Gregory Gloor, PhD

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1   Expertise and Research Interests

Composition and function of the human and other microbiomes. I use and develop tools to examine 16S rRNA gene composition, gene expression of mixed population samples, and metabolomic analysis of clinical samples. I teach a graduate course on the use of compositional data analysis techniques to examine transcriptomes, microbiomes and other types of complex data sets derived from high throughput sequencing.

Protein evolution. We use and develop tools to examine how protein structure and function is maintained in response to sequences changes. We have a special interest in identifying the role that variable positions play in protein evolution. I teach an undergraduate course in protein sequence alignment and proteins sequence-structure alignment.

Computational biology and that application of techniques for compositional data analysis to the above problems. Our primary contributions so far have been the ALDEx2 tool in Bioconductor for the analysis of high throughput experiments that generate counts per sequence tag: 16S rRNA gene sequencing, transcriptomics and selex-type experiments. I have further tools under development, and have contributed new visualization methods (effect-size plots) to the field.

2   Education and Training

1988-1990 Postdoctoral Fellow. University of Wisconsin - Madison - Laboratory of Genetics. Supervisor: Dr. William Engels.

1988 Ph.D, University of Western Ontario, Department of Biochemistry. Supervisor: Dr. George Chaconas. Dissertation: *Characterization of the Integrative Precursor Protein-DNA Complex of Bacteriophage Mu.*

1983 HBSc, University of Western Ontario, Genetics

3   Employment

2002-present , Professor of Biochemistry
University of Western Ontario, Faculty of Medicine
now the Schulich School of Medicine and Dentistry

1997-2002, Associate Professor of Biochemistry
University of Western Ontario, Faculty of Medicine

1993-1997, Assistant Professor of Biochemistry
University of Western Ontario, Faculty of Medicine

1990-1992, Assistant Professor Medical Genetics
Memorial University of Newfoundland, Faculty of Medicine

4   Faculty Development

2014, Five day theory and applied course on Compositional Data Analysis (UdG, Spain)
   Accredited by European Statistical Society

2007, Leadership Workshop
   Offered by Continuing Education of Shulich School of Medicine and Dentistry for Medical School
   Accreditation Leaders

1995, Course on Teaching at the University Level
   Offered through the Faculty of Medicine Development Office.

1990, Faculty Orientation Day Memorial University of Newfoundland
   This covered teaching tips and grant writing skills for new faculty at MUN

5   Awards, Honours, Fellowships

2014, Faculty Development Award: Attended week-long course on Compositional Data Analysis (UdG,
   Spain)

2011-2013, Faculty Scholar

2009, University Student's Council Teaching Honor Roll

2007, University Student's Council Teaching Honor Roll

2005, Schulich School of Medicine Teaching Award

2004, WL Magee Teaching Award, Biochemistry, UWO

1993 - 1998, Salary Award, Medical Research Council of Canada (MRC)
   Development Grant in Molecular Biology

1984 -1988, K. M. Hunter Fellowship, National Cancer Institute of Canada.

1983, Graduate Entrance Scholarship, UWO.

6   HQP Training Summary

Graduate Student: 10; Undergraduate Student: 30; Postdoctoral Fellow: 2;

Graduate Advisory Committee: 30; Thesis Defence: 68; Qualifying Examiner: 46.

7   Scholarly and Professional Activities Summary

7.1   Grants and Awards Panels, Editorial membership

2017-present, Chair, CIHR Project Grant Scheme (Genomics/Genetics)

2017-present, Member, CIHR College of Reviewers (First round invitee)

2017, Member, Canadian Crohns and Colitis Review panel

2016, Member, Agence Nationale de la Recherche, Preindustrial Biotechnology Demonstrator, Paris,
   France

2016-present, Senior Editor, Microbiome

2016, Western Science and Engineering Review Board Member

2016, CIHR Operating Grant Review Panel Chair

2015-2016, Associate Editor, Microbiome

2015, Ontario Genomics Institute: SPARC and Genome Canada review panel

2014-present, CRC College of Reviewers

2012-2015, Editorial Board member Microbiome

2010-2014, Member CIHR Genetics panel

2008-present, IODE Doctoral Scholarship committee

2006-2010, NCIC Model Organisms Panel B2

1998, 1999, 2000, 2003, 2004, 2005, 2006, 2007, 2008 MRC/CIHR BMB/Genetics/Genomics invitee
item 1999, Chair OGS Biochemistry/Biophysics panel item 1997-1999, OGS Biochemistry/Biophysics panel

1997–2000, NCIC Virology and Molecular Biology Committee
Panel F

1995-2001, Foundation for Gene and Cell Therapy (Jesse's Journey)
Chair and Review Organizer 1995 - 2001

7.2 Board memberships

2001-2002, Member, Board of Directors for Partners in Research

1995-2001 Member, Board of Directors, The Foundation for Gene and Cell Therapy (FFGCT).
I was the lead negotiator for the FFGCT in working out a partnership with the MRC to fund up to 9 post-doctoral fellows in the area of gene therapy. This partnership provided approximately $900,000 in new money to the MRC.

1995, Member of the Home Team for Jesse's Journey (Internet and Science Advisor).
I posted and updated a World Wide Web map page so that people from around the world could follow John and Jesse's progress.

