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I 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 HBS, University of Western Ontario, Genetics

3 Employment

2019-present, Chair-Department of Biochemistry

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

2018, Four day applied course on Resolving Microbial Communities At Strain-Level using Metagenomic Assembly, University of Exeter, UK

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 Schulich 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

2016-17, University Student's Council Teaching Honor Roll

2011-12, University Student's Council Teaching Honor Roll

2010-11, University Student's Council Teaching Honor Roll

2009-10, 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 Scholarly and Professional Activities

6.1 Scholarly Presentations and Invitations

2019, Invited workshop speaker, Computational and Methodological Statistics 2019, London, England

2019, Invited Participant/Speaker, Emerging Challenges in Microbiome Data Analysis, BIRS, Banff, Canada

2019, Invited Speaker, Barcelona Microbiome Debates, Barcelona, Spain

2019, Invited Speaker, Department of Bioinformatics, North Carolina State University, Charlotte

2019, Invited Speaker, Department of Biology, North Carolina State University,

2019, Invited Speaker, Program in Bioinformatics, Duke University,

2019, Invited Webinar Presenter, International Society for the Application of Probiotics and Probiotics (ISAPP)

2019, Invited Speaker, North American Microbiome Congress, Washington, USA

2018, Invited Webinar Presenter, International Life Sciences Institute (ILSI)

2018, Invited industrial speaker (KGK Biosciences), Supply Side West, Las Vegas, USA

2018, Invited speaker, Department of Physiology and Pharmacology, UWO

2018, Invited speaker, Department of Epidemiology, SUNY Buffalo, USA

2018, Invited speaker, EMBL-EBI, EBI Seminar Series, Hinxton, Cambridgeshire, UK

2018, Invited speaker, Gairdner Foundation Symposium on health through food and microbes, London, CA

2018, Invited speaker Gynecological Research Symposium, The Society of Gynecologic Oncology of Canada, Toronto, CA

2018, Workshop organizer and presenter, Compositional Data analysis methods, NGS'18, Barcelona, Catalonia

2017, Keynote, Microbial Ecology 2017, Toronto, Ontario

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

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, Tromsø, NO

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

2015, Invited visiting scholar, Tiyan Health Sciences Research Institute, Zenjiang, China

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 Janeway Hospital Residents Training seminar series, Faculty of Medicine, MUN

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

6.2 Media Interviews and Public Presentations

I : radio or TV interview

W : written interview

P : press release

S : social media

R : public presentation or outreach

W Western News, Oct 2019: The promise of CRISPR for microbiome modulation

I Western News, Mar 2019: Study betters health by expanding gut knowledge

I Western News, Jan 2018: Molecular weapon targets bad bacteria

I BBC Radio, Oct 2017: *The Science Hour* <http://www.bbc.co.uk/programmes/w3csv1fg>

I BBC Radio, Oct 2017: *Health Check* <http://www.bbc.co.uk/programmes/w3csty7v>

I CTV Health, Oct 2017: <http://www.ctvnews.ca/health/healthy-gut-linked-to-healthy-aging-in-new-research-1.3629433>

W Medical News Today, Oct 2017 <https://www.medicalnewstoday.com/articles/319756.php>

W Medicalresearch.com, Oct 2017 <https://medicalresearch.com/author-interviews/gut-microbiome-of-health-very-old-similar-to-younger-adults/37533/>

P Science Daily, Oct 2017 <https://www.sciencedaily.com/releases/2017/10/171011123728.htm>

P Medscape, Oct 2017 <https://www.medscape.com/viewarticle/887559>

P Good Times, Oct 2017 <https://goodtimes.ca/trust-gut-might-key-healthy-aging/>

P Psychology Today, Oct 2017 <https://www.psychologytoday.com/blog/the-athletes-way/201710/study-links-gut-microbiome-ridiculously-healthy-aging>

I CTV London TV, Oct 2017 CTV *video* <http://london.ctvnews.ca/video?clipId=1229909>

I HealthLine, Oct 2017 <https://www.healthline.com/health-news/does-healthy-gut-equal-long-healthy-life>

I CBC Radio London, Oct 2017 - *Afternoon Drive with host Chris Delatorre*

I AM1290-London/AM800 Windsor, Oct 2017: *TKO SHOW with Kara Ro*

P Reader's Digest, Oct 2017: <https://www.rd.com/health/wellness/healthy-gut-microbiome-longevity/>

W Oxygen Magazine: Date of publication to be determined

S Science Reddit (to Nov 7, 2017) (196 comments, 3064 upvotes, 94% upvoted):
https://www.reddit.com/r/science/comments/764rbg/ridiculously_healthy_elderly_have_the_same_gut/

S Reddit AMA (to Nov 7, 2017) (99 comments, 184 upvotes, 89% upvoted):
https://www.reddit.com/r/science/comments/79myv8/science_ama_series_were_the_researchers_from/

S SchulichMedDent Twitter (to Nov 7, 2017) (10 retweets, 13 likes):
<https://twitter.com/SchulichMedDent/status/918117822865264641>

S Lawson Twitter (to Nov 7, 2017) (6 retweets, 12 likes):
<https://twitter.com/lawsonresearch/status/918222731849748480>

- S Western Facebook post (to Nov 7, 2017) (109 shares, 371 reactions – this also had a reach of 50.4K, and 2.1K clicks): <https://www.facebook.com/WesternUniversity/>
- I CTV London, Dec 2012:
<http://london.ctvnews.ca/video?clipId=1015906>
- P Globe and Mail Jan 2013:
<http://www.theglobeandmail.com/life/health-and-fitness/health/fake-poop-created-to-treat-c-diff/article7190494/>
- I CTV Kitchener, London, Kingston Jan 2016:
<http://kitchener.ctvnews.ca/video?playlistId=1.1111065>
- R 2000-2004: Tour Organizer for Regina Mundi College Gr12 students (~30 per year)
- R Nov 2001: Presentation on Emerging Career Opportunities in Biotechnology to the post-graduate Corporate Communications and Public Relations course at Fanshawe College
- R March 2001: Presentation on Genetic Research opportunities to entire A.B. Lucas Secondary School Student body (1400 students)
- I CBC TV Nov 1996: *Undercurrents* Documentary program: interviewed and hosted by Wendy Mesley. Rebroadcast on CBC News world
- R Nov 1996: Presentation on Gene Therapy at the joint meeting of National Science Teachers Association- Science Teachers of Ontario Meeting
- R June 1996: Presentation on Medical Research to Students at Tilsonburg High school
- I Feb 1996: Led press conference outlining partnership between the FFGCT and the MRC for the funds raised by Jesse's Journey
- R Nov 1995: Presentation on Molecular Genetic Research to Saunder's Secondary School students
- R Oct 1995: Presentation to South London Chapter of Phi-delta- epsilon on Duchenne Muscular Dystrophy and the promise of gene therapy
- R Sept 1995: Presentation at Jesse Davidson Appreciation Night at the London City Press Club
- R Aug 1995: Presentation at the corporate fundraising launch for Jesse's Journey
- R Aug 1991: *Gene Therapy, Approaches and Limitations* Resident's Rounds, Janeway Children's Hospital, St. John's Newfoundland

