Florian **Wünnemann**

Postdoc in the group of Denis Schapiro

Im Neuenheimer Feld 130, 69120 Heidelberg, Germany

flowuenne@gmail.com

florianwuennemann.com | flowuenne | flowuenne

***Research and scientific interests**: Spatial OMICS, Cardiovascular disease, Human genetics, Bioinformatics, Machine Learning, Computer vision*

Research experience

University Hospital Heidelberg
Heidelberg, Germany

Postdoc in the Schapiro Lab — *22-Jan-22 - ongoing*

- Investigation of cellular neighbourhoods and tissue architecture in myocardial infarction models using spatial OMICS technologies

Montreal Heart Institute
Montreal, Canada

Postdoc in the Lettre lab — *18-Aug-22 - 21-Aug-22*

- 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
Remote work

Professionnel recherche niv. II — *19-Jan-22 - 16-Jan-22*

- 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
Münster, Germany

Student Research assistant — *11-Sep-22 - 12-Jul-22*

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

IEB, University of Münster
Münster, Germany

Student assistant — *11-Mar-22 - 11-May-22*

- Bornberg-Bauer group

Education

University of Münster / CHU Sainte Justine Research Center
Münster, Germany / Montreal, Canada

Ph.D. (Dr.rer.nat) - Life sciences — *Apr.2014 - Apr.2018*

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

University of Münster
Münster, Germany

MSc in Life sciences — *Oct.2011 - Feb.2014*

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

University of Münster
Münster, Germany

BSc in Life sciences — *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

Walter-Benjamin Postdoctoral position for 24 months, Deutsche Forschungsgemeinschaft (DFG) — *2022 - ongoing*

Postdoctoral Training scholarship (Canadian citizens and permanent residents) , 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)	*Montreal,Canada*
2019/06	Best oral presentation award, 22nd Montreal Heart Institute research day	*Montreal,Canada*
2017/05	Best oral presentation award, 32nd student congress at the CHU Sainte-Justine	*Montreal, Canada*
2016/05	Markwald award for best oral presentation, Weinstein Cardiovascular Development and Regeneration Conference 2016	*Durham, USA*

Invited Presentations

Resolve Biosciences - Immersive Spatial Biology Experience — *Basel, Switzerland*

Molecular cartography helps reveal immune cell infiltration routes and their microenvironments during acute myocardial infarction.

29.09 - 29.09

Resolve Biosciences - Immersive Spatial Biology Experience — *Heidelberg, Germany*

Molecular cartography helps reveal immune cell infiltration routes and their microenvironments during acute myocardial infarction.

26.09 - 26.09

Presentations

American Society of Human Genetics (ASHG) Meeting 2019 — *Houston, Texas, USA*

Prioritization of genomic loci for coronary artery disease using targeted CRISPR screens for endothelial dysfunction

15.10.2019 - 19.10.2019

XXIIe Journée de la recherche ICM — *Montreal, Canada*

Validation of genome-wide polygenic risk scores for coronary artery disease in French Canadians

06.06.2019 - 06.06.2019

7th annual MGSE Symposium — *Münster, Germany*

Single cell landscape of mammalian heart maturation

21.03.2018 - 22.03.2018

American Society of Human Genetics (ASHG) Meeting 2017 — *Orlando, Florida, USA*

Identification of a novel marker for valve maturation: Loss of ADAMTS19 function causes progressive valve disease in mice and men

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 — *Montreal, Canada*

Heart valve dysfunction in men and mice is caused by loss of function mutations in Adamts19, a novel marker for valvular interstitial cells

26.05.2017 - 26.05.2017

Weinstein Cardiovascular Development and Regeneration Conference 2016 — *Durham, North Carolina, USA*

Loss of Adamts19, a novel marker for valvular interstitial cell populations during valve maturation, causes aortic valve dysfunction

18.05.2016 - 21.05.2016

Evolgen, collaborative meeting on genome evolution — *Ciążeń, Poland*

ACTransDB: An online database for Acanthamoeba castellani transcripts,

27.06.2012 - 28.06.2012

2nd Muenster graduate school evolution symposium — *Münster, Germany*

Biogeochemistry meets molecular evolution via metagenomics: tracing nitrogen fluxes from ecosystems to genomes in microbial communities

18.06.2012 - 19.06.2012

Poster presentations

XXIIIe Journée de la recherche ICM — *Montreal, Canada*

CRISPR perturbations at many coronary artery disease loci impair vascular endothelial cell functions

17.06.2021 - 17.06.2021

Cold Spring Harbor Laboratories: The Biology of Genomes — *Virtual*

CRISPR perturbations at many coronary artery disease loci impair vascular endothelial cell functions

11.05.2021 - 14.05.2021

Weinstein Cardiovascular Development and Regeneration Conference — *Nara, Japan*

A single-cell perspective on growth and maturation pathways in the mouse heart.

