Stanford

Erik Ingelsson

Professor of Medicine (Cardiovascular Medicine) and, by courtesy, of Health Research and Policy (Epidemiology)

Medicine - Cardiovascular Medicine

NIH Biosketch available Online Curriculum Vitae available Online

CONTACT INFORMATION

- **Administrative Contact**

  Alyssa Sacro - Administrative Assistant

  Email asacro@stanford.edu

Bio

BIO

Dr. Ingelsson obtained his MD (2000) and PhD (2005) at Uppsala University, Sweden. After internship, he did a residency in general medicine (2003-2006) and took up a postdoctoral research fellowship at the Framingham Heart Study (2006-2007). He moved to Karolinska Institutet (Stockholm, Sweden) in 2007 and was appointed Professor of Cardiovascular Epidemiology in 2010. From 2013-2016, he was a Professor of Molecular Epidemiology at Uppsala University. He was also a Visiting Professor at the Wellcome Trust Centre for Human Genetics at University of Oxford in 2012-2015. Since May 2016, he is Professor of Medicine at Stanford University.

For the past fifteen years, Dr. Ingelsson has been doing cardiovascular research with a special focus on the role of obesity and insulin resistance in development of subclinical and clinical cardiovascular disease. His research is translational and interdisciplinary, combining big data approaches, such as -omics in population-based cohorts, with gene editing in functional model systems to reach new insights into the pathophysiology of cardiovascular disease and related conditions, identification of new biomarkers for improved risk prediction, and discovery of novel targets for drug development.

He has had a leading role in many of the large efforts identifying new genetic loci associated with cardiovascular and metabolic traits, and has extensive experience from research on biomarkers and -omics methods, including development and application of prediction metrics and Mendelian randomization. He has served as PI of numerous –omics efforts in several Swedish cohort studies, including ULSAM, PIVUS, TwinGene and EpiHealth. Since 2013, his laboratory has refocused much of their research efforts towards characterization of genes discovered in genome-wide association studies using a combination of in-depth studies in human (including various -omics methods), in vitro studies (primarily adipocytes, hepatocytes and skeletal myocytes) and in vivo models (mice and zebrafish).

He has published over 300 peer-reviewed original articles (>110 as lead author), and >60 in journals with impact factor over 30. Before relocating to the U.S, he received many large European research grants, and after joining the Stanford faculty in May 2016, he has built a strong and well-funded research program. He has won several prestigious awards, such as the AHA Trudy Bush Fellowship for Cardiovascular Research in Women’s Health, ERC starting grant, Wallenberg Academy Fellow and the Göran Gustafsson Prize in Medicine in 2015 (to the most successful medical researcher in Sweden under age 45).

ACADEMIC APPOINTMENTS

- Professor, Medicine - Cardiovascular Medicine
- Professor (By courtesy), Health Research & Policy

- Member, Bio-X
- Member, Cardiovascular Institute

ADMINISTRATIVE APPOINTMENTS

- Committee Member, Department of Medicine's Professoriate Appointments and Promotions Committee, (2018- present)
- Affinity Group Leader, Stanford Diabetes Research Center, (2017- present)
- National Director, EATRIS.se (Swedish node of the European Infrastructure for Translational Medicine), (2015-2016)
- Board Member, Faculty Board of the Disciplinary Domain of Medicine and Pharmacy, Uppsala University, (2014-2015)
- Executive Group Member, Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, (2010-2012)

HONORS AND AWARDS

- Göran Gustafsson Prize in Medicine, Göran Gustafsson Foundation (2015)
- Wallenberg Academy Fellow, Knut och Alice Wallenberg Foundation (2013)
- ERC Starting Grant Award, European Research Council (2013)
- Fellow of the American Heart Association (FAHA), American Heart Association (2010)
- Ingvar Carlsson Award, Swedish Foundation for Strategic Research (2009)
- Trudy Bush Fellowship for Cardiovascular Research in Women's Health, American Heart Association (2009)
- Young Investigator Award, EuroPRevent 2008, European Association of Cardiovascular Prevention and Rehabilitation (2008)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Scientific advisor, Precision Wellness (2016 - present)
- Scientific advisor, Olink Proteomics (2017 - present)

