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### ACADEMIC APPOINTMENTS

**1998-1999**      **Research Assistant, Natural History Museum, London**  
**2000**            **Chief Science Officer, ANARE station Davis, Antarctica.**  
**2005-2010**      **Molecular Ecologist, Senior Scientist**  
                         **Plymouth Marine Laboratory, Plymouth, UK**  
**2010-Present**   **Environmental microbiologist Grade 707 Argonne National Laboratory,**  
                         **and Assistant Professor in Dept of Ecology and Evolution, University of**  
                         **Chicago, USA**

### ACADEMIC TRAINING

**1999-2002**   **University of Nottingham / Unilever Colworth Laboratories – Ph.D.**  
                         **‘Cold Adaptation and Biodiversity of Antarctic Lake Bacteria’**  
                         *PhD Life and Environmental Science/Food Microbiology*  
**1995-1998**   **Kings College, University of London**  
                         *BSc with First Class Honours in Biological Sciences with specialization in Marine*  
                         *Biology*  
**2002-2005**   **Post-Doctoral Fellowship - Biochemistry**  
                         *Department of Biochemistry, Queen’s University, Ontario, Canada*

### SCHOLARSHIP

#### Peer-reviewed publications in the primary literature, exclusive of abstracts:

1. Roy A-S, Gibbons, SM, Shunck H, Owens S, Caporaso JG, Sperling M, Nissimov, JI, Romac, S, Bittner L, Riebesell U, LaRoche J, **Gilbert JA**. 2012. Ocean acidification shows negligible impacts on high-latitude bacterial community structure in coastal pelagic mesocosms. **Biogeosciences Discussions**. 9, 13319-13349
2. Zarraonaindia I, Smith D, **Gilbert JA**. 2012. Beyond the genome: community-level analysis of the microbial world. **Biology & Philosophy**. 10.1007/s10539-012-9357-8
3. Fierer N, Leff JW, Adams BJ, Nielsen UN, Bates ST, Lauber CL, Owens S, **Gilbert JA**, Wall DH, Caporaso JG. 2012. Cross-biome metagenomic analyses of soil microbial communities and their functional attributes. **PNAS**. 109 (52), 21390-21395.
4. Trimble WL, Phung LT, Meyer F, **Gilbert JA**, Silver S. 2012. Draft Genome Sequence of *Agrobacterium albertimagni* Strain AOL15. **Journal of Bacteriology**. 194 (24) 6986-6987.

5. Robbins R, Amaral-Zettler L, Bik H, Blum S, Edwards J, Field D, Garrity G, **Gilbert JA**, Kottmann R, Krishtalka L, Lapp H, Lawrence C, Morrison N, Tuama EO, Parr C, San Gil I, Schindl D, Schriml L, Vieglas D, Wooley J. RCN4GSC Workshop Report: Managing Data at the Interface of Biodiversity and (Meta) Genomics, March 2011. **Standards in Genomic Sciences** 7 (1)
6. Trimble WL, Phung LT, Meyer F, Silver S, **Gilbert JA**. 2012. Draft Genome Sequence of *Achromobacter piechaudii* Strain HLE. **Journal of Bacteriology** 194 (22), 6355-6355.
7. Sangwan N, Lata P, Dwivedi V, Singh A, Niharika N, Kaur J, Anand S, Malhortra J, Jindal S, Nigam A, Lai D, Dua A, Saxena A, Garg N, Verma M, Kaur J, Mukherjee U, **Gilbert JA**, Dowd SE, Raman R, Khurana P, Khurana JP, Lal R. 2012 Comparative Metagenomic Analysis of Soil Microbial Communities across Three Hexachlorocyclohexane Contamination Levels. **PLoS ONE** 7(9): e46219. doi:10.1371/journal.pone.0046219
