

Florian Wünnemann

POSTDOC IN THE SCHAPIRO LAB

Im Neuenheimer Feld 130, 69120 Heidelberg, Germany

✉ flowuenne@gmail.com

🏠 florianwuennemann.com | 📷 flowuenne | 🐦 flowuenne

Research and scientific interests: Human genetics, Single cell OMICS, Heart development, Bioinformatics, Machine Learning, Computer vision, Open source software

🔬 Research experience

University Hospital Heidelberg

POSTDOC IN THE SCHAPIRO LAB

Heidelberg, Germany

Jan2022 - ongoing

- Defining and modulating cellular neighbourhoods in myocardial infarction models using spatial OMICS technologies

Montreal Heart Institute

POSTDOC IN THE LETTRE LAB

Montreal, Canada

Aug2018 - Aug2021

- Projects focused on high-throughput CRISPR screens, polygenic risk scores, genetics of heart valve disease and development of single-cell screens to investigate human cellular traits.

Universite de Sherbrooke

PROFESSIONNEL RECHERCHE NIV. II

Sherbrooke, Canada

Jan 2019 - ongoing

- Part of the GenAP initiative (www.genap.ca) as single-cell expert, to include single-cell tools into the GenAP2 platform. Development of Galaxy tools, Rshiny applications and docker containers for single-cell analysis.

IEB, University of Münster

STUDENT RESEARCH ASSISTANT

Münster, Germany

Sept2011 - Jul2012

- Acquisti group: Analysis of genomes and metagenomes in the context of nutrient limitation and fertilization.

IEB, University of Münster

STUDENT ASSISTANT

Münster, Germany

Mar2011 - May 2011

- Bornberg-Bauer group

🎓 Education

University of Münster / CHU Sainte Justine Research Center

PH.D. (DR.RER.NAT) - LIFE SCIENCES

Münster, Germany / Montreal,

Canada

Apr.2014 - Apr.2018

- Thesis title: The role of genetic factors in pathogenesis and progression of cardiac malformations

University of Münster

MSC IN LIFE SCIENCES

Münster, Germany

Oct.2011 - Feb.2014

- Thesis title: Functional and genetic characterization of a novel arrhythmic syndrome

University of Münster

BSC IN LIFE SCIENCES

Münster, Germany

Oct.2008 - Sep.2011

- Thesis title: Impact of nutrient limitation in insects: Comparative genomics of the pea aphid and the human body louse

\$ Funding History

POSTDOCTORAL TRAINING (CANADIAN CITIZENS AND PERMANENT RESIDENTS) SCHOLARSHIP, FONDS DE RECHERCHE QUÉBEC

SANTÉ (FRQS)

2019 - 2021

🏆 Achievements and Awards

2021/06	Poster prize: Prix Fonds de recherche du Québec (FRQS) (Recherche fondamentale doctorale / Postdoc)	<i>Montreal, Canada</i>
2019/06	Best oral presentation award, 22nd Montreal Heart Institute research day	<i>Montreal, Canada</i>
2017/05	Best oral presentation award, 32nd student congress at the CHU Sainte-Justine	<i>Montreal, Canada</i>
2016/05	Markwald award for best oral presentation, Weinstein Cardiovascular Development and Regeneration Conference 2016	<i>Durham, USA</i>

Presentations

American Society of Human Genetics (ASHG) Meeting 2019

PRIORITIZATION OF GENOMIC LOCI FOR CORONARY ARTERY DISEASE USING TARGETED CRISPR SCREENS FOR ENDOTHELIAL DYSFUNCTION

Houston, Texas, USA

15.10.2019 - 19.10.2019

XXIIe Journée de la recherche ICM

VALIDATION OF GENOME-WIDE POLYGENIC RISK SCORES FOR CORONARY ARTERY DISEASE IN FRENCH CANADIANS

Montreal, Canada

06.06.2019 - 06.06.2019

7th annual MGSE Symposium

SINGLE CELL LANDSCAPE OF MAMMALIAN HEART MATURATION

Münster, Germany

21.03.2018 - 22.03.2018

American Society of Human Genetics (ASHG) Meeting 2017

IDENTIFICATION OF A NOVEL MARKER FOR VALVE MATURATION: LOSS OF ADAMTS19 FUNCTION CAUSES PROGRESSIVE VALVE DISEASE IN MICE AND MEN