7.3 Presentations and Invitations

2017, Keynote, Microbial Ecology 2017, Toronto, Ontario

2017, Workshop, Compositional Data analysis methods, Microbial Ecology 2017, Toronto, Ontario

2017, Invited speaker, EMBL-EBI Industrial Program Workshop - The human microbiome: challenges and opportunities for novel therapeutics, Hinxton, England

2017, Invited speaker Canadian Society of Microbiology, Waterloo, Ontario

2017, Canadian Statistical Sciences Institute Microbiome Planning Meeting speaker and discussion leader, Winnipeg,Manitoba

2017, Contributed Oral Presentation (2), Great Lakes Bioinformatics, Chicago, Illinois

2017, Invited speaker in the Microbiology & Immunology Department, Western University, London, CA

2017, Invited speaker in the Health Sciences Department, Carleton University, Ottawa, CA

2016, Invited speaker in the Biostatistics and Epidemiology Department, Western University, London, CA

2016, Invited speaker at Exploring Human Host-Microbiome Interactions in Health and Disease 2016, Cambridge, UK

2016, Invited workshop organizer at Exploring Human Host-Microbiome Interactions in Health and Disease 2016, Cambridge, UK

2016, Invited speaker at Symposium on Synthetic Biology, Western University, London, CA

2016, Invited workshop presenter, The Human Microbiome and Epidemiology, 2016 Epidemiology Congress of the Americas, Miami, USA

2016, Invited presentation/workshop, Infection, Inflammation and Immunity course, The Arctic University of Norway, Tromso, NO

2016, Oral Presentation, Great Lakes Bioinformatics/Canadian Computational Biology Conference, Toronto, CA

2015, Invited speaker at Exploring Human Host-Microbiome Interactions in Health and Disease 2015, Cambridge, UK

2015, Invited paper at CoDaWork 2015, Girona, Spain

2015, Applying compositional data framework to microbiome datasets, Canadian Society of Microbiology workshop 2015, Saskatoon, Canada

2015, Invited speaker, University of Guelph Bioinformatics group

2014, Invited seminar, Dept. of Biochemistry, University of Calgary

2014, Invited participant at NIH sponsored Microbiome Quality Control Initiative: only Canadian group invited, Rockville, MD, USA

2013, Invited speaker at Fondation Merieux Conference on Better Foods for Better Health, Annecy, France

2013, Invited speaker at the Institute of Genome Sciences seminar series, University of Maryland, Baltimore, USA

2013, Invited expert participant at African International Conference and Workshop on the Microbiome and Probiotics, Nairobi, Kenya

2011, Invited speaker at the RePOOPulating the gut: therapeutic microbial preparations to eradicate recurrent C.difficile infections in Canada, Toronto

2011, Invited expert participant at International Society for the Application of Probiotics and Prebiotics, Berkley, CA

2010, Invited platform speaker at the Ontario Illumina Users Group, Toronto Ontario

2008, Invited speaker at University of North Carolina-Charlotte Department of Bioinformatics Seminar Series

2003, Invited speaker at First Canadian Workshop on Statistical Genomics, The Fields Institute, Toronto

2000, Department of Genetics seminar series, Harvard Medical School, Boston, Mass.

1999, London and Regional Cancer Center seminar series, London Ontario

1997 Department of Molecular Biology and Genetics seminar series, University of Guelph

1994 Mogenson Research Forum, UWO Faculty of Medicine

1992 Department of Genetics, University of Alberta seminar series
    Alberta Heritage Foundation for Medical Research Sponsored Speaker

1992 Lunchtime Seminar Series, Faculty of Medicine, Memorial University of Newfoundland

1992 Department of Biochemistry seminar series, Queens University

1992 Department of Biochemistry seminar series, UWO

1991 Molecular Biology Research Discussion Group seminar series, Faculty of Medicine, MUN

1991 Department of Biochemistry seminar series, MUN

1990 Faculty of Medicine seminar series, MUN

7.4   Peer Reviewed Papers:

Academic trivia

- H-index: 34, i10 index: 75 (Google Scholar)

- Erdos number 3 (two ways)

- Aitchison number 1 (two ways)

- Academic lineage: T.H. Morgan

[111] Gregory B. Gloor, Jean M. Macklaim, Vera Pawlowsky-Glahn, and Juan J. Egozcue. Microbiome datasets are compositional: And this is not optional. *Frontiers in Microbiology*, 8:2224, 2017.

[110] Gaorui Bian, Gregory B Gloor, Aihua Gong, Changsheng Jia, Wei Zhang, Jun Hu, Hong Zhang, Yumei Zhang, Zhenqing Zhou, Jiangao Zhang, Jeremy P Burton, Gregor Reid, Yongliang Xiao, Qiang Zeng, Kaiping Yang, and Jiangang Li. The gut microbiota of healthy aged chinese is similar to that of the healthy young. *mSphere*, 2(5):e00327–17, 2017.

[109] Sarah Lynn Martz, Mabel Guzman-Rodriguez, Shu-Mei He, Curtis Noordhof, David John Hurlbut, Gregory Brian Gloor, Christian Carlucci, Scott Weese, Emma Allen-Vercoe, Jun Sun, Erika Chiong Claud, and Elaine Olga Petrof. A human gut ecosystem protects against c. difficile disease by targeting tcda. *Journal of Gastroenterology*, 52(4):452–465, Apr 2017.

