Paul Stothard

Professor, Department of Agricultural, Food & Nutritional Science

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Work Experience

Professor, Department of Agricultural, Food and Nutritional Science, University of Alberta 2018-present

Associate Professor, Department of Agricultural, Food and Nutritional Science, University of Alberta 2012-2018

Assistant Professor, Department of Agricultural, Food and Nutritional Science, University of Alberta 2006-2012

Academic and Training Background

PhD, Molecular Biology and Genetics, University of Alberta 2002

Postdoctoral Fellow, Bioinformatics, University of Alberta 2006

BSc, Biology, University of Victoria 1994

Research Output Summary

183	30,436	62	155
Peer-reviewed publications	Google Scholar citations	H-index	i10-index

Research translation: trait discoveries incorporated into DNA tests used in cattle and pig breeding, including Dominant Red testing in Holsteins; genomic research contributing to feed efficiency genetic evaluations released by Lactanet Canada; bison SNP array available through Neogen Canada; Holstein structural variant database supporting applied genomics.

Selected Software and Research Resources

DrugBank, co-author on the original NAR database paper for a widely used drug, target, and drug-action knowledgebase. 4,788 citations

HMDB, contributor to the original Human Metabolome Database resource. 4,094 citations

CGView family, creator/co-developer of genome visualization tools for circular and comparative genome maps. 2,719 citations

Sequence Manipulation Suite, creator of web-based DNA and protein sequence utilities used in research and teaching. 2,261 citations

Proksee, co-developer of a modern platform for bacterial genome assembly, annotation, analysis, and visualization. 1,808 citations

Selected Publications

Vandiver AR, Herbst A, **Stothard P**, and Wanagat J. 2025. Chimeric mitochondrial RNA transcripts predict mitochondrial genome deletion mutations in mitochondrial genetic diseases and aging. *Genome Research*, 35, 55-65.

Kalbfleisch TS et al. (including **Stothard P**). 2024. The Ruminant Telomere-to-Telomere (RT2T) Consortium. *Nature Genetics*, 56, 1566-1573.

Grant JR, Herman EK, Barlow LD, Miglior F, Schenkel FS, Baes CF, and **Stothard P**. 2024. A large structural variant collection in Holstein cattle and associated database for variant discovery, characterization, and application. *BMC Genomics*, 25, 903.

Grant JR, Enns E, Marinier E, Mandal A, Herman EK, Chen CY, Graham M, Van Domselaar G, and **Stothard P**. 2023. Proksee: in-depth characterization and visualization of bacterial genomes. *Nucleic Acids Research*, 51(W1), W484-W492.

Stothard P, Liao X, Arantes AS, et al. 2015. A large and diverse collection of bovine genome sequences from the Canadian Cattle Genome Project. *GigaScience*, 4, 49.

Daetwyler HD et al. (including **Stothard P**). 2014. Whole-genome sequencing of 234 bulls facilitates mapping of monogenic and complex traits in cattle. *Nature Genetics*, 46, 858-865.

Selected Research Funding

Genome Canada, A comprehensive analytical toolkit and high-performance genome browser for rapid, reliable and in-depth characterization of bacterial genomes. PIs: Stothard and Van Domselaar. — 2018-2022 $940,000

NSERC, An integrative genomics approach to uncover genetic mechanisms underlying susceptibility to important infectious diseases in pigs. PI: Stothard. — 2016-2024 $205,000

Genome Canada, Leveraging genomics to achieve Dairy Net Zero. PIs: Baes, Gervais, Miglior, and Stothard. — 2023-2027 $2,999,515

Genome Canada GAPP, Bison Integrated Genomics. PIs: Adams and Shury. — 2022-2026 $5,147,192

Selected Honors and Awards

Faculty of ALES Teacher of the Year Award, University of Alberta — 2023

Faculty of ALES Teaching Hall of Fame Award, University of Alberta — 2022

Earlier recognition and fellowships, Letter of Commendation for Teaching Excellence; NSERC Postdoctoral Fellowship and postgraduate scholarships; Alberta Heritage Foundation for Medical Research Studentship. — Selected

Research Expertise

Animal genomics and breeding: genomics of managed animal populations, genotype-to-phenotype discovery, genetic evaluation, feed efficiency, methane efficiency, fertility, health, and production traits.

Genome variation and trait biology: structural variation, copy number variation, SNP discovery and panel design, sequence imputation, comparative genomics, and functional interpretation of trait-associated variants.

Translational bioinformatics: genomic databases, breeder-facing resources, bacterial genome interpretation, metagenomic diagnostics, and scalable computing workflows for genome-scale biological data.

Teaching and Training

AFNS 508: Applied Bioinformatics, graduate instruction in sequence databases, DNA and protein analysis, high-throughput sequencing, command-line bioinformatics, R/Bioconductor, workflow systems, and high-performance computing. — Graduate

AN SC 485: Animal Genetics and Breeding, undergraduate instruction in genetic and genomic methods for livestock and poultry improvement, including R-based analysis of phenotype, pedigree, and genotype data. — Undergraduate

AN SC 384: Principles of Animal Genetics, introductory instruction in animal genetics, selection strategies, breeding systems, quantitative traits, heritability, inbreeding, heterosis, genome editing, and reproductive technologies. — Undergraduate

Selected Invited Talks

Livestock genomics and genetic improvement, invited and keynote presentations on bison conservation genomics, feed efficiency, methane emissions, causative mutation discovery, and genotype-to-phenotype analysis. — Selected topics

Bioinformatics tools and research data, invited presentations on cattle genome data management, SNP annotation, genome visualization, and comparative genome analysis. — Selected topics

Professional Service and Engagement

Editorial, review, and advisory service for *BMC Genomics*, Canadian and international funding agencies, genetics-related litigation, livestock genomics initiatives, and scientific conference planning. — Selected