Orlando, Florida, USA

18.10.2017 - 18.10.2017

Congrès de la recherche des étudiantes des cycles supérieurs et des post-doctorants en recherche au CHU Sainte-Justine

HEART VALVE DYSFUNCTION IN MEN AND MICE IS CAUSED BY LOSS OF FUNCTION MUTATIONS IN ADAMTS19, A NOVEL MARKER FOR VALVULAR INTERSTITIAL CELLS

Montreal, Canada

26.05.2017 - 26.05.2017

Weinstein Cardiovascular Development and Regeneration Conference 2016

LOSS OF ADAMTS19, A NOVEL MARKER FOR VALVULAR INTERSTITIAL CELL POPULATIONS DURING VALVE MATURATION, CAUSES AORTIC VALVE DYSFUNCTION

Durham, North Carolina, USA

18.05.2016 - 21.05.2016

Evolgen, collaborative meeting on genome evolution

ACTRANSD: AN ONLINE DATABASE FOR ACANTHAMOEBA CASTELLANI TRANSCRIPTS,

Ciążeń, Poland

27.06.2012 - 28.06.2012

2nd Muenster graduate school evolution symposium

BIOGEOCHEMISTRY MEETS MOLECULAR EVOLUTION VIA METAGENOMICS: TRACING NITROGEN FLUXES FROM ECOSYSTEMS TO GENOMES IN MICROBIAL COMMUNITIES

Münster, Germany

18.06.2012 - 19.06.2012

Poster presentations

XXIIIe Journée de la recherche ICM

CRISPR PERTURBATIONS AT MANY CORONARY ARTERY DISEASE LOCI IMPAIR VASCULAR ENDOTHELIAL CELL FUNCTIONS

Montreal, Canada

17.06.2021 - 17.06.2021

Cold Spring Harbor Laboratories: The Biology of Genomes

CRISPR PERTURBATIONS AT MANY CORONARY ARTERY DISEASE LOCI IMPAIR VASCULAR ENDOTHELIAL CELL FUNCTIONS

Virtual

11.05.2021 - 14.05.2021

Weinstein Cardiovascular Development and Regeneration Conference

A SINGLE-CELL PERSPECTIVE ON GROWTH AND MATURATION PATHWAYS IN THE MOUSE HEART.

Nara, Japan

16.05.2018 - 18.05.2018

American Society of Human Genetics (ASHG) 2014

DE NOVO MUTATION IN SOX18 CAUSES A NOVEL FORM OF HYPOTRICHOSIS-LYPHEDEMA-TELANGIECTASIA WITH SEVERE VASCULAR DEFECTS

San Diego, California, USA

18.10.2014 - 22.10.2014

42nd Annual Meeting of the Ecological Society of Germany, Austria and Switzerland 2012

SOIL METAGENOMICS TO UNRAVEL THE SIGNATURE OF FERTILIZERS ON THE MOLECULAR COMPOSITION OF THE BACTERIAL RIBOSOME

Lueneburg, Germany

10.09.2012 - 14.09.2012

Preprints

1. Wünnemann, F., Tadjó, T. F., Beaudoin, M., Lalonde, S., Lo, K. S., & Lettre, G. (2021). CRISPR perturbations at many coronary artery disease loci impair vascular endothelial cell functions. *bioRxiv*.
2. Audain, E., Wilsdon, A., Breckpot, J., Izarzugaza, J. M., Fitzgerald, T. W., Kahlert, A., Sifrim, A., Wünnemann, F., Perez-Riverol, Y., Abdul-Khaliq, H. others. (2020). Integrative analysis of genomic variants reveals new associations of candidate haploinsufficient genes with congenital heart disease. *bioRxiv*.
3. Churakov, G., Kuritzin, A., Chukharev, K., Zhang, F., Wünnemann, F., Ulyantsev, V., & Schmitz, J. (2020). A 4-lineage statistical suite to evaluate the support of large-scale retrotransposon insertion data to reconstruct evolutionary trees. *bioRxiv*.