8. Trimble WL, Keegan KP, D'Souza M, Wilke A, Wilkening J, **Gilbert JA**, Meyer F. 2012. Short-read reading-frame predictors are not created equal: sequence error causes loss of signal. **BMC bioinformatics** 13 (1), 183
9. Sperling M, Piontek J, Gerdtts G, Wichels A, Schunck H, Roy AS, La Roche J, **Gilbert JA**, Bittner L, Romac S, Riebesell U, Engel A. 2012. Effect of elevated CO<sub>2</sub> on the dynamics of particle attached and free living bacterioplankton communities in an Arctic fjord. **Biogeosciences Discuss**, 9, 10725-10755
10. Olivas AD, Shogan BD, Valuckaite V, Zaborin A, Belogortseva N, Musch M, Meyer F, Trimble WL, An G, **Gilbert JA**, Zaborina O, Alverdy JC. 2012. Intestinal Tissues Induce an SNP Mutation in *Pseudomonas aeruginosa* That Enhances Its Virulence: Possible Role in Anastomotic Leak. **PLoS ONE** 7(8): e44326. doi:10.1371/journal.pone.0044326
11. Phung LT, Trimble WL, Meyer F, **Gilbert JA**, Silver S. 2012. Draft Genome Sequence of *Alcaligenes faecalis* subsp. *faecalis* NCIB 8687 (CCUG 2071). **Journal of Bacteriology** 194 (18), 5153-5153
12. Davies N, Meyer C, **Gilbert JA**, Amaral-Zettler L, Deck J, Bicak M, Rocca-Serra P, Sansone S-A, Willis K, Field D. 2012. A Call for an International Network of Genomic Observatories (GOs). **GigaScience**. 1(1) 5.
13. **Gilbert JA**, Bao Y, Wang H, Sansone, S-A, Edmunds, SC, Morrison N, Meyer F, Schriml LM, Davies N, Sterk P, Wilkening J, Garrity GM, Field D, Robbins R, Smith D, Mizrahi I, Moreau C. 2012. Report of the 13<sup>th</sup> Genomic Standards Consortium Meeting, Shenzhen China, March 4-7<sup>th</sup> 2012. **Standards in Genomic Science**. 6(2): 276–286.
14. Larsen, P, Gibbons S, **Gilbert JA**. 2012. Bacterial diversity and function across time and space: modeling microbial community structure. **FEMS Microbiology Letters**. Volume 332, Issue 2, pages 91–98,
15. Knight R, Jansson J, Field D, Fierer N, Desai N, Fuhrman J, Hugenholtz P, Meyer F, Stevens R, Bailey M, Gordon JI, Kowalchuk G, **Gilbert JA**. 2012. Designing Better Metagenomic Surveys: The role of experimental design and metadata capture in making useful metagenomic datasets for ecology and biotechnology. **Nature Biotechnology**. 30 (6), 513–520
16. Larsen PE, Field D, **Gilbert JA**. 2012. Predicting bacterial community assemblages using an artificial neural network approach. **Nature Methods**. 9 621-625 doi:10.1038/nmeth.1975
17. **Gilbert JA**, Catlett C, Desai, N, Field D, Knight R, White O, Robbins R, Sankaran R, Meyer F. 2012. White Paper: Conceptualizing a Genomics Software Institute (GSI). **Standards in Genomic Science**. 6:1.
18. Larsen PE, Hamada Y, **Gilbert JA**. Modeling Microbial Communities. **Journal of Biotechnology**. 160 (1–2) 17–24.
19. Willetts A, Joint I, **Gilbert JA**, Trimble W, Muhling M. Isolation and initial characterization of a novel type of Baeyer-Villiger monooxygenase activity from a marine microorganism. **Microbial Biotechnology**. 5(4) 549-559.

