Niek de Klein

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

Education

May 2015 – **PhD Functional Genomics**
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

Employment and 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

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

Dec 2012 – Aug 2013 **Assistant Webmining**
Company TextKernel, Amsterdam, Netherlands

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

Oct 2011 – Oct 2012 **Junior Developer**
Company iVention, Amesfoort, Netherlands

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 8/10
https://github.com/npklein/miP3

Teaching

Courses and seminars

Sep 2019 — **Lecture + workshop gene expression**
Lecture on gene expression + workshop differential gene expression and pathway analysis
Data Science for Life Sciences Master students of the Hanze University of Applied Sciences Groningen
Course material at `npklein.github.io/Teaching-modules/`.

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

Apr 2019 – — Fabian VogelPohl
Bachelor internship
Unraveling the brain specific molecular network of the SCGE gene, the major gene for myoclonus dystonia.

Sep 2018 – Apr 2019 — Omar El Garwany
Master thesis
Brain eQTLs show more enrichment for neuro-psychotic diseases than blood eQTLs

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

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

Miscellaneous Experience

Conference (poster) presentations

17 October 2019 — **eQTL analysis in brain cortex samples of 3,833 individuals and 31,684 blood samples reveals distinct regulatory effects of disease-associated genetic variants**
ASHG (Poster)

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

Okt 2019 – Dec 2019 — **Research visit at Biogen**

Sep 2019 – — **Oncode Investigator**

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

Research Publications (Reverse chronological order)

Journal Articles

1. Aguirre-Gamboa, R., de **Klein**, N., di Tommaso, J., Claringbould, A., Vosa, U., Zorro, M., … Ricano-Ponce, I. et al. (2019). Deconvolution of bulk blood eqtl effects into immune cell subpopulations. *bioRxiv*, 548669. (*Underlined authors contributioned equally.*)

2. 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.

3. Parmar, P., Lowry, E., Cugliari, G., Suderman, M., Wilson, R., Karhunen, V., … Guarrera, S. et al. (2018). Association of maternal prenatal smoking gfi1-locus and cardio-metabolic phenotypes in 18,212 adults. *EBioMedicine*, *38*, 206–216.

4. Claringbould, A., de **Klein**, N. & Franke, L. (2017). The genetic architecture of molecular traits. *Current Opinion in Systems Biology*, *1*, 25–31. (*Underlined authors contributioned equally.*)

5. 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.

6. 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.

7. Rodius, S., Androsova, G. & G. (2016). Analysis of the dynamic co-expression network of heart regeneration in the zebrafish. *Scientific reports*, *6*, 26822.

8. 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.

9. 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*.

10. 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.