Publications

1. Wünnemann, F., Ta-Shma, A., Preuss, C., Leclerc, S., Vliet, P. P. van, Oneglia, A., Thibeault, M., Nordquist, E., Lincoln, J., Scharfenberg, F.others. (2020). Loss of ADAMTS19 causes progressive non-syndromic heart valve disease. *Nature Genetics*, 52(1), 40–47.
2. Gould, R. A., Aziz, H., Woods, C. E., Seman-Senderos, M. A., Sparks, E., Preuss, C., Wünnemann, F., Bedja, D., Moats, C. R., McClymont, S. A.others. (2019). ROBO4 variants predispose individuals to bicuspid aortic valve and thoracic aortic aneurysm. *Nature Genetics*, 51(1), 42–50.
3. Luyckx, I., Kumar, A. A., Reyniers, E., Dekeyser, E., Vanderstraeten, K., Vandeweyer, G., Wünnemann, F., Preuss, C., Mazzella, J.-M., Goudot, G.others. (2019). Copy number variation analysis in bicuspid aortic valve-related aortopathy identifies TBX20 as a contributing gene. *European Journal of Human Genetics*, 27(7), 1033–1043.
4. Wünnemann, F., Sin Lo, K., Langford-Avelar, A., Busseuil, D., Dubé, M.-P., Tardif, J.-C., & Lettre, G. (2019). Validation of genome-wide polygenic risk scores for coronary artery disease in french canadians. *Circulation: Genomic and Precision Medicine*, 12(6), e002481.
5. Preuss, C., Wünnemann, F., & Andelfinger, G. (2017). At the heart of a complex disease “molecular genetics of congenital heart disease.” *eLS*, 1–9.
6. Gillis, E., Kumar, A. A., Luyckx, I., Preuss, C., Cannaerts, E., Van De Beek, G., Wieschendorf, B., Alaerts, M., Bolar, N., Vandeweyer, G.others. (2017). Candidate gene resequencing in a large bicuspid aortic valve-associated thoracic aortic aneurysm cohort: SMAD6 as an important contributor. *Frontiers in Physiology*, 8, 400.
7. Wünnemann, F., Kokta, V., Leclerc, S., Thibeault, M., McCuaig, C., Hatami, A., Stheneur, C., Grenier, J.-C., Awadalla, P., Mitchell, G. A.others. (2016). Aortic dilatation associated with a de novo mutation in the SOX18 gene: Expanding the clinical spectrum of hypotrichosis-lymphedema-telangiectasia syndrome. *Canadian Journal of Cardiology*, 32(1), 135–e1.
8. Preuss, C., Capredon, M., Wünnemann, F., Chetaille, P., Prince, A., Godard, B., Leclerc, S., Sobreira, N., Ling, H., Awadalla, P.others. (2016). Family based whole exome sequencing reveals the multifaceted role of notch signaling in congenital heart disease. *PLoS Genetics*, 12(10), e1006335.
9. Wünnemann, F., & Andelfinger, G. U. (2016). Molecular pathways and animal models of hypoplastic left heart syndrome. In *Congenital heart diseases: The broken heart* (pp. 649–664). Springer, Vienna.
10. Chetaille, P., Preuss, C., Burkhard, S., Côté, J.-M., Houde, C., Castilloux, J., Piché, J., Gosset, N., Leclerc, S., Wünnemann, F.others. (2014). Mutations in SGOL1 cause a novel cohesinopathy affecting heart and gut rhythm. *Nature Genetics*, 46(11), 1245.

Computational skills

- **General:** GWAS analysis, Exome/Genome variant calling, Plink, bedtools
- **R:** Rshiny application development, Rmarkdown, Package development, OMICS data analysis (RNA-seq, single-cell OMICS), reticulate
- **Python:** Jupyter notebooks, basic computer vision applications, single-cell OMICS analysis
- **Containers:** Docker container creation, Singularity usage, Nextflow
- **Galaxy project:** Creation of galaxy tools and wrappers

Languages

- German (mother-language)
- English (fluent)
- French (fluent)