

# Danang Crysnanto

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## Education

<b>ETH Zurich</b> <i>Doctoral in Animal Genomics</i>	Dec 2017 – Present Zurich, Switzerland
<b>The University of Edinburgh</b> <i>Msc in Quantitative Genetics and Genome Analysis with <b>Distinction</b></i>	Aug 2016 – Aug 2017 Edinburgh, UK
<b>Bandung Institute of Technology</b> <i>Bsc in Biology (Genetics) with <b>Cum Laude</b></i>	Oct 2010 – Oct 2014 Bandung, Indonesia

## Publications

### First-author publications

1. **Crysnanto D.**, A. S. Leonard, Z. H. Fang, and H. Pausch, 2021. Novel functional sequences uncovered through a bovine multi-assembly graph. Accepted *Proceedings of the National Academy of Sciences USA*
2. **Crysnanto D.**, and H. Pausch, 2020. Bovine breed-specific augmented reference graphs facilitate accurate sequence read mapping and unbiased variant discovery. *Genome Biology*. 21:184
3. **Crysnanto D.**, C. Wurmser, and H. Pausch, 2019. Accurate sequence variant genotyping in cattle using variation-aware genome graphs. *Genetics Selection Evolution* 51:21
4. **Crysnanto D.**, and D. J. Obbard, 2019 Widespread gene duplication and adaptive evolution in the RNA interference pathways of the *Drosophila obscura* group. *BMC Evolutionary Biology* 19:1

### Co-authored publications

5. Nosková A., C. Wurmser, **D. Crysnanto**, A. Sironen, P. Uimari, et al., 2020 Deletion of porcine BOLL is associated with defective acrosomes and subfertility in Yorkshire boars. *Animal Genetics* 51: 945–949
6. Fang Z. H., A. Nosková, **D. Crysnanto**, S. Neuenschwander, P. Vögeli, et al., 2020 A 63-bp insertion in exon 2 of the porcine KIF21A gene is associated with arthrogryposis multiplex congenita. *Animal Genetics* 51: 820–823
7. Hiltbold M., G. Niu, N. K. Kadri, **D. Crysnanto**, Z. H. Fang, et al., 2020 Activation of cryptic splicing in bovine WDR19 is associated with reduced semen quality and male fertility. *PLoS Genetics*. 16: 1–27
8. Bhati M., N. K. Kadri, **D. Crysnanto**, and H. Pausch, 2020 Assessing genomic diversity and signatures of selection in Original Braunvieh cattle using whole-genome sequencing data. *BMC Genomics* 21(1)

## Invited Talks

<b>CIGENE Seminar Series</b> Talk title: Bovine pangenomics	March 2021 NMBU Norway
<b>International Virtual Animal Breeding Journal Club</b> Talk title: Bovine pangenomics	Sept 2020 USDA USA
<b>Plant and Animal Genome Conference (PAG)</b> Talk title: Bovine pangenome graph enables unbiased genetic variants discovery	Jan 2020 San Diego USA
<b>Livestock Genomics session - Genome Informatics</b> Talk title: Development of graph-based genotyping pipelines for bovine whole-genome data	Sept 2018 Cambridge UK
<b>Population Genetics (PopGroup) Conference</b> Talk title: Widespread gene duplications in <i>Drosophila</i> immune system pathways	Jan 2018 Oxford UK

## Awards

<b>Sir Kenneth Mather Memorial Prize</b> Annual award for a MSc or PhD student of any UK University or Research Institutions which shown an outstanding performance in the area of quantitative and population genetics.	Jan 2018 The Genetics Society
<b>The Douglas Falcone Prize</b> Annual award for the best master's thesis in Quantitative Genetics and Genome Analysis	Oct 2017 The University of Edinburgh
<b>Bronze Medalist 21st International Biology Olympiad</b> Winning a medal on a highly prestigious International bioscience Olympiad	Aug 2010 International Biology Olympiad