Niek de Klein

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

Education

May 2015 – Sep 2021	**PhD Functional Genomics**
	Genetics Department of University Medical Center Groningen, Groningen, Netherlands.
	Thesis title Genetic regulation of gene expression in brain and blood
	DOI: 10.33612/diss.178049845
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

After PhD

Sep 2020 – *Aug 2023*	**Postdoctoral researcher**
	Company Wellcome Sanger, Cambridge, United Kingdom
	keywords Single cell RNA-seq, VDJ, and CITE-seq; eQTLs; Lupus; immune traits

After M.Sc.

Mar 2015 – May 2015	**Assistant Webmining**
	Company TextKernel, Amsterdam, Netherlands

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

16 Jun 2022   ▐ **Lecture basics of eQTL analysis and colocalisations**
Wellcome Sanger departmental retret

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 (co)-supervision

Mar 2021 –   ▐ Ziying Ke
PhD student
Metabolic pathway perturbation in single cells

May 2022 – Jul 2022   ▐ Haerin Jang
PhD rotation project
Drug target identification through single cell eQTL mapping of immune response regulation in health and SLE

Teaching (continued)

Haerin Jang
PhD rotation project
Drug target identification through single cell eQTL mapping of immune response regulation in health and SLE

Mar 2021 – May 2021
Isaac Garcia-Salinas
PhD rotation project
Determining putative causal genes of neuropsychiatric lupus through genotype and brain gene expression data

Jan 2020 – Jun 2020
Martijn Vochteloo
Master thesis
Investigation of Cell Type Mediated eQTL Regulatory Effects in Psychiatric and Neurodegenerative Diseases

Apr 2019 – Jun 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

Misc

Jun 2022
Marking students for M.Sc. course Genomics of complex disease
Cambridge University, United Kingdom

Aug 2020, 2021
External examiner for various bachelor thesis projects
H.A.N., Nijmgen, the Netherlands

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. Boulogne, F., Claus, L., Wiersma, H., Oelen, R., Schukking, F., de **Klein**, N., Li, S., Westra, H.-J., van der Zwaag, B., van Reekum, F., et al. (2022). Kidneynetwork: Using kidney-derived gene expression data to predict and prioritize novel genes involved in kidney disease.

2. Bakker, O. B., & Ram. (2021). Potential impact of celiac disease genetic risk factors on t cell receptor signaling in gluten-specific cd4+ t cells. *Scientific reports*, *11*(1), 1–15.

3 de **Klein**, N., Tsai, E. A., Vochteloo, M., Baird, D., Huang, Y., Chen, C.-Y., van Dam, S., Deelen, P., Bakker, O. B., El Garwany, O., et al. (2021). Brain expression quantitative trait locus and network analysis reveals downstream effects and putative drivers for brain-related diseases. *bioRxiv*.

4 Karabegovic, I., Portilla-Fernandez, E., Li, Y., Ma, J., Maas, S. C., Sun, D., Hu, E. A., & K. (2021). Epigenome-wide association meta-analysis of dna methylation with coffee and tea consumption. *Nature communications*, *12*(1), 1–13.

5 Schlosser, P., Tin, A., Matias-Garcia, P. R., Thio, C. H., Joehanes, R., Liu, H., Weihs, A., Yu, Z., Hoppmann, A., Grundner-Culemann, F., et al. (2021). Meta-analyses identify dna methylation associated with kidney function and damage. *Nature communications*, *12*(1), 1–16.

6 Van Rheenen, W., Van Der Spek, R. A., Bakker, M. K., Van Vugt, J. J., Hop, P. J., Zwamborn, R. A., de **Klein**, N., Westra, H.-J., Bakker, O. B., Deelen, P., et al. (2021). Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. *Nature genetics*, *53*(12), 1636–1648.

7 Zhang, Z., van Dijk, F., de **Klein**, N., & van Gijn, M. (2021). Feasibility of predicting allele specific expression from dna sequencing using machine learning. *Scientific reports*, *11*(1), 1–11.

8 Aguirre-Gamboa, R. (2020). Deconvolution of bulk blood eqtl effects into immune cell subpopulations. *BMC bioinformatics*, *21*(1), 1–23.

9 de **Klein**, N., van Dijk, F., Deelen, P., Urzua, C. G., Claringbould, A., & V. (2020). Imbalanced expression for predicted high-impact, autosomal-dominant variants in a cohort of 3,818 healthy samples. *bioRxiv*.

10 Rodius, S., de **Klein**, N., & Jeanty, C. (2020). Fisetin protects against cardiac cell death through reduction of ros production and caspases activity. *Scientific reports*, *10*(1), 1–12.

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

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

13 Zhernakova, D. V., Deelen, P., Vermaat, M., Van Iterson, M., Van Galen, M., Arindrarto, W., Van't Hof, P., Mei, H., Van Dijk, F., Westra, H.-J., et al. (2017). Identification of context-dependent expression quantitative trait loci in whole blood. *Nature genetics*, *49*(1), 139–145.

14 Graham, D. B., Lefkovith, A., Deelen, P., de **Klein**, N., Varma, M., Boroughs, A., Desch, A. N., Ng, A. C., Guzman, G., 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.

15 Rodius, S., Androsova, G., & G. (2016). Analysis of the dynamic co-expression network of heart regeneration in the zebrafish. *Scientific reports*, *6*(1), 1–12.

16 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.

17 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*.

18 Magnani, E., de **Klein**, N., Nam, H.-I., Kim, J.-G., Pham, K., Fiume, E., Mudgett, M. B., & Rhee, S. Y. (2014). A comprehensive analysis of microproteins reveals their potentially widespread mechanism of transcriptional regulation. *Plant physiology*, *165*(1), 149–159.