6.3 Peer Reviewed Papers:

- [135] S. Yang, G. Reid, J. R. G. Challis, G. B. Gloor, E. Asztalos, D. Money, S. Seney, and A. D. Bocking, "Effect of oral probiotic lactobacillus rhamnosus gr-1 and lactobacillusreuteri rc-14 on the vaginal microbiota, cytokines and chemokines in pregnant women," *Nutrients*, vol. 12, Jan 2020.
- [134] D. J. Giguere, J. M. Macklaim, B. Y. Lieng, and G. B. Gloor, "omiclotr: visualizing omic datasets as compositions," *BMC Bioinformatics*, vol. 20, p. 580, Nov 2019.
- [133] L. Grieves, G. Gloor, M. Bernards, and E. MacDougall-Shackleton, "Songbirds show odour-based discrimination of similarity and diversity at the major histocompatibility complex," *Animal Behaviour*, vol. 158, pp. 131 – 138, 2019.
- [132] T. A. Hamilton, G. M. Pellegrino, J. A. Therrien, D. T. Ham, P. C. Bartlett, B. J. Karas, G. B. Gloor, and D. R. Edgell, "Efficient inter-species conjugative transfer of a crispr nuclease for targeted bacterial killing," *Nat Commun*, vol. 10, p. 4544, Oct 2019.
- [131] M. Laforet, T. A. McMurrough, M. Vu, C. M. Brown, K. Zhang, M. S. Junop, G. B. Gloor, and D. R. Edgell, "Modifying a covarying protein-dna interaction changes substrate preference of a site-specific endonuclease," *Nucleic Acids Res*, vol. 47, pp. 10830–10841, Nov 2019.
- [130] T. P. Quinn, I. Erb, G. Gloor, C. Notredame, M. F. Richardson, and T. M. Crowley, "A field guide for the compositional analysis of any-omics data," *Gigascience*, vol. 8, Sep 2019.
- [129] C. Elwood, A. Y. K. Albert, E. McClymont, E. Wagner, D. Mahal, K. Devakandan, B. L. Quigley, Z. Pakzad, M. H. Yudin, J. E. Hill, D. Money, VOGUE Research Group, A. Bocking, T. Dumonceaux, G. Gloor, S. Hemmingsen, J. E. Hill, M. Links, D. Money, K. O'Doherty, G. Reid, J. van Schalkwyk, P. Tang, and M. H. Yudin, "Different and diverse anaerobic microbiota were seen in women living with hiv with unsuppressed hiv viral load and in women with recurrent bacterial vaginosis: a cohort study," *BJOG*, Sep 2019.
- [128] M. D. Berg, D. J. Giguere, J. S. Dron, J. T. Lant, J. Genereaux, C. Liao, J. Wang, J. F. Robinson, G. B. Gloor, R. A. Hegele, P. O'Donoghue, and C. J. Brandl, "Targeted sequencing reveals expanded genetic diversity of human transfer rnas," *RNA Biol*, vol. 16, pp. 1574–1585, Aug 2019.
- [127] Z. Awamleh, G. B. Gloor, and V. K. M. Han, "Placental micrnas in pregnancies with early onset intrauterine growth restriction and preeclampsia: potential impact on gene expression and pathophysiology," *BMC Med Genomics*, vol. 12, p. 91, 06 2019.
- [126] D. G. Wootton, M. J. Cox, G. B. Gloor, D. Litt, K. Hoschler, E. German, J. Court, O. Eneje, L. Keogan, L. Macfarlane, S. Wilks, P. J. Diggle, M. Woodhead, M. F. Moffatt, W. O. C. Cookson, and S. B. Gordon, "A haemophilus sp. dominates the microbiota of sputum from uk adults with non-severe community acquired pneumonia and chronic lung disease," *Sci Rep*, vol. 9, p. 2388, Feb 2019.
- [125] A. Almeida, A. L. Mitchell, M. Boland, S. C. Forster, G. B. Gloor, A. Tarkowska, T. D. Lawley, and R. D. Finn, "A new genomic blueprint of the human gut microbiota," *Nature*, vol. 568, p. 499, Feb 2019.
- [124] B. R. Joris and G. B. Gloor, "Unaccounted risk of cardiovascular disease: the role of the microbiome in lipid metabolism," *Curr Opin Lipidol*, Jan 2019.
- [123] M. D. Berg, J. Genereaux, Y. Zhu, S. Mian, G. B. Gloor, and C. J. Brandl, "Acceptor stem differences contribute to species-specific use of yeast and human tRNAs^{er}," *Genes (Basel)*, vol. 9, p. 612, Dec 2018.

- [122] T. A. McMurrough, C. M. Brown, K. Zhang, G. Hausner, M. S. Junop, G. B. Gloor, and D. R. Edgell, "Active site residue identity regulates cleavage preference of LAGLIDADG homing endonucleases," *Nucleic Acids Res*, vol. 46, pp. 11990–12007, Oct 2018.
- [121] M. I. Petrova, J. M. Macklaim, S. Wuyts, T. Verhoeven, J. Vanderleyden, G. B. Gloor, S. Lebeer, and G. Reid, "Comparative genomic and phenotypic analysis of the vaginal probiotic lactobacillus rhamnosus GR-1," *Front Microbiol*, vol. 9, p. 1278, 2018.
- [120] G. B. Gloor, R. G. Wong, E. Allen-Vercoe, V. Dinculescu, M. Pignanelli, C. Bogiatzi, G. Reid, and J. D. Spence, "Data on the gut and saliva microbiota from a cohort of atherosclerosis patients determined by 16s rna gene sequencing," *Data Brief*, vol. 19, pp. 481–485, Aug 2018.
- [119] M. Pignanelli, C. Bogiatzi, G. Gloor, E. Allen-Vercoe, G. Reid, B. L. Urquhart, K. N. Ruetz, T. J. Velenosi, and J. D. Spence, "Moderate renal impairment and toxic metabolites produced by the intestinal microbiome: Dietary implications," *J Ren Nutr*, vol. 29, pp. 55–64, Aug 2018.
- [118] M. Pignanelli, C. Just, C. Bogiatzi, V. Dinculescu, G. B. Gloor, E. Allen-Vercoe, G. Reid, B. L. Urquhart, K. N. Ruetz, T. J. Velenosi, and J. D. Spence, "Mediterranean diet score: Associations with metabolic products of the intestinal microbiome, carotid plaque burden, and renal function," *Nutrients*, vol. 10, Jun 2018.
- [117] A. McMillan, S. Rulisa, G. B. Gloor, J. M. Macklaim, M. Sumarah, and G. Reid, "Pilot assessment of probiotics for pregnant women in rwanda," *PLoS One*, vol. 13, no. 6, p. e0195081, 2018.
- [116] J. M. Macklaim and G. B. Gloor, "From RNA-seq to biological inference: Using compositional data analysis in meta-transcriptomics," *Methods Mol Biol*, vol. 1849, pp. 193–213, 2018.
- [115] C. Bogiatzi, G. Gloor, E. Allen-Vercoe, G. Reid, R. G. Wong, B. L. Urquhart, V. Dinculescu, K. N. Ruetz, T. J. Velenosi, M. Pignanelli, and J. D. Spence, "Metabolic products of the intestinal microbiome and extremes of atherosclerosis," *Atherosclerosis*, vol. 273, pp. 91–97, Jun 2018.
- [114] K. F. Al, J. E. Bisanz, G. B. Gloor, G. Reid, and J. P. Burton, "Evaluation of sampling and storage procedures on preserving the community structure of stool microbiota: A simple at-home toilet-paper collection method," *J Microbiol Methods*, vol. 144, pp. 117–121, Jan 2018.
- [113] J. J. Egozcue, V. Pawlowsky-Glahn, and G. B. Gloor, "Linear association in compositional data analysis," *Austrian Journal of Statistics*, vol. 47, pp. 3–31, january 2018.
- [112] G. B. Gloor, J. M. Macklaim, V. Pawlowsky-Glahn, and J. J. Egozcue, "Microbiome datasets are compositional: And this is not optional," *Front Microbiol*, vol. 8, p. 2224, 2017.
- [111] R. Sinha, G. Abu-Ali, E. Vogtmann, A. A. Fodor, B. Ren, A. Amir, E. Schwager, J. Crabtree, S. Ma, Microbiome Quality Control Project Consortium, C. C. Abnet, R. Knight, O. White, and C. Huttenhower, "Assessment of variation in microbial community amplicon sequencing by the microbiome quality control (mbqc) project consortium," *Nat Biotechnol*, vol. 35, pp. 1077–1086, Nov 2017.
- [110] G. Bian, G. B. Gloor, A. Gong, C. Jia, W. Zhang, J. Hu, H. Zhang, Y. Zhang, Z. Zhou, J. Zhang, J. P. Burton, G. Reid, Y. Xiao, Q. Zeng, K. Yang, and J. Li, "The gut microbiota of healthy aged chinese is similar to that of the healthy young," *mSphere*, vol. 2, no. 5, pp. e00327–17, 2017.
- [109] S. L. Martz, M. Guzman-Rodriguez, S.-M. He, C. Noordhof, D. J. Hurlbut, G. B. Gloor, C. Carlucci, S. Weese, E. Allen-Vercoe, J. Sun, E. C. Claud, and E. O. Petrof, "A human gut ecosystem protects against c. difficile disease by targeting tcda," *Journal of Gastroenterology*, vol. 52, pp. 452–465, Apr 2017.