PROFESSIONAL EDUCATION

- PhD, Uppsala University , Epidemiology (2005)
- MD, Uppsala University , Medicine (2000)

PATENTS

- Lindholm D, Fukaya E, Leeper NJ, Ingelsson E. "United States Patent 62/522,601 Systems and Methods for Predicting Heart Failure Using Leg Bioimpedance", Leland Stanford Junior University, Jun 20, 2017

LINKS

- Ingelsson Lab Homepage: http://med.stanford.edu/ingelssonlab.html

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Our research area is cardiovascular medicine with a special focus on metabolic disturbances, such as obesity and insulin resistance and their role in the development of subclinical and clinical cardiovascular disease. The methods used are from the molecular epidemiology field where we use -omics studies of how cardiovascular disease and related conditions varies with DNA variation, RNA expression, and circulating biomarkers such as proteins and metabolites; but also functional characterization of candidate genes using CRISPR-Cas9 gene editing in cell and animal models. Our research is translational, trying to bridge population studies with molecular biology to reach new important insights into the pathophysiology of cardiovascular diseases, identification of new biomarkers for improved risk prediction, and discovery of novel targets for drug development.

Population-based studies

We are performing many population-based projects in the UK Biobank, which is an excellent example of science in the new era of open science initiatives and big data analytics. In 2006-2010, the UK Biobank recruited 502,650 participants aged 37-73 years to undergo physical measurements, detailed assessments about risk factors and future disease events, and sampling of blood, urine and saliva. Genome-wide genotyping on the UK Biobank Axiom Array and imputation to ~80 million variants has been performed in all participants. They have also been extensively examined, and outcome events are recorded in a longitudinal fashion.

We are working on a wide range of projects using this excellent cohort, including traditional epidemiological studies and GWAS addressing important, but understudied conditions, such as peripheral vascular disease and heart failure – including risk prediction studies to improve patient stratification, as well as studies of environmental risk factors, genetic determinants and their interactions; but also more novel approaches which aims at addressing causality of risk factors and biomarkers and importantly, at finding druggable targets using genomic approaches. The statistical power, as well as the opportunities to study new research questions, are unprecedented given the very large sample size (ten- to hundred-fold larger than all previous studies) and the extreme richness of the data.

In addition to UK Biobank, we are also working with several other datasets. I am still the PI for a range of –omics projects in several Swedish cohorts – ULSAM, PIVUS, TwinGene and EpiHealth. These include genomics, transcriptomics, epigenomics, proteomics and metabolomics, often used in combination - aiming at increasing the biological knowledge of obesity, insulin resistance and CVD, and to identify new biomarkers for risk prediction and novel drug targets.

Wet-lab approaches

To further characterize gene function after various –omics studies and use of in silico data on gene regulation and transcription from public resources, we proceed to studies of gene function in model systems. We use CRISPR-Cas9 techniques for gene editing in human SGBS adipocytes, HepG2 hepatocytes, HMCL-7304 skeletal myocytes, and murine 3T3-L1 adipocytes to study phenotypes related to obesity and insulin resistance. We transfect cells using our custom-built lentivirus CRISPR-Cas9 constructs, and assess the effect of knockdown or overexpression of candidate genes on basal and insulin-stimulated glucose uptake (using 14C-labeled deoxyglucose) and lipolysis (measuring glycerol after insulin and isoprenaline exposure), as well as insulin signaling proteins and adipogenesis. We address downstream effects of gene knockdown using transcriptomic and metabolomic profiling on cell lysates.

