



Katedry genetiky a biochémie PriF UK  
a občianske združenie *NATURA*



Vás pozývajú na **104. prednášku** v rámci Kuželových seminárov:

## **Andrea Pauli**

The Research Institute of Molecular Pathology  
Vienna, Austria

# **FOUND IN TRANSLATION: FROM GENOMICS TO NOVEL GENE FUNCTIONS**

ktorá sa uskutoční **18. mája 2016** (streda) o **14:00**

v miestnosti CH1-222 Prírodovedeckej fakulty UK

<http://www.naturaoz.org/seminare.html>  
<http://www.naturaoz.org/KuzeloveSeminare.html>

Hostiteľ: Juraj Gregáň, Katedra genetiky PriF UK

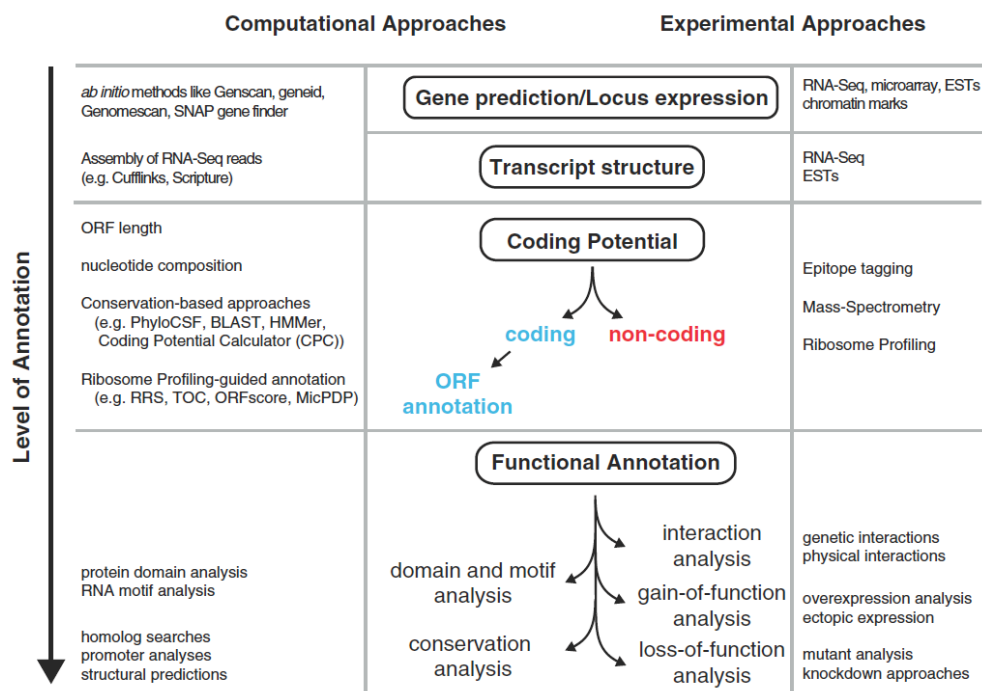
## Curriculum vitae

2015 - present: Group Leader, Research Institute of Molecular Pathology (IMP)  
 2009-2015: Postdoc, Harvard University, Department of Molecular and Cellular Biology, USA (Laboratory of Alex Schier)  
 2006-2009: PhD student, Oxford University, UK (Laboratory of Kim Nasmyth)  
 2004-2005: PhD student, Research Institute of Molecular Pathology (IMP), Austria (Laboratories of Kim Nasmyth and Barry Dickson)  
 2004: M.Sc. in Molecular and Cellular Biology, University of Heidelberg, Germany (Laboratory of Ed Hurt)



## Research Interests

Recent genome-wide analyses have spurred the notion of ‘pervasive translation’ outside of known protein-coding genes. Some of these translated regions have been predicted to encode short, conserved proteins, while others lack signatures of protein conservation and might have regulatory roles. We aim to identify functions for these newly discovered short translated open reading frames (ORFs) during embryogenesis by employing genetic, molecular, cellular and genomics approaches in zebrafish embryos.



Levels of gene annotation. At the most basic level the presence of a gene is indicated by evidence of expression of the locus or by computational prediction of its locus (top). The next level of annotation is the determination of a transcript’s exon–intron structure, which is usually followed by the prediction of its coding potential (middle). The ultimate level of annotation is reached by discovering a gene’s function (bottom). The computational methods (left) and experimental approaches (right) that can be used to reach each level of gene annotation are outlined (from Pauli et al., 2015).

## Selected Publications

- Pauli, A., Valen, E., Schier, AF. (2015). Identifying (non-)coding RNAs and small peptides: challenges and opportunities. *Bioessays* 37(1):103-112
- Pauli, A., Norris, ML., Valen, E., Chew, GL., Gagnon, JA., Zimmerman, S., Mitchell, A., Ma, J., Dubrulle, J., Reyon, D., Tsai, SQ., Joung, JK., Saghatelian, A., Schier, AF. (2014). Toddler: an embryonic signal that promotes cell movement via Apelin receptors. *Science* 343(6172): 1248636
- Pauli, A., Valen, E., Lin, MF., Garber, M., Vastenhouw, NL., Levin, JZ., Fan, L., Sandelin, A., Rinn, JL., Regev, A., Schier, AF. (2012). Systematic identification of long noncoding RNAs expressed during zebrafish embryogenesis. *Genome Res.* 22(3):577-591
- Pauli, A., Rinn, JL., Schier, AF. (2011). Non-coding RNAs as regulators of embryogenesis. *Nat. Rev. Genet.* 12(2): 136-149