.
72. Singh, G., Srinivasen, R., Cheng, J.F., Peng, Z., Fujimura, K., Baek, M.S., Panzer, A.R., **Tringe, S.G.**, Chen, F., Sorek, R., Weng, L., Bristow, J., Wiener-Kronish, J.P., Lynch, S.V. Rearrangement of a Large Novel *Pseudomonas aeruginosa* Gene Island in Strains Isolated from a Patient Developing Ventilator-Associated Pneumonia. *Journal of Clinical Microbiology* 52:2430-2438, 2014.
73. Coleman-Derr, D., **Tringe, S.G.** Building the crops of tomorrow: advantage of symbiont-based approaches to improving abiotic stress tolerance. *Frontiers in Microbiology* 5: 283, 2014.
74. Hawley, E.R., Malfatti, S.A., Pagani, I., Huntemann, M., Chen, A., Foster, B., Copeland, A., Glavina del Rio, T., Pati, A., Jansson, J., Gilbert, J.A., **Tringe, S.G.**, Lorenson, T., Hess, M. Metagenomes from two microbial consortia associated with Santa Barbara seep oil. *Marine Genomics* 18 Pt B: 97-99, 2014.
75. Piao, H., Lachman, M., Malfatti, S., Sczyrba, A., Knierim, B., Auer, M., **Tringe, S.G.**, Mackie, R.I., Yeoman, C.J., Hess, M. Temporal dynamics of fibrolytic and methanogenic rumen microorganisms during in situ incubation of switchgrass determined by 16S rRNA gene profiling. *Frontiers in Microbiology* 5:307, 2014.
76. Wu, Y.W., Tang, Y.T., **Tringe, S.G.**, Simmons, B.A., Singer, S.W. MaxBin: an automated binning method to recover individual genomes from metagenomes using an expectation-maximization algorithm. *Microbiome* 2:26, 2014.
77. Hawley, E.R., Piao, H., Scott, N.M., Malfatti, S., Pagani, I., Huntemann, M., Chen, A., Glavina del Rio, T., Foster, B., Copeland, A., Jansson, J., Pati, A., **Tringe, S.**, Gilbert, J.A., Lorenson, T.D., Hess, M. Metagenomic

analysis of microbial consortium from natural crude oil that seeps into the marine ecosystem offshore Southern California. *Standards in Genomic Science* 9: 1259-74, 2014.

78. Prestat, E., David, M.M., Hultman, J., Tas, N., Lamendella, R., Dvornik, J., Mackelprang, R., Myrold, D.D., Jumpponen, A., **Tringe, S.**, Holman, E., Mavromatis, K., Jansson, J.K. FOAM (Functional Ontology Assignments for Metagenomes): A Hidden Markov Model (HMM) database with environmental focus. *Nucleic Acids Research* 42:e145, 2014.
79. O'Connor, R.M., Fung, J.M., Sharp, K.H., Benner, J., McClung, C., Cushing, S., Lamkin, E., Fomenkov, A., Henrissat, B., Londer, Y., Scholz, M.B., Posfai, J., Malfatti, S., **Tringe, S.G.**, Woyke, T., Malmstrom, R.R., Coleman-Derr, D., Altamia, M.A., Dedrick, S., Kaluziak, S.T., Haygood, M.G., Distel, D.L. Gill bacteria enable a novel digestive strategy in a wood-feeding mollusk. *Proceedings of the National Academy of Sciences* 111: E5096-104, 2014.
80. Aylward, F.O., Suen, G., Biedermann, P., Adams, A., Scott, J., Malfatti, S., Glavina del Rio, T., **Tringe, S.G.**, Poulsen, M., Raffa, K., Klepzig, K., Currie, C. Convergent Bacterial Microbiotas in the Fungal Agricultural Systems of Insects. *mBio* 5: e02077, 2014.
81. Nobu, M.K., Narihiro, T., Rinke, C., Kamagata, Y., **Tringe, S.G.**, Woyke, T., Liu, W.T. Microbial dark matter ecogenomics reveals complex synergistic networks in a methanogenic bioreactor. *ISME Journal* 9: 1710-1722, 2015.
82. Zhou, J., He, Z., Yang, Y., Deng, Y., **Tringe, S.G.**, Alvarez-Cohen, L. High-throughput metagenomic technologies for complex microbial community analysis: open and closed formats. *MBio* 6: e02288-14, 2015.
83. Hug, L.A., Thomas, B.C., Brown, C.T., Frischkorn, K.R., Williams, K.H., **Tringe, S.G.**, Banfield, J.F. Aquifer environment selects for microbial species cohorts in sediment and groundwater. *ISME Journal* 9: 1846-1856, 2015.
84. Sharon, I., Kertesz, M., Hug, L.A., Pushkarev, D., Blauwkamp, T.A., Castelle, C.J., Amirebrahimi, M., Thomas, B.C., **Tringe, S.G.**, Williams, K.H., Banfield, J.F. Accurate, multi-kb synthetic reads resolve complex populations and detect rare microorganisms. *Genome Research* 25: 534-43, 2015.
85. Castelle, C.J., Wrighton, K.C., Thomas, B.C., Hug, L.A., Brown, C.T., Wilkins, M.J., Frischkorn, K.R., **Tringe, S.G.**, Singh, A., Markillie, M., Williams, K.H., Banfield, J.F. Genomic Expansion of Domain Archaea highlights roles for organisms from new phyla in subsurface anaerobic carbon cycling. *Current Biology* 25:690-701, 2015.
86. Luef, B., Frischkorn, K.R., Wrighton, K.C., Holman, H.Y.N., Birarda, G., Thomas, B.C., Singh, A., Williams, K.H., Siegerist, C.E., **Tringe, S.G.**, Downing, K.H., Comolli, L.R., Banfield, J.F. Diverse, uncultivated ultra-small bacterial cells in groundwater. *Nature Communications* 6:6372, 2015.
87. Cantor, M., Nordberg, H., Smirnova, T., Hess, M., **Tringe, S.**, Dubchak, I. Elviz – exploration of metagenome assemblies with an interactive visualization tool. *BMC Bioinformatics* 16:130, 2015.
88. He, S., Malfatti, S.A., McFarland, J.W., Anderson, F.E., Pati, A., Huntemann, M., Tremblay, J., Glavina del Rio, T., Waldrop, M., Windham-Myers, L., **Tringe, S.G.** Patterns in wetland microbial community composition and functional gene repertoire associated with methane emissions. *Mbio* 6: e00066-15, 2015.
89. Beam, J.P., Jay, Z.J., Schmid, M.C., Rusche, D.B., Romine, M.F., dem Jennings, R., Kozubal, M.A., **Tringe, S.G.**, Wagner, M., Inskeep, W.P. Ecophysiology of an uncultivated lineage of Aigarchaeota from an oxic, hot spring filamentous 'streamer' community. *ISME Journal*, 2015.
90. Tremblay, J., Singh, K., Fern, A., Kirton, E.S., He, S., Lee, J., Woyke, T., Chen, F., Dangl, J.L., **Tringe, S.G.** Primer and platform effects on 16S rRNA tag sequencing. *Frontiers in Microbiology* 6: 771, 2015.