Teaching

STANFORD ADVISEES

Postdoctoral Faculty Sponsor

Laeya Abdoli Najmi, Sylwia Figarska, Hyun-Jung Kim, Jiehan Li, Peter Saliba Gustafsson, Alberta Yen

Postdoctoral Research Mentor

Lee Chang, Sylwia Figarska, Hyun-Jung Kim, Joanna Lankester, Jiehan Li, Peter Saliba Gustafsson, Alberta Yen

Publications

PUBLICATIONS

- **Publisher Correction: Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits.** *Nature genetics*
  Evangelou, E., Warren, H. R., Mosen-Ansorena, D., Mifsud, B., Pazoki, R., Gao, H., Ntritsos, G., Dimou, N., Cabrera, C. P., Karaman, I., Ng, F. L., Evangelou, M., Witkowska, et al
  2018

- **Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders.** *American journal of human genetics*
  Ligthart, S., Vaez, A., Vosa, U., Stathopoulou, M. G., de Vries, P. S., Prins, B. P., Van der Most, P. J., Tanaka, T., Naderi, E., Rose, L. M., Wu, Y., Karlsson, R., Barbalic, et al
  2018; 103 (5): 691–706

- **Proteomic profiling of endothelium-dependent vasodilation.** *Journal of hypertension*
  Lind, L., Sundstrom, J., Arnlov, J., Ingelsson, E.
  2018

- **Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps.** *Nature genetics*
  Mahajan, A., Taliun, D., Thurner, M., Robertson, N. R., Torres, J. M., Rayner, N. W., Payne, A. J., Steinthorsdottir, V., Scott, R. A., Grarup, N., Cook, J. P., Schmidt, E. M., Wuttke, et al
  2018

- **Genome-wide association study of coronary artery disease among individuals with diabetes: the UK Biobank** *DIABETOLOGIA*
  Fall, T., Gustafsson, S., Orho-Melander, M., Ingelsson, E.
  2018; 61 (10): 2174–79

- **A Phenome- Wide Association Study of Patatin-like Phospholipase Domain Containing 3 (PNPLA3) I148M Variant in 337,536 Participants of the UK Biobank Study**
  Yeo, Y., Rao, A., Liu, B., Nguyen, M. H., Ingelsson, E.
  WILEY.2018: 65A–66A

- **Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits** *NATURE GENETICS*
  Evangelou, E., Warren, H. R., Mosen-Ansorena, D., Mifsu, B., Pazoki, R., Gao, H., Ntritsos, G., Dimou, N., Cabrer, C. P., Karaman, I., Ng, F., Evangelou, M., Witkowska, et al
  2018; 50 (10): 1412-+

- **Associations of Circulating Protein Levels With Lipid Fractions in the General Population** *ARTERIOSCLEROSIS THROMBOSIS AND VASCULAR BIOLOGY*
  Figarska, S. M., Gustafsson, S., Sundstrom, J., Arnlov, J., Malarstig, A., Elmstahl, S., Fall, T., Lind, L., Ingelsson, E.
  2018; 38 (10): 2505–18

- **Epigenetic influences on aging: a longitudinal genome-wide methylation study in old Swedish twins.** *Epigenetics*
  Wang, Y., Karlsson, R., Lampa, E., Zhang, Q., Hedman, A. K., Almgren, M., Almqvist, C., McRae, A. F., Marioni, R. E., Ingelsson, E., Visscher, P. M., Deary, I. J., Lind, et al
  2018: 1–13

- **Genetic predictors of testosterone and their associations with cardiovascular disease and risk factors: A Mendelian randomization investigation** *INTERNATIONAL JOURNAL OF CARDIOLOGY*
  Schooling, C., Luo, S., Yeung, S., Thompson, D. J., Karthikeyan, S., Bolton, T. R., Mason, A. M., Ingelsson, E., Burgess, S.
  2018; 267: 171–76

- **Multi-ethnic genome-wide association study for atrial fibrillation** *NATURE GENETICS*
  Roselli, C., Chaffin, M. D., Weng, L., Aeschbacher, S., Ahlberg, G., Albert, C. M., Almgren, P., Alonso, A., Anderson, C. D., Aragam, K. G., Arking, D. E., Barnard, J., Bartz, et al
  2018; 50 (9): 1225-+

