James R. Brown, B.Sc., M.Sc., PhD

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Google Scholar: https://scholar.google.com/citations?user=NuEw1YoAAAAJ&hl=en)

Professional Summary

- Ph.D. scientist with over 28 years experience leading computational biology and multidisciplinary R&D teams in pharma, vaccine and consumer health from early target discovery to launched products in major pharma and biotech companies.
- Experienced leader of computational teams at the levels of Director, Executive Director and VP for the companies GSK, Kaleido Biosciences and Novasenta, respectively.
- Currently, independent consultant for data science, disease biology and drug discovery.
- Expertise in developing strategic drug discovery solutions using advanced data analytics (i.e., multivariate, AI/ML) to multidimensional datasets including human genetics, next generation sequencing (NGS – transcriptomics, single-cell genomics, whole genome sequencing [WGS]), microbial WGS, microbiome metagenomics, molecular evolution and host-pathogen interactions.
- In-depth biological knowledge of diverse therapy areas including viral, bacterial and parasite infections, oncology and metabolic, respiratory, neuro-degenerative and autoimmune diseases.
- Initiated and lead diverse therapeutic discovery projects related to the gut, lung, urogenital and skin microbiome and overall human immune system-microbial interactions at GSK and Kaleido.
- Dedicated manager and mentor of early career scientists with a strong record of positive and inclusive recruitment and dedication to talent development.
- Significant external scientific profile with 123 publications including *Nature* journals, *PNAS* and *EMBO* as well as numerous invited speaker and advisory roles for NIH + other panels.

Employment Experience

Principal Consultant & Founder. JRBrown Bio Consulting LLC. Jun. 16, 2023 – present**.**

- Computational biology and data science support to pharma, vaccines and consumer health R&D.
- Multi-year consultancy to Cambrian Bio for clinical multi-omics and computational analyses.
- Consultant to biopharma / investor panels for AlphaSights, Arbolus, GLG & Quadrant Strategies.

Visiting Scholar. *College of Engineering, Drexel University, Philadelphia PA.* May 8, 2023 – present.

- Visiting member of the Ecological and Evolutionary Signal-processing and Informatics (EESI) Lab of Dr. Gail Rosen with a focus on applying AI to large-scale genomic / multi-omics datasets.
- Co-author on four AI/genomics manuscripts (published or in press).
- Technical Lead for Drexel EESI NSF I-Corps Team – AI-powered multi-omics analysis agent

Courtesy Professor. *College of Medicine, University of Florida, Gainesville FL.* Jun. 21, 2023 – present.

- Visiting Professor of Department of Medicine, Division of Pulmonary Systems Medicine contributing to systems biology and computational approaches to drug and discovery.

Vice President & Head. *Computational Sciences, Novasenta, Pittsburgh PA*. May 2 – Dec. 5, 2022.

- R&D leadership team member providing input into overall R&D and company-wide strategy.
- Head of a high achieving team of data scientists and software engineers focused on advancing novel immune-oncology (IO) therapeutics using single-cell genomics.
- Responsible for new staff recruitment and setting the strategic direction for the team.
- Coordinated the development and support of two novel computational platforms for: 1) data-mining proprietary and public single cell transcriptomics (scRNA-seq) datasets; 2) decision-making based on public data and literature through multiple analytic methods including NLP and ML.

- Supported drug discovery teams with target validation and translational analyses for three preclinical phase projects.

Executive Director & Head. *Computational Biology & Integrated Data Science (CB & IDS). Discovery, R&D, Kaleido Biosciences, Lexington MA.* Feb. 3/22 – April 8/22. (company closure in April/22).
Senior Director & Head. *CB & IDS. Kaleido Biosciences.* Jan. 19/21 – Feb. 2/22

- Leader of a high functioning team of computational biologists and software engineers, in support of preclinical and clinical studies of microbiome targeted therapeutics (proprietary foodstuff-derived glycan compound libraries) for immune-inflammatory and infectious diseases.
- Expanded and enhanced the team through new recruitment and facilitating the development of technical and managerial skillsets among existing staff members.
- Provided strategic vision of computational biology for functional genomics, system biology and advanced data analytics to identify microbiome effectors of host immunity and mechanisms of action.
- Broadly contributed to R&D strategy as a member of the Discovery leadership team, reporting to the Chief Science Officer (CSO).
- Founder and co-leader of a Phase 2A clinical program targeting the gut-lung axis in chronic obstructive pulmonary disease (COPD) which was partnered with the COPD Foundation. Responsible for preclinical discovery, design of clinical biomarker strategy and exploratory 'omics analyses.

Scientific Director & Senior Fellow. (1996-2021 [retired])**.** *Computational Biology, Human Genetics, GlaxoSmithKline (GSK), R&D, Collegeville, PA.* Specific role descriptions are below:

- Computational Biology Leadership Team Member. Accountable for overall strategy, staff recruitment and development and the supervision of multiple, diverse drug pipeline projects.

- Infectious Disease Therapy Area Lead for Human Genetics (2017-2021). Accountable for coordinating projects spanning new target discovery through late-stage pipeline for infectious diseases using human genetics (i.e. GSK collaboration with 23andMe), functional genomics (i.e. Vir Biotechnology alliance) and computational biology for the Infectious Disease Research Unit (IDRU) and Global Health Unit.
- Designed and lead a strategic initiative to identify novel host-pathogen targets and rapidly progress through drug development by integrating 23andMe and Vir Biotechnology data with GSK resources.
- Played an important role in GSK's response to COVID-19 by coordinating the evaluation and prioritization of dozens of proposals to repurpose infectious diseases and chronic disease drugs.
- Co-developed human host-target strategy for HCV, RSV, TB, respiratory viral/bacterial infections and urinary tract infections.
- Designed and lead genomics analyses for anti-bacterial clinical trials (Phase I, II & III).
- Identified human host targets shared by neurodegenerative diseases and herpes viral infections.
- Significant external profile in host-pathogen immunity with 5 peer-reviewed papers and invited member of NIH Review Panels for Genomics Centers for Infectious Diseases (2018) and TB Immunology and Drug Discovery (2017), both focused on host-pathogen interactions.

- Microbiome Research. Initiated microbiome research in GSK in 2010 and remained the in-house expert of microbiome applications across GSK Pharma, Consumer Health (Cx) and Vaccines (Vx).
- Leader of multiple lung, gut, skin and urogenital microbiome clinical study arms in respiratory, metabolic and infectious diseases, including gepotidacin (Phase 2A) and bacterial FimH inhibitor (Phase 1A).
- Led project that identified hundreds of novel human receptor and microbial metabolites interactions as a source of potential immuno-modulators and drug targets for inflammatory bowel disease and other autoimmune diseases.
- Scientific and technical lead on 3 early development microbiome therapeutics programs.
- External profile in the microbiome includes 20 papers and several speaker invitations.

- Global Health Unit. Identified pathogen and human targets for TB, malaria and enteric infections.
- Led novel bioinformatics analyses of whole cell compound screening results of malaria, TB and Leishmania which resulted in dozens of new target hypotheses against these global diseases.
- Contributed to microbiome strategy for treating childhood malnutrition and enteric infections.

- GSK Vaccines (Vx) and Consumer Health (Cx): Research relationships with Vx and Cx R&Ds.
- Co-inventor for 3 TB vaccine patents and in silico validation for TB vaccine in Phase 2.
- Collaborations on endogenous microbiome metabolites as adjuvants and immune-modulators.

- Previous Therapy Area Contact Lead roles include: 1) ViiV [HIV therapies] (2002-19); 2) Oncology [kinases, immune-oncology and epigenetics (2002-17)] and; 3) Alternative Drug Discovery R&D [virtualized unit focused on biotech alliances] (2006-13).