- [108] A. McMillan, A. E. Orimadegun, M. W. Sumarah, J. Renaud, M. M. da Encarnacao, G. B. Gloor, O. O. Akinyinka, G. Reid, and S. J. Allen, "Metabolic derangements identified through untar-geted metabolomics in a cross-sectional study of nigerian children with severe acute malnutrition," *Metabolomics*, vol. 13, p. 13, Dec 2016.
- [107] G. Ettinger, J. P. Burton, G. B. Gloor, and G. Reid, "Lactobacillus rhamnosus GR-1 attenuates induc-tion of hypertrophy in cardiomyocytes but not through secreted protein msp-1 (p75)," *PLoS One*, vol. 12, no. 1, p. e0168622, 2017.
- [106] K. Al, O. Sarr, K. Dunlop, G. B. Gloor, G. Reid, J. Burton, and T. R. H. Regnault, "Impact of birth weight and postnatal diet on the gut microbiota of young adult guinea pigs," *PeerJ*, vol. 5, p. e2840, 2017.
- [105] J. M. Wolfs, T. A. Hamilton, J. T. Lant, M. Laforet, J. Zhang, L. M. Salemi, G. B. Gloor, C. Schild-Poulter, and D. R. Edgell, "Biasing genome-editing events toward precise length deletions with an rna-guided tevca9 dual nuclease," *Proc Natl Acad Sci U S A*, Dec 2016.
- [104] J. W. G. Slade, Y. Sarquis-Adamson, G. B. Gloor, M.-A. Lachance, and E. A. MacDougall-Shackleton, "Population differences at mhc do not explain enhanced resistance of song sparrows to local para-sites," *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 simi-larity in songbirds," *Proc Biol Sci*, vol. 283, Nov 2016.
- [101] M. I. Petrova, E. Lievens, T. L. A. Verhoeven, J. M. Macklaim, G. Gloor, D. Schols, J. Vanderleyden, G. Reid, and S. Lebeer, "The lectin-like protein 1 in lactobacillus rhamnosus gr-1 mediates tissue-specific adherence to vaginal epithelium and inhibits urogenital pathogens," *Sci Rep*, vol. 6, p. 37437, Nov 2016.
- [100] G. B. Gloor, J. M. Macklaim, M. Vu, and A. D. Fernandes, "Compositional uncertainty should not be ignored in high-throughput sequencing data analysis," *Austrian Journal of Statistics*, vol. 45, pp. 73–87, September 2016.
- [99] G. B. Gloor and G. Reid, "Compositional analysis: a valid approach to analyze microbiome high-throughput sequencing data," *Can J Microbiol*, vol. 62, pp. 692–703, Aug 2016.
- [98] C. Urbaniak, G. B. Gloor, M. Brackstone, L. Scott, M. Tangney, and G. Reid, "The microbiota of breast tissue and its association with breast cancer," *Appl Environ Microbiol*, vol. 82, pp. 5039–48, Aug 2016.
- [97] G. B. Gloor, J. R. Wu, V. Pawlowsky-Glahn, and J. J. Egozcue, "It's all relative: analyzing microbiome data as compositions," *Ann Epidemiol*, vol. 26, pp. 322–9, May 2016.
- [96] G. B. Gloor, J. M. Macklaim, and A. D. Fernandes, "Displaying variation in large datasets: Plotting a visual summary of effect sizes," *Journal of Computational and Graphical Statistics*, vol. 25, no. 3C, pp. 971–979, 2016.
- [95] R. G. Wong, J. R. Wu, and G. B. Gloor, "Expanding the UniFrac toolbox," *PLoS One*, vol. 11, no. 9, p. e0161196, 2016.

