

# Stanford

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## Thomas Quertermous, MD

William G. Irwin Professor of Cardiovascular Medicine  
Medicine - Cardiovascular Medicine

### CONTACT INFORMATION

- **Alternate Contact**

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### Bio

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#### 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

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#### 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.

#### CLINICAL TRIALS

- Permission to Collect Blood Over Time for Research, Not Recruiting

### Teaching

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#### STANFORD ADVISEES

**Doctoral Dissertation Reader (AC)**

Ronghao Zhou

**Postdoctoral Faculty Sponsor**

Wenduo Gu, João Pinho Monteiro, Markus Ramste, Matthew Worssam

#### Postdoctoral Research Mentor

Wenduo Gu, João Pinho Monteiro, Markus Ramste

## Publications

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### PUBLICATIONS

- **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  
2015; 11 (5)
  - **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  
2015; 11 (5)
  - **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  
2015; 11 (5)
  - **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
  - **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

- **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: 101161ATVBHAHA122317381
- **Author Correction: Single-nucleus chromatin accessibility profiling highlights regulatory mechanisms of coronary artery disease risk.** *Nature genetics*  
Turner, A. W., Hu, S. S., Mosquera, J. V., Ma, W. F., Hodonsky, C. J., Wong, D., Auguste, G., Song, Y., Sol-Church, K., Farber, E., Kundu, S., Kundaje, A., Lopez, et al  
2022
- **Single-nucleus chromatin accessibility profiling highlights regulatory mechanisms of coronary artery disease risk.** *Nature genetics*  
Turner, A. W., Hu, S. S., Mosquera, J. V., Ma, W. F., Hodonsky, C. J., Wong, D., Auguste, G., Song, Y., Sol-Church, K., Farber, E., Kundu, S., Kundaje, A., Lopez, et al  
2022
- **Human Coronary Plaque T Cells Are Clonal and Cross-React to Virus and Self.** *Circulation research*  
Roy Chowdhury, R., D'Addabbo, J., Huang, X., Veizades, S., Sasagawa, K., Louis, D. M., Cheng, P., Sokol, J., Jensen, A., Tso, A., Shankar, V., Wendel, B. S., Bakerman, et al  
2022: 101161CIRCRESAHA121320090

- **Integration of genetic colocalizations with physiological and pharmacological perturbations identifies cardiometabolic disease genes.** *Genome medicine*  
Gloudemans, M. J., Balliu, B., Nachun, D., Schnurr, T. M., Durrant, M. G., Ingelsson, E., Wabitsch, M., Quertermous, T., Montgomery, S. B., Knowles, J. W., Carcamo-Orive, I.  
2022; 14 (1): 31
- **Integration of genetic colocalizations with physiological and pharmacological perturbations identifies cardiometabolic disease genes**  
Gloudemans, M. J., Balliu, B., Nachun, D., Durrant, M. G., Ingelsson, E., Wabitsch, M., Quertermous, T., Montgomery, S. B., Knowles, J., Carcamo-Orive, I.  
W B SAUNDERS CO-ELSEVIER INC.2022: S24-S25
- **Osteomodulin attenuates smooth muscle cell osteogenic transition in vascular calcification.** *Clinical and translational medicine*  
Skenteris, N. T., Seime, T., Witasp, A., Karlof, E., Wasilewski, G. B., Heuschkel, M. A., Jaminon, A. M., Oduor, L., Dzhanayev, R., Kronqvist, M., Lengquist, M., Peeters, F. E., Soderberg, et al  
