Stanford



# Thomas Quertermous, MD

William G. Irwin Professor of Cardiovascular Medicine

Medicine - Cardiovascular Medicine

### CONTACT INFORMATION


- **Alternate Contact**

  MARIAH J. ROBERTS - Administrative Asst.

  **Email** mariahr@stanford.edu

  **Tel** (650) 497-6234


## Bio

### ACADEMIC APPOINTMENTS

- Professor, Medicine - Cardiovascular Medicine
- Member, Bio-X
- Member, Cardiovascular Institute
- Member, Maternal & Child Health Research Institute (MCHRI)

### LINKS

- Quertermous Lab homepage: http://quertermous.stanford.edu

## Research & Scholarship

### CURRENT RESEARCH AND SCHOLARLY INTERESTS

The Quertermous laboratory employs two basic approaches of study to better understand the genetic basis of atherosclerotic heart disease. One approach uses basic molecular biology methodology, primarily working with cellular and genetic mouse models, and is focused on the recently identified apelin-APJ pathway. A second approach employs the power of modern human genetics. Informative cohorts have been collected that allow investigation of risk factors such as hypertension and insulin resistance as well as coronary heart disease. Initial studies have employed the candidate gene approach, and more recently whole genome association studies, to identify allelic variation that is associated with risk factor and disease susceptibility.

## Teaching

### STANFORD ADVISEES

**Doctoral Dissertation Reader (AC)**

Tony Zeng

**Postdoctoral Faculty Sponsor**

Matteo Cartura, Yunyun Wang, Matthew Worssam

# Publications

## PUBLICATIONS

- **Single-Cell Studies Advance Understanding of the Genetic and Molecular Basis of Atherosclerosis.** *Circulation research*
  Li, D. Y., Monteiro, J. P., Zhao, Q., Stitziel, N. O., Quertermous, T.
  2026

- **Vascular smooth muscle cell state trajectories mediate molecular mechanisms of coronary disease risk.** *Nature communications*
  Li, D. Y., Kundu, S., Cheng, P., Gu, W., Worssam, M. D., Jackson, W. R., Zhao, Q., Nguyen, T., Yu, A. M., Monteiro, J. P., Caceres, R. D., Dale, S., Palmisano, et al
  2026

- **Vascular smooth muscle cell atherosclerosis trajectories characterized at single cell resolution identify causal transcriptomic and epigenomic mechanisms of disease risk**
  Li, D., Kundu, S., Cheng, P., Gu, W., Jackson, W., Zhao, Q., Nguyen, T., Worssam, M., Monteiro, J., Palmisano, B., Weldy, C., Kundu, R., Kundaje, et al
  LIPPINCOTT WILLIAMS & WILKINS.2025

- **Decoding human cardiovascular development and disease through single-cell transcriptomic and epigenomic profiling.** *Trends in cell biology*
  Dunkenberger, L., Li, D. Y., Karakikes, I., Quertermous, T.
  2025

- **Spatial transcriptomic mapping of coronary atherosclerosis in the luminal plaque and beyond.** *Nature cardiovascular research*
  Cheng, P., Quertermous, T.
  2025

- **Single cell variant to enhancer to gene map for coronary artery disease.** *medRxiv : the preprint server for health sciences*
  Amrute, J. M., Lee, P. C., Eres, I., Lee, C. J., Bredemeyer, A., Sheth, M. U., Yamawaki, T., Gurung, R., Anene-Nzelu, C., Qiu, W. L., Kundu, S., Li, D. Y., Ramste, et al
  2024

- **Deciphering the impact of genomic variation on function.** *Nature*
  2024; 633 (8028): 47-57

- **Genome-Wide Genetic Associations Prioritize Evaluation of Causal Mechanisms of Atherosclerotic Disease Risk.** *Arteriosclerosis, thrombosis, and vascular biology*
  Quertermous, T., Li, D. Y., Weldy, C. S., Ramste, M., Sharma, D., Monteiro, J. P., Gu, W., Worssam, M. D., Palmisano, B. T., Park, C. Y., Cheng, P.
  2024; 44 (2): 323-327