[108] Amy McMillan, Adebola E. Orimadegun, Mark W. Sumarah, Justin Renaud, Magdalena Muc da Encarnacao, Gregory B. Gloor, Olusegun O. Akinyinka, Gregor Reid, and Stephen J. Allen. Metabolic derangements identified through untargeted metabolomics in a cross-sectional study of nigerian children with severe acute malnutrition. *Metabolomics*, 13(2):13, Dec 2016.

[107] Grace Ettinger, Jeremy P Burton, Gregory B Gloor, and Gregor Reid. Lactobacillus rhamnosus gr-1 attenuates induction of hypertrophy in cardiomyocytes but not through secreted protein msp-1 (p75). *PLoS One*, 12(1):e0168622, 2017.

[106] Kait Al, Ousseynou Sarr, Kristyn Dunlop, Gregory B Gloor, Gregor Reid, Jeremy Burton, and Timothy R H Regnault. Impact of birth weight and postnatal diet on the gut microbiota of young adult guinea pigs. *PeerJ*, 5:e2840, 2017.

[105] Jason M Wolfs, Thomas A Hamilton, Jeremy T Lant, Marcon Laforet, Jenny Zhang, Louisa M Salemi, Gregory B Gloor, Caroline Schild-Poulter, and David R Edgell. Biasing genome-editing events toward precise length deletions with an rna-guided tevcas9 dual nuclease. *Proc Natl Acad Sci U S A*, Dec 2016.

[104] Joel W G Slade, Yanina Sarquis-Adamson, Gregory B Gloor, Marc-André Lachance, and Elizabeth A MacDougall-Shackleton. Population differences at mhc do not explain enhanced resistance of song sparrows to local parasites. *J Hered*, Dec 2016.

[103] S Rahat-Rozenbloom, J Fernandes, J Cheng, G B Gloor, and T M S Wolever. The acute effects of inulin and resistant starch on postprandial serum short-chain fatty acids and second-meal glycemic response in lean and overweight humans. *Eur J Clin Nutr*, Dec 2016.

[102] J W G Slade, M J Watson, T R Kelly, G B Gloor, M A Bernards, and E A MacDougall-Shackleton. Chemical composition of preen wax reflects major histocompatibility complex similarity in song-birds. *Proc Biol Sci*, 283(1842), Nov 2016.

[101] Mariya I Petrova, Elke Lievens, Tine L A Verhoeven, Jean M Macklaim, Gregory Gloor, Dominique Schols, Jos Vanderleyden, Gregor Reid, and Sarah Lebeer. The lectin-like protein 1 in lactobacillus rhamnosus gr-1 mediates tissue-specific adherence to vaginal epithelium and inhibits urogenital pathogens. *Sci Rep*, 6:37437, Nov 2016.

[100] Gregory B Gloor, Jean M Macklaim, Michael Vu, and Andrew D Fernandes. Compositional un-certainty should not be ignored in high-throughput sequencing data analysis. *Austrian Journal of Statistics*, 45:73–87, September 2016.

[99] Gregory B Gloor and Gregor Reid. Compositional analysis: a valid approach to analyze microbiome high-throughput sequencing data. *Can J Microbiol*, 62(8):692–703, Aug 2016.

[98] Camilla Urbaniak, Gregory B Gloor, Muriel Brackstone, Leslie Scott, Mark Tangney, and Gregor Reid. The microbiota of breast tissue and its association with breast cancer. *Appl Environ Microbiol*, 82(16):5039–48, Aug 2016.

[97] Gregory B Gloor, Jia Rong Wu, Vera Pawlowsky-Glahn, and Juan José Egozcue. It's all relative: analyzing microbiome data as compositions. *Ann Epidemiol*, 26(5):322–9, May 2016.

[96] Gregory B. Gloor, Jean M. Macklaim, and Andrew D. Fernandes. Displaying variation in large datasets: a visual summary of effect sizes. *Journal of Computational and Graphical Statistics*, 25(3):971–9, 2016.

[95] Ruth G Wong, Jia R Wu, and Gregory B Gloor. Expanding the UniFrac toolbox. *PLoS One*, 11(9):e0161196, 2016.

[94] Camilla Urbaniak, Michelle Angelini, Gregory B Gloor, and Gregor Reid. Human milk microbiota profiles in relation to birthing method, gestation and infant gender. *Microbiome*, 4:1, Jan 2016.

[93] Asma Asemaninejad, Nimalka Weerasuriya, Gregory B Gloor, Zoë Lindo, and R Greg Thorn. New primers for discovering fungal diversity using nuclear large ribosomal dna. *PLoS One*, 11(7):e0159043, 2016.

[92] A McMillan, J B Renaud, G B Gloor, G Reid, and M W Sumarah. Post-acquisition filtering of salt cluster artefacts for lc-ms based human metabolomic studies. *J Cheminform*, 8(1):44, 2016.