20. Thomas T, **Gilbert JA**, Meyer F. 2012. Metagenomics – a guide from sampling to data analysis. **Microbial Informatics and Experimentation**. 2:3; doi:10.1186/2042-5783-2-3.
21. Delmont TO, Prestat E, Keegan KP, Faubladiere M, Robe P, Clark IM, Pelletier E, Hirsch PR, Meyer F, **Gilbert JA**, Le Paslier D, Simonet P, Vogel TM. 2012. Structure, Fluctuation and Magnitude of a Natural Prairie Soil Metagenome. **ISME J**. advance online publication 2 February 2012; doi: 10.1038/ismej.2011.197.
22. Caporaso JG, Lauber CL, Walters WA, Berg-Lyons D, Huntley J, Fierer N, Owens SM, Betley J, Fraser L, Bauer M, Gormley N, **Gilbert JA**, Smith G, Knight R. 2012. Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. **ISME J**. 6, 1621-1624.
23. **Gilbert JA**, Meyer F. 2012. Modeling the Earth's Microbiome: A real world deliverable for microbial ecology. **ASM Microbe Magazine**. 7 (2), 64
24. Amaro F, **Gilbert JA**, Owens S, Trimble W, Shuman HA. 2012. Whole-genome sequence of the human pathogen *Legionella pneumophila* Serotype 12 strain 570-CO-H. **Journal of Bacteriology**. 194 (6), 1613-1614
25. Desai N, Antonopoulos D, **Gilbert JA**, Glass E, and Meyer F. 2012. From genomics to metagenomics. **Current Opinions in Biotechnology**. 23(1): 72-6.
26. Sansone S-A, Rocca-Serra P, Field D, Maguire E, Taylor C, Hofmann O, Fang H, Neumann S, Tong W, Amaral-Zettler L, Begley K, Booth T, Bougueleret L, Burns G, Chapman B, Clark T, Coleman L, Copeland J, Das S, de Daruvar A, de Matos P, Dix I, Edmunds S, Evelo CT, Forster MJ, Gaudet P, **Gilbert JA**, Goble C, Griffin JL, Jacob D, Kleinjans J, Harland L, Haug K, Hermjakob H, Ho Sui SJ, Laederach A, Liang S, Marshall S, McGrath A, Merrill E, Reilly D, Roux M, Shamu CE, Shang CA, Steinbeck C, Trefethen A, Williams-Jones B, Wolstencroft K, Xenarios I & Hide W. 2012. Toward interoperable bioscience data. **Nature Genetics** 44, 121–126 (2012) doi:10.1038/ng.1054.
27. **Gilbert JA**, Steele J, Caporaso JG, Steinbruck L, Somerfield PJ, Reeder J, Temperton B, Huse S, Joint I, McHardy AC, Knight R, Fuhrman JA, Field D. 2012. Defining seasonal marine microbial community dynamics. **ISME J**. 6, 298-308.
28. Phung L, Silver S, Trimble W, **Gilbert JA**. 2012. Draft genome of Halomonas strain GFAJ-1 (ATCC BAA-2256). **Journal of Bacteriology**. 194 (7), 1835-1836.
29. Foster J, Bunge J, **Gilbert JA**, Moore J. 2012. Measuring the Microbiome: perspective on advances in exploring microbial life. **Briefings in Bioinformatics**. 13(4):420-9
30. Davies N, Field D, Meyer C, **Gilbert JA** et al 2012. Sequencing data: A genomic network to monitor Earth. **Nature**. 481, 145.
31. Caporaso JG, Field D, Paszkiewicz K, Knight R, **Gilbert JA**. 2012. Evidence for a persistent microbial community in the Western English Channel. **ISME J**. 6, 1089–1093 doi: 10.1038/ismej.2011.162.