- **Comprehensive Integration of Multiple Single-Cell Transcriptomic Datasets Defines Distinct Cell Populations and Their Phenotypic Changes in Murine Atherosclerosis.** *Arteriosclerosis, thrombosis, and vascular biology*
  Sharma, D., DeForest Worssam, M., Pedroza, A. J., Dalal, A. R., Alemany, H., Kim, H. J., Kundu, R., Fischbein, M., Cheng, P., Wirka, R., Quertermous, T.
  2023

- **Discovery of Transacting Long Noncoding RNAs That Regulate Smooth Muscle Cell Phenotype.** *Circulation research*
  Shi, H., Nguyen, T., Zhao, Q., Cheng, P., Sharma, D., Kim, H. J., Brian Kim, J., Wirka, R., Weldy, C. S., Monteiro, J. P., Quertermous, T.
  2023

- **Molecular mechanisms of coronary artery disease risk at the PDGFD locus.** *Nature communications*
  Kim, H., Cheng, P., Travisano, S., Weldy, C., Monteiro, J. P., Kundu, R., Nguyen, T., Sharma, D., Shi, H., Lin, Y., Liu, B., Haldar, S., Jackson, et al
  2023; 14 (1): 847

- **Integrative single-cell analysis of cardiogenesis identifies developmental trajectories and non-coding mutations in congenital heart disease.** *Cell*
  Ameen, M., Sundaram, L., Shen, M., Banerjee, A., Kundu, S., Nair, S., Shcherbina, A., Gu, M., Wilson, K. D., Varadarajan, A., Vadgama, N., Balsubramani, A., Wu, et al
  2022; 185 (26): 4937

- **Smad3 regulates smooth muscle cell fate and mediates adverse remodeling and calcification of the atherosclerotic plaque.** *Nature cardiovascular research*
  Cheng, P., Wirka, R. C., Kim, J. B., Kim, H. J., Nguyen, T., Kundu, R., Zhao, Q., Sharma, D., Pedroza, A., Nagao, M., Iyer, D., Fischbein, M. P., Quertermous, et al
  2022; 1 (4): 322-333

- **ZEB2 Shapes the Epigenetic Landscape of Atherosclerosis** *Circulation*
  Cheng, P., Wirka, R. C., Clarke, L., Zhao, Q., Kundu, R., Nguyen, T., Nair, S., Sharma, D., Kim, H., Shi, H., Assimes, T., Kim, J., Kundaje, et al
  2022; 145 (6): 469–485

- **ZEB2 Shapes the Epigenetic Landscape of Atherosclerosis.** *Circulation*
  Cheng, P., Wirka, R. C., Clarke, L. S., Zhao, Q., Kundu, R., Nguyen, T., Nair, S., Sharma, D., Kim, H. J., Shi, H., Assimes, T., Kim, J. B., Kundaje, et al
  2022

- **Molecular mechanisms of coronary disease revealed using quantitative trait loci for TCF21 binding, chromatin accessibility, and chromosomal looping.** *Genome biology*
  Zhao, Q. n., Dacre, M. n., Nguyen, T. n., Pjanic, M. n., Liu, B. n., Iyer, D. n., Cheng, P. n., Wirka, R. n., Kim, J. B., Fraser, H. B., Quertermous, T. n.
  2020; 21 (1): 135

- **The Environment-Sensing Aryl-Hydrocarbon Receptor Inhibits the Chondrogenic Fate of Modulated Smooth Muscle Cells in Atherosclerotic Lesions.** *Circulation*
  Kim, J. B., Zhao, Q. n., Nguyen, T. n., Pjanic, M. n., Cheng, P. n., Wirka, R. n., Travisano, S. n., Nagao, M. n., Kundu, R. n., Quertermous, T. n.
  2020

- **Coronary Disease Associated Gene TCF21 Inhibits Smooth Muscle Cell Differentiation by Blocking the Myocardin-Serum Response Factor Pathway.** *Circulation research*
  Nagao, M., Lyu, Q., Zhao, Q., Wirka, R. C., Bagga, J., Nguyen, T., Cheng, P., Kim, J. B., Pjanic, M., Miano, J. M., Quertermous, T.
  2019