[91] David M Walton, James M Elliott, Joshua Lee, Eldon Loh, Joy C MacDermid, Siobhan Schabrun, Walter L Siqueira, Brian D Corneil, Bill Aal, Trevor Birmingham, Amy Brown, Lynn K Cooper, James P Dickey, S Jeffrey Dixon, Douglas D Fraser, Joseph S Gati, Gregory B Gloor, Gordon Good, David Holdsworth, Samuel A McLean, Wanda Millard, Jordan Miller, Jackie Sadi, David A Semi-nowicz, J Kevin Shoemaker, Gunter P Siegmund, Theodore Vertseegh, and Timothy H Wideman. Research priorities in the field of posttraumatic pain and disability: Results of a transdisciplinary consensus-generating workshop. *Pain Res Manag*, 2016:1859434, 2016.

[90] Jordan E Bisanz, Praema Suppiah, W Murray Thomson, Trudy Milne, Nigel Yeoh, Anita Nolan, Grace Ettinger, Gregor Reid, Gregory B Gloor, Jeremy P Burton, Mary P Cullinan, and Simon M Stebbings. The oral microbiome of patients with axial spondyloarthritis compared to healthy indi-viduals. *PeerJ*, 4:e2095, 2016.

[89] Jordan E Bisanz, Megan K Enos, George PrayGod, Shannon Seney, Jean M Macklaim, Stephanie Chilton, Dana Willner, Rob Knight, Christoph Fusch, Gerhard Fusch, Gregory B Gloor, Jeremy P Burton, and Gregor Reid. Microbiota at multiple body sites during pregnancy in a rural tanzanian population and effects of moringa-supplemented probiotic yogurt. *Appl Environ Microbiol*, 81(15):4965–75, Aug 2015.

[88] Nicole St-Denis, Michelle Gabriel, Jacob P Turowec, Gregory B Gloor, Shawn S-C Li, Anne-Claude Gingras, and David W Litchfield. Systematic investigation of hierarchical phosphorylation by protein kinase ck2. *J Proteomics*, 118:49–62, Apr 2015.

[87] Lee W Goneau, Thomas J Hannan, Roderick A MacPhee, Drew J Schwartz, Jean M Macklaim, Gregory B Gloor, Hassan Razvi, Gregor Reid, Scott J Hultgren, and Jeremy P Burton. Subinhibitory antibiotic therapy alters recurrent urinary tract infection pathogenesis through modulation of bacterial virulence and host immunity. *MBio*, 6(2), Mar 2015.

[86] Amy McMillan, Stephen Rulisa, Mark Sumarah, Jean M Macklaim, Justin Renaud, Jordan E Bisanz, Gregory B Gloor, and Gregor Reid. A multi-platform metabolomics approach identifies highly specific biomarkers of bacterial diversity in the vagina of pregnant and non-pregnant women. *Sci Rep*, 5:14174, 2015.

[85] Sarah-Lynn E Martz, Julie A K McDonald, Jun Sun, Yong-Guo Zhang, Gregory B Gloor, Curtis Noordhof, Shu-Mei He, Teklu K Gerbaba, Michael Blennerhassett, David J Hurlbut, Emma Allen-Vercoe, Erika C Claud, and Elaine O Petrof. Administration of defined microbiota is protective in a murine salmonella infection model. *Sci Rep*, 5:16094, 2015.

[84] Jean M Macklaim, Jose C Clemente, Rob Knight, Gregory B Gloor, and Gregor Reid. Changes in vaginal microbiota following antimicrobial and probiotic therapy. *Microb Ecol Health Dis*, 26:27799, 2015.

[83] Siwen Yang, Gregor Reid, John R G Challis, Sung O Kim, Gregory B Gloor, and Alan D Bocking. Is there a role for probiotics in the prevention of preterm birth? *Front Immunol*, 6:62, 2015.

[82] S Rahat-Rozenbloom, J Fernandes, G B Gloor, and T M S Wolever. Evidence for greater production of colonic short-chain fatty acids in overweight than lean humans. *Int J Obes (Lond)*, 38(12):1525–31, Dec 2014.

[81] Thomas A McMurrough, Russell J Dickson, Stephanie M F Thibert, Gregory B Gloor, and David R Edgell. Control of catalytic efficiency by a coevolving network of catalytic and noncatalytic residues. *Proc Natl Acad Sci U S A*, 111(23):E2376–83, Jun 2014.

[80] Camilla Urbaniak, Joanne Cummins, Muriel Brackstone, Jean M Macklaim, Gregory B Gloor, Chwanrow K Baban, Leslie Scott, Deidre M O'Hanlon, Jeremy P Burton, Kevin P Francis, Mark Tangney, and Gregor Reid. Microbiota of human breast tissue. *Appl Environ Microbiol*, 80(10):3007–14, May 2014.

[79] Xiaohong Tracey Gan, Grace Ettinger, Cathy X Huang, Jeremy P Burton, James V Haist, Venkatesh Rajapurohitam, James E Sidaway, Glynn Martin, Gregory B Gloor, Jonathan R Swann, Gregor Reid, and Morris Karmazyn. Probiotic administration attenuates myocardial hypertrophy and heart failure after myocardial infarction in the rat. *Circ Heart Fail*, 7(3):491–9, May 2014.