- **Multiplex proteomics for prediction of major cardiovascular events in type 2 diabetes** *DIABETOLOGIA*
  Nowak, C., Carlsson, A. C., Ostgren, C., Nystrom, F. H., Alam, M., Feldreich, T., Sundstrom, J., Carrero, J., Leppert, J., Hedberg, P., Henriksen, E., Cordeiro, A. C., Giedraitis, et al
  2018; 61 (8): 1748–57

- **Large-Scale Phenome-Wide Association Study of PCSK9 Variants Demonstrates Protection Against Ischemic Stroke** *CIRCULATION-GENOMIC AND PRECISION MEDICINE*
  Rao, A. S., Lindholm, D., Rivas, M. A., Knowles, J. W., Montgomery, S. B., Ingelsson, E.
  2018; 11 (7): e002162

- **Glucose challenge metabolomics implicates medium-chain acylcarnitines in insulin resistance** *SCIENTIFIC REPORTS*
  Nowak, C., Hetty, S., Salihovic, S., Castillejo-Lopez, C., Ganna, A., Cook, N. L., Broeckling, C. D., Prenni, J. E., Shen, X., Giedraitis, V., Arnlov, J., Lind, L., Berne, et al
  2018; 8: 8691

- **Human Genetics of Obesity and Type 2 Diabetes Mellitus: Past, Present, and Future.** *Circulation. Genomic and precision medicine*
  Ingelsson, E., McCarthy, M. I.
  2018; 11 (6): e002090

- **Clinical and genetic determinants of varicose veins: a prospective, community-based prospective study of similar to 500,000 individuals**
  Fukaya, E., Flores, A., Lindholm, D., Gustafsson, S., Ingelsson, E., Leeper, N.
  SAGE PUBLICATIONS LTD.2018: 300

- **A genome-wide association study of IgM antibody against phosphorylcholine: shared genetics and phenotypic relationship to chronic lymphocytic leukemia** *HUMAN MOLECULAR GENETICS*
  Chen, X., Gustafsson, S., Whitington, T., Borne, Y., Lorentzen, E., Sun, J., Almgren, P., Su, J., Karlsson, R., Song, J., Lu, Y., Zhan, Y., Hagg, et al
  2018; 27 (10): 1809–18

- **Habitual coffee consumption and cognitive function: a Mendelian randomization meta-analysis in up to 415,530 participants** *SCIENTIFIC REPORTS*
  Zhou, A., Taylor, A. E., Karhunen, V., Zhan, Y., Rovio, S. P., Lahti, J., Sjogren, P., Byberg, L., Lyall, D. M., Auvinen, J., Lehtimaki, T., Kahonen, M., Hutri-Kahonen, et al
  2018; 8: 7526

- **Biological Insights Into Muscular Strength: Genetic Findings in the UK Biobank** *SCIENTIFIC REPORTS*
  Tikkanen, E., Gustafsson, S., Amar, D., Shcherbina, A., Waggott, D., Ashley, E. A., Ingelsson, E.
  2018; 8: 6451

- **Medical relevance of protein-truncating variants across 337,205 individuals in the UK Biobank study** *NATURE COMMUNICATIONS*
  DeBoever, C., Tanigawa, Y., Lindholm, M. E., McInnes, G., Lavertu, A., Ingelsson, E., Chang, C., Ashley, E. A., Bustamante, C. D., Daly, M. J., Rivas, M. A.
  2018; 9: 1612

- **Associations of Fitness, Physical Activity, Strength, and Genetic Risk With Cardiovascular Disease: Longitudinal Analyses in the UK Biobank Study.** *Circulation*
  Tikkanen, E., Gustafsson, S., Ingelsson, E.
  2018

- **Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes** *NATURE GENETICS*
  Malik, R., Chauhan, G., Traylor, M., Sargurupremraj, M., Okada, Y., Mishra, A., Rutten-Jacobs, L., Giese, A., van der Laan, S. W., Gretarsdottir, S., Anderson, C. D., Chong, M., Adams, et al
  2018; 50 (4): 524-+