- **Atheroprotective roles of smooth muscle cell phenotypic modulation and the TCF21 disease gene as revealed by single-cell analysis.** *Nature medicine*
  Wirka, R. C., Wagh, D., Paik, D. T., Pjanic, M., Nguyen, T., Miller, C. L., Kundu, R., Nagao, M., Coller, J., Koyano, T. K., Fong, R., Woo, Y. J., Liu, et al
  2019

- **TCF21 and AP-1 interact through epigenetic modifications to regulate coronary artery disease gene expression** *GENOME MEDICINE*
  Zhao, Q., Wirka, R., Trieu Nguyen, Nagao, M., Cheng, P., Miller, C. L., Kim, J., Pjanic, M., Quertermous, T.
  2019; 11

- **Genetic Regulatory Mechanisms of Smooth Muscle Cells Map to Coronary Artery Disease Risk Loci.** *American journal of human genetics*
  Liu, B. n., Pjanic, M. n., Wang, T. n., Nguyen, T. n., Gloudemans, M. n., Rao, A. n., Castano, V. G., Nurnberg, S. n., Rader, D. J., Elwyn, S. n., Ingelsson, E. n., Montgomery, S. B., Miller, et al
  2018

- **Circulating peptide prevents preeclampsia** *SCIENCE*
  Wirka, R. C., Quertermous, T.
  2017; 357 (6352): 643–44

- **Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements.** *Nature genetics*
  Mumbach, M. R., Satpathy, A. T., Boyle, E. A., Dai, C. n., Gowen, B. G., Cho, S. W., Nguyen, M. L., Rubin, A. J., Granja, J. M., Kazane, K. R., Wei, Y. n., Nguyen, T. n., Greenside, et al
  2017

- **Integrative functional genomics identifies regulatory mechanisms at coronary artery disease loci.** *Nature communications*
  Miller, C. L., Pjanic, M., Wang, T., Nguyen, T., Cohain, A., Lee, J. D., Perisic, L., Hedin, U., Kundu, R. K., Majmudar, D., Kim, J. B., Wang, O., Betsholtz, et al
  2016; 7: 12092-?

- **Coronary Artery Disease and Its Risk Factors: Leveraging Shared Genetics to Discover Novel Biology.** *Circulation research*
  Quertermous, T. n., Ingelsson, E. n.
  2016; 118 (1): 14–16

- **Coronary Artery Disease Associated Transcription Factor TCF21 Regulates Smooth Muscle Precursor Cells that Contribute to the Fibrous Cap.** *Genomics data*
  Nurnberg, S. T., Cheng, K., Raiesdana, A., Kundu, R., MILLER, C. L., Kim, J. B., Arora, K., Carcamo-Oribe, I., Xiong, Y., Tellakula, N., Nanda, V., Murthy, N., Boisvert, et al
  2015; 5: 36-37

- **Characterization of TCF21 Downstream Target Regions Identifies a Transcriptional Network Linking Multiple Independent Coronary Artery Disease Loci** *PLOS GENETICS*
  Sazonova, O., Zhao, Y., Nuernberg, S., Miller, C., Pjanic, M., Castano, V. G., Kim, J. B., Salfati, E. L., Kundaje, A. B., Bejerano, G., Assimes, T., Yang, X., Quertermous, et al
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- **Coronary Artery Disease Associated Transcription Factor TCF21 Regulates Smooth Muscle Precursor Cells That Contribute to the Fibrous Cap** *PLOS GENETICS*
  Nurnberg, S. T., Cheng, K., Raiesdana, A., Kundu, R., Miller, C. L., Kim, J. B., Arora, K., Carcamo-Oribe, I., Xiong, Y., Tellakula, N., Nanda, V., Murthy, N., Boisvert, et al
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- **Coronary Artery Disease Associated Transcription Factor TCF21 Regulates Smooth Muscle Precursor Cells That Contribute to the Fibrous Cap.** *PLoS genetics*
  Nurnberg, S. T., Cheng, K., Raiesdana, A., Kundu, R., Miller, C. L., Kim, J. B., Arora, K., Carcamo-Oribe, I., Xiong, Y., Tellakula, N., Nanda, V., Murthy, N., Boisvert, et al
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- **A long noncoding RNA protects the heart from pathological hypertrophy.** *Nature*
  Han, P., Li, W., Lin, C., Yang, J., Shang, C., Nurnberg, S. T., Jin, K. K., Xu, W., Lin, C., Lin, C., Xiong, Y., Chien, H., Zhou, et al
  2014; 514 (7520): 102-106