[78] Gregor Reid, Nicholas Nduti, Wilbert Sybesma, Remco Kort, Tobias R Kollmann, Rod Adam, Hamadi Boga, Eric M Brown, Alexandra Einerhand, Hani El-Nezami, Gregory B Gloor, Irene I Kavere, Johanna Lindahl, Amee Manges, Wondu Mamo, Rocio Martin, Amy McMillan, Jael Obiero,

Pamela A Ochieng, Arnold Onyango, Stephen Rulisa, Eeva Salminen, Seppo Salminen, Antony Sije, Jonathan R Swann, William van Treuren, Daniel Waweru, and Steve J Kemp. Harnessing microbiome and probiotic research in sub-Saharan Africa: recommendations from an African workshop. *Microbiome*, 2(1):12, Apr 2014.

[77] S Rahat-Rozenbloom, J Fernandes, G B Gloor, and T M S Wolever. Evidence for greater production of colonic short chain fatty acids in overweight than lean humans. *Int J Obes (Lond)*, Mar 2014.

[76] Chantalle Brace, Gregory B Gloor, Mark Ropeleski, Emma Allen-Vercoe, and Elaine O Petrof. Microbial composition analysis of *Clostridium difficile* infections in an ulcerative colitis patient treated with multiple fecal microbiota transplantations. *J Crohns Colitis*, 8:1113–7, Feb 2014.

[75] Jordan E Bisanz, Shannon Seney, Amy McMillan, Rebecca Vongsa, David Koenig, LungFai Wong, Barbara Dvoracek, Gregory B Gloor, Mark Sumarah, Brenda Ford, Dorli Herman, Jeremy P Burton, and Gregor Reid. A systems biology approach investigating the effect of probiotics on the vaginal microbiome and host responses in a double blind, placebo-controlled clinical trial of post-menopausal women. *PLoS One*, 9(8):e104511, 2014.

[74] Kristin D Kernohan, Douglas Vernimmen, Gregory B Gloor, and Nathalie G Bérubé. Analysis of neonatal brain lacking ATRX or MeCP2 reveals changes in nucleosome density, CTCF binding and chromatin looping. *Nucleic Acids Res*, 42(13):8356–68, 2014.

[73] Russell J Dickson and Gregory B Gloor. Bioinformatics identification of coevolving residues. *Methods Mol Biol*, 1123:223–43, 2014.

[72] Camilla Urbaniak, Amy McMillan, Michelle Angelini, Gregory B Gloor, Mark Sumarah, Jeremy P Burton, and Gregor Reid. Effect of chemotherapy on the microbiota and metabolome of human milk, a case report. *Microbiome*, 2:24, 2014.

[71] Mariana Rosenthal, Allison E Aiello, Carol Chenoweth, Deborah Goldberg, Elaine Larson, Gregory Gloor, and Betsy Foxman. Impact of technical sources of variation on the hand microbiome dynamics of healthcare workers. *PLoS One*, 9(2):e88999, 2014.

[70] Jordan E Bisanz, Megan K Enos, Joseph R Mwanga, John Changalucha, Jeremy P Burton, Gregory B Gloor, and Gregor Reid. Randomized open-label pilot study of the influence of probiotics and the gut microbiome on toxic metal levels in Tanzanian pregnant women and school children. *MBio*, 5(5):e01580–14, 2014.

[69] Andrew D Fernandes, Jennifer Ns Reid, Jean M Macklaim, Thomas A McMurrough, David R Edgell, and Gregory B Gloor. Unifying the analysis of high-throughput sequencing datasets: characterizing RNA-seq, 16S rRNA gene sequencing and selective growth experiments by compositional data analysis. *Microbiome*, 2:15.1–15.13, 2014.

[68] Julia M Di Bella, Yige Bao, Gregory B Gloor, Jeremy P Burton, and Gregor Reid. High throughput sequencing methods and analysis for microbiome research. *J Microbiol Methods*, 95(3):401–14, Dec 2013.

[67] Lance F DaSilva, Samantha Pillon, Julie Genereaux, Megan J Davey, Gregory B Gloor, Jim Karagiannis, and Christopher J Brandl. The C-terminal residues of *Saccharomyces cerevisiae* Mec1 are required for its localization, stability, and function. *G3 (Bethesda)*, 3(10):1661–74, Oct 2013.

[66] A. D. Fernandes, J. M. Macklaim, T.G Linn, G. Reid, and G. B. Gloor. ANOVA-like differential expression (ALDEx) analysis for mixed population RNA-seq. *PLoS ONE*, 8(7):e67019, July 2013.

[65] Mi Seong Kim, Gregory B Gloor, and Donglin Bai. The distribution and functional properties of Pelizaeus-Merzbacher-like disease-linked Cx47 mutations on Cx47/Cx47 homotypic and Cx47/Cx43 heterotypic gap junctions. *Biochem J*, 452(2):249–58, Jun 2013.

[64] Roderick A MacPhee, Wayne L Miller, Gregory B Gloor, John K McCormick, Jo-Anne Hammond, Jeremy P Burton, and Gregor Reid. Influence of the vaginal microbiota on toxic shock syndrome toxin 1 production by staphylococcus aureus. *Appl Environ Microbiol*, 79(6):1835–42, Mar 2013.

[63] E O Petrof, E C Claud, G B Gloor, and E Allen-Vercoe. Microbial ecosystems therapeutics: a new paradigm in medicine? *Benef Microbes*, 4(1):53–65, Mar 2013.