- [94] C. Urbaniak, M. Angelini, G. B. Gloor, and G. Reid, "Human milk microbiota profiles in relation to birthing method, gestation and infant gender," *Microbiome*, vol. 4, p. 1, Jan 2016.
- [93] A. Asemaninejad, N. Weerasuriya, G. B. Gloor, Z. Lindo, and R. G. Thorn, "New primers for discovering fungal diversity using nuclear large ribosomal dna," *PLoS One*, vol. 11, no. 7, p. 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*, vol. 8, no. 1, p. 44, 2016.
- [91] D. M. Walton, J. M. Elliott, J. Lee, E. Loh, J. C. MacDermid, S. Schabrun, W. L. Siqueira, B. D. Corneil, B. Aal, T. Birmingham, A. Brown, L. K. Cooper, J. P. Dickey, S. J. Dixon, D. D. Fraser, J. S. Gati, G. B. Gloor, G. Good, D. Holdsworth, S. A. McLean, W. Millard, J. Miller, J. Sadi, D. A. Seminowicz, J. K. Shoemaker, G. P. Siegmund, T. Vertseegh, and T. H. Wideman, "Research priorities in the field of posttraumatic pain and disability: Results of a transdisciplinary consensus-generating workshop," *Pain Res Manag*, vol. 2016, p. 1859434, 2016.
- [90] J. E. Bisanz, P. Suppiah, W. M. Thomson, T. Milne, N. Yeoh, A. Nolan, G. Ettinger, G. Reid, G. B. Gloor, J. P. Burton, M. P. Cullinan, and S. M. Stebbings, "The oral microbiome of patients with axial spondyloarthritis compared to healthy individuals," *PeerJ*, vol. 4, p. e2095, 2016.
- [89] J. E. Bisanz, M. K. Enos, G. PrayGod, S. Seney, J. M. Macklaim, S. Chilton, D. Willner, R. Knight, C. Fusch, G. Fusch, G. B. Gloor, J. P. Burton, and G. Reid, "Microbiota at multiple body sites during pregnancy in a rural tanzanian population and effects of moringa-supplemented probiotic yogurt," *Appl Environ Microbiol*, vol. 81, pp. 4965–75, Aug 2015.
- [88] N. St-Denis, M. Gabriel, J. P. Turowec, G. B. Gloor, S. S.-C. Li, A.-C. Gingras, and D. W. Litchfield, "Systematic investigation of hierarchical phosphorylation by protein kinase ck2," *J Proteomics*, vol. 118, pp. 49–62, Apr 2015.
- [87] L. W. Goneau, T. J. Hannan, R. A. MacPhee, D. J. Schwartz, J. M. Macklaim, G. B. Gloor, H. Razvi, G. Reid, S. J. Hultgren, and J. P. Burton, "Subinhibitory antibiotic therapy alters recurrent urinary tract infection pathogenesis through modulation of bacterial virulence and host immunity," *MBio*, vol. 6, Mar 2015.
- [86] A. McMillan, S. Rulisa, M. Sumarah, J. M. Macklaim, J. Renaud, J. E. Bisanz, G. B. Gloor, and G. Reid, "A multi-platform metabolomics approach identifies highly specific biomarkers of bacterial diversity in the vagina of pregnant and non-pregnant women," *Sci Rep*, vol. 5, p. 14174, 2015.
- [85] S.-L. E. Martz, J. A. K. McDonald, J. Sun, Y.-G. Zhang, G. B. Gloor, C. Noordhof, S.-M. He, T. K. Gerbaba, M. Blennerhassett, D. J. Hurlbut, E. Allen-Vercoe, E. C. Claud, and E. O. Petrof, "Administration of defined microbiota is protective in a murine salmonella infection model," *Sci Rep*, vol. 5, p. 16094, 2015.
- [84] J. M. Macklaim, J. C. Clemente, R. Knight, G. B. Gloor, and G. Reid, "Changes in vaginal microbiota following antimicrobial and probiotic therapy," *Microb Ecol Health Dis*, vol. 26, p. 27799, 2015.
- [83] S. Yang, G. Reid, J. R. G. Challis, S. O. Kim, G. B. Gloor, and A. D. Bocking, "Is there a role for probiotics in the prevention of preterm birth?," *Front Immunol*, vol. 6, p. 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)*, vol. 38, pp. 1525–31, Dec 2014.
- [81] T. A. McMurrough, R. J. Dickson, S. M. F. Thibert, G. B. Gloor, and D. R. Edgell, "Control of catalytic efficiency by a coevolving network of catalytic and noncatalytic residues," *Proc Natl Acad Sci U S A*, vol. 111, pp. E2376–83, Jun 2014.
- [80] C. Urbaniak, J. Cummins, M. Brackstone, J. M. Macklaim, G. B. Gloor, C. K. Baban, L. Scott, D. M. O'Hanlon, J. P. Burton, K. P. Francis, M. Tangney, and G. Reid, "Microbiota of human breast tissue," *Appl Environ Microbiol*, vol. 80, pp. 3007–14, May 2014.
- [79] X. T. Gan, G. Ettinger, C. X. Huang, J. P. Burton, J. V. Haist, V. Rajapurohitam, J. E. Sidaway, G. Martin, G. B. Gloor, J. R. Swann, G. Reid, and M. Karmazyn, "Probiotic administration attenuates myocardial hypertrophy and heart failure after myocardial infarction in the rat," *Circ Heart Fail*, vol. 7, pp. 491–9, May 2014.
- [78] G. Reid, N. Nduti, W. Sybesma, R. Kort, T. R. Kollmann, R. Adam, H. Boga, E. M. Brown, A. Einerhand, H. El-Nezami, G. B. Gloor, I. I. Kavere, J. Lindahl, A. Manges, W. Mamo, R. Martin, A. McMillan, J. Obiero, P. A. Ochieng, A. Onyango, S. Rulisa, E. Salminen, S. Salminen, A. Sije, J. R. Swann, W. van Treuren, D. Waweru, and S. J. Kemp, "Harnessing microbiome and probiotic research in sub-Saharan Africa: recommendations from an African workshop," *Microbiome*, vol. 2, p. 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] C. Brace, G. B. Gloor, M. Ropeleski, E. Allen-Vercoe, and E. O. Petrof, "Microbial composition analysis of *Clostridium difficile* infections in an ulcerative colitis patient treated with multiple fecal microbiota transplantations," *J Crohns Colitis*, vol. 8, pp. 1113–7, Feb 2014.
- [75] J. E. Bisanz, S. Seney, A. McMillan, R. Vongsa, D. Koenig, L. Wong, B. Dvoracek, G. B. Gloor, M. Sumarah, B. Ford, D. Herman, J. P. Burton, and G. 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*, vol. 9, no. 8, p. e104511, 2014.
- [74] K. D. Kernohan, D. Vernimmen, G. B. Gloor, and N. G. Bérubé, "Analysis of neonatal brain lacking ATRX or MeCP2 reveals changes in nucleosome density, CTCF binding and chromatin looping," *Nucleic Acids Res*, vol. 42, no. 13, pp. 8356–68, 2014.
- [73] R. J. Dickson and G. B. Gloor, "Bioinformatics identification of coevolving residues," *Methods Mol Biol*, vol. 1123, pp. 223–43, 2014.
- [72] C. Urbaniak, A. McMillan, M. Angelini, G. B. Gloor, M. Sumarah, J. P. Burton, and G. Reid, "Effect of chemotherapy on the microbiota and metabolome of human milk, a case report," *Microbiome*, vol. 2, p. 24, 2014.
- [71] M. Rosenthal, A. E. Aiello, C. Chenoweth, D. Goldberg, E. Larson, G. Gloor, and B. Foxman, "Impact of technical sources of variation on the hand microbiome dynamics of healthcare workers," *PLoS One*, vol. 9, no. 2, p. e88999, 2014.