16.05.2018 - 18.05.2018

American Society of Human Genetics (ASHG) 2014 — *San Diego, California, USA*

De novo mutation in SOX18 causes a novel form of Hypotrichosis-Lymphedema-Telangiectasia with severe vascular defects

18.10.2014 - 22.10.2014

Preprints

1. Lavertu-Jolin, M., Chattopadhyaya, B., Chehrazi, P., Carrier, D., Wunnemann, F., Leclerc, S., Dumouchel, F., Robertson, D., Affia, H., Saba, K., et al. (2022). Enhancing adult neuroplasticity by epigenetic regulation of parvalbumin-expressing GABAergic cells. *bioRxiv*.
2. Creason, A. L., Watson, C., Gu, Q., Persson, D., Sargent, L. L., Chen, Y.-A., Lin, J.-R., Sivagnanam, S., Wünnemann, F., Nirmal, A. J., et al. (2022). A web-based software resource for interactive analysis of multiplex tissue imaging datasets. *bioRxiv*.
3. Lerma-Martin, C., Badia-i-Mompel, P., Flores, R. O. R., Sekol, P., Hofmann, A., Thaewel, T., Riedl, C. J., Wuennemann, F., Ibarra-Arellano, M. A., Trobisch, T., et al. (2022). Spatial cell type mapping of multiple sclerosis lesions. *bioRxiv*.
4. Wünnemann, F., Tadjo, 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*.
5. 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. Kuppe, C., Ramirez Flores, R. O., Li, Z., Hayat, S., Levinson, R. T., Liao, X., Hannani, M. T., Tanevski, J., Wünnemann, F., Nagai, J. S., Halder, M., Schumacher, D., Menzel, S., Schäfer, G., Hoeft, K., Cheng, M., Ziegler, S., Zhang, X., Peisker, F., … Kramann, R. (2022). Spatial multi-omic map of human myocardial infarction. *Nature*, 1–12. `https://doi.org/10.1038/s41586-022-05060-x`
2. Biermann, J., Melms, J. C., Amin, A. D., Wang, Y., Caprio, L. A., Karz, A., Tagore, S., Barrera, I., Ibarra-Arellano, M. A., Andreatta, M., Fullerton, B. T., Gretarsson, K. H., Sahu, V., Mangipudy, V. S., Nguyen, T. T. T., Nair, A., Rogava, M., Ho, P., Koch, P. D., … Izar, B. (2022). Dissecting the treatment-naive ecosystem of human melanoma brain metastasis. *Cell*, *185*(14), 2591–2608.e30.
3. Heckel, E., Cagnone, G., Agnihotri, T., Cakir, B., Das, A., Kim, J. S., Kim, N., Lavoie, G., Situ, A., Pundir, S., et al. (2022). Triglyceride-derived fatty acids reduce autophagy in a model of retinal angiomatous proliferation. *JCI Insight*, *7*(6).
4. Audain, E., Wilsdon, A., Breckpot, J., Izarzugaza, J. M., Fitzgerald, T. W., Kahlert, A.-K., Sifrim, A., Wünnemann, F., Perez-Riverol, Y., Abdul-Khaliq, H., et al. (2021). Integrative analysis of genomic variants reveals new associations of candidate haploinsufficient genes with congenital heart disease. *PLoS Genetics*, *17*(7), e1009679.
5. Wünnemann, F., Ta-Shma, A., Preuss, C., Leclerc, S., Vliet, P. P. van, Oneglia, A., Thibeault, M., Nordquist, E., Lincoln, J., Scharfenberg, F., et al. (2020). Loss of ADAMTS19 causes progressive non-syndromic heart valve disease. *Nature Genetics*, *52*(1), 40–47.
6. 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., et al. (2019). ROBO4 variants predispose individuals to bicuspid aortic valve and thoracic aortic aneurysm. *Nature Genetics*, *51*(1), 42–50.
7. Luyckx, I., Kumar, A. A., Reyniers, E., Dekeyser, E., Vanderstraeten, K., Vandeweyer, G., Wünnemann, F., Preuss, C., Mazzella, J.-M., Goudot, G., et al. (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.
8. 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.
9. Preuss, C., Wünnemann, F., & Andelfinger, G. (2017). At the heart of a complex disease “molecular genetics of congenital heart disease.” *eLS*, 1–9.
10. Gillis, E., Kumar, A. A., Luyckx, I., Preuss, C., Cannaerts, E., Van De Beek, G., Wieschendorf, B., Alaerts, M., Bolar, N., Vandeweyer, G., et al. (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.
11. Wünnemann, F., Kokta, V., Leclerc, S., Thibeault, M., McCuaig, C., Hatami, A., Stheneur, C., Grenier, J.-C., Awadalla, P., Mitchell, G. A., et al. (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.
12. Preuss, C., Capredon, M., Wünnemann, F., Chetaille, P., Prince, A., Godard, B., Leclerc, S., Sobreira, N., Ling, H., Awadalla, P., et al. (2016). Family based whole exome sequencing reveals the multifaceted role of notch signaling in congenital heart disease. *PLoS Genetics*, *12*(10), e1006335.
13. 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.

14. Chetaille, P., Preuss, C., Burkhard, S., Côté, J.-M., Houde, C., Castilloux, J., Piché, J., Gosset, N., Leclerc, S., Wünnemann, F., et al. (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, Image analysis (Fiji, Napari, QuPath)
- **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 workflow creation and execution
- **Galaxy project**: Creation of galaxy tools and wrappers, setup of `https://spatialomics.usegalaxy.eu/`

Languages

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