[62] Piya Lahiry, Lemuel Racacho, Jian Wang, John F Robinson, Gregory B Gloor, C Anthony Rupar, Victoria M Siu, Dennis E Bulman, and Robert A Hegele. A mutation in the serine protease TMPRSS4 in a novel pediatric neurodegenerative disorder. *Orphanet J Rare Dis*, 8:126, 2013.

[61] M Jean Macklaim, D Andrew Fernandes, M Julia Di Bella, Jo-Anne Hammond, Gregor Reid, and Gregory B Gloor. Comparative meta-RNA-seq of the vaginal microbiota and differential expression by *Lactobacillus iners* in health and dysbiosis. *Microbiome*, 1:15, 2013.

[60] Kingsley C Anukam, Jean M Macklaim, Gregory B Gloor, Gregor Reid, Jos Boekhorst, Bernadet Renckens, Sacha A F T van Hijum, and Roland J Siezen. Genome sequence of *Lactobacillus pentosus* KCA1: Vaginal isolate from a healthy premenopausal woman. *PLoS One*, 8(3):e59239, 2013.

[59] Philip A. Wescombe, Jean M. Macklaim, Melissa H. C. Chai, Kyle MacDonald, John D. F. Hale, John Tagg, Gregor Reid, Gregory B. Gloor, and Peter A. Cadieux. Persistence of the oral probiotic *Streptococcus salivarius* M18 is dose dependent and megaplasmid transfer can augment their bacteriocin production and adhesion characteristics. *PLoS ONE*, 8:e65991, 2013.

[58] Elaine O Petrof, Gregory B Gloor, Stephen J Vanner, J Scott Weese, David Carter, Michelle C Daigneault, Eric M Brown, Kathleen Schroeter, and Emma Allen-Vercoe. Stool substitute transplant therapy for the eradication of *Clostridium difficile* infection: "RePOOPulating" the gut. *Microbiome*, 1:3, 2013.

[57] Emma Allen-Vercoe, Gregor Reid, Norman Viner, Gregory B Gloor, Susy Hota, Peter Kim, Christine Lee, Kieran O'Doherty, Stephen J Vanner, J Scott Weese, and Elaine O Petrof. A Canadian working group report on fecal microbial therapy: microbial ecosystems therapeutics. *Can J Gastroenterol*, 26(7):457–62, Jul 2012.

[56] Jean M Macklaim, Craig R Cohen, Gilbert Donders, Gregory B Gloor, Janet E Hill, Groesbeck P Parham, Jacques Ravel, Gregory Spear, Janneke van de Wijgert, and Gregor Reid. Exploring a road map to counter misconceptions about the cervicovaginal microbiome and disease. *Reprod Sci*, May 2012.

[55] Tao Li, Jack Liang, Alexandre Ambrogelly, Tim Brennan, Guy Gloor, Gjalt Huisman, James Lalonde, Azzeddine Lekhal, Ben Mijts, Sheela Muley, Lisa Newman, Matt Tobin, George Wong, Aleksey Zaks, and Xiyun Zhang. Efficient, chemoenzymatic process for manufacture of the boceprevir bicyclic [3.1.0]proline intermediate based on amine oxidase-catalyzed desymmetrization. *J Am Chem Soc*, 134(14):6467–72, Apr 2012.

[54] Julie Genereaux, Stephanie Kvas, Dominik Dobransky, Jim Karagiannis, Gregory B Gloor, and Christopher J Brandl. Genetic evidence links the ASTRA protein chaperone component Tti2 to the SAGA transcription factor Tra1. *Genetics*, Apr 2012.

[53] Stephanie Kvas, Gregory B Gloor, and Christopher J Brandl. Loss of nonsense mediated decay suppresses mutations in *Saccharomyces cerevisiae* TRA1. *BMC Genet*, 13(1):19, Mar 2012.

[52] Russell J Dickson and Gregory B Gloor. Protein sequence alignment analysis by local covariation: coevolution statistics detect benchmark alignment errors. *PLoS One*, 7(6):e37645, 2012.

[51] Jacob P Turowec, James S Duncan, Greg B Gloor, and David W Litchfield. Regulation of caspase pathways by protein kinase CK2: identification of proteins with overlapping CK2 and caspase consensus motifs. *Mol Cell Biochem*, 356(1-2):159–67, Oct 2011.

[50] Ryo Takeuchi, Abigail R Lambert, Amanda Nga-Sze Mak, Kyle Jacoby, Russell J Dickson, Gregory B Gloor, Andrew M Scharenberg, David R Edgell, and Barry L Stoddard. Tapping natural reservoirs of homing endonucleases for targeted gene modification. *Proc Natl Acad Sci U S A*, 108(32):13077–82, Aug 2011.

[49] Jean M Macklaim, Gregory B Gloor, Kingsley C Anukam, Sarah Cribby, and Gregor Reid. At the crossroads of vaginal health and disease, the genome sequence of *Lactobacillus iners* AB-1. *Proc Natl Acad Sci U S A*, 108 Suppl 1:4688–95, Mar 2011.

[48] James S Duncan, Jacob P Turowec, Kelly E Duncan, Greg Vilk, Chenggang Wu, Bernhard Lüscher, Shawn S-C Li, Greg B Gloor, and David W Litchfield. A peptide-based target screen implicates the protein kinase CK2 in the global regulation of caspase signaling. *Sci Signal*, 4(172):ra30, 2011.

