Curriculum Vitae

Name
Alisdair “Al” Boraston

Current Position
Professor
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Education & Professional Experiences

Alisdair (“Al”) Boraston received his BSc. in Microbiology and Immunology from the University of British Columbia (UBC) and completed his Ph.D. in Microbiology and Immunology under the supervision of Professors Doug Kilburn and Tony Warrren at UBC. Then, after a brief post-doctoral research appointment in the UBC Biotechnology Laboratory, he trained in England as an NSERC-funded Post-Doctoral Fellow in the York Structural Biology Laboratory, University of York, UK, under the supervision of Professor Gideon Davies. Al took up his faculty position at the University of Victoria (UVic), Victoria, British Columbia, Canada, in 2003. As of 2014 he is a full Professor in the Department of Biochemistry and Microbiology at UVic. Past recognitions include an EWR Steacie Memorial Fellowship, a Michael Smith Foundation for Health Research Scholar award, and a Tier 2 Canada Research Chair.

Research Interests

Al’s research interest is in structural glycobiology and its application to the analysis of protein-carbohydrate interactions in proteins that modify and/or bind to glycans or glycoconjugates. An area of focus is the enzymatic breakdown of marine algal polysaccharides by microbes and how the unique building blocks of these polymerized sugars are funneled through novel metabolic pathways. A second key topic of study is host-microbe interactions where the roles of bacterial proteins in recognizing and/or modifying host glycoconjugates during colonization and/or infection are examined.

Selected Publications

Boraston, A.B., Bolam, D.N., Gilbert, H.J., G.J. Davies, 2004. Carbohydrate-binding modules: fine tuning polysaccharide recognition. Biochem. J. 382, 769-81.

Noach, I., Ficko-Blean, E., Pluvinage, B., Stuart, C., Jenkins, M.L., Brochu, D., Buenbrazo, N., Wakarchuk, W., Burke, J.E., Gilbert, M., and A.B. Boraston. (2017) Recognition of protein-linked glycans as a determinant of peptidase activity. Proc Natl Acad Sci U S A. 114: E679-E688.

Pluvinage B, Ficko-Blean E, Noach I, Stuart C, Thompson N, McClure H, Buenbrazo N, Wakarchuk W, AB Boraston. (2021). Architecturally complex *O*-glycopeptidases are customized for mucin recognition and hydrolysis. Proc Natl Acad Sci U S A. 118: e2019220118.

Medley BJ, Leclaire L, Thompson N, Mahoney KE, Pluvinage B, Parson MAH, Burke JE, Malaker S, Wakarchuk W, AB Boraston. (2022). A previously uncharacterized O-glycopeptidase from *Akkermansia muciniphila* requires the Tn-antigen for cleavage of the peptide bond. J Biol Chem. 298: 102439.

Lecture Title

Advances in understanding *O*-glycopeptidases from host-adapted bacteria: the complex role of ancillary modules.

Abstract

O-glycopeptidases are metal-dependent proteases that selectively hydrolyze peptide bonds proximal to *O*-linked glycans. While catalytic domains within families such as the peptidase_M60 superfamily have received significant attention, far less emphasis has been placed on the architectural logic of the full-length enzymes in which they reside. Strikingly, most characterized *O*-glycopeptidases are multimodular proteins, frequently containing ancillary carbohydrate-binding modules (CBMs) or glycan-recognition domains.

In this presentation, I will explore how this modularity is not merely decorative but functionally integrated. Structural and biochemical evidence suggests that appended CBMs often adopt conformations that fold toward the catalytic cleft, positioning their glycan-binding sites adjacent to the active site. Rather than simply tethering the enzyme to glycosylated substrates, these domains appear to engage *O*-glycosylation sites distal to the site of *O*-glycosylation where cleavage occurs. This mode of action suggests a model in which distal glycan recognition potentiates catalysis by orienting extended glycopeptide substrates and stabilizing cleavage-competent conformations.

This integrated recognition strategy provides a mechanistic framework for understanding substrate selectivity, catalytic efficiency, and the evolution of *O*-glycopeptidase multimodularity in host-associated bacteria. More broadly, it highlights how glycan-binding domains can act as regulators of proteolysis within complex glycoprotein environments.