- **Clinical interpretation and implications of whole-genome sequencing.** *JAMA*
  Dewey, F. E., Grove, M. E., Pan, C., Goldstein, B. A., Bernstein, J. A., Chaib, H., Merker, J. D., Goldfeder, R. L., Enns, G. M., David, S. P., Pakdaman, N., Ormond, K. E., Caleshu, et al
  2014; 311 (10): 1035-1045

- **Apelin signaling antagonizes Ang II effects in mouse models of atherosclerosis** *JOURNAL OF CLINICAL INVESTIGATION*
  Chun, H. J., Ali, Z. A., Kojima, Y., Kundu, R. K., Sheikh, A. Y., Agrawal, R., Zheng, L., Leeper, N. J., Pearl, N. E., Patterson, A. J., Anderson, J. P., Tsao, P. S., Lenardo, et al
  2008; 118 (10): 3343-3354

- **Transient Activation of the Interferon-Stimulated Gene Program Drives Persistent Smooth Muscle Cell Reprogramming and Alters Cell Fate in Atherosclerosis**
  Rad, L., Monteiro, J. P., Worssam, M., Li, D., Gu, W., Nguyen, T., Kundu, R. K., Kim, J. B., Cheng, P., Quertermous, T., Weldy, C.
  LIPPINCOTT WILLIAMS & WILKINS.2026: A10656

- **An Atlas-Scale, Gene-Program Guided Framework for Functional Translation of Coronary Artery Disease Mechanisms**
  Karius, A., Worssam, M., Monteiro, J. P., Yu, A., Boluk, A., Cheng, P., Amrute, J., Kaikkonen, M. U., Quertermous, T., Li, D.
  LIPPINCOTT WILLIAMS & WILKINS.2026: A11459

- **TRANSCRIPTOMIC, SPECIFIC MARKER, AND PATHWAY ANALYSIS OF SMOOTH MUSCLE CELL FOAM CELLS IN HUMAN ATHEROSCLEROSIS**
  Allahverdian, S., Mao, Y., Xiang, P., Hart, P., Cheng, P., Miller, C., Boluk, A., Ord, T., Kaikkonen-Maatta, M., Quertermous, T., Chan, T., Francis, G.
  ELSEVIER IRELAND LTD.2026

- **Transcriptomic, Specific Marker, and Pathway Analysis of Smooth Muscle Cell Foam Cells Compared to Macrophage Foam Cells in Human Atherosclerosis.** *bioRxiv : the preprint server for biology*
  Allahverdian, S., Mao, Y., Xiang, P., Blanchard, V., Bölük, A., Hart, P. A., Cheng, P., Li, D. Y., Worssam, M. D., Arasu, U. T., Taipale, M., Kiema, M., Laakkonen, et al
  2026

- **FOXC1 Controls Smooth Muscle Cell Differentiation and Plasticity in Vascular Disease.** *JACC. Basic to translational science*
  Rykaczewska, U., Suur, B. E., Narayanan, S., Sundman, S., Auguste, G., Zhao, Q., Zhang, X., Prasad, I., Hedman, Å., Lengquist, M., Kronqvist, M., Swärd, K., Razuvaev, et al