- **Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes** *NATURE GENETICS*
  Mahajan, A., Wessel, J., Willems, S. M., Zhao, W., Robertson, N. R., Chu, A. Y., Gan, W., Kitajima, H., Taliun, D., Rayner, N., Guo, X., Lu, Y., Li, et al
  2018; 50 (4): 559-+

- **CONGENITAL HEART DISEASE CONFERS SUBSTANTIAL RISK OF ACQUIRED CARDIOVASCULAR DISEASE AMONGST BRITISH ADULTS**
  Saha, P., Potiny, P., Tcheandjieu, C., Fernandes, S. M., Romfh, A., Bernstein, D., Lui, G. K., Ingelsson, E., Priest, J.
  ELSEVIER SCIENCE INC.2018: 553

- **Methylation-based estimated biological age and cardiovascular disease** *EUROPEAN JOURNAL OF CLINICAL INVESTIGATION*
  Lind, L., Ingelsson, E., Sundstrom, J., Siegbahn, A., Lampa, E.
  2018; 48 (2)

- **Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels** *NATURE COMMUNICATIONS*
  Jiang, X., O'Reilly, P. F., Aschard, H., Hsu, Y., Richards, J., Dupuis, J., Ingelsson, E., Karasik, D., Pilz, S., Berry, D., Kestenbaum, B., Zheng, J., Luan, et al
  2018; 9: 260

- **Genome-wide Study of Atrial Fibrillation Identifies Seven Risk Loci and Highlights Biological Pathways and Regulatory Elements Involved in Cardiac Development** *AMERICAN JOURNAL OF HUMAN GENETICS*
  Nielsen, J. B., Fritsche, L. G., Zhou, W., Teslovich, T. M., Holmen, O. L., Gustafsson, S., Gabrielsen, M. E., Schmidt, E. M., Beaumont, R., Wolford, B. N., Lin, M., Brummett, C. M., Preuss, et al
  2018; 102 (1): 103–15

- **Circulating proteins as predictors of incident heart failure in the elderly** *EUROPEAN JOURNAL OF HEART FAILURE*
  Stenemo, M., Nowak, C., Byberg, L., Sundstrom, J., Giedraitis, V., Lind, L., Ingelsson, E., Fall, T., Arnlov, J.
  2018; 20 (1): 55–62

- **Birthweight, Type 2 Diabetes Mellitus, and Cardiovascular Disease: Addressing the Barker Hypothesis With Mendelian Randomization.** *Circulation. Genomic and precision medicine*
  Zanetti, D., Tikkanen, E., Gustafsson, S., Priest, J. R., Burgess, S., Ingelsson, E.
  2018; 11 (6): e002054

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

- **Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity** *NATURE GENETICS*
  Turcot, V., Lu, Y., Highland, H. M., Schurmann, C., Justice, A. E., Fine, R. S., Bradfield, J. P., Esko, T., Giri, A., Graff, M., Guo, X., Hendricks, A. E., Karaderi, et al
  2018; 50 (1): 26-+

- **Dog ownership and the risk of cardiovascular disease and death - a nationwide cohort study** *SCIENTIFIC REPORTS*
  Mubanga, M., Byberg, L., Nowak, C., Egenvall, A., Magnusson, P. K., Ingelsson, E., Fall, T.
  2017; 7: 15821

- **Large meta-analysis of genome-wide association studies identifies five loci for lean body mass (vol 8, 80, 2017)** *NATURE COMMUNICATIONS*
  Zillikens, M., Demissie, S., Hsu, Y., Yerges-Armstrong, L. M., Chou, W., Stolk, L., Livshits, G., Broer, L., Johnson, T., Koller, D. L., Kutalik, Z., Luan, J., Malkin, et al
  2017; 8: 1414

- **Identification of a novel proinsulin-associated SNP and demonstration that proinsulin is unlikely to be a causal factor in subclinical vascular remodelling using Mendelian randomisation** *ATHEROSCLEROSIS*
  Strawbridge, R. J., Silveira, A., den Hoed, M., Gustafsson, S., Luan, J., Rybin, D., Dupuis, J., Li-Gao, R., Kavousi, M., Dehghan, A., Haljas, K., Lahti, J., Gadin, et al
  2017; 266: 196–204

