Niek de Klein

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🌐 https://github.com/npklein
🌐 https://scholar.google.com/citations?user=QNwjBnwAAAAJ&hl

Education

May 2015 –	🔖	**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-Santeé, 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 Institue 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.

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*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