[47] Gregor Reid, Jessica A Younes, Henny C Van der Mei, Gregory B Gloor, Rob Knight, and Henk J Busscher. Microbiota restoration: natural and supplemented recovery of human microbial communities. *Nat Rev Microbiol*, 9(1):27–38, Jan 2011.

[46] Ruben Hummelen, Jean M Macklaim, Jordan E Bisanz, Jo-Anne Hammond, Amy McMillan, Rebecca Vongsa, David Koenig, Gregory B Gloor, and Gregor Reid. Vaginal microbiome and epithelial gene array in post-menopausal women with moderate to severe dryness. *PLoS One*, 6(11):e26602, 2011.

[45] Stephen M T Hoke, A Irina Mutiu, Julie Genereaux, Stephanie Kvas, Michael Buck, Michael Yu, Gregory B Gloor, and Christopher J Brandl. Mutational analysis of the C-terminal FATC domain of *Saccharomyces cerevisiae* Tra1. *Curr Genet*, 56(5):447–65, Oct 2010.

[44] Russel J Dickson, Linda M Wahl, Andrew D Fernandes, and Gregory B Gloor. Identifying and seeing beyond multiple sequence alignment errors using molecular covariation. *PLoS ONE*, 5(6):e11082, June:2010 2010.

[43] Gregory B Gloor, Gaurav Tyagi, Dana M Abrassart, Andrew J Kingston, Andrew D Fernandes, Stanley D Dunn, and Christopher J Brandl. Functionally compensating coevolving positions are neither homoplasic nor conserved in clades. *Mol Biol Evol*, 27(5):1181–91, May 2010.

[42] Andrew D Fernandes and Gregory B Gloor. Mutual information is critically dependent on prior assumptions: would the correct estimate of mutual information please identify itself? *Bioinformatics*, 26(9):1135–9, May 2010.

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7.5   Non Peer Reviewed Manuscripts

Russell J Dickson and Gregory B Gloor. Xorro: Rapid paired-end read overlapper. arXiv preprint arXiv:1304.4620, 2013.

Russell J Dickson and Gregory B Gloor. The MIp toolset:an efficient algorithm for calculating mutual information in protein alignments. arXiv preprint arXiv:1304.4573, 2013.

7.6   Software releases

ALDEx2. ALDEx tool to examine compositional high-throughput sequence data with Welch's t-test and Wilcoxon rank test. https://github.com/ggloor/ALDEx2, and
http://www.bioconductor.org/packages/release/bioc/html/ALDEx2.html last update Oct 2017

Languages and utilities: R, bash, Perl, awk, LaTeX, Markdown, HTML, git, svn

8   Research Funding History

NSERC Discovery, 2015-2020: Molecular covariation in protein families

PI: Gloor, GB

Goal is to examine how covarying positions affect the structure and function of protein families that can be used as gene editing reagents.

total: $155000 - pays for student and supplies

NIH R21 Dec 2015-2017, NIH R33 2017-2018: Microbes that matter

PI: Elaine Petrof (Queen's U), Allen-Vercoe (Guelph), Gloor (UWO)

Developing a synthetic stool substitute for the treatment of recurrent *C. difficile* infection

direct to Gloor: $70000 - partially pays for one student and sequencing costs

CIHR 2013-2016: Role of intestinal microbiota in non-alcoholic fatty liver disease pre and post bariatric surgery

PI: ALLARD, Johane P (U. Toronto): , Comelli Elena M; GLOOR, Gregory B; JACKSON, Timothy D; LOU, Wen-Yi W; OKRAINEC, Allan

Characterization of the stool microbiota in a cohort of patients undergoing treatment for non-alcoholic fatty liver disease

total: 522169, direct to Gloor: $25000/yr - partially paid for one student and sequencing costs

CIHR 2014-1016: Intestinal microbiome and extremes of atherosclerosis

PI: SPENCE, J. David , ALLEN-VERCOE, Emma; GLOOR, Gregory B; REID, Gregor

Characterization of the stool microbiota in a cohort of patients screened for risk of atherosclerosis

total: 211600, direct to Gloor: $25000 - partially paid for one student and sequencing costs

CIHR 2013-1016: Non-Alcoholic Fatty Liver Disease: Role of Intestinal Microbiota and n-3 Polyunsaturated Fatty Acid Supplementationtle

PI: ALLARD, Johane P , COMELLI, Elena M; GLOOR, Gregory B; LOU, Wen-Yi W

Characterization of the stool microbiota in a cohort of patients treated for non-alcoholic fatty liver disease with fish oils

total 211600, direct to Gloor: $17000 - partially paid for one student

CIHR Team grant, 2010-2015: The Vaginal Microbiome Project Team

PI: MONEY, Deborah M, BOCKING, Alan D; HEMMINGSEN, Sean M; HILL, Janet E; REID, Gregor (Co-PIs), co-investigators: DUMONCEAUX, Timothy J; GLOOR, Gregory B; LINKS, Matthew G; O'DOHERTY, Kieran C; TANG, Patrick K; VAN SCHALKWYK, Julianne E; YUDIN, Mark H

Collection and analysis of large vaginal microbiota cohorts to identify determinants of health and disease in the Canadian population

total:1745341, direct to Gloor: 15000/year - partially paid for one student. My role was tool development

