

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

Postdoctoral Fellow , Bioinformatics, University of Alberta	2006
PhD , Molecular Biology and Genetics, University of Alberta	2002
BSc , Biology, University of Victoria	1994

Research Output Summary

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

Proksee , co-developer of a modern platform for bacterial genome assembly, annotation, analysis, and visualization.	1,808 citations
Sequence Manipulation Suite , creator of web-based DNA and protein sequence utilities used in research and teaching.	2,261 citations
DrugBank , contributor to the original 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

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.
- Yang T, Miller M, Forgacs D, Derr JN, and **Stothard P**. 2020. Development of SNP-based genomic tools for genetic monitoring and management of bison. *Frontiers in Genetics*, 11, 585999.
- 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 , Leveraging genomics to achieve Dairy Net Zero. PIs: Baes, Gervais, Miglior, and Stothard.	2023-2027 \$2,999,515
Genome Canada , Bison Integrated Genomics. PIs: Adams and Shury.	2022-2026 \$5,147,192
AKC Canine Health Foundation , Candidate genetic variants for copper-associated hepatopathy in the Dalmatian. PI: Mason.	2023-2025 \$79,369
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 , Proksee bacterial genome analysis and visualization platform. PIs: Stothard and Van Domselaar.	2018-2022 \$940,000

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 genetic improvement: genomic analysis for managed animal and aquaculture populations, including genetic evaluation, parentage, SNP panels, feed and methane efficiency, fertility, health, and production traits.

Variant discovery and trait interpretation: WGS analysis, GWAS/association mapping, copy number variation, sequence imputation, functional annotation, and genotype-to-phenotype interpretation.

Applied bioinformatics infrastructure: large-scale bacterial assembly/comparative genomics, metagenomic diagnostics, genomic databases and visualization tools, breeder-facing resources, and high-performance workflows.

Teaching and Training

AFNS 508: Applied Bioinformatics , 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 , 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 , animal genetics, selection strategies, breeding systems, quantitative traits, heritability, inbreeding, heterosis, genome editing, and reproductive technologies.	Undergraduate
Graduate mentoring and research supervision in genomics and bioinformatics across MSc, PhD, postdoctoral, and research staff roles.	Mentoring

Selected Invited Talks

Invited and keynote presentations across Canada, the United States, Europe, and Australia on livestock genomics, bison conservation genomics, feed efficiency, methane emissions, causative mutation discovery, genome data management, SNP annotation, and genome visualization.

Selected Professional Service and Consulting

Editorial, review, advisory, and consulting: journal editing and grant review; genetics-related litigation; applied genomics consulting across animal, aquaculture, biomedical, microbial, and technology projects.