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32. **Gilbert JA**, Bailey M, Field D, Fierer N, Fuhrman JA, Hu B, Jansson J, Knight R, Kowalchuk GA, Kyrpides NC, Meyer F, Stevens R. 2011. The Earth Microbiome Project: The Meeting Report for the 1st International Earth Microbiome Project Conference, Shenzhen, China, June 13th-15th 2011. **Standards in Genomic Science**. 5(2).
33. Jeffries TC, Seymour JR, **Gilbert JA**, Dinsdale E, Newton K, Leterne SSC, Roudnew B, Smith RJ, Seuront L, Mitchell JG. Substrate type determines metagenomic profiles from diverse chemical habitats. **PLoS ONE** 6(9): e25173. doi:10.1371/journal.pone.0025173 PMID: 21966446
34. **Gilbert JA**. 2011. The Smallest Champions in the World. **Marine Scientist**. 34:16-19
35. Kulakova AN, Simthen M, Pavlov E, **Gilbert JA**, Quinn JP, McGrath JW. Direct quantification of inorganic polyphosphate in microbial cells using 4'-6-diamidino-2-phenylindole (DAPI). **Environmental Science and Technology**. *In Press*.
36. O'Brien SL, Glass EM, Brulc JM, **Gilbert JA**, Antonopoulos DA, Meyer F. 2011. Meeting

- Report: The 2<sup>nd</sup> Annual Argonne Soils Workshop, Argonne National Laboratory, Chicago USA, October 6-8, 2010. **Standards in Genomic Science**. 5(2)
37. **Gilbert JA**, O'Dor R, King N, Vogel T. 2011. The importance of metagenomic surveys to microbial ecology: or why Darwin would have been a metagenomic scientist. **Microbial Informatics and Experimentation**, 1:5
  38. Larsen PE, Collart F, Field D, Meyer F, Keegan KP, Henry CS, McGrath J, Quinn J, **Gilbert JA**. 2011. Predicted Relative Metabolomic Turnover (PRMT): determining metabolic turnover from a coastal marine metagenomic dataset. **Microbial Informatics and Experimentation**. 1:4
  39. White J, **Gilbert JA**, Hill G, Hill E, Huse SM, Weightman AJ, and Mahenthalingam E. 2011. Culture-independent analysis of bacterial fuel contamination provides insights into the level of concordance with the standard industry practice of aerobic cultivation. **Applied and Environmental Microbiology** 77:13, 4527-4538.
  40. Jansson J, Neufeld J, Moran MA, **Gilbert JA**. 2011. Omics for Understanding Microbial Functional Dynamics. **Environmental Microbiology: Special Issue: OMICS Driven Microbial Ecology**. 14(1), 1-3.
  41. Field D, Amaral-Zettler L, Cochrane G, Cole JR, Dawyndt P, Garrity GM, **Gilbert JA**, Glöckner FO, Hirschman L, Karsch-Mizrachi I, Klenk H-P, Knight R, Kottmann R, Kyrpides N, Meyer F, San Gil I, Sansone S-A, Schriml LM, Sterk P, Tatusova T, Ussery DW, White O, Wooley J. 2011. The Genomic Standards Consortium. **PLoS Biology** 9(6): e1001088.
  42. Best A, DeJongh M, Devold S, **Gilbert JA**, Glass E, Henry CS, Larsen P, Meyer F, Overbeek R, Stevens RL, Vonstein V, Wilke A, Wilkening J, Xia F. 2011. Connecting Genotype to Phenotype in the Era of High-Throughput Sequencing. **Biochimica et Biophysica Acta General Subjects**. 1810(10): 967-977
  43. Amanda Birmingham, Jose C Clemente, Narayan Desai, **Jack A. Gilbert**, Antonio Gonzalez, Nikos Kyrpides, Folker Meyer, Eric Nawrocki, Peter Sterk, Jesse Stombaugh, Zasha Weinberg, Doug Wendel, Neocles B Leontis, Craig Zirbel, Rob Knight, Alain Laederach. 2011. Meeting report of the RNA Ontology Consortium January 8-9, 2011. **Standards in Genomic Science**, 4:2.
  44. Temperton B, Thomas S, Tait K, Parry H, Emery M, Allen M, Quinn J, McGrath J, **Gilbert JA**. 2011. Permanent draft genome sequence of *Vibrio tubiashii* strain NCIMB 1337 (ATCC19106). **Standards in Genomic Science**. 4:2
  45. Laverock B, **Gilbert JA**, Tait K, Osborn AM, Widdicombe S. 2011. Bioturbation: impact on the marine nitrogen cycle. **Biochem Soc Trans**. 39(1):315-20.
  46. Yilmaz P, **Gilbert JA**, Knight R, Amaral-Zettler L, Mizrachi I, Chochrane G, Nakamura Y, Assunta-Sansone S, Glockner F-O, Field D. 2011. The Genomic Standards Consortium: Bringing Standards to Life for Microbial Ecology. **ISME J**. 5, 1565-1567 doi:10.1038/ismej.2011.39
  47. Yilmaz P, Kottmann R, Field D, Knight R, Cole JR, Amaral-Zettler L, **Gilbert JA** et al. 2011. Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. **Nature Biotechnology**, 29, 415-420.
  48. Cooley NA, Kulakova AN, Villareal-Chiu JF, **Gilbert JA**, McGrath JW, Quinn JP. 2011. Phosphonoacetate Biosynthesis: In vitro Detection of a Novel NADP+ Dependent Phosphonoacetaldehyde Oxidizing Activity in Cell Extracts of a Marine *Roseobacter*. **Microbiology**, 80(3), 335-340.
  49. Turk K, Pereira N, Swift P, Shelley R, Zehr J, Lohan M, Woodward EMS, Rees A, **Gilbert JA**. 2011. Nitrogen fixation across a gradient of primary productivity. **ISME J**. 5, 1201-1212 doi:10.1038/ismej.2010.205
  50. **Gilbert JA**, Meyer F and Bailey M. 2011. The Future of microbial metagenomics (or is ignorance bliss?). **ISME J**. 5, 777-779 doi:10.1038/ismej.2010.178