Associate Director / Senior Manager. *Bioinformatics, GSK*. Feb. 08/02 – Oct. 26/09.

- Led teams of bioinformatics analysts and software developers supporting multiple therapeutic areas including musculoskeletal diseases, oncology and infectious disease from early-stage gene target validation to translational clinical studies and launched product support.
- Pioneered whole genome sequencing for the surveillance of clinically relevant mutations in bacterial pathogens. Senior author of a highly cited paper describing genome-level mutations that caused bacterial resistance to a GSK antibiotic in Phase 2 leading to its termination.

Research Leader. *Center for Excellence External Drug Discovery, GSK,* Jun. 01/06 – Jun. 01/07.

- One year secondment to provide genomics-oriented analysis in support of due diligences teams reviewing new biotech partnerships in oncology and other therapeutic areas.
- Innovated the integration of genomics and target analyses for business partnership decisions.

Assistant Director / Manager. *Microbial Bioinformatics, Bioinformatics Division, GSK/SmithKline Beecham (SB) R&D.* Sept. 25/00 – Feb. 08/02.

- Responsible for overall computational biology support for the Antimicrobial R&D division.
- Built a bioinformatics team focused on a large portfolio of anti-bacterial and anti-viral targets.

Senior Investigator, *Microbial Bioinformatics, Bioinformatics Division, SB R&D.* Dec. 2/96 - Sept. 25/00.

- Pioneered the use of molecular evolution to identify targets and assist in assay design.
- Conceived and led an innovative genomics-based target engine that identified over 300 broad spectrum anti-bacterial targets for subsequent validation using site-directed mutagenesis and functional assays.

Medical Research Council of Canada Postdoctoral Fellow. Lab of *W. Ford Doolittle, Dept. of Biochemistry, Dalhousie University, Halifax, Nova Scotia, Canada.* Jul./91- Nov./96.

- Highly competitive three-year post-doctoral national fellowship (Ranked 8th highest nationally).
- Phylogenomic studies of early cellular evolution and horizontal gene transfer which resulted in 9 papers including two *PNAS* publications.

Tutorial Lecturer. *Biology Dept., Dalhousie University, Halifax, Nova Scotia.* Sept. 92 - Nov. 96.

- Instructor in second year course, Genetics and Molecular Biology 2030, for 5 semesters.

Aquaculture Development Consultant. *Multiple contracts with First Nations (Nanaimo Indian Band, Kalhoose Indian Band), British Columbia Ministry of Agriculture and Fisheries, Aquaculture and Commercial Branch and B C Research, Applied Biology Division*, *Vancouver, BC* Nov.86 – Apr. 91.

- Developed a habitat selection model for oyster aquaculture in coastal management plans.
- Worked with First Nations to develop business model for sustainable shellfish farms.

Lecturer/Teaching Assistant. *Primary lecturer or tutorial leader in Dept. of Biological Sciences, Simon Fraser University, Burnaby, BC; Vancouver Community College, King Edward Campus, Vancouver, BC; Malaspina College, Nanaimo, BC and Capilano College, Sechelt, BC* Jun. 83 - Jan. 90.

- Tutorial / lab Instructor for courses in Marine Invertebrate Ecology and Fisheries, Invertebrate Biology and Ecology. Lecturer for introductory college courses in biology and oyster aquaculture.

Biological Consultant. *Hough, Stansbury and Michalski Ltd, Rexdale, Ontario* May 31-Sept. 15/83.

- Managed ship-board field-work to monitor Great Lakes water quality for the Province of Ontario.

Marine Technologist. *Environment Canada, Institute Canada Center for Inland Waters, Burlington, Ontario*, July 4/78-July 1/83.

- Provided technical support for ship-board and remote field studies on Great Lakes water quality.
- Member of SCUBA team responsible for underwater recovery, construction and scientific studies.

Student Technician. *Dept. of Fisheries and Oceans, Arctic Biological Station, Ste Anne de Bellevue, Quebec & Baffin Island, NWT.* May 15-Aug. 15/77.

- Summer field work to study the effects of pollution on Arctic marine phytoplankton communities.

Education

Ph.D., Molecular Biology, Jan. 87 - Jul. 91. Dept. of Biological Sciences, Simon Fraser University (SFU), British Columbia (BC), Canada. *Ph.D. Thesis:* **Molecular Evolution and Population Genetics of Sturgeon (Genus *Acipenser*) based on Mitochondrial DNA Analysis.** 191 pp. (w/ Dr. Michael J Smith).

M.Sc., Biology, Jan. 83 - Sept. 86. Dept. of Biological Sciences, SFU. *M.Sc. Thesis:* **The Influence of Environmental Factors Upon the Growth and Survival of the Pacific Oyster, *Crassostrea gigas* Thunberg.** 146 pp. (w/ Dr. Brian Hartwick).

B.Sc., Marine Biology, Sept. 75 – Jun. 78. McGill University, Graduated 1978.

Fellowships and Awards

GSK

- 2020. Gold Impact Award for genomics and genetics support to GSK COVID-19 response.
- 2016. Elected GSK Senior Fellow and reaccreditation in 2018.
- 2010. Goldfish Award for Gut Microbiome and Obesity. Competitive GSK grant (1 of 6 awards selected from 140 company-wide applications).
- 1996-2021. 14 other GSK Impact Awards for excellence in support of drug discovery support.

Post-doctoral Fellow

- 1991-94. Medical Research Council of Canada. With Doolittle WF, Dept. of Biochemistry, Dalhousie University. Ranked 8th in a national competition of 176 applications.

PhD / MSc.

- 1984-86 and1987-90. Grad. Res. Engineering & Technology Award, Science Council of BC
- 1988-90. Simon Fraser University (SFU) Special Research Grant
- 1988-90. Spring Semester. SFU Graduate Fellowship & President's Research Stipend.
- 1990. Molecular Evolution Workshop Tuition Stipend
- 1991. Spring Semester. J. Abbott/M. Fretwell Graduate Fellowship in Fisheries Biology.
- 1991. Spring Semester. BC Packers Ltd. Fellowship
- 1984-1986. Special Research Grant BC Ministry of Fisheries and Aquaculture

Professional Advisory Panels and Boards – Last 10 Years

- 2001-present. External Advisory Committee, Chair, NIH Puerto Rico IDeA Network Biomedical Research Excellence Program
- 2023-24. Board of Editors. mSystems journal of the American Society of Microbiology (ASM)
- 2023-25. Careers in Microbiology Panelist. Eastern PA ASM Branch. Drexel U., Philadelphia, PA
- 2021. NIH Special Emphasis Panel: Immune Development in Early Life (IDEaL)
- 2018. NIH Special Emphasis Panel: Genomics Centers for Infectious Diseases
- 2014-21. Temple University Bioinformatics Professional Science Master Program
- 2017-20. Preclinical Human Mechanisms committee, Crohn's and Colitis Foundation
- 2017. NIH NIAD P01 Review Panel TB Immunology and Drug Discovery
- 2014-16. GSK Early Talent Post-doctoral Program Ops Committee
- 2011-14. Chair of Scientific Advisory Board, TB Compound Mechanism of Action (GeMoA), ERA-NET PathoGenoMics Consortium

Publications *(Descending Chronology; * = senior and/or corresponding author)*

1. Yoo H, Sokhansanj BA, Brown JR, Rosen GL. 2025. Predicting anti-microbial resistance using large language models. https://arxiv.org/pdf/2401.00642

2. Refahi MS, Yoo H, Hearne GLA, Allegra C, Brown JR, Sokhansanj BA, Ramjattun K, Allipilli SR, Polikar R, Rosen GL. 2025. Genomic Language Models: A review of experimental validation, multi-omics integration, and ethical-legal challenges. **Signal Processing in Medicine and Biology Genomics**. In press.

