



<https://github.com/andreyhgl>

andreyhgl.github.io/doc/cv.pdf

Andrey Höglund

PhD in Genetic
Bioinformatician

Profile

I develop omics computational pipelines in nextflow with reproducibility and reusability in mind. I am highly organised, enjoy problem-solving, collaborative and a golf enthusiast!

Professional experiences

| **Bioinformatician in Toxicogenomics** | 2022 Jan – on-going | [Karlssonlab](#) | Stockholm University |

- I lead the omics analysis for two projects investigating the effects of [DBP](#) and [PFOS](#).
- Analyse Next-Generation Sequencing (NGS) omics datasets generated in mouse and human cell lines with pipelines built in **Nextflow** and **R**.
- Develop [transcriptome analysis pipeline](#) for **RNA-seq**.
- Develop [methylome analysis pipeline](#) for **RRBS**, **EM-seq** and **BS-seq**.
- Mentor group members in bioinformatic tools (**R**, **Nextflow**, **git**, **Quarto**, **package managers** and **containers**).
- Co-author peer-reviewed manuscripts elucidating the effects of DBP and PFOS (*see my publication list below*).

| **Postdoctoral researcher in Evolutionary Biology** | 2020 Nov – 2022 Jan | Linköping University |

- I analysed NGS omics datasets generated in chickens to understand the mammalian version of dosage compensation process in birds.
- Developed [linkage mapping pipeline](#) based on single nucleotide polymorphisms (SNPs).
- Developed pipelines to understand the landscape of gene expression and DNA methylation based on Microarrays and MeDIP-seq.
- Mentored group members in R coding.
- Authored peer-reviewed manuscripts (*see my publication list below*).

Education

| **PhD in Genetics** | [My thesis](#) | 2020-10-23 | Linköping University |

- I investigated the effects of gene expression and DNA methylation on the domestication process in chickens.
- Developed pipelines for linkage mapping of single nucleotide polymorphisms (SNPs).
- Optimized MeDIP-seq protocol and produced DNA methylation NGS data.
- Taught university level courses on cell biology, physiology and gene expression analysis, with laboratory techniques such as RNA/DNA extractions, Microarray, PCR and immunoprecipitation protocols.

Projects

- [Methylome nextflow pipeline](#), analysis of differentially methylated regions.
- [Transcriptome nextflow pipeline](#), analysis of differentially expressed genes.
- Singularity containers packaged with R libraries for omics analysis of the [transcriptome](#), [methylome](#) and [gene ontology](#).
- [Python webscraper](#) extracting the loan interest rate.
- Cheat sheets for working with [git](#), [nextflow](#) and [computing clusters](#).

Peer-reviewed scientific publications

| [ORCiD](#) | [Google Scholar](#) |

Pierozan, **Höglund**, Theodoropoulou, Karlsson (2024) Perfluorooctanesulfonic acid (PFOS) induced cancer related DNA methylation alterations in human breast cells: A whole genome methylome study. *The Science of the total environment* | [DOI](#) | [Computational pipeline](#)

Abele, Perez, **Höglund**, Pierozan, Breitholtz, Karlsson (2024) Automated Image-Based Fluorescence Screening of Mitochondrial Membrane Potential in *Daphnia magna*: An Advanced Ecotoxicological Testing Tool. *Environmental science & technology* | [DOI](#) | [Computational pipeline](#)

Strand, Nylander, **Höglund**, Lundgren, Martin, Karlsson (2024) Screening persistent organic pollutants for effects on testosterone and estrogen synthesis at human-relevant concentrations using H295R cells in 96-well plates. *Cell biology and toxicology* | [DOI](#) | [Computational pipeline](#)

Höglund, Henriksen, Churcher, Guerrero-Bosagna, Martinez-Barrio, Johnsson, Jensen, Wright (2024) The regulation of methylation on the Z chromosome and the identification of multiple novel Male Hyper-Methylated regions in the chicken. *PLoS genetics* | [DOI](#) | [Computational pipeline](#)

Theodoropoulou, Pierozan, Marabita, **Höglund**, Karlsson (2024) Persistent effects of di-n-butyl phthalate on liver transcriptome: impaired energy and lipid metabolic pathways. *Chemosphere* | [DOI](#)

Bakovic, Martin-Cerezo, **Höglund**, Fogelholm, Henriksen, Hargeby, Wright (2021) The genomics of phenotypically differentiated *Asellus aquaticus* cave, surface stream and lake ecotypes *Molecular Ecology* | [DOI](#)

Höglund, Henriksen, Fogelholm, Churcher, Guerrero-Bosagna, Martinez-Barrio, Johnsson, Jensen, Wright (2020) The methylation landscape and its role in domestication and gene regulation in the chicken *Nature Ecology & Evolution* | [DOI](#)

Höglund, Strempl, Fogelholm, Wright, Henriksen (2020) The genetic regulation of size variation in the transcriptome of the cerebrum in the chicken and its role in domestication and brain size evolution *BMC Genomics* | [DOI](#)

Henriksen, **Höglund**, Fogelholm, Abbey-Lee, Johnsson, Dingemanse, Wright (2020) Intra-Individual Behavioural Variability: A Trait under Genetic Control *Int J Mo. Sci* | [DOI](#)

Fogelholm, Henriksen, **Höglund**, Huq, Johnsson, Lenz, Jensen, Wright (2020) CREBBP and WDR 24 Identified as Candidate Genes for Quantitative Variation in Red-Brown Plumage Colouration in the Chicken *Scientific Reports* | [DOI](#)

Fogelholm, Inkabi, **Höglund**, Abbey-Lee, Johnsson, Jensen, Henriksen, Wright (2019) Genetical Genomics of Tonic Immobility in the Chicken *Genes* | [DOI](#)

Johnsson, Henriksen, **Höglund**, Fogelholm, Jensen, Wright (2018) Genetical genomics of growth in a chicken model *BMC Genomics* | [DOI](#)

Johnsson, Henriksen, Fogelholm, **Höglund**, Jensen, Wright (2018) Genetics and Genomics of Social Behavior in a Chicken Model *Genetics* | [DOI](#)

Edstam, Laurila, **Höglund**, Raman, Dahlström, Salminen, Edqvist, Blomqvist (2014) Characterization of the GPI-anchored lipid transfer proteins in the moss *Physcomitrella patens* *Plant Physiology and Biochemistry* | [DOI](#)

Johnsson, Rubin, **Höglund**, Sahlqvist, Jonsson, Kerje, Ekwall, Kämpe, Andersson, Jensen, Wright (2014) The role of pleiotropy and linkage in genes affecting a sexual ornament and bone allocation in the chicken *Molecular Ecology* | [DOI](#)