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- **A Perturb-seq screen guided by species divergence uncovers pathways for collateral artery formation.** *bioRxiv : the preprint server for biology*
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  2026
- **Adenosine-to-Inosine (A-to-I) RNA Editing by ADAR1 to Control RNA Sensing in Cardiovascular Disease.** *Arteriosclerosis, thrombosis, and vascular biology*
  Weldy, C. S., Li, J. B., Quertermous, T.
  2026
- **Targeting modulated vascular smooth muscle cells in atherosclerosis via FAP-directed immunotherapy.** *Science (New York, N.Y.)*
  Amrute, J. M., Jung, I. H., Yamawaki, T., Lin, W. L., Bredemeyer, A., Diekmann, J., Hayat, S., Zhang, X., Wakefield, D. L., Luo, X., Maryam, S., Heo, G. S., Yang, et al
  2026: eadx1736
- **Functional Genomics Link REST to Endothelial Plasticity and Atherosclerosis.** *Circulation research*
  Viskadourou, M., Chaudhry, S., Scalco, A., Reventun, P., Toledano-Sanz, P., An, R., Alcharani, N., Delgado Marin, M., Fennell, A., Zhao, Q., Osburn, W., McCallion, A. S., Quertermous, et al
  2025
- **ZEB1 Regulates Coronary Disease Risk Through Epigenetic Control of Smooth Muscle Cell Identity**
  Li, D., Jackson, W., Gu, W., Yu, A., Zhu, S., Zhao, Q., Nguyen, T., Cheng, P., Quertermous, T.
  LIPPINCOTT WILLIAMS & WILKINS.2025
- **The epigenomic landscape of single vascular cells reflects developmental origin and identifies disease risk loci**
  Weldy, C., Kundu, S., Monteiro, J., Gu, W., Pedroza, A., Dalal, A., Worssam, M., Li, D., Palmisano, B., Zhao, Q., Sharma, D., Nguyen, T., Kundu, et al
  LIPPINCOTT WILLIAMS & WILKINS.2025
- **GREGoR: accelerating genomics for rare diseases.** *Nature*
  Dawood, M., Heavner, B., Wheeler, M. M., Ungar, R. A., LoTempio, J., Wiel, L., Berger, S., Bernstein, J. A., Chong, J. X., Délot, E. C., Eichler, E. E., Lupski, J. R., Shojaie, et al
  2025; 647 (8089): 331-342
- **A cell and transcriptome atlas of human arterial vasculature.** *Cell genomics*
  Zhao, Q., Pedroza, A., Sharma, D., Gu, W., Dalal, A., Weldy, C., Jackson, W., Li, D. Y., Ryan, Y., Nguyen, T., Shad, R., Palmisano, B. T., Monteiro, et al
  2025: 101034
- **Smooth muscle expression of RNA editing enzyme ADAR1 controls activation of the RNA sensor MDA5 in atherosclerosis.** *Nature cardiovascular research*
  Weldy, C. S., Li, Q., Monteiro, J. P., Peters, T. S., Guo, H., Galls, D., Gu, W., Cheng, P. P., Ramste, M., Li, D., Palmisano, B. T., Sharma, D., Worssam, et al
  2025
- **Epigenomic landscape of single vascular cells reflects developmental origin and disease risk loci.** *Molecular systems biology*
  Weldy, C. S., Kundu, S., Monteiro, J., Gu, W., Pedroza, A. J., Dalal, A. R., Worssam, M. D., Li, D., Palmisano, B., Zhao, Q., Sharma, D., Nguyen, T., Kundu, et al
  2025
- **Enhancer-targeting CRISPR screens at coronary artery disease loci suggest shared mechanisms of disease risk.** *medRxiv : the preprint server for health sciences*
  Ramste, M., Weldy, C., Kundu, S., Zhao, Q., Li, D., Brand, K., Sharma, D., Ramste, A., Jagoda, E., Ray, J., Caceres, R. D., Galante, J., Gschwind, et al
  2025
- **The epigenomic landscape of single vascular cells reflects developmental origin and identifies disease risk loci.** *bioRxiv : the preprint server for biology*

Weldy, C. S., Kundu, S., Monteiro, J., Gu, W., Pedroza, A. J., Dalal, A. R., Worssam, M. D., Li, D., Palmisano, B., Zhao, Q., Sharma, D., Nguyen, T., Kundu, et al

2025

- **Loss of conserved long non-coding RNA MIR503HG leads to altered NOTCH pathway signalling and left ventricular non-compaction cardiomyopathy.** *Cardiovascular research*

  Monteiro, J. P., Saha, D., Spiroski, A. M., Mahesh, S., Kaltzis, P., Nadavallil, A., Janbandhu, V., Murray, N. J., Severi, F., De Pace, A. L., Sánchez-Esteban, S., Rodor, J., Beqqali, et al

  2025

- **Chemokine (C-C Motif) Ligand 2 Expressing Adventitial Fibroblast Expansion During Loeys-Dietz Syndrome Aortic Aneurysm Formation.** *Arteriosclerosis, thrombosis, and vascular biology*