3. Refahi MS, Sokhansanj BA, Mell JC, Brown JR, Yoo H, Hearne G, Rosen GL. 2025. Scorpio: Enhancing embeddings to improve downstream analysis of DNA sequences. **Communications Biology (Nature)**. 8:517. https://www.nature.com/articles/s42003-025-07902-6

4. Yoo H, Refahi MS, Polikar R, Sokhansanj BA, Brown JR, Rosen GL. 2025. iSeqSearch: Incremental Protein Search for iBlast/iMMSeqs2/iDiamond. **PeerJ Life & Environment.** In press.

5. Hearne GLA, Refahi MS, Duan HN, Brown JR, Rosen GL. 2024. Normalized Compression Distance for DNA Classification. **Proceedings of the 15th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics.** Article No.: 93, Page 1 https://doi.org/10.1145/3698587.3701490 .

6. Nuzzo A, Van Horn S, Traini C, Perry CR, Dumont EF, Scangarella-Oman NE Gardiner DF, Brown JR*. 2021. Microbiome recovery in adult females with uncomplicated urinary tract infections in a randomised phase 2A trial of the novel antibiotic gepotidacin (GSK140944). **BMC Microbiology** 21:181. doi: 10.1186/s12866-021-02245-8

7. Nuzzo A, Saha S, Berg E, Jayawickreme C, Tocker J, Brown JR*. 2021. Expanding the drug discovery space with predicted metabolite-target interactions. **Communications Biology (Nature)**. 4:288. doi: 10.1038/s42003-021-01822-x

8. Inflammatory endotype associated airway microbiome in COPD clinical stability and exacerbations. 2020. Wang Z, Locantore N, Haldar K, Ramsheh MY, Beech AS, Ma W, Brown JR, Tal-Singer R, Barer MR, Bafadhel M, Donaldson GC, Wedzicha JA, Singh D, Wilkinson TMA, Miller BE, Brightling CE. **American Journal of Respiratory And Critical Care Medicine.** doi: 10.1164/rccm.202009-3448OC

9. Wang Z, Yang Y, Yan Z, Liu H, Chen B, Liang Z, Wang F, Miller BE, Tal-Singer R, Yi X, Li J-t, Stampfli MR, Zhou H, Brightling CE, Brown JR, Wu M, Chen R, Shu W. 2020. Multi-omic meta-analysis identifies functional signatures of airway microbiome in chronic obstructive pulmonary disease. **The ISME Journal**. doi: 10.1038/s41396-020-0727-y

10. Haldar K, George L, Wang Z, Mistry V, Ramsheh MY, Free RC, John C, Reeve NF, Miller BE, Tal-Singer R, Webb AJ, Brookes AJ, Tobin MD, Singh D, Donaldson GC, Wedzicha JA, Brown JR, Barer MR, Brightling CE. 2020. The sputum microbiome is distinct between COPD and health, independent of smoking history. **BMC Respiratory Research.** 21:183. doi: 10.1186/s12931-020-01448-3

11. Douglas GM, Maffei VJ, Zaneveld J, Yurgel SN, Brown JR, Taylor CM, Huttenhower C, Langille MGI. 2020. PICRUSt2: An improved and extensible approach for metagenome inference. **Nature Biotechnology.** 38:685-88. doi: 10.1038/s41587-020-0548-6.

12. Nuzzo A, Brown JR*. 2020. Microbiome metabolite mimics accelerate drug discovery. **Trends in Molecular Medicine.** 26:435-437 doi: 10.1016/j.molmed.2020.03.006

13. Nuzzo A, Brown JR*. 2020. The microbiome factor in drug discovery and development. **Chemical Research in Toxicology**. doi: full/10.1021/acs.chemrestox.9b00333

14. Scangarella-Oman N, Ingraham K, Tiffany C, Tomsho L, Van Horn S, Mayhew D, Perry C, Ashton T, Dumont E, Huang J, Brown JR, Miller L. 2020. In vitro activity and microbiological efficacy of gepotidacin from a Phase 2, randomized, multicenter, dose-ranging study in patients with acute bacterial skin and skin structure infections. **Antimicrobial Agents and Chemotherapy.** 64:e01301-19.

15. Washburn WL, Wang Z, Walton AH, Goedegebuure SP, Figueroa DJ, Van Horn S, Grossman J, Remlinger K, Madsen H, Brown JR, Srinivasan R, Wolf AI, Berger SB, Yi V, Hawkins WG, Fields RC, Hotchkiss RS. 2019. T cell and monocyte specific RNAseq analysis in septic and non-septic critically-ill patients and in patients with cancer. **Journal of Immunology**. 203:1897 doi.org/10.4049/jimmunol.1900560.

16. Michalovich D, Rodriguez-Perez N, Smolinska S, Pirozynski M, Mayhew D, Uddin S, Van Horn S, Sokolowska M, Altunbulakli C, Eljaszewicz A, Pugin B, Barcik W, Kurnik-Lucka M, Saunders K, Simpson K, Schmid-Grendelmeier P, Ferstl R, Frei R, Sievi N, Kohler M, Gajdanowicz P, Graversen K, Bøgh K, Jutel M, Brown JR, Akdis C, Hessel E, O'Mahony L. 2019. Obesity and disease severity magnify disturbed microbiome-immune interactions in asthma patients. **Nature Communications.** 10:5711. doi: 10.1038/s41467-019-13751-9.

17. Costa Sa AC, Madsen H, Brown JR*. 2019. Shared molecular signatures across neurodegenerative diseases and herpes virus infections highlights potential mechanisms for maladaptive innate immune responses. **Scientific Reports (Nature)**. 9:8795. doi: 10.1038/s41598-019-45129-8.

18. Wang Z, Maschera B, Lea S, Kolsum U, Michalovich D, Van Horn S, Traini C, Brown JR*, Hessel EM, Singh D. 2019. Airway host-microbiome interactions in chronic obstructive pulmonary disease. **BMC Respiratory Research**. 20:113. doi: 10.1186/s12931-019-1085-z.

19. Brown JR*, Baker SJ, Barros-Aquirre D, Payne D. 2018. The ninth commandment -- Better incentives to promote investment for new drugs and improving existing ones. **Microbiologist, Society for Applied Microbiology.** 19:42.

20. Wang Z, Arat S, Magid-Slav M, Brown JR*. 2018. Meta-analysis of human gene expression in response to *Mycobacterium tuberculosis* infection reveals potential therapeutic targets. **BMC Systems Biology**. 12:3. doi:10.1186/s12918-017-0524-z.

21. Mayhew D, Devos N, Lambert C, Brown JR, Clarke S, Kim V, Magid-Slav M, Miller BE, Ostridge K, Patel R, Sathe G, Simola DF, Staples KJ, Sung R, Tal-Singer R, Tuck AC, Van Horn S, Weynants V, Williams N, Devaster J-M, Wilkinson TM. 2018. Lung microbiome analysis and stochastic modeling of COPD exacerbations in the AERIS study. **Thorax.** doi: 10.1136/thoraxjnl2017-210741.

22. Wang Z, Saha S, Van Horn S, Thomas E, Traini C, Sathe G, Rajpal DK, Brown JR*. 2017. Gut microbiome differences between metformin and liraglutide treated T2DM subjects. **Endocrinology, Diabetes & Metabolism** doi: 10.1002/edm2.9.