- [70] J. E. Bisanz, M. K. Enos, J. R. Mwanga, J. Chagalucha, J. P. Burton, G. B. Gloor, and G. 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*, vol. 5, no. 5, pp. e01580–14, 2014.
- [69] A. D. Fernandes, J. N. Reid, J. M. Macklaim, T. A. McMurrough, D. R. Edgell, and G. 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*, vol. 2, pp. 15.1–15.13, 2014.
- [68] J. M. Di Bella, Y. Bao, G. B. Gloor, J. P. Burton, and G. Reid, "High throughput sequencing methods and analysis for microbiome research," *J Microbiol Methods*, vol. 95, pp. 401–14, Dec 2013.
- [67] L. F. DaSilva, S. Pilon, J. Genereaux, M. J. Davey, G. B. Gloor, J. Karagiannis, and C. J. Brandl, "The C-terminal residues of *Saccharomyces cerevisiae* Mec1 are required for its localization, stability, and function," *G3 (Bethesda)*, vol. 3, pp. 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*, vol. 8, no. 7, p. e67019, 2013.
- [65] M. S. Kim, G. B. Gloor, and D. 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*, vol. 452, pp. 249–58, Jun 2013.
- [64] R. A. MacPhee, W. L. Miller, G. B. Gloor, J. K. McCormick, J.-A. Hammond, J. P. Burton, and G. Reid, "Influence of the vaginal microbiota on toxic shock syndrome toxin 1 production by staphylococcus aureus," *Appl Environ Microbiol*, vol. 79, pp. 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*, vol. 4, pp. 53–65, Mar 2013.
- [62] P. Lahiry, L. Racacho, J. Wang, J. F. Robinson, G. B. Gloor, C. A. Rupar, V. M. Siu, D. E. Bulman, and R. A. Hegele, "A mutation in the serine protease TMPRSS4 in a novel pediatric neurodegenerative disorder," *Orphanet J Rare Dis*, vol. 8, p. 126, 2013.
- [61] J. M. Macklaim, A. D. Fernandes, J. M. Di Bella, J.-A. Hammond, G. Reid, and G. B. Gloor, "Comparative meta-RNA-seq of the vaginal microbiota and differential expression by lactobacillus iners in health and dysbiosis," *Microbiome*, vol. 1, p. 12, Apr 2013.
- [60] K. C. Anukam, J. M. Macklaim, G. B. Gloor, G. Reid, J. Boekhorst, B. Renckens, S. A. F. T. van Hijum, and R. J. Siezen, "Genome sequence of *Lactobacillus pentosus* KCA1: Vaginal isolate from a healthy premenopausal woman," *PLoS One*, vol. 8, no. 3, p. e59239, 2013.
- [59] P. A. Wescombe, J. M. Macklaim, M. H. C. Chai, K. MacDonald, J. D. F. Hale, J. Tagg, G. Reid, G. B. Gloor, and P. 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*, vol. 8, p. e65991, 2013.
- [58] E. O. Petrof, G. B. Gloor, S. J. Vanner, S. J. Weese, D. Carter, M. C. Daigneault, E. M. Brown, K. Schroeter, and E. Allen-Vercoe, "Stool substitute transplant therapy for the eradication of clostridium difficile infection: 'repopulating' the gut," *Microbiome*, vol. 1, p. 3, Jan 2013.
- [57] E. Allen-Vercoe, G. Reid, N. Viner, G. B. Gloor, S. Hota, P. Kim, C. Lee, K. O'Doherty, S. J. Vanner, J. S. Weese, and E. O. Petrof, "A Canadian working group report on fecal microbial therapy: microbial ecosystems therapeutics," *Can J Gastroenterol*, vol. 26, pp. 457–62, Jul 2012.

- [56] J. M. Macklaim, C. R. Cohen, G. Donders, G. B. Gloor, J. E. Hill, G. P. Parham, J. Ravel, G. Spear, J. van de Wijgert, and G. Reid, "Exploring a road map to counter misconceptions about the cervico-vaginal microbiome and disease," *Reprod Sci*, May 2012.
- [55] T. Li, J. Liang, A. Ambrogelly, T. Brennan, G. Gloor, G. Huisman, J. Lalonde, A. Lekhal, B. Mijts, S. Muley, L. Newman, M. Tobin, G. Wong, A. Zaks, and X. 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*, vol. 134, pp. 6467–72, Apr 2012.
- [54] J. Genereaux, S. Kvas, D. Dobransky, J. Karagiannis, G. B. Gloor, and C. J. Brandl, "Genetic evidence links the ASTRA protein chaperone component Tti2 to the SAGA transcription factor Tra1," *Genetics*, Apr 2012.
- [53] S. Kvas, G. B. Gloor, and C. J. Brandl, "Loss of nonsense mediated decay suppresses mutations in *Saccharomyces cerevisiae* TRA1," *BMC Genet*, vol. 13, p. 19, Mar 2012.
- [52] R. J. Dickson and G. B. Gloor, "Protein sequence alignment analysis by local covariation: coevolution statistics detect benchmark alignment errors," *PLoS One*, vol. 7, no. 6, p. e37645, 2012.
- [51] J. P. Turowec, J. S. Duncan, G. B. Gloor, and D. W. Litchfield, "Regulation of caspase pathways by protein kinase CK2: identification of proteins with overlapping CK2 and caspase consensus motifs," *Mol Cell Biochem*, vol. 356, pp. 159–67, Oct 2011.
- [50] R. Takeuchi, A. R. Lambert, A. N.-S. Mak, K. Jacoby, R. J. Dickson, G. B. Gloor, A. M. Scharenberg, D. R. Edgell, and B. L. Stoddard, "Tapping natural reservoirs of homing endonucleases for targeted gene modification," *Proc Natl Acad Sci U S A*, vol. 108, pp. 13077–82, Aug 2011.
- [49] J. M. Macklaim, G. B. Gloor, K. C. Anukam, S. Cribby, and G. Reid, "At the crossroads of vaginal health and disease, the genome sequence of *Lactobacillus iners* AB-1," *Proc Natl Acad Sci U S A*, vol. 108 Suppl 1, pp. 4688–95, Mar 2011.
- [48] J. S. Duncan, J. P. Turowec, K. E. Duncan, G. Vilks, C. Wu, B. Lüscher, S. S.-C. Li, G. B. Gloor, and D. W. Litchfield, "A peptide-based target screen implicates the protein kinase CK2 in the global regulation of caspase signaling," *Sci Signal*, vol. 4, no. 172, p. ra30, 2011.
- [47] G. Reid, J. A. Younes, H. C. Van der Mei, G. B. Gloor, R. Knight, and H. J. Busscher, "Microbiota restoration: natural and supplemented recovery of human microbial communities," *Nat Rev Microbiol*, vol. 9, pp. 27–38, Jan 2011.
- [46] R. Hummelen, J. M. Macklaim, J. E. Bisanz, J.-A. Hammond, A. McMillan, R. Vongsa, D. Koenig, G. B. Gloor, and G. Reid, "Vaginal microbiome and epithelial gene array in post-menopausal women with moderate to severe dryness," *PLoS One*, vol. 6, no. 11, p. e26602, 2011.
- [45] S. M. T. Hoke, A. Irina Mutiu, J. Genereaux, S. Kvas, M. Buck, M. Yu, G. B. Gloor, and C. J. Brandl, "Mutational analysis of the C-terminal FATC domain of *Saccharomyces cerevisiae* Tra1," *Curr Genet*, vol. 56, pp. 447–65, Oct 2010.
- [44] R. J. Dickson, L. M. Wahl, A. D. Fernandes, and G. B. Gloor, "Identifying and seeing beyond multiple sequence alignment errors using molecular covariation," *PLoS ONE*, vol. 5, p. e11082, June:2010 2010.
- [43] G. B. Gloor, G. Tyagi, D. M. Abrassart, A. J. Kingston, A. D. Fernandes, S. D. Dunn, and C. J. Brandl, "Functionally compensating coevolving positions are neither homoplastic nor conserved in clades," *Mol Biol Evol*, vol. 27, pp. 1181–91, May 2010.

