China Scholarship Councel – University Maastricht PhD Programme

Application form

Basic information
---

1. Information on prospective UM supervisors and Promotor

1a. First Supervisor and Promoter"

- Name: ***Prof Dr Erik A.L. Biessen***
- Research group: *Experimental Vascular Pathology*
- Address for correspondence: *Department of Pathology, MUMC, P. Debyelaan 25, 6229 HX Maastricht, The Netherlands*
- Telephone: *0031-43-3874635*
- E-mail: *erik.biessen@mumc.nl*

1b. Second Supervisor:

- Name: ***Prof Dr Guanghou Shui***
- Research group: *Lipidomics and metabolomics*
- Address for correspondence: *Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing 100101, PRC*
- Telephone: *86-010-64807781*
- E-mail: *ghshui@genetics.ac.cn*

2. Information on University Maastricht Faculty / Department/ Institute/ School contact person:

Email contact person: Carim-office@maastrichtuniversity.nl
Research group: CARIM

3. Details of applicant's home university

- Name of home university:
- Address:
- Telephone:
- E-mail:
- Website (if available):

4. Research field(s)

AI, data mining, bioinformatics, gene regulatory and genome scale metabolic network analysis; machine learning, multiomics (metabolites, genes)

人类健康与疾病的生物学基础 / Biological Foundations of Human Health and Diseases 重大新药创制 / Major New Drugs Discovery 前沿技术 / Frontier Technologies • 信息技术 / Information Technology • 基础研究 / Basic Research • 人类健康与疾病的生物学基础 / Biological Foundations of Human Health and Diseases • 支撑信息技术发展的科学基础 / Scientific Basis for Development of Information Technology

5. Title of research plan for CSC-UM PhD Programme

Computational strategies to dissect and locate metabolic and genetic pathways in cardiovascular diseases

6. Short summary of research plan (max. 250 words) (A full plan has to be submitted later)

Background: Aberrant macrophage function has been shown to underlie a range of chronic diseases. Macrophages are therefore broadly viewed as intervention target. Drug design is however frustrated by their notorious plasticity and by failure of animal models to represent macrophage function in human disease. Therefore, a need exists for robust and comprehensive computational models of human macrophage in disease, as first step in drug screening.

Aim and objectives: the PhD will, based on own and open-access mRNA and metabolic datasets of a variety of human macrophages

1. **Build** genome scale metabolic and transcriptional networks of human macrophages in vitro and in vivo (healthy organ Mf populations)
2. **Link** *in vitro* Mf phenotypes to *in vivo* populations based on similarity of expression signature
3. **Design** "shortest path" algorithms for identifying drugs or genes with a high likelihood of interfering with specific transcriptional and metabolic networks in macrophages.

Models and their outcome will subsequently be validated by biomedical scientists in the team; conversely, the PhD will provide bioinformatics support in the integrative analysis of omics datasets by the Biessen team, augmenting the PhD's output. Thus, both project and working environment are highly interdisciplinary. Career guidance, training opportunities, and dissemination support, provided by the supervision team will further complement the PhD's training.

Requirements: MSc degree in Computation biology or similar, and prior experience with bioinformatic languages (R and/or python) is crucial. Team spirit, perseverance, a curious nature, and adequate English communication skills are important assets.

Group's performance (Biessen):

Publications:	250
H-Index:	71
Number of citations:	17,000

Five key publications of Biessen group relevant to the topic (> 2017)

1. van der Vorst, E. P. C.*, … Biessen, E. A. L. & Donners, M.* High-Density Lipoproteins Exert Pro-inflammatory Effects on Macrophages via Passive Cholesterol Depletion and PKC- NF-kappaB/STAT1-IRF1 Signaling. **Cell Metabolism** 2016; 25: 197-207 (**IF=27,3**) (* PhD/staff member from Biessen's group)
2. Jin H, … Biessen EAL. Integrative multiomics analysis of human atherosclerosis reveals a serum response factor-driven network associated with intraplaque hemorrhage. **Clin Transl Med.** 2021 Jun;11(6):e458. **(IF=8,6)**
3. van der Vorst EPC, Theodorou K, Biessen EAL, Donners MMPC. Disease- or Storage-Associated Structural Modifications Are Unlikely to Explain HDL Pro-inflammatory Effects on Macrophages. **Cell Metab**. 2017 Jul 5;26(1):4-5**. (IF=27,3)**
4. Jin H[#], Mees BME, Biessen EAL*, Sluimer JC*. Transcriptional Sex Dimorphism in Human Atherosclerosis Relates to Plaque Type. **Circ Res.** 2021 Dec 3;129(12):1175-1177**. IF=17.6) (* shared seniors; # PhD Biessen group)**
5. Goossens P, Lu C, … Biessen EAL. Integrating multiplex immunofluorescent and mass spectrometry imaging to map myeloid heterogeneity in its metabolic and cellular context. **Cell Metab**. 2022 Aug 2;34(8):1214-1225.e6. **(IF-27,3**)

Group's performance (Guanghou Shui):

Publications:	200
H-Index:	68
Number of citations:	17,000

Five key publications of Guanghou group (> 2017)

1. Lu J#, Lam SM#, Wan Q, Shi L, Huo Y, Chen L, Tang X, Li B, Wu X, Peng K, Li M, Wang S, Xu Y, Xu M, Bi Y, Ning G, Shui G*, Wang W*. High-Coverage Targeted Lipidomics Reveals Novel Serum Lipid Predictors and Lipid Pathway Dysregulation Antecedent to Type 2 Diabetes Onset in Normoglycemic Chinese Adults. **Diabetes Care,** 2019**,** 42:2117-2126.
2. Song JW#, Lam SM#, Fan X#, Cao WJ, Wang SY, Tian H, CHUA GH, Zhang C, Meng FP, Xu Z, Fu JL, Huang L, Xia P, Yang T, Zhang SH, Li BW, Jiang TJ, Wang RX, Wang ZH, Shi M, Zhang JY*, Wang FS*, Shui G*. Omics-driven systems interrogation of metabolic dysregulation in COVID-19 pathogenesis. **Cell Metabolism**, 2020, 32: 188-202**. (IF=27.3)**
3. Lam SM, Zhang Chao, Wang Z, Ni Z , Zhang S, Yang S, Huang X, Mo L, Li J, Lee B, Mei M, Huang L, Shi M, Xu Z, Meng FP, Cao WJ, Zhou MJ, Shi L, Chua GH, Li B, Cao J, Wang J, Bao S, Wang Y, Song JW*, Zhang F, Wang FS, Shui G*. A multi-omics investigation on the composition and function of extracellular vesicles along the temporal trajectory of COVID-19. **Nature Metabolism**: 2021, 7:909-922.
4. Lam SM#, Zhou TX#, Li J#, Zhang SH, Chua GH, Li BW, Shui G*. A robust, integrated platform for comprehensive analyses of acyl-coenzyme As and acyl-carnitines revealed chain length-dependent disparity in fatty acyl metabolic fates across Drosophila development. **Science Bulletin**, 65(2020), 1840-1848**. (IF=11.0)**
5. Tian H, Ni Z, Lam SM, Jiang W, Li F, Du J, Wang Y, Shui G*. Precise Metabolomics Reveals a Diversity of Aging-Associated Metabolic Features. **Small Methods,** 2022, 6(7):e2200130**. (IF=14.1)**