23. Wang Z, Singh R, Miller BE, Tal-Singer R, Van Horn S, Tomsho L, Mackay A, Allinson JP, Webb AJ, Brookes AJ, George LM, Barker B, Kolsum U, Donnelly LE, Belchamber K, Barnes PJ, Singh D, Brightling CE, Donaldson GC, Wedzicha JA, Brown JR*. 2017. Sputum microbiome temporal variability and dysbiosis in chronic obstructive pulmonary disease exacerbations: an analysis of the COPDMAP study. **Thorax** 73:331-338 doi: 10.1136/thoraxjnl-2017-210741.

24. Brown JR*. 2017. The Microbiome in Health and Disease. In Bornstein MH, ed. **The SAGE Encyclopedia of Lifespan and Human Development.**

25. Saha S, Rajpal DK, Brown JR*. 2016. Human microbial metabolites as a source of new drugs. **Drug Discovery Today.** 21: 692-698. DOI: 10.1016/j.drudis.2016.02.009

26. Wang Z, Bafadhel M, Haldar K, Spivak A, Mayhew D, Miller BE, Tal-Singer R, Johnston SL, Ramsheh MY, Barer MR, Brightling CE, Brown JR*. 2016. Lung microbiome dynamics in chronic obstructive pulmonary disease exacerbations. **European Respiratory Journal.** 47:1082-92.

27. Rajpal D, Klein J-L, Mayhew D, Boucheron J, Spivak A, Kumar V, Ingraham K, Paulik M, Chen L, Van Horn S, Thomas E, Sathe G, Livi GP, Holmes DJ, Brown JR*. 2015. Selective spectrum antibiotic modulation of the gut microbiome in obesity and diabetes rodent models. **PLoS One.** 10: e0145499.

28. Rebollo-Lopez MJ, Lelièvre J, Alvarez-Gomez D, Castro-Pichel J, Martínez-Jiménez F, Papadatos G, Mugumbate G, Kumar V, Colmenarejo G, Hurle M, Barroso V, Young R, Bates RH. Maria Lopez-Roman E, Mendoza-Losana A, Brown JR, Alvarez-Ruiz E, Marti-Renom MA, Overington JP, Cammack N, Ballell L, Barros D. 2015. Release of 50 new, drug-like compounds and their computational target predictions for open source anti-tubercular drug discovery. **PLoS One** 10:e0142293.

29. Peña I, Manzano MP, Cantizani J, Kessler A, Alonso-Padilla J, Bardera AI, Alvarez E, Colmenarejo G, Cotillo I, Roquero I, de Dios-Anton F, Barroso V, Rodriguez A, Gray DW, Navarro M, Kumar V, Sherstnev A, Drewry D, Brown JR, Fiandor JM, Martin JJ. 2015. New compound sets identified from high throughput phenotypic screening against three kinetoplastid parasites: An open resource. **Scientific Reports (Nature).** 5:8771.

30. Arat S, Spivak A, Van Horn S, Thomas E, Traini C, Sathe G, Livi GP, Ingraham K, Jones L, Aubart K, Holmes DJ, Naderer O, Brown JR. 2015. Microbiome changes in healthy volunteers treated with GSK1322322, a novel antibiotic targeting bacterial peptide deformylase. **Antimicrobial Agents and Chemotherapy.** 59:1182-1192.

31. O'Dwyer K, Spivak A, Ingraham K, Min S, Holmes DJ, Jakielaszek C, Rittenhouse S, Kwan A, Livi GP, Sathe G, Thomas E, Van Horn S, Miller LA, Twynholm M, Tomayko J, Dalessandro M, Caltabiano M, Scangarella-Oman NE, Brown JR*. 2015. Bacterial resistance to leucyl-tRNA synthetase inhibitor GSK2251052 develops during treatment of complicated urinary tract infections. **Antimicrobial Agents and Chemotherapy.** 59:289-298.

32. Brown JR, Drewry D, Gamo F-J, Garcia-Bustos JF. 2015. Kinase inhibitors among hits from malaria cellular screens. In Doerig C, Wiese M, Spaeth G, ed. **Protein phosphorylation in eukaryotic parasites: potential for chemotherapy.** Wiley-Blackwell.

33. Napolitano A, Miller S, Nicholls AW, Baker D, Van Horn S, Thomas E, Rajpal D, Spivak A, Brown JR*, Nunez DJ. 2014. Novel gut-based pharmacology of metformin in patients with Type 2 Diabetes Mellitus. **PLoS One**. 9:e100778.

34. Irlbeck DM, Vernon SD, McCleary KK, Bateman L, Klimas NG, Lapp CW, Peterson DL , Brown JR, Wilfret DA, Gerondelis P. 2014. No association found between the detection of either Xenotropic Murine Leukemia Virus-Related Virus or Polytropic Murine Leukemia Virus and Chronic Fatigue Syndrome in a blinded, multi-site, prospective study. **BMC Research Notes**. 7:461.

35. Ross LL, Horton J, Hasan S, Brown JR, Murphy D, DeJesus E, Potter M, LaMarca A, MelendezRivera I, Ward D, Uy J, Shaefer MS. 2014. HIV-1 transmission patterns in antiretroviral therapy naïve, HIV-infected North Americans based on phylogenetic analysis by population level and ultra-deep DNA sequencing. **PLoS One.** 9:e89611.

36. Smith SB, Magid-Slav M, Brown JR*. 2013. Host response to respiratory bacterial pathogens as identified by integrated analysis of human gene expression data. **PLoS One.** 8:e75607.

37. Martínez-Jiménez F, Papadatos G, Yang L, Wallace IM, Kumar V, Pieper U, Sali A, Brown JR, Overington JP, Marti-Renom MA. 2013. Target prediction for an open access set of compounds active against *Mycobacterium tuberculosis*. **PLoS Computational Biology**. 9:e1003253.

38. Rajpal DK, Brown JR*. 2013. The microbiome as a therapeutic target for metabolic diseases. **Drug Development Research.** 74:376-394.

39. Rajpal DK, Brown JR*. 2013. Modulating the human gut microbiome as an emerging therapeutic paradigm. **Science Progress.** 96:224-236.

40. Vamathevan JJ, Hall MD, Hasan S, Woollard PM, Xu M, Yang Y, Li X, Wang X, Kenny S, Brown JR, Huxley-Jones J, Lyon J, Haselden J, Min J, Sanseau P. 2013. Minipig and beagle animal model genomes aid species selection in pharmaceutical discovery and development. **Toxicology and Applied Pharmacology**. 270:149-157.

41. Brown JR, de Vos WM, DiStefano PS, Doré J, Huttenhower C, Knight R, Lawley, TD, Raes J, Turnbaugh, P. 2013 Translating the human microbiome. **Nature Biotechnology**. 31:304–308.

42. Collison M, Hirt RP, Wipat A, Nakjang S, Sanseau P, Brown JR*. 2012. Data mining the human gut microbiota for therapeutic targets. **Briefings in Bioinformatics**. Mar. 24 EPub.

43. Smith SB, Dampier W, Tozeren A, Brown JR*, Magid-Slav M. 2012. Identification of common biological pathways and drug targets across multiple respiratory viruses based on human host gene expression analysis. **PLoS One.** 7(3):e33174.

44. Kumar V, Sun P, Vamathevan J, Li Y, Ingraham K, Palmer L, Huang J, Brown JR*. 2011. Comparative genomics of *Klebsiella pneumoniae* strains with different antibiotic resistance profiles. **Antimicrobial Agents and Chemotherapy.** 55:4267-4276.

45. Brown JR*, Magid-Slav M, Sanseau P, Rajpal D. 2011. Computational biology approaches for selecting host-pathogen drug targets. **Drug Discovery Today.** 16:229-236.