51. Temperton B, **Gilbert JA**, Quinn JP, McGrath JW (2011) Novel Analysis of Oceanic Surface Water Metagenomes Suggests Importance of Polyphosphate Metabolism in Oligotrophic Environments. **PLoS ONE** 6(1): e16499. doi:10.1371/journal.pone.0016499
52. **Gilbert JA** and Dupont C. 2011. Marine Metagenomics. **Annual Review of Marine Science**. Volume 3: 347-371.
53. **Gilbert JA**, O'Dor R, Vogel T. 2011. Survey studies are still vital to science. **Nature**. 469, 162.

## 2010

54. **Gilbert JA**, Meyer F, Knight R, Field D, Kyrpides N, Yilmaz P, Wooley J. 2010. Meeting report: GSC M5 roundtable at the 13<sup>th</sup> International Society for Microbial Ecology meeting in Seattle, WA, USA, August 22-27<sup>th</sup> 2010. **Standards in Genomic Science**. 3:3
55. **Gilbert JA**, Meyer F, Antonoploulos D, Balaji P, Brown CT, Brown CT, Desai N, Eisen JA, Evers D, Feng W, Huson D, Jasson J, Knight R, Knight J, Kolker E, Kostantindis K, Kostka J, Kyrpides, N, Mackelprang R, McHardy A, Quince C, Raes J, Sczyrba A, Shade A, Stevens R. 2010. Meeting Report. The Terabase Metagenomics Workshop and the Vision of an Earth Microbiome Project. **Standards in Genomic Science**. 3:3.
56. **Gilbert JA**, Meyer F, Jansson J, Gordon J, Pace N, Tiedje J, Ley R, Fierer N, Field D, Kyrpides N, Glockner F-O, Klenk H-P, Wommack KE, Glass E, Docherty K, Gallery R, Stevens R, Knight R. 2010. The Earth Microbiome Project: Meeting report of the "1<sup>st</sup> EMP meeting on sample selection and acquisition" at Argonne National Laboratory October 6<sup>th</sup> 2010. **Standards in Genomic Science**. 3:3.
57. Glass E, Meyer F, **Gilbert JA**, Field D, Hunter S, Kottman R, Kyrpides N, Sansone S, Schriml L, Sterk P, White O, Wooley J. 2010. Meeting report from the Genomics Standards Consortium (GSC) workshop 10. **Standards in Genomic Science** 3:3.
58. Davidsen T, Madupu R, Sterk P, Field D, Garrity G, **Gilbert JA**, Glöckner F-O, Hirschman L, Kolker E, Kottmann R, Kyrpides N, Meyer F, Morrison N, Schriml L, Tatusova T, Wooley J. 2010. Meeting Report from the Genomic Standards Consortium (GSC) Workshop 9. **Standards in Genomic Science**. 3:3.
59. **Gilbert JA**, Field D, Swift P, Thomas S, Cummings D, et al. (2010) The Taxonomic and Functional Diversity of Microbes at a Temperate Coastal Site: A 'Multi-Omic' Study of Seasonal and Diel Temporal Variation. **PLoS ONE** 5(11): e15545. doi:10.1371/journal.pone.0015545.
60. Mitra S, Rupek P, Urich T, **Gilbert JA**, Meyer F, Huson DH. 2010. Functional analysis of meta-genomes and -transcriptomes using SEED and KEGG. **BMC Bioinformatics**. 12(Suppl 1):S12+.
61. **Gilbert JA**, Meyer F, Joint I, Mühlhling M, Field D. 2010. Short Metagenome Report: Metagenomes and metatranscriptomes from the L4 long term coastal monitoring station in the Western English Channel. **Standards in Genomic Science**. Vol 3 (2).
62. **Gilbert JA**, Meyer F, Field D, Schriml LM, Garrity GM. 2010. Metagenomics: A founding finds its feet. **Standards in Genomic Science**. Vol 3 (2).
63. Heidelberg KB, **Gilbert JA** and Joint I. 2010. Mini Review: Marine genomics: at the interface of marine microbial ecology and biodiscovery. **Microbial Biotechnology**. 3(5), 531–543
64. Laverock B., Widdicombe S, Tait K, Smith C, Osborn M, **Gilbert JA**. 2010. The impact of burrowing shrimp on bacterial diversity in temperate coastal sediments. **ISME J**. 4, 1531–1544.
65. Hirschman L., Sterk P., Field D., Wooley J., Cochrane G., **Gilbert JA**., Kolker E., Kyrpides N., Meyer F., Mizrahi I., Nakamura Y., Sansone S., Schriml L., Tatusova T., White O. and Yilmaz P. 2010. Meeting Report: "Metagenomics, Metadata and Meta-analysis" (M3)

Workshop at the Pacific Symposium on Biocomputing 2010. **Standards in Genomic Sciences**, Vol 2, No 3

66. **Gilbert JA**. 2010. Beyond the Infinite – tracking bacterial gene expression. **Microbiology Today**. 37:2; 82-85.
67. Mitra S, **Gilbert JA**, Field D & Huson DH. 2010. Comparison of multiple metagenomes using phylogenetic networks based on ecological indices. **ISME J**. 4, 1236-1242
68. Field D, Friedberg I, Sterk P, Kottmann R, Glöckner FO, Hirschman L, Garrity G, Cochrane G, Wooley J, and **Gilbert J.A.** 2010. Meeting Report: “Metagenomics, Metadata and Meta-analysis” (M3) Special Interest Group at ISMB 2009. **Standards in Genomic Science**. Vol 1, No 3.
69. Craft J., **Gilbert JA**, Temperton B., Dempsey KA, Ashelford K, Tiwari B, Hutchinson T & Chipman K. 2010. The mussel transcriptome: analysis using pyrosequencing. **PLoS One** 5(1): e8875.
70. Thomas S, Burdett H, Temperton B, Wick R, Snelling D, Woodward M, McGrath J, Quinn J, Munn C and **Gilbert JA**. 2010. The diversity of *phnA* gene homologues in temperature-stressed Cnidarian-associated Bacteria. **ISME J**. 4, 459-461 doi:10.1038/ismej.2009.129

## 2009

71. **Gilbert JA**, Field D, Swift P, Newbold L, Oliver A, Smyth T, Somerfield P, Huse S, Joint I. 2009. Seasonal succession of microbial communities in the Western English Channel using 16S rDNA-tag pyrosequencing. **Environmental Microbiology**. 11(12), 3132–3139
72. Temperton B, Field D, Oliver A, Tiwari B, Joint I and **Gilbert JA**. 2009. Bias in assessments of marine microbial biodiversity in fosmid libraries as evaluated by pyrosequencing. **ISME J** 3: 792-96.
73. Quinn J, Kulakova A, Kulakov L, Villarreal-Chiu J, **Gilbert JA**, McGrath J. 2009. Expression of the Phosphonoalanine Degradative Gene Cluster from *Variovorax* sp. Pal2 is induced by Growth on Phosphonoalanine and Phosphonopyruvate. **FEMS Microbiology Letters**. 292(1):100-6.
74. **Gilbert JA**, Thomas S, Cooley NA, Kulakova A, Field D, Booth T, McGrath JW, Quinn JP, Joint I. 2009. Potential for Phosphonate utilisation by marine bacteria in temperate coastal waters. **Environmental microbiology**. 11(1):111-25