  Dalal, A. R., Pedroza, A. J., Kim, J., Gilles, C., Gu, W., Kusadokoro, S., Shad, R., Mitchel, O., Jackson, W., Hiesinger, W., Berry, G., Gallo MacFarlane, E., Quertermous, et al

  2025

- **Single-Cell Transcriptomics Identifies Selective Lineage-Specific Regulation of Genes in Aortic Smooth Muscle Cells in Mice.** *Arteriosclerosis, thrombosis, and vascular biology*

  Shukla, S., Jana, S., Sanford, N., Lee, C. Y., Liu, L., Cheng, P., Quertermous, T., Dichek, D. A.

  2025

- **Molecular convergence of risk variants for congenital heart defects leveraging a regulatory map of the human fetal heart.** *medRxiv : the preprint server for health sciences*

  Ma, X. R., Conley, S. D., Kosicki, M., Bredikhin, D., Cui, R., Tran, S., Sheth, M. U., Qiu, W. L., Chen, S., Kundu, S., Kang, H. Y., Amgalan, D., Munger, et al

  2024

- **Atheroma transcriptomics identifies ARNTL as a smooth muscle cell regulator and with clinical and genetic data improves risk stratification.** *European heart journal*

  Narayanan, S., Vuckovic, S., Bergman, O., Wirka, R., Verdezoto Mosquera, J., Chen, Q. S., Baldassarre, D., Tremoli, E., Veglia, F., Lengquist, M., Aherahrrou, R., Razuvaev, A., Gigante, et al

  2024

- **A functional genomic framework to elucidate novel causal metabolic dysfunction-associated fatty liver disease genes.** *Hepatology (Baltimore, Md.)*

  Saliba-Gustafsson, P., Justesen, J. M., Ranta, A., Sharma, D., Bielczyk-Maczynska, E., Li, J., Najmi, L. A., Apodaka, M., Aspichueta, P., Björck, H. M., Eriksson, P., Schurr, T. M., Franco-Cereceda, et al

  2024

- **Genetic and functional analysis of Raynaud's syndrome implicates loci in vasculature and immunity.** *Cell genomics*

  Tervi, A., Ramste, M., Abner, E., Cheng, P., Lane, J. M., Maher, M., Valliere, J., Lammi, V., Strausz, S., Riikonen, J., Nguyen, T., Martyn, G. E., Sheth, et al

  2024: 100630

- **A functional genomic framework to elucidate novel causal non-alcoholic fatty liver disease genes.** *medRxiv : the preprint server for health sciences*

  Saliba-Gustafsson, P., Justesen, J. M., Ranta, A., Sharma, D., Bielczyk-Maczynska, E., Li, J., Najmi, L. A., Apodaka, M., Aspichueta, P., Björck, H. M., Eriksson, P., Franco-Cereceda, A., Gloudemans, et al

  2024

- **Alpha-2A adrenergic receptor (ADRA2A) modulates susceptibility to Raynaud's disease**

  Tervi, A., Rasanen, M., Lammi, V., Abner, E., Esko, T., Lane, J., Maher, M., Heckman, C. A., Quertermous, T., Jones, S., Ollila, H., FinnGen Consortium

  SPRINGERNATURE.2024: 786

- **Single-nuclei multiomic analyses identify human cardiac lymphatic endothelial cells associated with coronary arteries in the epicardium.** *Cell reports*

  Travisano, S. I., Harrison, M. R., Thornton, M. E., Grubbs, B. H., Quertermous, T., Lien, C. L.

  2023; 42 (9): 113106

- **INTEGRATION OF GENETIC AND CLINICAL DATA, WITH SINGLE-CELL TRANSCRIPTOMICS OF ATHEROSCLEROTIC PLAQUES IDENTIFIES NOVEL SMOOTH MUSCLE CELL GENES**

Narayanan, S., Vuckovic, S., Bergman, O., Wirka, R., Lengquist, M., Quertermous, T., Hedin, U., Matic, L.
ELSEVIER IRELAND LTD.2023