46. Brown JR*, Auger KR. 2011. Phylogenomics of phosphoinositide lipid kinases: Perspectives on the evolution of second messenger signaling and drug discovery. **BMC Evolutionary Biology**. 11:4.

47. Gamo F-J, Sanz LM, Vidal J, de Cozar C, Alvarez E, Lavandera J-L, Vanderwall DE, Green DVS, Kumar V, Hasan S, Brown JR, Peishoff CE, Cardon LR, Garcia-Bustos JF. 2010. Thousands of chemical starting points for antimalarial lead identification. **Nature**. 465:305-310.

48. Zhang Y, Italia MJ, Auger KR, Halsey WS, Van Horn SF, Sathe GM, Magid-Slav M, Brown JR*, Holbrook JD. 2010. Molecular evolutionary analysis of cancer cell lines. **Molecular Cancer Therapeutics.** 9:279-291.

49. Brown JR*. 2010. Next generation sequencing for antibacterial drug discovery. **International Drug Discovery**. 6:42-45.

50. Brown JR*, Deharo S, Dancis B, Barnes MR, Sanseau P. 2007. Non-coding RNA bioinformatics. In Barnes MR, Gray IC, ed. **Bioinformatics for Geneticists** 2nd edition. Wiley Press.

51. Murphy DM, Dancis B, Brown JR*. 2006. Evolution of MicroRNA Biogenesis. In Clarke N, Sanseau P, ed. **microRNAs: Biology, Function and Expression.** DNA Press.

52. Brown JR*, Murphy DM. 2009. Computational biology in anti-tuberculosis drug discovery. **Infectious Disorders – Drug targets.** 9:319-326.

53. Murphy DM, Brown JR*. 2008. Novel drug target strategies against *Mycobacterium tuberculosis*. **Current Opinion Microbiology.** 11:422-427.

54. Murphy DM, Dancis B, Brown JR*. 2008. The evolution of core proteins involved in microRNA biogenesis. **BMC Evolutionary Biology.** 8:92.

55. Brown JR*, Editor. 2008. **Comparative Genomics: Basic and Applied Research.** CRC / Taylor and Francis Press. 383 pages.

56. Brown JR*. 2008. The Broad Horizons of Comparative Genomics. In Brown, JR, ed. **Comparative Genomics: Basic and Applied Research**. CRC/Taylor & Francis Press.

57. Brown JR*. 2008. Comparative Genomics in Drug Discovery. In Brown, JR, ed. **Comparative Genomics: Basic and Applied Research**. CRC/Taylor & Francis Press.

58. Murphy DM, Brown JR*. 2007. Identification of gene targets against dormant phase *Mycobacterium tuberculosis* infections. **BMC Infectious Diseases** 7:84**.**

59. Barnes MR, Deharo S, Grocock RJ, Brown JR, Sanseau P. 2007 The micro RNA target paradigm: a fundamental and polymorphic control layer of cellular expression. **Expert Opinion Biol. Ther.** 9:1387-99.

60. Huang J, Van Aller GS, Taylor AN, Kerrigan JJ, Liu W-S, Trulli JM, Lai Z, Holmes D, Payne DJ, Aubart KM, Brown JR, Zalacain M. 2006. Phylogenomic and biochemical characterization of three *Legionella pneumophila* polypeptide deformylases. **J. Bacteriol.** 188:5249-5257.

61. Stanhope MJ, Walsh SL, Becker JA, Italia MJ, Ingraham KA, Gwynn MN, Mathie T, Poupard JA, Miller LA, Brown JR, Amrine-Madsen H. 2005. Molecular evolution perspectives on intraspecific lateral DNA transfer of topoisomerase and gyrase loci in *Streptococcus pneumoniae*, with implications for fluoroquinolone resistance development and spread. **Antimicrobial Agents and Chemotherapy.** 49:4315-4326.

62. Brown JR, Sanseau P. 2005. A computational view of microRNAs and their targets. **Drug Discovery Today** 10:595-601.

63. Brown JR*, Koretke KK, Birkeland ML, Sanseau P, Patrick, DR. 2004. Aurora kinase evolution: Implications for model organism studies and the development of anti-cancer drugs. **BMC Evolutionary Biology** 4:39.

64. Brown JR*, Volker CJ. 2004. Phylogeny of g-proteobacteria: resolution of one branch of the universal tree? **BioEssays**. 26:463-468.

65. Stanhope MJ, Brown JR, Armine-Madsen H. 2004. Evidence from the evolutionary analysis of nucleotide sequences for a recombinant history of the SARS virus. **Infection, Genetics and Evolution.** 4:15-19.

66. Brown JR*. 2004. Putting the "Bio" back in bioinformatics. **The Scientist** 18:44-45.

67. Brown JR*. 2004. Horizontal Gene Transfer and Bacterial Genomic Legacies. In Mullany L. **The Dynamic Bacterial Genome and its Biological Consequences.** Advances in Molecular and Cellular Microbiology. Cambridge University Press.

68. Brown JR*. 2003. Ancient horizontal gene transfer. **Nature Reviews Genetics.** 4:119-130.

69. Brown JR*, Gentry DR, Becker JA, Ingraham K, Holmes DJ, Stanhope MJ. 2003. Horizontal transfer of drug resistant aminoacyl-tRNA synthetases of anthrax and Gram-positive pathogens. **EMBO reports.** 4:692-698.

70. Zalacain M, Biswas S, Ingraham KA, Ambrad J, Bryant A, Chalker AF, Iordanescu S, Fan J, Fan F, Lunsford RD, O'Dwyer K, Palmer LM, So C, Sylvester D, Volker C, Warren P, McDevitt D, Brown JR, Holmes DJ, Burnham MKR. 2003. A global approach to identify novel broad spectrum antibacterial targets among proteins of unknown function. **J Molecular Microbiology and Biotechnology.** 6:109-126.

71. Choudhry AE, Mandichak TL, Broskey JP, Egolf RW, Kinsland C, Begley TP, Seefeld MA, Ku TW, Brown JR, Zalacain M, Ratnam K. 2003. Inhibitors of pantothenate kinase: novel antibiotics for Staphylococcal infections. **Antimicrobial Agents and Chemotherapy.** 47:2051-2055.

72. Gentry DR, Ingraham KA, Stanhope MJ, Rittenhouse S, Jarvest RL, O'Hanlon PJ, Brown JR, Holmes DJ. 2003. Variable sensitivity to bacterial methionyl-tRNA synthetase inhibitors reveals sub populations of *Streptococcus pneumoniae* with two distinct methionyl tRNA synthetase genes. **Antimicrobial Agents and Chemotherapy.** 47:1784-1789.

73. Brown JR*. 2003. Reconstructing the universal tree of life. In Ribas de Pouplana L, ed. **The Genetic Code and the Origin of Life.** Landes Biosciences Press.

74. Volker CJ, Brown JR*. 2002. Bioinformatics and the discovery of novel anti-microbial targets. **Current Drug Targets - Infectious Disorders.** 2:279-290.

75. Noordewier M, Brown JR*. 2002. Comparing the genomes of *Salmonella enterica* serovars: Differences and similarities among the closest of relatives. **Trends in Pharmacological Sciences**. 23:397-399.

76. Poupard J, Brown JR, Gagnon R, Stanhope M, Stewart C. 2002. Methods of data mining from large multi-national surveillance studies. **Antimicrobial Agents and Chemotherapy.** 46:24092419.

