
KRIS GEVAERT

CV

SPEAKER AT:

THE DEATH OF PLANT CELLS. FROM PROTEASES TO FIELD APPLICATIONS



October, 2nd and 3rd, 2013, Barcelona

Kris Gevaert, Director of the Department of Medical Protein Research, [VIB](#), [Ghent University](#), Ghent, Belgium

Gevaert obtained his PhD in Biotechnology in 2000 at Ghent University (Belgium). He was a post-doctoral fellow with the Fund for Scientific Research (Flanders, Belgium) until 2006 and got appointed Professor in Functional Proteomics at Ghent University in 2004. Since 2005 he heads the Functional Proteomics group of the VIB Department of Medical Protein Research and also the VIB Proteomics Expertise Centre which is part of the FP7-funded PRIME-XS research infrastructures consortium. In 2010 he got appointed Full Professor at Ghent University and is currently acting director of the VIB Department of Medical Protein Research. Together with Joël Vandekerckhove he has introduced the suite of COFRADIC proteomics technologies which his group applies to the deep analysis of protein modifications, including protein processing by proteases. Further, the COFRADIC platform was the basis for establishing the VIB/UGhent spin-off company Pronota that focuses on protein biomarkers for various human diseases. His group published more than 180 papers and several book chapters on the development and applications of proteomics techniques in several areas of biomedical and life sciences research.

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Positional Proteomics Approaches for Protease Degradomics

Proteases polish proteomes after activating or inactivating their substrates. Proteomic approaches for studying protease substrates aged over the past decade and now allow for detailed characterizations of protease degradomes. Our lab developed positional proteomics approaches that enrich for the novel protein termini that are generated upon protein processing by proteases. I will here discuss our latest developments which include strategies to distinguish efficiently processed substrates from inefficiently cleaved ones, more automated identification of protease substrates and the identification of carboxypeptidase substrates and characterization of their specificities using natural peptide libraries.

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