2022; 12 (2): e682
- **Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease.** *Cell*  
de Goede, O. M., Nachun, D. C., Ferraro, N. M., Gloudemans, M. J., Rao, A. S., Smail, C., Eulalio, T. Y., Aguet, F., Ng, B., Xu, J., Barbeira, A. N., Castel, S. E., Kim-Hellmuth, et al  
2021
- **Multi-omics analysis identifies CpGs near G6PC2 mediating the effects of genetic variants on fasting glucose.** *Diabetologia*  
Chung, R., Chiu, Y., Wang, W., Hwu, C., Hung, Y., Lee, I., Chuang, L., Quertermous, T., Rotter, J. I., Chen, Y. I., Chang, I., Hsiung, C. A.  
2021
- **Generation of Vascular Smooth Muscle Cells From Induced Pluripotent Stem Cells: Methods, Applications, and Considerations.** *Circulation research*  
Shen, M., Quertermous, T., Fischbein, M. P., Wu, J. C.  
2021; 128 (5): 670–86
- **AMPA-Type Glutamate Receptors Associated With Vascular Smooth Muscle Cell Subpopulations in Atherosclerosis and Vascular Injury.** *Frontiers in cardiovascular medicine*  
Gallina, A. L., Rykaczewska, U., Wirka, R. C., Caravaca, A. S., Shavva, V. S., Youness, M., Karadimou, G., Lengquist, M., Razuvaev, A., Paulsson-Berne, G., Quertermous, T., Gistera, A., Malin, et al  
2021; 8: 655869
- **An integrated approach to identify environmental modulators of genetic risk factors for complex traits.** *American journal of human genetics*  
Balliu, B., Carcamo-Orive, I., Gloudemans, M. J., Nachun, D. C., Durrant, M. G., Gazal, S., Park, C. Y., Knowles, D. A., Wabitsch, M., Quertermous, T., Knowles, J. W., Montgomery, S. B.  
2021
- **Predictive network modeling in human induced pluripotent stem cells identifies key driver genes for insulin responsiveness.** *PLoS computational biology*  
Carcamo-Orive, I., Henrion, M. Y., Zhu, K., Beckmann, N. D., Cundiff, P., Moein, S., Zhang, Z., Alamprese, M., D'Souza, S. L., Wabitsch, M., Schadt, E. E., Quertermous, T., Knowles, et al  
2020; 16 (12): e1008491
- **Apelin increases atrial conduction velocity, refractoriness, and prevents inducibility of atrial fibrillation.** *JCI insight*  
Kim, Y. M., Lakin, R., Zhang, H., Liu, J., Sachedina, A., Singh, M., Wilson, E., Perez, M., Verma, S., Quertermous, T., Olgin, J., Backx, P. H., Ashley, et al  
2020; 5 (17)
- **Single-Cell Transcriptomic Profiling of Vascular Smooth Muscle Cell Phenotype Modulation in Marfan Syndrome Aortic Aneurysm.** *Arteriosclerosis, thrombosis, and vascular biology*  
Pedroza, A. J., Tashima, Y., Shad, R., Cheng, P., Wirka, R., Churovich, S., Nakamura, K., Yokoyama, N., Cui, J. Z., Iosef, C., Hiesinger, W., Quertermous, T., Fischbein, et al  
2020: ATVBHA120314670
- **Discovery and quality analysis of a comprehensive set of structural variants and short tandem repeats.** *Nature communications*  
Jakubosky, D., Smith, E. N., D'Antonio, M., Jan Bonder, M., Young Greenwald, W. W., D'Antonio-Chronowska, A., Matsui, H., i2QTL Consortium, Stegle, O., Montgomery, S. B., DeBoever, C., Frazer, K. A., Bonder, M. J., et al  
2020; 11 (1): 2928
- **Properties of structural variants and short tandem repeats associated with gene expression and complex traits.** *Nature communications*  
Jakubosky, D., D'Antonio, M., Bonder, M. J., Smail, C., Donovan, M. K., Young Greenwald, W. W., Matsui, H., i2QTL Consortium, D'Antonio-Chronowska, A., Stegle, O., Smith, E. N., Montgomery, S. B., DeBoever, C., et al