77. Sousa S, McLaughlin MM, Pereira SA, VanHorn S, Knowlton R, Brown JR, Nicholas RO, Livi GP. 2002. The ARO4 gene of *Candida albicans* encodes a tyrosine-sensitive DAHP synthase: evolution, functional conservation and phenotype of Aro3p, /Aro4p-deficient mutants. **Microbiology**. 148:1291-1303.

78. Brown JR*, Italia MJ, Douady CJ, Stanhope MJ. 2002. Horizontal gene transfer and the universal tree of life. pp. 305-349. In Syvanen M, Kado CI. Horizontal Gene Transfer, 2nd Edition. Academic Press.

79. Stanhope MJ, Lupas A, Italia MJ, Koretke K, Volker C, Brown JR. 2001. Phylogenetic analyses of genomic and EST sequences do not support horizontal gene transfers between bacteria and vertebrates. **Nature** 411:940-944.

80. Brown JR*, Douady CJ, Italia MJ, Marshall WE, Stanhope MJ. 2001. Universal trees based on large combined protein sequence datasets. **Nature Genetics**. 28:281-285.

81. Brown JR*. 2001. Genomic and phylogenetic perspectives on the evolution of prokaryotes. **Systematic Biology.** 50:497-512.

82. Ribas de Pouplana L, Brown JR, Schimmel P. 2001. Structure-based phylogeny of class IIa tRNA synthetases in relation to an unusual biochemistry. **J. Molecular Evolution.** 53:261-268.

83. Petit, CM, Brown JR, Ingraham K, Bryant AP, Holmes D. 2001. Lipid modification of prelipoproteins is dispensable for growth in vitro but essential for virulence in *Streptococcus pneumoniae*. **FEMS Microbiology Letters.** 9987:1-5.

84. Savopoulos JW, Hibbs M, Jones EJ, Mensah L, Richardson C, Fosberry A, Downes R, Fox SG, Brown JR, Jenkins O. 2001. Identification, cloning and expression of a functional phenylalanyltRNA synthetase (pheRS) from *Staphylococcus aureus*. **Protein Expression and Purification.** 21:470-484.

85. Chalker AF, Minehart HW, Birks NJ, Koretke KK, Lonetto MA, Warren PV, Stanhope MJ, Lupas AN, Brinkmann K, Brown JR, Hoffman PS. 2001. Systematic identification of unique essential genes in *Helicobacter pylori* by genome prioritization and allelic replacement mutagenesis. **J. Bacteriology.** 183:1259-1268.

86. Robb FT, Maeder DL, Brown JR, Weiss RB, DiRuggiero J, Dunn DM, Yeh RK. 2001. The genomic sequence of the hyperthermophile, *Pyrococcus furiosus*: implications for physiology and enzymology. pp. 134-157. In Adams, MWW, Kelly RM. **Hyperthermophilic Enzymes Pt A.** Methods in Enzymology. Academic Press.

87. Chihade J, Brown JR, Schimmel P, Ribas de Pouplana L. Origin of mitochondria in relation to evolutionary history of eukaryotic alanyl-tRNA synthetase. 2000. **Proceedings of the National Academy of Sciences USA.** 97:12153-12157.

88. Koretke KK, Lupas AN, Warren PV, Rosenberg M, Brown JR*. 2000. Evolution of two component signal transduction. **Mol. Biol. Evol.** 17:1956-1970.

89. Du W, Brown JR, Sylvester DR, Huang J, Chalker AF, So C-Y, Holmes DJ, Payne DJ, Wallis NG. 2000. Two active forms of UDP-*N*-acetylglucosamine enolpyruvyl transferase in Gram-positive bacteria. **J. Bacteriology** 182:4146-4152.

90. Wilding EI, Brown JR, Bryant A, Chalker AF, Holmes D, Ingraham K, So CY, Iordanescu S, Rosenberg M, Gwynn MN. 2000. Identification, essentiality and evolution of the mevalonate pathway for isopentenyl diphosphate biosynthesis in Gram-positive cocci. **J. Bacteriology** 182:4319-4327.

91. Throup JP, Koretke KK, Bryant AP, Ingraham K.A., Chalker AF, Ge Y, Marra A, Wallis NG, Brown JR, Holmes DJ, Rosenberg M, Burnham, MKR. 2000. A genomic analysis of two component signal transduction in *Streptococcus pneumoniae*. **Molecular Microbiology** 35:566-576.

92. Brown JR*, Koretke KK. 2000. Universal trees: discovering the archaeal and bacterial legacies. pp. 19-55. In Priest FG, Goodfellow M. **Applied Microbial Systematics.** Chapman and Hall Publishers.

93. Leroux MR, Fändrich M, Klunker D, Siegers K, Lupas AN, Brown JR, Schiebel E, Dobson CM, Hartl FU. 1999. MtGimC, a novel archaeal chaperone related to the eukaryotic chaperonin cofactor GimC/prefoldin. **EMBO J.** 18:6730-43.

94. Brown JR*, Doolittle WF. 1999. Gene descent, duplication and horizontal transfer in the evolution of glutamyl- and glutaminyl-tRNA synthetases. **J. Molecular Evolution** 49:485-495.

95. DiRuggiero J, Brown JR, Bogert AM, Robb FT. 1999. DNA repair systems in Archaea: mechanisms from the last universal common ancestor? **J. Molecular Evolution** 49:474-484.

96. Brown JR*. 1999. Universal tree of life. In the **Encyclopedia of Life Sciences**. Nature Publishing Group, London, www.els.net.

97. Brown JR*, Warren PV. 1998. Antibiotic discovery: Is it in the genes? **Drug Discovery Today.** 3:564-566.

98. Brown JR*, Lupas AN. 1998. What makes a thermophile? **Trends in Microbiology**. 6:349-351.

99. Brown JR*, Zhang J, Hodgson JE. 1998. A bacterial antibiotic resistance gene with eukaryotic origins. **Current Biology.** 8:R365-R367.

100. Brown JR*. 1998. Aminoacyl-tRNA synthetases: Evolution of a troubled family. pp. 217-230. In Wiegel J, Adams M. **Thermophiles - the keys to molecular evolution and the origin of life?** Taylor and Francis Group.

101. Brown JR*, Doolittle WF. 1997. Archaea and the prokaryote-eukaryote transition. **Microbiology and Molecular Biology Reviews.** 61:456-502.

102. Brown JR*, Robb FT, Weiss R, Doolittle WF. 1997. Evidence for the early divergence of tryptophanyl- and tyrosyl-tRNA synthetases. **J. Molecular Evolution.** 45:9-16.

103. Charlebois RL, Sensen CW, Doolittle WF, Brown JR*. 1997. Evolutionary analysis of the *hisCGAB$_d$FD$_o$D$_a$EHI* operon from the archaeon *Sulfolobus solfataricus* P2. **J. Bacteriology** 179: 4429-4432.

104. Bochar D, Brown JR, Doolittle WF, Klenk H-P, Lam W, Schenk M, Stauffacher CV, Rodwell VM. 1997. Cloning, sequencing, and expression in *Escherichia coli* of the biosynthetic HMGCoA reductase of *Sulfolobus solfataricus.* **J. Bacteriology**. 179:3632-3638.

105. Crnogorac-Jurcevic T, Brown JR, Lehrach H, Schalkwyk L. 1997. *Tetraodon fluviatilis*, an additional puffer fish model for genome studies. **Genomics**. 41:177-184.

106. Brown JR* 1996. Preparing for the flood: evolutionary biology in the age of genomics. **Trends in Ecology and Evolution**. 11:510-513.

107. Roger A, Brown JR*. 1996. A chimeric origin for eukaryotes re-examined. **Trends in Biochemical Sciences.** 21:370-371.