- **Vitamin D and cognitive function: A Mendelian randomisation study** *SCIENTIFIC REPORTS*
  Maddock, J., Zhou, A., Cavadino, A., Kuzma, E., Bao, Y., Smart, M. C., Saum, K., Schoettker, B., Engmann, J., Kjaergaard, M., Karhunen, V., Zhan, Y., Lehtimaki, et al
  2017; 7: 13230

- **New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475000 Individuals** *CIRCULATION-CARDIOVASCULAR GENETICS*
  Kraja, A. T., Cook, J. P., Warren, H. R., Surendran, P., Liu, C., Evangelou, E., Manning, A. K., Grarup, N., Drenos, F., Sim, X., Smith, A., Amin, N., Blakemore, et al
  2017; 10 (5)

- **Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis** *PLOS MEDICINE*
  Wheeler, E., Leong, A., Liu, C., Hivert, M., Strawbridge, R. J., Podmore, C., Li, M., Yao, J., Sim, X., Hong, J., Chu, A. Y., Zhang, W., Wang, et al
  2017; 14 (9): e1002383

- **Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney** *HYPERTENSION*
  Wain, L. V., Vaez, A., Jansen, R., Joehanes, R., van der Most, P. J., Erzurumluoglu, A., O'Reilly, P. F., Cabrera, C. P., Warren, H. R., Rose, L. M., Verwoert, G. C., Hottenga, J., Strawbridge, et al
  2017; 70 (3): E4-+

- **Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation.** *Nature genetics*
  Christophersen, I. E., Rienstra, M., Roselli, C., Yin, X., Geelhoed, B., Barnard, J., Lin, H., Arking, D. E., Smith, A. V., Albert, C. M., Chaffin, M., Tucker, N. R., Li, et al
  2017; 49 (6): 946-952

- **Ranking and characterization of established BMI and lipid associated loci as candidates for gene-environment interactions** *PLOS GENETICS*
  Shungin, D., Deng, W. Q., Varga, T. V., Luan, J., Mihailov, E., Metspalu, A., Morris, A. P., Forouhi, N. G., Lindgren, C., Magnusson, P. E., Pedersen, N. L., Hallmans, G., Chu, et al
  2017; 13 (6): e1006812

- **An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans.** *Diabetes*
  Scott, R. A., Scott, L. J., Mägi, R., Marullo, L., Gaulton, K. J., Kaakinen, M., Pervjakova, N., Pers, T. H., Johnson, A. D., Eicher, J. D., Jackson, A. U., Ferreira, T., Lee, et al
  2017

- **Leveraging Human Genetics to Understand the Relation of LDL Cholesterol with Type 2 Diabetes.** *Clinical chemistry*
  Ingelsson, E., Knowles, J. W.
  2017

- **Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function** *JOURNAL OF CLINICAL INVESTIGATION*
  Wild, P. S., Felix, J. F., Schillert, A., Teumer, A., Chen, M., Leening, M. J., Voelker, U., Grossmann, V., Brody, J. A., Irvin, M. R., Shah, S. J., Pramana, S., Lieb, et al
  2017; 127 (5): 1798-1812

- **Locus Due to Gene-Smoking Interactions.** *Circulation*
  Saleheen, D., Zhao, W., Young, R., Nelson, C. P., Ho, W. K., Ferguson, J. F., Rasheed, A., Ou, K., Nurnberg, S. T., Bauer, R. C., Goel, A., Do, R., Stewart, et al
  2017

- **Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits** *NATURE COMMUNICATIONS*
  Justice, A. E., Winkler, T. W., Feitosa, M. F., Graff, M., Fisher, V. A., Young, K., Barata, L., Deng, X., Czajkowski, J., Hadley, D., Ngwa, J. S., Ahluwalia, T. S., Chu, et al
  2017; 8