## 2008

75. Rees AP, **Gilbert JA**, Kelly-Gerreyn BA. 2008. Evidence of Nitrogen fixation in a temperate coastal sea (western English Channel). **Marine Ecology Progress Series** Vol. 374: 7–12
76. **Gilbert JA**, Field D, Huang Y, Edwards R, Li W, et al. (2008) Detection of Large Numbers of Novel Sequences in the Metatranscriptomes of Complex Marine Microbial Communities. **PLoS ONE** 3(8): e3042. doi:10.1371/journal.pone.0003042
77. **Gilbert JA**, Muhling M & Joint I. 2008. A SAR11 fosmid clone with coding sequences not present in the “*Candidatus* Pelagibacter ubique” genome. **ISME J**. 2(7):790-3
78. Susanna-Assunta Sansone, Philippe Rocca-Serra, Dawn Field, **Jack Gilbert**, et al. 2008. The first RSBI (ISA-TAB) workshop: “can a simple format work for complex studies?”. **OMICS**. 12(2):143-9.
79. Field D, Joint I, **Gilbert JA** et al. 2008. Towards a richer description of our complete collection of genomes and metagenomes: the “Minimum Information about a Genome Sequence” (MIGS) specification. **Nature Biotechnology**. 26(5):541-7.
80. Garnham C.P.<sup>†</sup>, **Gilbert JA**<sup>\*</sup>, Hartman C<sup>†</sup>, Campbell RL<sup>†</sup>, Laybourn-Parry J.<sup>‡</sup> and Davies PL. 2008. Ca<sup>2+</sup>-dependent bacterial antifreeze protein domain has a novel beta-helical ice-binding fold. **Biochemistry Journal**. 411, 171-180

## 2007

81. Booth T, **Gilbert JA**, Neufeld JD, Ball J, Thurston M, Chipman K Joint I & Field D. 2007. Handlebar: a flexible, web-based inventory manager for handling barcoded samples. **Biotechniques**. 42(3):300-02

## 2006

82. Scotter AJ, Marshall CB, Graham LA, **Gilbert JA**, Garnham CP, Davies PL. (2006). The basis for hyperactivity of antifreeze proteins. **Cryobiology**. 53(2). 229-239.

## 2005

83. **Gilbert, J. A.**; Davies, P.L.; Laybourn-Parry, J. (2005). A hyperactive, Ca<sup>2+</sup>-dependent antifreeze protein in an Antarctic bacterium. **FEMS Microbiology Letters**. 245(1), 67-72.

## 2004

84. **Gilbert, J. A.**; Hill, P. J.; Dodd, C. E. R. and Laybourn-Parry, J. (2004). Demonstration of antifreeze protein activity in Antarctic lake bacteria. **Microbiology**, 150, 171-180.

## 2003

85. Tomczak, M. M.; Marshall, C. B.; **Gilbert, J. A.** and Davies, P. L. (2003). A facile method for determining ice recrystallisation inhibition by antifreeze proteins. **Biochemical and Biophysical Research Communications**, 311 (4), 1041-1046.

### Book chapters:

86. **Gilbert JA**, Zhang K & Neufeld J. 2010. Multiple Displacement Amplification. **In: HANDBOOK OF HYDROCARBON AND LIPID MICROBIOLOGY**. Ed. Timmis, K. Springer-Verlag Berlin Heidelberg. 10.1007/978-3-540-77587-4\_333. 4255-4263
87. **Gilbert JA**. 2010. Aquatic metagenome library (archive; expression) generation and analysis. **In: HANDBOOK OF HYDROCARBON AND LIPID MICROBIOLOGY**. Ed. Timmis, K. . Springer-Verlag Berlin Heidelberg. 10.1007/978-3-540-77587-4\_340. 4347-4352
88. **Gilbert JA**, Field D, Huang Y, Edwards R, Li W, et al. (2010) Detection of Large Numbers of Novel Sequences in the Metatranscriptomes of Complex Marine Microbial Communities. **In Volume 2 of "Handbook of Molecular Microbial Ecology II: Metagenomics in Different Habitats"** edited by Frans J. de Bruijn. John Wiley & Sons, Inc.
89. **Gilbert J.A.**, Laverock B, Temperton B, Thomas S, Mühling M and Hughes M. Metagenomic protocols. 2011. In: *Methods in Molecular Biology, Vol 733: High-throughput Sequencing: Applications to Microbiology*. Kwon, Young Min; Ricke, Steven C. (Eds.) Springer. ISBN: 978-1-61779-088-1.
90. **Gilbert J.A.** and Hughes M. 2011. Gene Expression Profiling: Metatranscriptomics. In: *Methods in Molecular Biology, Vol 733: High-throughput Sequencing: Applications to Microbiology*. Kwon, Young Min; Ricke, Steven C. (Eds.) Springer. ISBN: 978-1-61779-088-1.
91. **Gilbert JA**, Li L-L, Taghavi S, McCorkle SM, Tringe S, van der Lelie N. 2012. Bioprospecting metagenomics for new glycoside hydrolases. In: **Methods in Molecular Biology Vol. 908 – Biomass Conversion**. Ed. Himmel, Michael E. Humana Press. ISBN 978-1-61779-955-6



## FUNDING

### Past:

1. PI: J A Gilbert. My Role: PI. Arthur P Sloan Foundation (2011-6-05). Total Direct Costs: \$145k. Title: "How personal is your home microbiome? Unraveling the relationship between human-associated and home-associated microbial signatures". Annual Salary recovery or effort: 20%. Period: 01/08/11-30/09/12.
2. PI: J A Gilbert. My Role: PI. Doe Travel Award GSC13. Total Direct Costs: \$15k. Title: Travel award for the Genomic Standards Consortium's 13<sup>th</sup> annual meeting. Annual salary recovery or effort: 0%. Period: 01/02/12-30/09/12.