108. Brown JR*, Beckenbach K, Beckenbach AT, Smith MJ. 1996. Length variation, heteroplasmy and sequence divergence in the mitochondrial DNA of four species of sturgeon (*Acipenser*). **Genetics** 142:525-535.

109. Brown JR*, Doolittle WF. 1995. Root of the universal tree of life based on ancient aminoacyltRNA synthetase gene duplications. **Proceedings of the National Academy of Sciences USA.** 92:2441-2445.

110. Doolittle WF, Brown JR*. 1994. Tempo, mode, the progenote and the universal root. **Proceedings of the National Academy of Sciences USA** 91:6721-6728.

111. Brown JR*, Masuchi Y, Robb FT,. Doolittle WF. 1994. Evolutionary relationships of bacterial and archaeal glutamine synthetase genes. **J. Molecular Evolution** 38:566-576.

112. Doolittle WF, Brown JR*. 1994. Tempo, mode, the progenote and the universal root. pp. 3-24. In Fitch WM and Ayala FJ. **Tempo and Mode in Evolution.** National Academy Press.

113. Brown JR*, Beckenbach AT, Smith MJ. 1993. Intraspecific DNA sequence variation of the mitochondrial D-loop region of the white sturgeon (*Acipenser transmontanus*). **Molecular Biology and Evolution** 10:326-341.

114. Brown JR*, Beckenbach AT, Smith MJ. 1992. Mitochondrial DNA length variation and heteroplasmy in populations of white sturgeon *(Acipenser transmontanus*). **Genetics** 132:221228.

115. Brown JR*, Beckenbach AT, Smith MJ. 1992. The effects of Pleistocene glaciations and human intervention upon mitochondrial DNA diversity in white sturgeon *(Acipenser transmontanus*) populations. **J. Canadian Fisheries and Aquatic Sciences** 49:358-367.

116. Buroker NE, Brown JR*, Gilbert TL, O'Hara PJ, Beckenbach AT, Thomas WK, Smith MJ. 1990. Length heteroplasmy of sturgeon mtDNA: an illegitimate elongation model. **Genetics** 124:157163.

117. Brown JR*, Gilbert TL, Kowbel DJ, O'Hara PJ, Buroker NE, Beckenbach AT, Smith MJ. 1989. Nucleotide sequence of the apocytochrome B gene in white sturgeon mitochondrial DNA. **Nucleic Acids Res.** 17:4389.

118. Gilbert TL, Brown JR*, O'Hara PJ, Buroker NE, Beckenbach AT, Smith MJ. 1988. Sequence of tRNA(Thr) and tRNA(Pro) from white sturgeon (*Acipenser transmontanus*) mitochondria. **Nucleic Acids Res.** 16:11825.

119. Roland WG, Brown JR*. 1990. A production model for suspended culture of the Pacific oyster, (*Crassostrea gigas*). **Aquaculture** 87:35-52.

120. Brown JR*. 1988. Multivariate analyses of the role of environmental factors in seasonal and siterelated growth variation in the Pacific oyster, *Crassostrea gigas*. **Marine Ecology Progress Series** 45:225-236.

121. Brown JR*, Hartwick EB. 1988. Influences of temperature, salinity and available food upon suspended culture of the Pacific oyster, *Crassostrea gigas*: I. Absolute and allometric growth. **Aquaculture** 70:231-251.

122. Brown JR*, Hartwick EB. 1988. Influences of temperature, salinity and available food upon suspended culture of the Pacific oyster, *Crassostrea gigas*: II. Condition and survival. **Aquaculture** 70:253-267.

123. Brown JR*, Hartwick EB. 1988. A habitat suitability index model for suspended tray culture of the Pacific oyster, *Crassostrea gigas* Thunberg. **Aquaculture and Fisheries Management** 19:107124.

Patents

Co-inventor for three patent filings on novel TB vaccine targets. Co-inventor of patent for biotherapeutic in respiratory disease. Co-author of 62 patents on novel bacterial gene sequences. Developed a novel patent strategy based on phylogenetic clustering of related sequences.

Reports and User Manuals

1. Brown JR. 1994. The postdoctoral fellow perspective of the Department of Biochemistry. Brief submitted to the Departmental Survey Committee. Dalhousie University. 3 pp.

2. Brown JR. 1991. A development strategy for the Nanaimo Indian Band shellfish project. Prepared for the Nanaimo Indian Band Council, Nanaimo, BC 15 pp.

3. Brown JR. 1989. The Klahoose Band shellfish project in Squirrel Cove: A development plan. Prepared for the Klahoose Indian Band Council, Squirrel Cove, Cortes Island, BC 33 pp.

4. Brown JR, Roland WG. 1988. Siting culture operations for the Pacific oyster, *Crassostrea gigas*. Fish. Tech. Rep. 34, BC Ministry of Agriculture and Fisheries, Victoria, BC 49 pp.

5. Brown JR. 1987. Current constraints on the development of shellfish aquaculture in British Columbia. BC Ministry of Agriculture and Fisheries, Victoria, BC 7 pp.

6. Brown JR, Gordon MR. 1987. An assessment of the Nimpkish Oyster Project. Applied Biology Division, B C Research, Vancouver, BC 24 pp.

7. Brown JR. 1984. A habitat evaluation model for the Pacific oyster in mariculture in BC waters. Marine Resources Branch, Ministry of Environment, Victoria, BC 41 pp.

Conference Abstracts and Presentations – Last 10 Years (* *Invited Speaker*)

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1. Brown JR. 2025. Computational Biology and AI - Accelerating Drug Development. GLG Consulting Teleconference.

2. Hearne G, Refahi MS, Duan H, Brown JR, Rosen GL. 2024. Normalized Compression Distances for DNA Classification. Proceedings of the 2024 ACM Conference on Bioinformatics, Computational Biology, and Health Informatics. Shenzhen, China.

3. Brown JR.* 2024. Computational Approaches to Drug Target Discovery and Validation Workshop. Organizer and Presenter. University of Puerto Rico Medical Sciences Campus, San Juan, PR.

4. Brown JR*. 2023. Targeting Human Host and Microbe Interactions in Drug Discovery. EMBL-EBI Industry Programme Workshop. Microbial Genomics. New York City, NY.

5. Brown JR*. 2023. Integrative Data Analysis for the Discovery of Novel Drug Targets for Infectious and Immune-related Diseases. Electrical and Computer Engineering, Drexel U., Philadelphia, PA.

6. Brown JR*. 2023. Integrative Data Analysis in Drug Discovery. Dept. of Medicine. U. Florida, Gainesville, FL.

7. Brown JR*. 2018. Targeting the Human Host-Microbiome Interface in Metabolic Disease. Microbiome Data Conference. On-line.

8. Brown JR*. 2018. The Human Microbiome: The Role of Our Second Genome in Health and Disease. Parlee Lecture Series. Ursinus College, Collegeville, PA.

9. Brown JR*. 2018. Respiratory Tract and Gut Microbiomes in Precision Medicine for Respiratory Diseases. Microbiome Drug Development Summit, Paris, France.

10. Brown JR*. 2017. The Microbiome in Respiratory Diseases. EMBL-EBI Industry Programme Workshop on The Human Microbiome: challenges and opportunities for novel therapeutics. Wellcome Genome Campus, Hinxton-Cambridge, UK.

11. Brown JR*. 2017. A Drug Discovery Perspective on the Microbiome. Microbiome 2 Workshop: Impacts on Toxicity and Risk Assessment. EUROTOX 2017. Bratislava, Slovak.

