# Associate Professor Loïc Yengo

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## Research Experience

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| *Jan 2025 – Dec 2032* | **Snow Fellow**<br>Institute for Molecular Bioscience, Brisbane, Australia. |
| *Jan 2023 – Dec 2026* | **ARC Future Fellow,** (Associate Professor – Level D)<br>Institute for Molecular Bioscience, Brisbane, Australia. |
| *Oct 2020 – Present* | **Group Leader -** Statistical Genomics Laboratory (Level C/D)<br>Institute for Molecular Bioscience, Brisbane, Australia. |
| *Jan 2020 – Dec 2022* | **ARC DECRA Research Fellow** (Level B/C)<br>Institute for Molecular Bioscience, Brisbane, Australia. |
| *May 2019 – May 2021* | **Visiting Scientist**<br>Broad Institute of MIT and Harvard, Boston, MA USA. |
| *Sep 2018 – Jan 2020* | **Senior Research Officer** (Level B)<br>Institute for Molecular Bioscience, Brisbane, Australia. |
| *Feb 2016 – Aug 2018* | **Postdoctoral Research Fellow** (Level A)<br>Institute for Molecular Bioscience, Brisbane, Australia. |

## Education

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| *Oct 2011 – Sep 2015* | **PhD in Applied Mathematics (Special. Statistics)**<br>University of Lille 1. Contribution to variable clustering in high-dimensional regression model. Lille, France (advised by Professor Christophe Biernacki). |
| *Sep 2005 – Nov 2008* | **MSc in Statistics**<br>Ecole Nationale de la Statistique et de l'Analyse de l'Information.<br>(part of France's "Grandes Ecoles" elite system), Rennes, France. |

## Teaching | Students

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| Since 2022 | UQ IMB Genetics & Genomics Winter School – (3 modules). |
| Since 2021 | Invited faculty – Computational Genomics Summer Institute, UCLA (USA). |
| Since 2020 | Invited faculty – Summer Institute in Statistical Genetics, Seattle (USA). Modules: *Advanced Quantitative Genetics / Genome-Wide Association Studies*. |
| Since 2019 | Invited faculty – International Statistical Genetics Workshop, University of Colorado (USA). Lectures (including course organisation): *Concepts in Quantitative and Population Genetics.* |
| Since 2017 | Statistical Analysis of Genetic Data – STAT3306/7306 at UQ. |

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| Past PhD supervision: | Ying Wang, PhD (2021) – Currently Postdoctoral Research at the Broad Institute; Pierrick Wainschtein, PhD (2022) – Currently Data Scientist at Illumina. |
| Current PhD supervision | Sam McEwan (first year), Mandy Moore (second year), Yuanxiang Wang (third Year) |

## Awards / Honours

2022: Australian Academy of Science, *Ruth Stephens Gani Medal* for exceptional contribution in human genetics
2022: Named among 11 early career researchers (only Australia-based researcher) "to watch" in *Nature Medicine*'s Yearbook
2021: UQ Foundation Research Excellence Award
2021: Named among Australia's rising stars of biomedical research by *The Australian* newspaper

## Keynote Talks

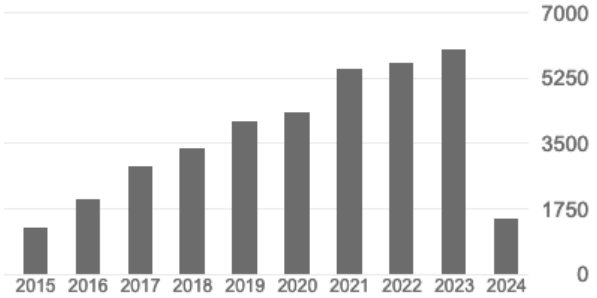
2024: International Congress in Quantitative Genetics (July), Vienna, Austria
2024: 52nd European Mathematical Genetics Meeting (April), Vienna, Austria
2024: Sydney Brenner Research Symposium (April), Johannesburg, South Africa
2023: Gordon Conference in Quantitative Genetics 2023 (February), Ventura, USA
2022: World Congress on Genetics Applied to Livestock Production 2022 (July), Rotterdam, The Netherlands
2021: Australian Polygenic risk Symposium 2021, Garvan Institute Sydney, Australia
2019: Nuffield College Sociology Seminar 2019, Oxford, UK
2018: Polygenic Prediction and its Application in the Social Sciences Conference, Los Angeles, USA

## Grants as principal (PI) and co-investigator (CI)

Snow Medical Fellowship (2025-2032): AUD $8,000,000 – PI
NIH R01 (2023-2028): USD $755,700 – (sub-contract) – CI
ARC Future Fellowship (2023-2026): AUD $904,843 – PI
MRFF 2021 Genomics Health Futures Mission Stream 5 (2022-2026): AUD $4,071,226 ($80,148 to Yengo) – CI
UQ Foundation Research Excellence Award (2022): AUD $71,604 – PI
NHMRC Ideas Grant (2021-2023): AUD $290,137 – PI
ARC DECRA (2020-2022): AUD $409,364 – PI
NIH R01 (2018-2021): AUD $301,131 – (sub-contract) – CI
UQ Early Career Researcher Grant (2019): AUD $15,360 – PI

## Research outputs

### Overview




My research has been cited more than 38,000 times to date (Jan 2024), from a total of 117 publications. My citation profile shows an upwards trajectory (**Fig. 1** from Google Scholar). I have 17 publications with >500 citations and 8 publications with >1000 citations. My research portfolio includes theoretical studies, various medical and non-medical applications, and software tools. My *h*-index is 73 (Google Scholar, March 2024).