2020; 11 (1): 2927

- **PCSK6 Is a Key Protease in the Control of Smooth Muscle Cell Function in Vascular Remodeling.** *Circulation research*  
Rykcaczevska, U., Suur, B. E., Rohl, S., Razuvaev, A., Lengquist, M., Sabater-Lleal, M., van der Laan, S. W., Miller, C. L., Wirka, R. C., Kronqvist, M., Gonzalez Diez, M., Vesterlund, M., Gillgren, et al  
2020
- **FAM13A affects body fat distribution and adipocyte function.** *Nature communications*  
Fathzadeh, M. n., Li, J. n., Rao, A. n., Cook, N. n., Chennamsetty, I. n., Seldin, M. n., Zhou, X. n., Sangwung, P. n., Gloude mans, M. J., Keller, M. n., Attie, A. n., Yang, J. n., Wabitsch, et al  
2020; 11 (1): 1465
- **Transcriptomic profiling of experimental arterial injury reveals new mechanisms and temporal dynamics in vascular healing response.** *JVS-vascular science*  
Rohl, S., Rykcaczevska, U., Seime, T., Suur, B. E., Diez, M. G., Gadin, J. R., Gainullina, A., Sergushichev, A. A., Wirka, R., Lengquist, M., Kronqvist, M., Bergman, O., Odeberg, et al  
2020; 1: 13-27
- **Genomic integrity of human induced pluripotent stem cells across nine studies in the NHLBI NextGen program.** *Stem cell research*  
Kanchan, K. n., Iyer, K. n., Yanek, L. R., Carcamo-Orive, I. n., Taub, M. A., Malley, C. n., Baldwin, K. n., Becker, L. C., Broeckel, U. n., Cheng, L. n., Cowan, C. n., D'Antonio, M. n., Frazer, et al  
2020; 46: 101803
- **Cardiovascular Risks in Patients with COVID-19: Potential Mechanisms and Areas of Uncertainty.** *Current cardiology reports*  
Cheng, P. n., Zhu, H. n., Witteles, R. M., Wu, J. C., Quertermous, T. n., Wu, S. M., Rhee, J. W.  
2020; 22 (5): 34
- **Genomic profiling of human vascular cells identifies TWIST1 as a causal gene for common vascular diseases.** *PLoS genetics*  
Nurnberg, S. T., Guerraty, M. A., Wirka, R. C., Rao, H. S., Pjanic, M. n., Norton, S. n., Serrano, F. n., Perisic, L. n., Elwyn, S. n., Pluta, J. n., Zhao, W. n., Testa, S. n., Park, et al  
2020; 16 (1): e1008538
- **Adiponectin Receptor 3 is Associated With Endothelial Nitric Oxide Synthase Dysfunction and Predicts Insulin Resistance in South Asians**  
Chandy, M., Sayed, N., Lau, E., Liu, C., Wei Tzu-Tang, Chen, I. Y., Thomas, D., Rhee, J., Oh, B., Pepic, L., Husain, M., Quertermous, T., Nallamshetty, S., et al  
LIPPINCOTT WILLIAMS & WILKINS.2019
- **The role of insulin as a key regulator of seeding, proliferation, and mRNA transcription of human pluripotent stem cells.** *Stem cell research & therapy*  
Shahbazi, M., Cundiff, P., Zhou, W., Lee, P., Patel, A., D'Souza, S. L., Abbasi, F., Quertermous, T., Knowles, J. W.  
2019; 10 (1): 228
- **IGF1 gene is associated with triglyceride levels in subjects with family history of hypertension from the SAPHIRE and TWB projects**  
Wang, W., Chiu, Y., Chung, R., Hwu, C., Lee, I., Lee, C., Chang, Y., Hung, K., Quertermous, T., Chen, Y. I., Hsiung, C. A.  
NATURE PUBLISHING GROUP.2019: 163
- **Stanford Cardiovascular Institute At the Forefront of Cardiovascular Research** *CIRCULATION RESEARCH*  
Wu, J. C., Woo, Y., Mayerle, M., Harrington, R. A., Quertermous, T.  
2019; 124 (10): 1420–24
- **Opportunities and challenges for transcriptome-wide association studies.** *Nature genetics*  
Wainberg, M., Sinnott-Armstrong, N., Mancuso, N., Barbeira, A. N., Knowles, D. A., Golan, D., Ermel, R., Ruusalepp, A., Quertermous, T., Hao, K., Björkegren, J. L., Im, H. K., Pasaniuc, et al  
2019; 51 (4): 592-599
- **Opportunities and challenges for transcriptome-wide association studies** *NATURE GENETICS*  
Wainberg, M., Sinnott-Armstrong, N., Mancuso, N., Barbeira, A. N., Knowles, D. A., Golan, D., Ermel, R., Ruusalepp, A., Quertermous, T., Hao, K., Björkegren, J. M., Im, H., Pasaniuc, et al  
2019; 51 (4): 592–99
- **Stanford Cardiovascular Institute.** *Circulation research*  
Wu, J. C., Woo, Y. J., Mayerle, M. n., Harrington, R. A., Quertermous, T. n.  
2019; 124 (10): 1420–24

- **CRISPR-Cas9-mediated knockout of SPRY2 in human hepatocytes leads to increased glucose uptake and lipid droplet accumulation.** *BMC endocrine disorders*  
Cook, N. L., Pjanic, M. n., Emmerich, A. G., Rao, A. S., Hetty, S. n., Knowles, J. W., Quertermous, T. n., Castillejo-López, C. n., Ingelsson, E. n.  
2019; 19 (1): 115
- **Detailed Functional Characterization of a Waist-Hip Ratio Locus in 7p15.2 Defines an Enhancer Controlling Adipocyte Differentiation.** *iScience*  
Castillejo-Lopez, C. n., Pjanic, M. n., Pirona, A. C., Hetty, S. n., Wabitsch, M. n., Wadelius, C. n., Quertermous, T. n., Arner, E. n., Ingelsson, E. n.  
2019; 20: 42–59
- **TCF21 and AP-1 interact through epigenetic modifications to regulate coronary artery disease gene expression.** *Genome medicine*  
Zhao, Q. n., Wirka, R. n., Nguyen, T. n., Nagao, M. n., Cheng, P. n., Miller, C. L., Kim, J. B., Pjanic, M. n., Quertermous, T. n.  
2019; 11 (1): 23
- **Genetic variation of SORBS1 gene is associated with glucose homeostasis and age at onset of diabetes: A SAPPHiRe Cohort Study** *SCIENTIFIC REPORTS*  
Chang, T., Wang, W., Hsiung, C. A., He, C., Lin, M., Sheu, W., Chang, Y., Quertermous, T., Chen, Y., Rotter, J. I., Chuang, L., SAPPHiRe Study Grp  
2018; 8: 10574
- **Large-Scale Single-Cell RNA-Seq Reveals Molecular Signatures of Heterogeneous Populations of Human Induced Pluripotent Stem Cell-Derived Endothelial Cells.** *Circulation research*  
Paik, D. T., Tian, L., Lee, J., Sayed, N., Chen, I. Y., Rhee, S., Rhee, J., Kim, Y., Wirka, R. C., Buikema, J. W., Wu, S. M., Red-Horse, K., Quertermous, et al  
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