- **Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease.** *PLoS genetics*
  Folkersen, L., Fauman, E., Sabater-Lleal, M., Strawbridge, R. J., Frånberg, M., Sennblad, B., Baldassarre, D., Veglia, F., Humphries, S. E., Rauramaa, R., de Faire, U., Smit, A. J., Giral, et al
  2017; 13 (4)

- **Alterations in Multiple Lifestyle Factors in Subjects with the Metabolic Syndrome Independently of Obesity** *METABOLIC SYNDROME AND RELATED DISORDERS*
  Roos, V., Elmstahl, S., Ingelsson, E., Sundstrom, J., Arnlov, J., Lind, L.
  2017; 15 (3): 118-123

- **Variant Enriched in the Finnish Population is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk.** *Diabetes*
  Manning, A., Highland, H. M., Gasser, J., Sim, X., Tukiainen, T., Fontanillas, P., Grarup, N., Rivas, M. A., Mahajan, A., Locke, A. E., Cingolani, P., Pers, T. H., Viñuela, et al
  2017

- **Association of Pregnancy Complications and Characteristics With Future Risk of Elevated Blood Pressure: The Västerbotten Intervention Program.** *Hypertension*
  Parikh, N. I., Norberg, M., Ingelsson, E., Cnattingius, S., Vasan, R. S., Domellöf, M., Jansson, J. H., Edstedt Bonamy, A.
  2017; 69 (3): 475-483

- **Association of Pregnancy Complications and Characteristics With Future Risk of Elevated Blood Pressure The Vasterbotten Intervention Program** *HYPERTENSION*
  Parikh, N. I., Norberg, M., Ingelsson, E., Cnattingius, S., Vasan, R. S., Domellof, M., Jansson, J. H., Bonamy, A. E.
  2017; 69 (3): 475-483

- **Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk** *NATURE GENETICS*
  Warren, H. R., Evangelou, E., Cabrera, C. P., Gao, H., Ren, M., Mifsud, B., Ntalla, I., Surendran, P., Liu, C., Cook, J. P., Kraja, A. T., Drenos, F., Loh, et al
  2017; 49 (3): 403-415

- **Rare and low-frequency coding variants alter human adult height.** *Nature*
  Marouli, E., Graff, M., Medina-Gomez, C., Lo, K. S., Wood, A. R., Kjaer, T. R., Fine, R. S., Lu, Y., Schurmann, C., Highland, H. M., Rüeger, S., Thorleifsson, G., Justice, et al
  2017; 542 (7640): 186-190

- **PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study.** *The lancet. Diabetes & endocrinology*
  Schmidt, A. F., Swerdlow, D. I., Holmes, M. V., Patel, R. S., Fairhurst-Hunter, Z., Lyall, D. M., Hartwig, F. P., Horta, B. L., Hyppönen, E., Power, C., Moldovan, M., van Iperen, E., Hovingh, et al
  2017; 5 (2): 97-105

- **Metabolic Syndrome Development During Aging with Special Reference to Obesity Without the Metabolic Syndrome** *METABOLIC SYNDROME AND RELATED DISORDERS*
  Roos, V., Elmstahl, S., Ingelsson, E., Sundstrom, J., Arnlov, J., Lind, L.
  2017; 15 (1): 36-43
- **Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution** *DIABETES*
  Ehrlund, A., Mejhert, N., Bjork, C., Andersson, R., Kulyte, A., Astrom, G., Itoh, M., Kawaji, H., Lassmann, T., Daub, C. O., Carninci, P., Forrest, A. R., Hayashizaki, et al
  2017; 66 (1): 218-230
- **Genotype-based recall to study metabolic effects of genetic variation: a pilot study of PPARG Pro12Ala carriers** *UPSALA JOURNAL OF MEDICAL SCIENCES*
  Kamble, P. G., Gustafsson, S., Pereira, M. J., Lundkvist, P., Cook, N., Lind, L., Franks, P. W., Fall, T., Eriksson, J. W., Ingelsson, E.
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