### Current:

1. PI: J A Gilbert. My Role: PI. U.S. Dept. of Energy (DE-AC02-06CH11357) – Total Direct costs: \$1.8M. Title "Simultaneous ecological assessment and characterization of novel proteins from a soil microbial community". Annual salary recovery or effort: 100%. Projected period 01/08/10-30/07/13
3. PI: J A Gilbert. My Role: PI. U.S. Dept. of Energy (2012-016-N0). Total Direct Costs: \$100k. Title "Knowledge discovery in microbial community composition and metabolite turnover using satellite remote sensing data". Annual Salary recovery or effort: 10%. Project Period 01/10/11-30/09/14.
4. PI: J A Gilbert. My Role: PI. DDRCC-Gilbert. Total Direct Costs: \$20k. Title: "A Metagenomic Understanding of the Causes of Acute Appendicitis". Annual Salary Recovery or Effort: 0%. Period. 01/06/11-30/05/13.
5. PI: J A Gilbert. My Role: PI. Arthur P Sloan Foundation (2012-3-25). Total Direct Costs: \$17.5k. Title "Convening a working group to design a sampling scheme, and building metadata acquisition, to characterize the source and succession of microbial and viral communities in a new hospital". Annual salary recovery or effort: 0%. Projected Period: 01/06/12-30/08/13.
6. PI: Folker Meyer. My Role: Co-PI. Gordon and Betty Moore Foundation. Total Direct Costs: \$450k. Title: "METAZen". Annual salary recovery or effort: 0%. Projected Period: 01/03/12-28/02/15.
7. PI: J A Gilbert. My Role: PI. Arthur P Sloan Foundation (2012-11-01). Total Direct Costs \$850,000. Title "The Hospital Microbiome Project". Annual salary recovery or effort: 10%. Project Period: 01/11/12-31/10/14.
8. PI: J A Gilbert. My Role: PI. Gulf of Mexico Research Institute. Total Direct Costs: \$266,000. Title "Creating a Predictive Model of Microbially Mediated Carbon Remediation in the Gulf of Mexico". Annual salary recovery or effort: 10%. Project Period: 01/01/13-31/12/14.

### Pending:

1. PI: J A Gilbert. My Role: PI. NSF Macrosystems Ecology (Submitted April 18th 2012). Total Direct Costs: \$6.5M. Title: "Collaborative Research: Creating a continent-scale terrestrial microbial bioclimatic envelope model for the US". Annual Salary Recovery: 5%. Project Period: 01/03/2013-28/02/18.

## EDUCATION

### The College (B.A., B.S.):

2011-2011 BIOS 13129, " Environmental Science: a Microbiology Toolkit for the Modern Age ", Spring Quarter, 20 lecturers, no discussion sections or laboratories, ~40 students



2011-2011 BIOS 20150, "Introductory Biology", Spring Quarter, 1 lecture, 300 students

Graduate programs (Ph.D.):

2009 Masters in Bioinformatics, 5 lectures, Oxford University, Zoology Department, 24 students.  
2010 Masters in Bioinformatics, 3 lectures, Oxford University, Zoology Department, 19 students.

Research trainees:

Graduate (Ph.D.)

2006-2009 Principal supervisor for Bonnie Laverock, PhD 2010. Currently: Postdoctoral Associate, University of Western Australia.  
2006-2009 Principal supervisor for Simon Thomas, PhD 2010. Currently Senior Principle Researcher, Plymouth Marine Laboratory, UK.  
2007-2010 Principal supervisor for Ben Temperton, PhD 2011. Currently: Postdoctoral Associate, Oregon State University, USA.  
2011 Principle supervisor for Sean Gibbons, Biophysical program, University of Chicago. Still in program.  
2012 Principle supervisor for Simon Lax, Ecology and Evolution, University of Chicago. Still in program.  
2009-2012 Ph.D. Committee member for Anna Klindworth (MPI Bremen), Jacobs University, Germany. PhD. 2012.  
2011 Ph.D. Committee member for Matthew Perisin, Ecology and Evolution, University of Chicago. Still in Program.

Postdoctoral

2010 Daniel Smith (PhD Oregon State University, USA). Projected to complete postdoc in 2014.  
2011 Iratxe Zarraonaindia (PhD University of the Basque Country, Spain). Projected to complete postdoc in 2015.  
2013 New postdoc – yet to be named. Project to complete postdoc in 2015.