- [42] A. D. Fernandes and G. B. Gloor, "Mutual information is critically dependent on prior assumptions: would the correct estimate of mutual information please identify itself?," *Bioinformatics*, vol. 26, pp. 1135–9, May 2010.
- [41] B. P. Kleinstiver, A. D. Fernandes, G. B. Gloor, and D. R. Edgell, "A unified genetic, computational and experimental framework identifies functionally relevant residues of the homing endonuclease I-BmoI," *Nucleic Acids Res*, vol. 38, pp. 2411–27, Apr 2010.
- [40] J. S. Duncan, J. P. Turowec, G. Vilk, S. S. C. Li, G. B. Gloor, and D. W. Litchfield, "Regulation of cell proliferation and survival: convergence of protein kinases and caspases," *Biochim Biophys Acta*, vol. 1804, pp. 505–10, Mar 2010.
- [39] R. Hummelen, A. D. Fernandes, J. M. Macklaim, R. J. Dickson, J. Chagalucha, G. B. Gloor, and G. Reid, "Deep sequencing of the vaginal microbiota of women with HIV," *PLoS One*, vol. 5, no. 8, p. e12078, 2010.
- [38] A. D. Fernandes, B. P. Kleinstiver, D. R. Edgell, L. M. Wahl, and G. B. Gloor, "Estimating the evidence of selection and the reliability of inference in unigenic evolution," *Algorithms Mol Biol*, vol. 5, p. 35, 2010.
- [37] G. B. Gloor, R. Hummelen, J. M. Macklaim, R. J. Dickson, A. D. Fernandes, R. MacPhee, and G. Reid, "Microbiome profiling by Illumina sequencing of combinatorial sequence-tagged PCR products," *PLoS One*, vol. 5, no. 10, p. e15406, 2010.
- [36] P. Lahiry, J. Wang, J. F. Robinson, J. P. Turowec, D. W. Litchfield, M. B. Lanktree, G. B. Gloor, E. G. Puffenberger, K. A. Strauss, M. B. Martens, D. A. Ramsay, C. A. Rupa, V. Siu, and R. A. Hegele, "A multiplex human syndrome implicates a key role for intestinal cell kinase in development of central nervous, skeletal, and endocrine systems," *Am J Hum Genet*, vol. 84, pp. 134–47, Feb 2009.
- [35] S. Dunn, L. Wahl, and G. Gloor, "Mutual information without the influence of phylogeny or entropy dramatically improves residue contact prediction," *Bioinformatics*, vol. 23, no. 3, pp. 333–340, 2008.
- [34] A. M. Holmes, K. A. Weedmark, and G. B. Gloor, "Mutations in the extra sex combs and Enhancer of Polycomb genes increase homologous recombination in somatic cells of *Drosophila melanogaster*," *Genetics*, vol. 172, no. 4, pp. 2367–77, 2006.
- [33] G. B. Gloor, L. C. Martin, L. M. Wahl, and S. D. Dunn, "Mutual information in protein multiple sequence alignments reveals two classes of coevolving positions," *Biochemistry*, vol. 44, no. 19, pp. 7156–7165, 2005.
- [32] L. C. Martin, G. B. Gloor, S. D. Dunn, and L. M. Wahl, "Using information theory to search for co-evolving residues in proteins," *Bioinformatics*, vol. 21, no. 22, pp. 4116–4124, 2005.
- [31] B. R. Dempsey, M. Wrona, J. M. Moulin, G. B. Gloor, F. Jalilehvand, G. Lajoie, G. S. Shaw, and B. H. Shilton, "Solution nmr structure and x-ray absorption analysis of the c-terminal zinc-binding domain of the seca atpase," *Biochemistry*, vol. 43, pp. 9361–71, Jul 2004.
- [30] H. Qin, A. Percival-Smith, C. Li, C. Y. H. Jia, G. Gloor, and S. S.-C. Li, "A novel transmembrane protein recruits numb to the plasma membrane during asymmetric cell division," *J Biol Chem*, vol. 279, pp. 11304–12, Mar 2004.
- [29] G. B. Gloor, "Gene targeting in drosophila," *Methods Mol Biol*, vol. 260, pp. 97–114, 2004.

- [28] A. M. Coveny, T. Dray, and G. B. Gloor, "The effect of heterologous insertions on gene conversion in mitotically dividing cells in drosophila melanogaster," *Genetics*, vol. 161, pp. 249–58, May 2002.
- [27] G. B. Gloor, "The role of sequence homology in the repair of DNA double-strand breaks in drosophila," *Adv Genet*, vol. 46, pp. 91–117, 2002.
- [26] G. B. Gloor, "Gene-targeting in drosophila validated," *Trends Genet*, vol. 17, pp. 549–51, Oct 2001.
- [25] L. Kari, R. Kitto, and G. Gloor, "A computer scientist's guide to molecular biology," *Soft Computing*, vol. 5, no. 2, pp. 95–101, 2001.
- [24] P. Krishna and G. Gloor, "The hsp90 family of proteins in arabidopsis thaliana," *Cell Stress Chaperones*, vol. 6, pp. 238–46, Jul 2001.
- [23] L. Kari, G. Gloor, and S. Yu, "Using dna to solve the bounded post correspondence problem," *Theoretical Computer Science*, vol. 231, no. 2, pp. 193–203, 2000.
- [22] G. B. Gloor, J. Moretti, J. Mouyal, and K. J. Keeler, "Distinct p-element excision products in somatic and germline cells of drosophila melanogaster," *Genetics*, vol. 155, pp. 1821–30, Aug 2000.
- [21] A. S. Bassi, D. N. Ding, G. B. Gloor, and A. Margaritis, "Expression of single chain antibodies (scfvs) for c-myc oncoprotein in recombinant escherichia coli membranes by using the ice-nucleation protein of pseudomonas syringae," *Biotechnol Prog*, vol. 16, no. 4, pp. 557–63, 2000.
- [20] M. Daley, L. Kari, G. Gloor, and R. Siromoney, "Circular contextual insertions / deletions with applications to biomolecular computation," in *String Processing and Information Retrieval Symposium, 1999 and International Workshop on Groupware*, pp. 47–54, IEEE, 1999.
- [19] G. B. Gloor, T. Dray, and K. Keeler, "Analyzing double-strand repair events in drosophila," *Methods Mol Biol*, vol. 113, pp. 425–38, 1999.
- [18] G. Gloor, L. Kari, M. Gaasenbeek, and S. Yu, "Towards a dna solution to the shortest common super-string problem," *International Journal on Artificial Intelligence Tools*, vol. 8, no. 04, pp. 385–399, 1999.
- [17] L. Kari, M. Daley, G. Gloor, R. Siromoney, and L. F. Landweber, "How to compute with dna," in *International Conference on Foundations of Software Technology and Theoretical Computer Science*, pp. 269–282, Springer Berlin Heidelberg, 1999.
- [16] D. H. Lankenau and G. B. Gloor, "In vivo gap repair in drosophila: a one-way street with many destinations," *Bioessays*, vol. 20, pp. 317–27, Apr 1998.
- [15] G. B. Gloor and D. H. Lankenau, "Gene conversion in mitotically dividing cells: a view from drosophila," *Trends Genet*, vol. 14, pp. 43–6, Feb 1998.
- [14] T. Dray and G. B. Gloor, "Homology requirements for targeting heterologous sequences during p-induced gap repair in drosophila melanogaster," *Genetics*, vol. 147, pp. 689–99, Oct 1997.
- [13] K. J. Keeler and G. B. Gloor, "Efficient gap repair in drosophila melanogaster requires a maximum of 31 nucleotides of homologous sequence at the searching ends," *Mol Cell Biol*, vol. 17, pp. 627–34, Feb 1997.
- [12] K. J. Keeler, T. Dray, J. E. Penney, and G. B. Gloor, "Gene targeting of a plasmid-borne sequence to a double-strand DNA break in drosophila melanogaster," *Mol Cell Biol*, vol. 16, pp. 522–8, Feb 1996.

