

Niek de Klein

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🌐 <https://github.com/npklein>

🌐 <https://scholar.google.com/citations?user=QNwjBnwAAAAJ&hl>

Education

- May 2015 – May 2019 **PhD Bioinformatics / Genetics**
Genetics Department of University Medical Center Groningen, Groningen, Netherlands.
- Sep 2012 – Aug 2014 **M. Sc. Bioinformatic**
Vrije Universiteit, Amsterdam, Netherlands
grade 8.6/10 (Cum laude)
- Sep 2008 – Aug 2012 **B. Sc. Bioinformatics**
HAN University of Applied Sciences, Nijmegen, Netherlands
grade 8.2/10

Teaching

Courses and seminars

- Sep – Oct 2017 **Introduction to Biomolecular Sciences**
Co-coordinated, created, and supervised various genetics workshops. Biomolecular Science Master students of the Rijksuniversiteit Groningen
Course material at npklein.github.io/iBMS.
- 26 Aug 2016 **Invited Talk + Workshop Genotyping from RNAseq**
Lecture + workshop on how to call genotypes from RNAseq data at the Estonian Genome Center.
- 22 Jun 2016 **Enriching biobanks using genotype data**
BIKE Summer School seminar

Student supervision

- Feb – Jul 2017 **Anne Tjallingii**
M.Sc. internship
Influence of a diabetes mellitus type II on the susceptibility of getting tuberculosis
- Jan – Jun 2016 **Carlos Urzua**
M.Sc. internship
Allele-specific signals in gluten sensitive t-cell clones

Internships

During M.Sc.

- Jan – Jun 2014 **Connecting multiple gene expression signatures with candidate drugs for boosting heart regeneration potential.**
Supervisor Dr. Francisco Azuaje
Institute CRD-Sant  , Luxembourg, Luxembourg
Grade 9/10
<https://github.com/npklein/drugFinder>

Internships (continued)

Aug – Dec 2013 ■ **Clustering of MS/MS spectra to improve peptide and protein identification.**
Supervisor Dr. Tham Pham
Institute Cancer Center Amsterdam, Amsterdam, Netherlands
Grade 9/10

During B.Sc.

Feb – Jun 2012 ■ **Methods to assess the reproducibility and coverage of tandem mass spectrometry data in phosphoproteomics experiments.**
Supervisor Dr. David Martin
Institute Wellcome Trust, Dundee, Scotland
Grade 9/10
<https://github.com/npklein/pyMSA>

Sep – Dec 2010 ■ **How widespread are microProteins and how did they evolve?**
Supervisor Dr. Sue Rhee
Institute Carnegie Institute for Life Sciences, Stanford, USA
Grade 9/10
<https://github.com/npklein/miP3>

Grants

07 Mar 2016 ■ **One tool to interpret and assess impact of genetic variants and predict disease-causing genes using the BBMRI – BIOS data (Co-Applicant)**
€ 60,000

Research Publications (Reverse chronological order)

Journal Articles

- 1 Barbieri, R., Uniken Venema, W., Vich Vila, A., Li, Y., Franke, L., van Dijk, F., ... Voskuil, M. et al. (2018). Op011 integration of whole-exome sequencing and rna sequencing of intestinal biopsies in inflammatory bowel disease identifies inflammation-dependent effects. *Journal of Crohn's and Colitis*, 12(supplement_1), S008–S009.
- 2 Claringbould*, A., **de Klein***, Niek & Franke, L. (2017). The genetic architecture of molecular traits. *Current Opinion in Systems Biology*, 1, 25–31.
- 3 Zhernakova, D. V., Deelen, P., Vermaat, M., van Iterson, M., van Galen, M., Arindrarto, W., ... Westra, H.-J. et al. (2017). Identification of context-dependent expression quantitative trait loci in whole blood. *Nature genetics*, 49(1), 139.
- 4 Graham, D. B., Lefkovith, A., Deelen, P., **de Klein, N.**, Varma, M., Boroughs, A., ... Schenone, M. et al. (2016). Tmem258 is a component of the oligosaccharyltransferase complex controlling er stress and intestinal inflammation. *Cell reports*, 17(11), 2955–2965.
- 5 Rodius, S., Androsova, G., Götz, L., Liechti, R., Crespo, I., Merz, S., ... González-Rosa, J. M. et al. (2016). Analysis of the dynamic co-expression network of heart regeneration in the zebrafish. *Scientific reports*, 6, 26822.
- 6 **de Klein, N.**, Ibberson, M., Crespo, I., Rodius, S. & Azuaje, F. (2015). A gene mapping bottleneck in the translational route from zebrafish to human. *Frontiers in genetics*, 5, 470.

*contributed equally



- 7 de **Klein**, N., Magnani, E., Banf, M. & Rhee, S. Y. (2015). Microprotein prediction program (mip3): A software for predicting microproteins and their target transcription factors. *International journal of genomics*, 2015.
- 8 Magnani, E., de **Klein**, N., Nam, H.-I., Kim, J.-G., Pham, K., Fiume, E., ... Rhee, S. Y. (2014). A comprehensive analysis of microproteins reveals their potentially widespread mechanism of transcriptional regulation. *Plant physiology*, 165(1), 149–159.

Books and Chapters



- 1 Fiume, E., de **Klein**, N., Rhee, S. Y. & Magnani, E. (2016). A framework for discovering, designing, and testing microproteins to regulate synthetic transcriptional modules. In *Plant synthetic promoters* (pp. 175–188). Humana Press, New York, NY.

Miscellaneous Experience





Conference (poster) presentations

- 17 June 2018  **Allele specific expression identifies rare variants as cause for extreme allelic imbalance**
ESHG (Poster)
- 25 May 2016  **Genotyping of all public RNA-sequencing data for large scale trans-QTL and ASE studies**
ESHG (Poster)
- 8 Sep 2014  **Connecting multiple gene expression signatures with candidate drugs for boosting heart regeneration potential**
ECCB (Poster)

Other

- Aug 2018  **Leena Peltonen Summer School**
Summer school
- Jul 2016  **Microsoft Research PhD Summer School**
Summer school

Skills

- Languages  Strong reading, writing and speaking competencies for English and Dutch.
- Coding  Python, R, Java, Bash
- Databases  MySQL, SQLite
- Misc.  Academic research, teaching

References

Available on Request