**PRESENTATIONS**

I have given >50 invited seminars, 20 offered talks, 5 television interviews, 10 radio interviews over the last 5 years, including:

- Invited Speaker at EU-US Microbial Community Dynamics Workshop, November 2012
- Invited Speaker at Loyola University, Chicago, IL, October 2012
- Invited Speaker at the SLOAN workshop, Boulder, Co, October 2012
- Invited Speaker at the Max Planck Institute, Bremen, Germany, October 2012
- Invited Speaker at University of Chicago, Gleecher Center, October 2012
- Invited Speaker at the GSC14, Oxford, UK, September 2012
- Invited Speaker at the Microbiota Conference, Basel, Switzerland, September 2012
- Invited Speaker at the SGM Conference, University of Warwick, UK, September 2012
- Invited Speaker at ISME14, Denmark, Copenhagen, August 2012
- Invited Speaker at MBL STAMPS Workshop, Falmouth, Ma, August 2012
- Invited Speaker at the Gordon Research Conference, Naples, Italy, June 2012
- Invited Speaker at the IOM forum on Microbial Threats, Washington, DC, June 2012
- Invited Speaker at KAUST, Jeddah, Saudi Arabia, June 2012

- Invited Speaker at the Research Triangle Institute, Raleigh NC, May 2012
- Invited Speaker at the Frontiers in Metagenomics Symposium, Columbia, Mo, May 2012
- Invited Speaker at the Bio Vision Alexandria, Alexandria, Egypt, April 2012
- Invited Speaker at the EMBRC workshop, Heidelberg, Germany, March 2012
- GSC13, Shenzhen China, March 2012
- Panel participant at the AAAS Annual Meeting, February 2012
- Invited Speaker at the BPC Seminar, December 2011
- Invited Speaker at the International Congress of Genomics, Shenzhen, China, November 2011
- Invited Speaker at Roche, New Delhi, India, November 2011
- Invited Speaker at GSC12, September 2011
- Invited Speaker at Max Planck Institute for Marine Microbiology, Bremen, September 2011
- Invited Speaker at CeBiTec Conference in Bielefeld University, July 2011
- Invited Speaker at ICiS Conference in Utah, July 2011.
- Invited Seminar for the 1<sup>st</sup> International EMP Conference, June 2011
- Plenary Lecture for Biogeography at ASM2011, April 2011
- Invited lecture for Oregon State University expert series, April 2011
- Special session, Waterloo University, Canada, April 2011
- GSC11, Wellcome Trust Campus, Cambridge, UK, March 2011
- CAMERA Inspirational Lecture Series – UCSD, January 2011
- BIOTA10 – Sao Paulo, Brazil, December 2010
- Soil Metagenomics 2010 – Braunschweig Germany, December 2010
- ICG V Shenzhen China, November 2010
- Departmental Seminar Miami University, Ohio, October 2010
- Departmental Seminar Colorado University Boulder, October 2010
- GSC10 – ANL, October 2010
- US-EU Special Taskforce meeting, Washington DC, October 2010
- Challenger Conference, UK – Invited Talk, September 2010.
- ISME 13 – Chair of Roundtable and Invited talk, August 2010
- Cambridge Next Generation Sequencing Bioinformatics Meeting, March 2010
- Metatranscriptomics for Microbes, REAL meeting, IGB Berlin, January 2010
- Genomic standards on microbial ecology, PSB10, January 2010
- 2<sup>nd</sup> Next Generation Sequencing Retreat 14<sup>th</sup> – Metagenomics, December 2009
- BBC Panorama – Britain’s Dirty Beaches, August 31<sup>st</sup> 2009
- AIMS Seminar Series, August 22<sup>nd</sup> 2009
- INTERCOL-10 – Genes in the Night, August 20<sup>th</sup> 2009
- BBC “Bang Goes the Theory” Science show <http://www.bbc.co.uk/bang/> - Dr. Venter in UK Waters, June 2009
- ICoMM meeting – Microbial biodiversity using pyrosequencing, April 2009
- “Using 16S rDNA pyrosequencing tag technology to investigate bacterial diversity changes over one year in the Western English Channel” offered speaker – ASLO, 2009.
- “Metagenomics and Metatranscriptomics in real world experiments” – invited speaker, Metagenomics, 2008
- “Metatranscriptomics and Ocean Acidification” – invited speaker, ISME, 2008
- “Phosphonate utilization in marine bacteria” – invited speaker, SGM, 2008

## **AFFILIATIONS:**

- I am senior editor for the ISME Journal.
- I am an academic editor for PLoS ONE.
- I am a member of the American Geophysical Union, Society for General Microbiology, the American Society for Microbiology, and the International Society for Microbial Ecology
- I am an associate editor for “Standards in Genomic Science” and “Microbial Informatics and Experimentation”.
- I am an associate editor for Frontiers in Marine Science
- I am on the board for the Genomic Standards Consortium non-for-profit organization.
- I am Co-PI for the Earth Microbiome Project.
- Special guest editor for Environmental Microbiology Reports, and Marine Drugs edition.