Southeastern Ontario Academic Medical Organization 2014-2015: Elucidating the factors that determine success in fecal transplant therapy for *C. difficile* infection

PI: PETROF, E, ROPELSKI, Mark, ALLEN-VERCOE, Emma, GLOOR, Gregory

Identifying mechanisms of microbial ecosystem inhibition of *C. difficile*

total:92000, direct to Gloor: %14000 - paid for sequencing costs

CIHR Network grant 2012-2015 Maternal-Infant Microbiome and Immunity (MIMI) Network

PI: KOLLMANN, Tobias R, GLOOR, Gregory B; REID, Gregor

Team grant to further training and planning of microbiome effects on proper health and development in Africa.

total:600000, direct to Gloor: 200000 - paid for PDF, student and conference costs

NSERC ENGAGE, 2014-2015: Function of maize endophytic microbiome

PI: GLOOR, GREGORY with A&L Biologicals

Total: $25000 - sequencing and sample processing costs

Determine the functional differences between high and normal yield sites by examining the endo-phytic corn sap meta-transcriptome.

Ontario Centre of Excellence, 2014-2015: Meta-transcriptome of high-yield corn endophytic microbiome

PI: GLOOR, GREGORY, with A&L Biologicals

Determine the functional differences between high and normal yield sites by examining the endo-phytic corn sap meta-transcriptome.

Total: $25000 - sequencing and sample processing costs

CIHR Team grant in Bariatric Care, 2014-2019: Exploiting the therapeutic effects of the fecal microbiome in bariatric care

PI: ALLARD, Johane P, GAISANO, Herbert Y , BANKS, Kate; COMELLI, Elena M; GLOOR, Gregory B; HOTA, Susy S; JACKSON, Timothy D; LOU, Wen- Yi W; OKRAINEC, Allan; PHILPOTT, Dana J; POUTANEN, Susan M

Fecal microbiome transplant as a treatment for obesity

direct to Gloor: $0 - I have chosen to withdraw from this research team

Agriculture and Agrifoods Canada, Agricultural Innovation Program, 2015-2017: Developing molecular methods as diagnostic tools to identify biological factors contributing to crop productivity and soil health

PI: Dr. George Lazarovitz (A&L Biologicals), Gloor, Gregory

Monitoring and understanding corn endophytic communities to maximize crop yield

Total: $600000, direct to Gloor: $120000 - pays for one PDF and sequencing costs

Academic Development Fund UWO, 2012: Major request for Illumina MiSeq Instrument

PI: Gloor, Hegele, Edgell, Singh

ADF money to buy an Illumina MiSeq for the Robarts sequencing core facility

Total: $132500 - Paid for purchase and installation.

Ontario Genomics Institute Summer Research, 2010: Metagenomic error rate analysis of rare biomes

PI: Gloor

Summer research project examining metagenomic sequencing error rates

Total: $5000 - partially paid for one summer student

NSERC Discovery, 2010-2015: Molecular covariation in protein families

PI: Gloor

Total: $255564 - Core Research Funding

Academic Development fund, UWO, 2010: Deep resequencing of single genes

PI: Gloor

Developing methodologies for resequencing on the Illumina MiSeq Sequencing Platform

direct to Gloor: $7500 - partially pays for one student and sequencing costs

CIHR Operating, 2006-2010: MODULATORS OF DOUBLE-STRAND BREAK REPAIR IN DROSOPHILA

PI: Gloor

Core research funding for examining DSB repair in Drosophila somatic cells

Total: $405312 - Core Lab Research funding

Academic Development Fund, UWO, 2008: IDENTIFYING AND VALIDATING COEVOLVING POSI-TIONS

PI: Gloor, Wahl, Dunn

direct to Gloor: $8500 - partially paid for one PDF

CANCER RESEARCH SOCIETY, 1997-1999: GENES INVOLVED IN SOMATIC-CELL DOUBLE-STRAND REPAIR

PI: Gloor

Core research lab funding

Total: $85145 - partially pays for one student and sequencing costs

CIHR Operating, 2005-2008: MODULATORS OF DOUBLE-STRAND BREAK REPAIR IN DROSOPHILA

PI: Gloor

Core research lab funding

Total: $361580 - partially pays for one student and sequencing costs

CIHR Operating, 2000-2006: Double strand break repair in Drosophila somatic and germline cells

PI: Gloor

Core research lab funding

Total: $148000 - Core Lab research funding

MRC of Canada, 1997-2000: TEMPLATE-DEPENDENT REPAIR OF DOUBLE STRAND CHROMOSOME BREAKS IN Drosophila

PI: Gloor

Total: $105005 - Core Lab research funding

MRC of Canada, 1993-1998: Transposon induced gene targeting

PI: Gloor

direct to Gloor: $156920 - Core Lab research funding

Cancer Research Society, 1992-1994: Gene targeting to arbitrary sites in the genome

PI: Gloor

Total: $96000 - Core Research Lab Funding

Where, years: Title

PI: , co-apps

Total: $70000 - Core Research Lab Funding

MRC of Canada, 1991-1994: P element regulation and double strand break repair in Drosophila

PI: Gloor

Total: $197806 - Core Research Lab Funding