- **FOXC1 CONTROLS SMOOTH MUSCLE CELL ACTIVATION IN VASCULAR DISEASE**
  Matic, L., Rykaczewska, U., Suur, B., Gaelle, A., Quanyi, Z., Xiang, Z., Narayanan, S., Hedman, A., Lengquist, M., Kronqvist, M., Vuckovic, S., Sward, K., Razuvaev, et al
  ELSEVIER IRELAND LTD.2023

- **Early clinical outcomes and molecular smooth muscle cell phenotyping using a prophylactic aortic arch replacement strategy in Loeys-Dietz syndrome.** *The Journal of thoracic and cardiovascular surgery*
  Pedroza, A. J., Cheng, P., Dalal, A. R., Baeumler, K., Kino, A., Tognozzi, E., Shad, R., Yokoyama, N., Nakamura, K., Mitchel, O., Hiesinger, W., MacFarlane, E. G., Fleischmann, et al
  2023

- **A single-cell CRISPRi platform for characterizing candidate genes relevant to metabolic disorders in human adipocytes.** *American journal of physiology. Cell physiology*
  Bielczyk-Maczynska, E., Sharma, D., Blencowe, M., Saliba Gustafsson, P., Gloudemans, M. J., Yang, X., Carcamo-Orive, I., Wabitsch, M., Svensson, K. J., Park, C. Y., Quertermous, T., Knowles, J. W., Li, et al
  2023

- **Single-cell transcriptome dataset of human and mouse in vitro adipogenesis models.** *Scientific data*
  Li, J., Jin, C., Gustafsson, S., Rao, A., Wabitsch, M., Park, C. Y., Quertermous, T., Knowles, J. W., Bielczyk-Maczynska, E.
  2023; 10 (1): 387

- **Single-cell transcriptome dataset of human and mouse in vitro adipogenesis models.** *bioRxiv : the preprint server for biology*
  Li, J., Jin, C., Gustafsson, S., Rao, A., Wabitsch, M., Park, C. Y., Quertermous, T., Bielczyk-Maczynska, E., Knowles, J. W.
  2023

- **Single-Cell Transcriptomic Census of Endothelial Changes Induced by Matrix Stiffness and the Association with Atherosclerosis.** *Advanced functional materials*
  Zamani, M., Cheng, Y. H., Charbonier, F., Gupta, V. K., Mayer, A. T., Trevino, A. E., Quertermous, T., Chaudhuri, O., Cahan, P., Huang, N. F.
  2022; 32 (47)

- **Single-Cell Transcriptomic Census of Endothelial Changes Induced by Matrix Stiffness and the Association with Atherosclerosis** *ADVANCED FUNCTIONAL MATERIALS*
  Zamani, M., Cheng, Y., Charbonier, F., Gupta, V., Mayer, A. T., Trevino, A. E., Quertermous, T., Chaudhuri, O., Cahan, P., Huang, N. F.
  2022

- **von Willebrand Factor Is Produced Exclusively by Endothelium, Not Neointima, in Occlusive Vascular Lesions in Both Pulmonary Hypertension and Atherosclerosis.** *Circulation*
  Steffes, L. C., Cheng, P., Quertermous, T., Kumar, M. E.
  2022; 146 (5): 429-431

- **INTEGRATION OF CAD-ASSOCIATED GWAS LOCI AND DECONVOLUTION FROM HUMAN CAROTID PLAQUES TO STUDY SMOOTH MUSCLE CELL FUNCTION IN ATHEROSCLEROSIS**
  Narayanan, S., Vuckovic, S., Wirka, R., Lengquist, M., Quertermous, T., Hedin, U., Matic, L. P.
  ELSEVIER IRELAND LTD.2022: E93

- **Embryologic Origin Influences Smooth Muscle Cell Phenotypic Modulation Signatures in Murine Marfan Syndrome Aortic Aneurysm.** *Arteriosclerosis, thrombosis, and vascular biology*
  Pedroza, A. J., Dalal, A. R., Shad, R., Yokoyama, N., Nakamura, K., Cheng, P., Wirka, R. C., Mitchel, O., Baiocchi, M., Hiesinger, W., Quertermous, T., Fischbein, M. P.
  2022: 101161ATVBAHA122317381

- **Author Correction: Single-nucleus chromatin accessibility profiling highlights regulatory mechanisms of coronary artery disease risk.** *Nature genetics*
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