91. Lebeis, S.L., Herrera Paredes, S., Lundberg, D.S., Breakfield, N., Gehring, J., McDonald, M., Malfatti, S., Glavina del Rio, T., Jones, C.D., **Tringe, S.G.**, Dangl, J.L. Salicylic acid modulates colonization of the root microbiome by specific bacterial taxa. *Science* 349: 860-4, 2015.
92. Oyserman, B.O., Noguera, D.R., Glavina del Rio, T., **Tringe, S.G.**, McMahon, K.D. Metatranscriptomic insights on gene expression and regulatory controls in *Candidatus Accumulibacter phosphatis*. *ISME Journal*, in press.
93. Coleman-Derr, D., Gross, S., North, G., Partida-Martinez, L., Clingenpeel, S., Woyke, T., DeAngelis, K., Visel, A., **Tringe, S.G.** Biogeography and cultivation affect microbiome composition in drought-adapted plants. *New Phytologist* 2015.
94. Singer, E., Coleman-Derr, D., Bowman, B., Bushnell, B., Gies, E., Cheng, J.F., Copeland, A., Hallam, S., **Tringe, S.G.**, Woyke, T. High-resolution phylogenetic microbial community profiling. Submitted.
95. Bowers, R.M., Clum, A., Tice, H., Lim, J., Singh, K., Ciobanu, D., Ngan, C.Y., Cheng, J.F., **Tringe, S.G.**, Woyke, T. How low can you go? Impact of low input library preparation protocols on the metagenomic reconstruction of a mock microbial community. *BMC Genomics*, in press.
96. Lamendella, R., Jesus, E., Grube, A., McClure, E., Liang, C., **Tringe, S.**, Tiedje, J., Jansson, J.K. Impact of cultivation on the native Great Prairie microbiome. Manuscript in preparation.

## **C. Research Support**

### **Ongoing Research Support**

“Systems Analysis of the Physiological and Molecular Mechanisms of Sorghum Nitrogen Use Efficiency, Water User Efficiency and Interactions with the Soil Microbiome” proposal to Department of Energy Systems Biology Research to Advance Sustainable Bioenergy Crops. PI for JGI subcontract, \$1,007,000 over 5 years, start date 10/1/2015.

“INSPIRE Track 2: Defining the Organizational Principles of Microbial Communities Colonizing Plant Roots” proposal to National Science Foundation, Co-PIs Jeff Dangl (University of North Carolina), Vladimir Jojic, Elizabeth Shank, Pieter Dorrestein and Ruth Ley. PI for JGI subcontract, \$412,436 over 3 years, start date 9/1/2014.

“Next Generation Ecosystem Experiments in the Arctic (NGEE-Arctic).” Proposal to DOE Joint Genome Institute Community Sequencing Program 2013, co-PI Janet Jansson. Start date 10/15/2012.

“Microbial communities in biological carbon sequestration.” DOE Early Career Research Program Award. \$2,500,013 over 5 years. Start date 8/15/11.

### **Past Research Support**

“PGRP-GEPR-Defining Plant-Associated Metagenomes” proposal to National Science Foundation, co-PIs Jeff Dangl (University of North Carolina) and Ruth Ley (Cornell University). PI for JGI subcontract, \$1,387,591, 5/6/2010 – 3/31/2015.

“Microbial community impact on carbon sequestration in managed wetland ‘carbon farming’” proposal to DOE Joint Genome Institute Community Sequencing Program 2011, co-PIs Susannah Tringe, Mark Waldrop, Lisamarie Windham-Myers and Tanja Woyke. 300 Gb sequence data on Illumina sequencing platform. 11/1/2010-10/31/2013.

“Meta-‘omics’ analysis of microbial carbon cycling responses to altered rainfall inputs in native prairie soils”  
proposal to DOE Office of Biological and Environmental Research, PI David Myrold. \$65,500 salary support.  
6/1/2010-5/31/2013.