- [11] J. D. Andrews and G. B. Gloor, "A role for the kp leucine zipper in regulating p element transposition in drosophila melanogaster," *Genetics*, vol. 141, pp. 587–94, Oct 1995.
- [10] N. Nassif, J. Penney, S. Pal, W. R. Engels, and G. B. Gloor, "Efficient copying of nonhomologous sequences from ectopic sites via p-element-induced gap repair," *Mol Cell Biol*, vol. 14, pp. 1613–25, Mar 1994.
- [9] G. B. Gloor, C. R. Preston, D. M. Johnson-Schlitz, N. A. Nassif, R. W. Phillis, W. K. Benz, H. M. Robertson, and W. R. Engels, "Type i repressors of p element mobility," *Genetics*, vol. 135, pp. 81–95, Sep 1993.
- [8] G. B. Gloor, N. A. Nassif, D. M. Johnson-Schlitz, C. R. Preston, and W. R. Engels, "Targeted gene replacement in drosophila via p element-induced gap repair," *Science*, vol. 253, pp. 1110–7, Sep 1991.
- [7] G. Gloor and G. Chaconas, "Sequence of bacteriophage mu n and p genes," *Nucleic Acids Res*, vol. 16, pp. 5211–2, Jun 1988.
- [6] G. Gloor and G. Chaconas, "The bacteriophage mu n gene encodes the 64-kda virion protein which is injected with, and circularizes, infecting mu DNA," *J Biol Chem*, vol. 261, pp. 16682–8, Dec 1986.
- [5] G. Chaconas, E. B. Giddens, J. L. Miller, and G. Gloor, "A truncated form of the bacteriophage mu b protein promotes conservative integration, but not replicative transposition, of mu DNA," *Cell*, vol. 41, pp. 857–65, Jul 1985.
- [4] G. Chaconas, G. Gloor, and J. L. Miller, "Amplification and purification of the bacteriophage mu encoded b transposition protein," *J Biol Chem*, vol. 260, pp. 2662–9, Mar 1985.
- [3] E. A. Faust, G. Gloor, M. F. MacIntyre, and R. Nagy, "Atp(gtp)-dependent conversion of mvm parvovirus single-stranded DNA to its replicative form by a purified 10 s species of mouse DNA polymerase alpha," *Biochim Biophys Acta*, vol. 781, pp. 216–24, Apr 1984.
- [2] E. A. Faust and G. Gloor, "Characterization of a metastable, partially replicated dimeric intermediate of minute virus of mice," *J Virol*, vol. 49, pp. 621–5, Feb 1984.
- [1] G. Chaconas, G. Gloor, J. L. Miller, D. L. Kennedy, E. B. Giddens, and C. R. Nagainis, "Transposition of bacteriophage mu dna: expression of the a and b proteins from lambda pl and analysis of infecting mu dna," *Cold Spring Harb Symp Quant Biol*, vol. 49, pp. 279–84, 1984.

6.4 Non Peer Reviewed Manuscripts

Giguere DJ, Bahcheli AT, Joris BR, Paulssen JM, Gieg LM, Flatley MW, Gloor GB (2020) Complete and validated genomes from a metagenome biorXIV: 10.1101/2020.04.08.032540

Toby Kenney, Glen Satten, Shyamal Peddada, Gregory Gloor, Hong Gu. Emerging Statistical Challenges and Methods for Analysis of Human Microbiome Data, 2019. Technical Report for the Banff International Research Centre (2019)

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.

6.5 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 December 2018

Languages and utilities: R, bash, Perl, awk, L^AT_EX, Markdown, HTML, git, svn

6.6 Patent filings

CIS CONJUGATIVE PLASMID SYSTEM, 2018, with David Edgell, Bogumil Karas

6.7 Academic trivia

- H-index: 47, past 5 years 39 (Google Scholar)
- mean iCite ratio: 2.5, past 10 years 2.8 (icite.od.nih.gov: 80th percentile NIH funded authors, 90th percentile of all authors)
- Erdos number 3 (Gloor - [Lila Kari - Solomon Marcus - Paul Erdos | Sheng Yu - Andrew Granville - Paul Erdos])
- Bacon number 4 (Gloor - Wendy Mesley (Undercurrents) - multiple paths - multiple paths - Kevin Bacon)
- Aitchison number 1 (two ways)
- Academic lineages: T.H. Morgan (Genetics through Engels), G. Khorana (Biochemistry through Chaconas)

6.8 Research Funding History

Mitacs Accelerate, 2020: Rapid scaling of viral spike protein production for SARS-CoV-2 testing using *Phaeodactylum tricornutum*

PI: Gloor GB, Co-PI Edgell DR, Partner organization: Suncor

total: \$40000

CIHR Project Grant, 2019-2024: Modulation of pain in IBD by microbial proteases

PI: Lomax, AEG, DE, Co-PI Gloor, GB, Allen-Vercoe E, Reed, DE, Ross, AC, Vanner, SJ

Basic research into the microbial causes of pain in IBD patients. Gloor role is metagenomic and meta-transcriptomic profiling of patient microbiome samples.

total: \$395990

CIHR Project Grant, 2018-2023: ConCRISPR: Conjugative delivery of a hybrid CRISPR/Tev nuclease system for specific microbiota modulation in the mammalian gut

PI: Edgell, DE, Co-PI Gloor, GB and Karas B

Basic research into the technology platform to target and eradicate specific taxa or genetic components of the human gut microbiome.

total: \$891000

Weston Family Foundation Microbiome Initiative, 2017-2018: Microbiota modulation with a hybrid CRISPR nuclease

PI: Gloor, GB, Co-PI Edgell, DE and Karas B

Developing technology to target and eradicate specific taxa or genetic components of the human gut microbiome.

total: \$149000

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 Supplementation

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 endophytic 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 endophytic 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 POSITIONS

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*

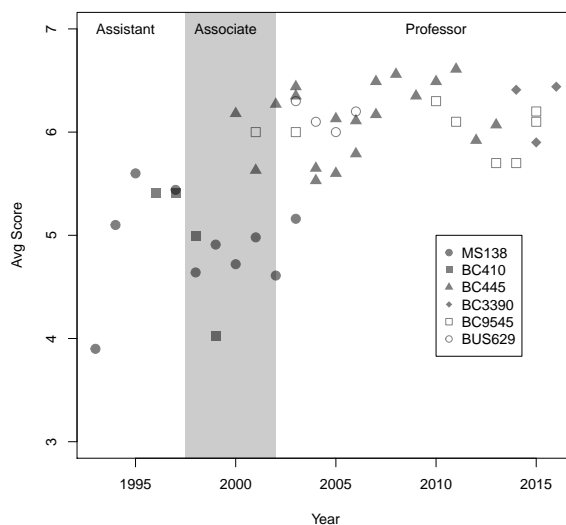
PI: Gloor

Total: \$197806 - Core Research Lab Funding

7 Teaching and Training

7.1 Course-based teaching

Figure 1: Teaching Ratings by Year and Course



I have been involved in teaching all or major portions of seven courses at Western, in addition to the occasional guest lecture. The six main courses are:

MS138: (1993-2003) First year medical school introduction to biochemistry. I taught 8-10 lectures that covered nucleotide metabolism, DNA replication and DNA repair as it related to cancer and HIV to first year medical students. I developed the material for delivery, following the broad theme given by the course co-ordinator at the time. The introductory didactic was removed from the undergraduate medical curriculum, along with most basic science, and replaced with small group teaching following a review of the undergraduate medical curriculum. I co-led a basic science review group for this process. I participated in small group teaching for several years afterward, but no evaluations were performed.

BC410: (1996-1999) I taught $\frac{1}{3}$ of this course, focussing on the basics of molecular biology pertaining to DNA structure, repair and recombination. The primary teaching tool was discussion of papers of current research interest with the objective of teaching the scientific discovery process. Included in this was one year of Biochemistry 453, the same course, different number.