12. Brown JR*. 2017. Human-Microbe Interactions and Drug Discovery. U. Connecticut. Farmington CT.

13. Brown JR*. 2017. Human-Microbe Interactions and Drug Discovery. Dalhousie University. Halifax NS.

14. Brown JR*. 2017. Human-Microbe Interactions in Target Discovery. From Basic Science to Clinical Benefits Seminar Series. Wellcome Genome Campus, Hinxton-Cambridge, UK.

15. Brown JR*. 2017. Human-Microbe Interactions in Drug Discovery. 4th Microbiome Forum Europe, Amsterdam, Netherlands.

16. Brown JR*. 2017. Human-Microbe Interactions in Drug Discovery. GSK/Wistar Institute Philadelphia Drug Discovery Forum. Philadelphia PA.

17. Brown JR*. 2017. Human-Microbe Interactions: A Drug Discovery Perspective. Microbiome Drug Development Summit Europe. Paris, France.

18. Brown JR*. 2016. Busting Silos: Host-Microbe Interactions in Infectious and Chronic Diseases. ReEntering Antibacterial Drug Development Summit. Boston, MA.

19. Brown JR*. 2016.The Microbiome in Respiratory Diseases. Microbiome Drug Development Summit. Boston, MA.

20. Brown JR*. 2016. Host-Microbe Interactions. 3rd Annual Drug Discovery USA Congress. San Diego, CA.

21. Brown JR*. 2016. A Drug Discovery Perspective on the Microbiome. The Delaware Valley Drug Metabolism Discussion Group Rozman Symposium. Langhorne PA.

22. Brown JR*. 2015. Invited industry panelist. Jefferies Microbiome Summit. Boston, MA.

23. Brown JR*. 2015. The human microbiome: A drug discovery perspective. American College of Toxicology 36th Annual Meeting. Summerlin, NV.

24. Brown JR*. 2015. Invited industry panelist. Microbiome Innovation: Roadmap to the Future. The White House Office of Science and Technology Policy. Washington, DC.

25. Brown JR*. 2015. Invited industry panelist. CIHR Microbiome Workshop. Ottawa, ON, Canada

26. Brown JR*. 2015. The lung microbiome in respiratory diseases. 13th Annual Discovery on Target. Boston, MA.

27. Brown JR*. 2015. Microbiome, microbial metabolites, and metabolic diseases. 13th Annual Discovery on Target. Boston, MA.

28. Brown JR*. 2015. Pathogen, host and microbiome interactions in drug discovery. U.S. Army Medical Research Institute of Infectious Diseases (USAMRIID), Fort Detrick, MD.

29. Brown JR*. 2015. Human-microbe interactions: Therapeutic opportunities and challenges. 1st Annual Translational Microbiome Conference, Boston MA.

30. Brown JR*. 2015. Better targets, better drugs: Human-microbe interactions in drug discovery. Genome Atlantic Seminar Series, Halifax, NS, Canada.

31. Brown JR*. 2015. The human microbiome. Guest lecturer. Ursinus College, Collegeville PA.

32. Brown JR*. 2014. Human-microbial Interactions in drug discovery. MidAtlantic Society of Toxicology, Raitan, NJ.

33. Brown JR*. 2014. NGS applications in infectious disease and microbiome research. The 6th Annual Global Drug Discovery and Development Innovation Summit, Woodbridge NJ.

34. Brown JR*. 2014. Integrating pathogen, human and microbiome genomics in antibacterial drug development. Cambridge Healthtech Institute's Inaugural Re-Entering Antibacterial Drug Development Summit, Boston, MA.

35. Brown JR*. 2014. Human-microbe interactions: Therapeutic opportunities and challenges. 2nd Microbiome/Microbiota R&D and Business Collaboration Forum, San Diego CA.

36. Brown JR*. 2014. Human-microbial interactions in drug discovery. Dalhousie University, Halifax, Canada.

37. Arat S, Spivak A, Ingraham K, Van Horn S, Thomas E, Traini C, Sathe G, Livi G, Soong D, Aubart K, Holmes DJ, Naderer O, Brown JR. 2014. Gut microbiome changes in healthy volunteers treated with a novel antibiotic peptide deformylase inhibitor GSK1322322. Keystone Symposia on Exploiting and Understanding Chemical Biotransformations in the Human Microbiome.

38. Brown JR*. 2014. Invited industry panelist. CIHR Canadian Microbiome Workshop 2014: From Research to Applications. Vancouver, BC, Canada. February 12-14.

Plus 72 other seminar and conference presentations since 1990 in drug discovery, evolutionary biology, mitochondrial DNA genetics, and aquaculture.

Student & Postdoctoral Fellow Supervision (since 2010)

- **Dr. Andrea Nuzzo** – GSK Early Talent Postdoctoral Fellow (2018-2020). Consumer Health & Pharma project on microbial metabolites as immuno-modulators. Two papers published in *Trends in Molecular Medicine*; *Chemical Research in Toxicology*; *Communications Biology (Nature)*, *BMC Microbiology*. Now at GSK as Association Director Computational Biologist.
- **Dr. Carol Sa** – GSK Early Talent Postdoctoral Fellow (2017-2020). Project on neuroinflammation targets. Paper published in *Scientific Reports (Nature)*. Hired by J&J.
- **Dr. Zhang Wang** – GSK Early Talent Postdoctoral Fellow (2014 – 2016). Lung microbiome. Eight papers in *European Respiratory Journal, Thorax, Journal of Immunology, BMC Respiratory Research, BMC Systems Biology, others.* GSK Computational Biologist; now full Professor, South China Normal University.
- **Dr. Somdutta Saha** – GSK Early Talent Postdoctoral Fellow (2014-2017). Project on microbiota metabolites and host receptors. Papers in *Drug Discovery Today*. Bioinformatician with Solid Bio.
- **Dr. Seda Arat** – PhD student intern (2013-2014) – Bacterial genomics. Papers in *BMC Systems Biology*, *Antimicrobial Agents and Chemotherapy*. Hired by Pfizer.
- **Dr. Steven Smith** – U. Pennsylvania BioEngineering MSc. (2011-2013). Project on host pathogen interactions. Two papers in *PLoS One***.** Later, completed PhD at U. Maryland with microbiome researcher Dr. Jacques Ravel. Bioinformatics position with Teva and Labcorp.
- **Ms Yan Zhang** – Pennsylvania State University intern (2010). Project on cancer evolution. Paper in *Molecular Cancer Therapeutics.* Data Analytics Scientist at Prudential Financial.

Symposium Organized / Sponsored

- Using Whole Genome Sequences to Understand Phylogenetic Relationships. 2003. American Society of Microbiology, Washington, DC.
- The Evolutionary Biology of Prokaryotes. 1999. Ann. Joint Mtg. of the Soc. of Systematic Biology/Soc. for the Study of Evolution/American Naturalists Soc. Madison, WI June 24-27.
- Symposia on the Evolution of Protein Function. 1998. Ann. Mtg. of the Soc. for Molecular Biology and Evolution, Vancouver, BC, Canada.

Journals and Books Refereed

American Naturalist, EMBO, Genetics, J. Bacteriology, J. of Molecular Evolution, Canadian J. of Microbiology, Canadian J. for Fisheries and Aquatic Sciences, Molecular Systematics of Fishes (book), Trends in Microbiology, Trends in Genetics, Molecular Biology and Evolution, Nucleic Acids Research, Microbiology and Molecular Biology Reviews, Drug Discovery Today, Nature Reviews Genetics, Science, Science Signalling, PLoS One, Scientific Reports (Nature), Nature Communications.

Personal information

Canadian citizen and naturalized US citizen. Married with two adult children. PADI and YMCA Certified SCUBA diver, golfer, skier, Rotarian member and Club Past-President (twice).