Florian **Wünnemann**

Postdoctoc at the Lettre lab

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***Research and scientific interests**: Human genetics, Single cell OMICS, Heart development, Bioinformatics, Open source software*

Research experience

Montreal Heart Institute — *Montreal, Canada*

Postdoc in the Lettre lab — *Aug.2018 - ongoing*

- 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 — *Sherbrooke, Canada*

Professionnel recherche niv. II — *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 — *Münster, Germany*

Student Research assistant — *Sep.2011 - Jul.2012*

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

IEB, University of Münster — *Münster, Germany*

Student assistant — *Mar.2011 - May 2011*

- Bornberg-Bauer group

Education

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

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

- 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*

- Functional and genetic characterization of a novel arrhythmic syndrome

University of Münster — *Münster, Germany*

BSc in Life sciences — *Oct.2008 - Sep.2011*

- 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

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*

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*

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 — *University of 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

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*

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

Soil metagenomics to unravel the signature of fertilizers on the molecular composition of the bacterial ribosome — *10.09.2012 - 14.09.2012*

Publications

1. 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*.
2. 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.
3. Audain, E., Wilsdon, A., Breckpot, J., Izarzugaza, J. M., Fitzgerald, T. W., Kahlert, A., Sifrim, A., Wuennemann, 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*.
4. 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*.
5. 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.
6. 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.

7. 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.

8. Gould, R., Aziz, H., Woods, C., Seman-Senderos, M., Sparks, E., Preuss, C., Wünnemann, F., Bedja, D., Moats, C., McClymont, S., & others. (2019). Baylor-hopkins center for mendelian genomics; MIBAVA leducq consortium. ROBO4 variants predispose individuals to bicuspid aortic valve and thoracic aortic aneurysm. *Nat Genet*, *51*(01), 42–50.

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., & 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.

11. Gillis, E., Kumar, A. A., Luyckx, I., Preuss, C., Cannaerts, E., Beek, G. van de, Wieschendorf, B., Alaerts, M., Bolar, N., Vandeweyer, G., & others. (2017). Corrigendum: Candidate gene resequencing in a large bicuspid aortic valve-associated thoracic aortic aneurysm cohort: SMAD6 as an important contributor. *Frontiers in Physiology*, *8*, 730.

12. 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.

13. 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.

14. 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.

15. 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

- **Ubuntu**: Bash scripting
- **R**: Rshiny application development, Rmarkdown, Package development, OMICS data analysis (RNA-seq, single-cell OMICS)
- **Python**: Basic usage, jupyter notebooks, basic computer vision applications
- **Containers**: Docker container creation, Singularity usage
- **Galaxy project**: Creation of galaxy tools and wrappers

Languages

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