BC445: (2000-2014) I developed and taught this course from scratch, often 2-3x per year. The course broadly covered 'bioinformatics' and had a focus on sequence and structure alignment, and at the time of development was rather novel being the first of its kind outside of a computer science department to cover the theory and practice of sequence alignment. The philosophy of the of this course was to teach how sequence alignment algorithms work in an intuitive way. The students would learn how the algorithm worked by doing it by hand, then we would move on to applying computers to make it faster. In addition, students learned the basics of Perl or Awk scripting and how to use a UNIX interface on a computer. Much of this material was rolled into BC3390.

BC3390: (2015 - now) A continuation, and simplification of the material in BC445 mandated when the undergraduate Biochemistry department curriculum was revamped.

BUS629: (2003-2006) I developed and taught this course in the Ivey MBA Biotechnology stream. I was responsible for all the material and for arranging guest experts. The thrust of the course was to teach non-science students in the MBA program how to quickly evaluate the business case for a biotechnology company based on the underlying science. This course was case-based and we discussed one case per week. I wish that Theranos was active at the time — it would have been a great example of foolish money chasing bad science. I received a citation from the Ivey Dean for teaching excellence.

BC9545: (2000 - now) This course initially was a more advance presentation of BC445 for graduate students. Since taking the course on compositional data analysis in 2014, I have redesigned it to be a course on the theory and practice of analyzing high throughput sequencing datasets — transcriptomics and metagenomics. I teach the theory and practice of probabilistic compositional data analysis for such datasets alongside the more traditional methods. My focus is on getting the students to understand and recognize when and why traditional methods go off the rails, and how they can use probabilistic compositional data analysis to double check their results.

The seventh course was a graduate computer science course.

CS881: (1996 - 2001) “Topics in computing and biology” Graduate Course. Six hours of lectures on the basics of DNA and on manipulations of DNA that could be used for primitive computational operations.

7.2 Summary of HQP

Graduate Students : 15; Undergraduate Student: 30; Postdoctoral Fellow: 2;

PhD Thesis Defence Examiner: 37

MSc Thesis Defence Examiner: 44

Thesis qualifying examiner: 48.

7.3 Graduate Students Supervised

Year	Student	Role	Description
2018-IPR	Joris	MSc (BC)	Defining correlated features in microbiomes
2017-IPR	Giguere	PhD (BC)	Integrative 'omic analysis of microbiomes
2017	Giguere	MSc (BC)	Visual exploration of multivariate multi-omic datasets
2017	Gajudhur	MSc (BC)	Visual exploration of multivariate multi-omic datasets
2013-2018	Macklaim	PDF	Microbial community composition of environmental datasets
2013-2016	Wong	MSc (BC)	Microbial community composition of patient cohorts
2012-2013	DiBella	MSc (MI, co)	Role of antisense transcription in bacterial gene regulation
2011-2017	McMurrough	PhD (BC, co)	Coevolution in LAGLIDAG endonucleases
2008-2013	Macklaim	PhD (BC)	Meta-omics of the vaginal microbiome
2008-2013	Dickson	PhD (BC)	Coevolution in protein families
2007-2012	Fernandes	PDF	Statistical tools for microbiome analysis
2002-2004	Gao	MSc (BCE, co)	Cell Surface Expression of <i>Vitreoscilla</i> Hemoglobin
2001-2008	Weedmark	PhD (BC)	DNA repair in <i>Drosophila</i>
1998-2005	Coveny	PhD (BC)	Polycomb genes and DSB
1997-1999	Ding	MSc (BCE, co)	Membrane display of an INP fusion protein
1994-1998	Dray	PhD (BC)	Targeting heterologous sequences in <i>Drosophila melanogaster</i>
1993-1998	Keeler	PhD (BC)	element induced double-strand break repair
1993-1995	Raynor	MSc (BC)	P element excision-induced double strand gap repair
1991-1995	Andrews	MSc (BC)	KP leucine zipper in the regulation of P transposition

8 Service to the University and Broader Community

8.1 University Committees

Year	Role	Description
2016	Member	Western NSERC Science Review Board
2012	Member	Law Graduate Program Review Committee
2011-2014	Member	Computer Science Promotion and Tenure Committee
2011-2013	Member	SUPR-G Committee
2011	Member	Faculty of Law and Ivey Business School Joint Promotion and Tenure Committee
2005-2006	Member	Ivey Business School Promotion and Tenure Committee
2005	Reviewer	External reviewer for Developmental Biology Graduate Program
2001-2004	Member	Promotion and Tenure - Biology Department
2001-2002	Member	UWO Bioinformatics Tier 2 CRC Search Committee
2000-2002	Member	Senate Subcommittee on Computing and Network Security
2000-2003	Chair	Senate Subcommittee on the WWW (SUWWW)
2000-2001	Member	Accessibility Subcommittee of SUWWW
1999-2000	Member	Biochemical Engineering Chair Selection Committee
1998-1999	Member	Senate Subcommittee on Computing and Network Services
1998-1999	Member	Senate Subcommittee on Computing and Information Technology
1997-1999	Member	Scientific Computing Research Advisory Subcommittee
1996-2000	Member	UWO Homepage Design and Implementation Subcommittee of SUWWW
1996-2000	Member	Senate Subcommittee on the WWW (SUWWW)
1995-2001	Chair	Molecular Biology Interfaculty Program Steering Committee
1995-2001	Chair	Molecular Biology Interfaculty Program Course Committee
1994	Co-Chair	Molecular Biology Interfaculty Program Open House
1993	Member	National Scholarship Selection Committee

8.2 Faculty Committees

Year	Role	Description
2010-2013	Member	Microbiology & Immunology Promotion and Tenure Committee
2007-2008	Member	Epidemiology and Biostatistics Chair Selection Committee
2007	Member	Ad hoc Faculty member disciplinary committee
2005-2007	Chair	Information Resources Institutional Self Study Task Force
2004-2006	Member	Promotion and Tenure - Pharmacology and Physiology Department
2001-2003	Member	Human Molecular Genetics Selection Committee
1999-2000	Chair	Information Resources Institutional Self Study Task Force
1997-2001	Member	UMEC Appeals Committee
1996-1998	Member	Medical Science Building Study Group
1996-1999	Member	Molecular Genetics Task Force
1996-1999	Co-Chair	Life Sciences group for the Medical School Curriculum renewal process
1996-2001	Member	ACMC Medical Informatics Group
1995-1996	Member	Computer and WWW Task Force
1994-2001	Member	Dean's advisory Committee on Genetics

8.3 Department Committees

Year	Role	Description
2019-present	Chair, Department of Biochemistry	Biochemistry Promotion and Research Committee
2015-2017	Member (Seconded)	Undergraduate Committee
2012-2015	Member	Biochemistry Promotion and Appointments Committee
2010-2013	Member	Biochemistry Graduate Studies
2009-2012	Member	Biochemistry Graduate Studies
2009-2012	Chair	Visiting Speakers Committee
2004-2008	Member	Department Outreach Committee
2002-2004	Chair	Biochemistry Promotion and Nominating Committee
2001-2004	CoChair	Ad hoc Computing Advisory Area, Safety, Equipment and Nominating Committee
1998-2004	Member	Graduate Studies Committee
1997	Chair	
1996	Member	
1995-2005	Member	
1995-1998	Member	
1993-1996	Member	
1993-1996	Member	

8.4 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.

8.5 Grants and Awards Panels, Editorial membership, External Committees

2019-2021, Member, CodaWorks Meetings Committee

2016-present, Chair, CIHR Project Grant Scheme (GMX committee)

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

2018-2019, Associate Editor, Microbiome

2016-2018, Section 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: Large Scale Applied Research Program 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

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