**Fig 1.** Citation counts between 2015 and 2024.

## Software Tools

2022: DGREML: software tool for estimating the contribution of gametic phase disequilibrium to the heritability of complex traits (https://github.com/loic-yengo/DRM)
2021: LDSCdom: software for estimating inbreeding depression (directional dominance) from additive-dominance GWAS summary statistics (https://github.com/loic-yengo/LDSCdom)
2016: R package clere (Cluster-wise Effect Regression): https://cran.r-project.org/web/packages/clere/index.html
2015: R package snpEnrichment: https://cran.r-project.org/web/packages/snpEnrichment/index.html
maintained by Dr Mickael Canouil
More open-source code (R/C++) available here: https://github.com/loic-yengo/

## Service and Engagement

2023 – present: Deputy Chair of the IMB Culture Committee.
2021 – 2022: Chair of an Invited Session at the 2022 American Society of Human Genetics meeting (>7,000 attendees). Co-organiser of the IMB Friday Seminar Series, which attracts both national and international speakers. Organising committee of the Australia and New Zealand's Statistical Genetics community conference (Gene Mappers). Member of IMB's Student Recruitment and Training (STAR) Committee. Member of IMB's Awards and Recognition Committee.

2020: Member of the organising committee of the Online International Conference in Quantitative Genetics (moderator and abstract reviewer).

2019 – 2022: Member of 15 PhD committees at UQ and 1 at the University of Amsterdam. Chair of Examiners of 3 PhD theses at UQ.

July 2017 – March 2019: Organisation of Journal Club in Complex Traits Genetics (IMB / UQ).

From 2012: Academic reviewer (3 to 5 articles per year) for a number of scientific journals including Nature, Science, Nature Genetics, Nature Human Behaviour, Nature Communications, Genetics, The European Journal of Human Genetics, The American Journal of Human Genetics, The Journal of Clinical Endocrinology and Metabolism, BMC Medical Genetics, Diabetes, The International Journal of Epidemiology.

## Career-best research outputs

I list below 13 studies that I led and published as (co)first- and (co)last-author over the past 8 years. Each of these studies introduced novel statistical approaches for analysing genomic data and led to significant discoveries regarding the genetic architecture of complex traits and diseases (ORCID: 0000-0002-4272-9305).

[*****] denotes co-first/last authorship.
[#] denotes corresponding author.

Campos A.I. et al., Yengo L[#]. (2023) *Boosting the power of genome-wide association studies within and across ancestries by using polygenic scores*. ***Nat. Genetics***. (published on September 18th 2023)

Qiao Z et al., Yengo L[#]. (2023) *Estimation and implications of the genetic architecture of fasting and non-fasting blood glucose*. ***Nat. Comm***. 14 (1), 451. (this study was published in January 2023 – no citation so far)

Yengo L[#] et al. (2022) *A Saturated Map of Common Genetic Variants Associated with human Height*. ***Nature*** 610(7933), 704 – 712. (>60 citations over 6 months).

Yengo L[#] et al. (2021) *Genomic Partitioning of Inbreeding Depression in Humans*. ***AJHG*** 108(8),1488–1501. (>4 citations)

Hivert V. et al., Yengo L*, Visscher P.M*. (2021). *Estimation of non-additive genetic variance in human complex traits from a large sample of unrelated individuals. AJHG* 108 (5), 786 – 798. (>63 citations).

Wang Y et al., Yengo L[#] (2020) *Theoretical and empirical quantification of the accuracy of polygenic scores in ancestry divergent populations*. ***Nat. Comm***. 11 (1), 3865. (>130 citations).

Yengo L[#] et al. (2019) *Extreme Inbreeding in a European ancestry sample from the contemporary UK population*. ***Nat. Comm***. 10 (1), 3719. (>29 citations).

Yengo L[#] et al. (2018) *Imprint of Assortative Mating on the Human Genome*. ***Nat. Hum. Behav***. 2, 948. (>94 citations).

Yengo L[#] et al. (2018) *Meta-analysis of genome-wide association studies for height and body mass index in ~700,000 individuals of European ancestry*. ***Hum. Mol. Genet***. 27, 3641-3649. (>1574 citations – **Clarivate Highly Cited paper**)

Abderrahmani A*, Yengo L* et al. (2018) *Increased Hepatic PDGF-AA Signalling Mediates Liver Insulin Resistance in Obesity-Associated Type 2 Diabetes*. ***Diabetes***. 67(7):1310-1321. (>66 citations)

Yengo L[#] et al. (2017) *Detection and quantification of inbreeding depression for complex traits*. ***PNAS*** 114, 8602-8607. (>49 citations).

Bonnefond A*, Yengo L* et al. (2017) *Relationship between salivary/pancreatic amylase and body mass index: A systems biology approach*. ***BMC Medicine*** 15(1):37. (>57 citations).

Yengo L*, Arredouani A* et al. (2016) *Impact of statistical models on the prediction of type 2 diabetes using non-targeted metabolomics profiling*. ***Molecular Metabolism*** 5(10):918-925. (>22 citations).

## Invited journal articles

Yengo L. (2023) Mate Choice Through a Genomic Lens. ***Nat. Rev. Genet***. **24**, 664 (2023).

Yengo L. & Colleran H. (2022) Constrained human genes under scrutiny. ***Nature***. (News and Views Forum)

## Other peer-reviewed journal articles

### 2024

Cabrera-Mendoza B., Wendt G.A, Pathak L., Yengo L*., Polimanti* R. (2024) The impact of assortative mating, participation bias and socioeconomic status on the polygenic risk of behavioural and psychiatric traits. ***Nature Human Behaviour***. (in press)

### 2023

Hawkes G., Yengo L. et al. (2023) Identification and analysis of individuals who deviate from their genetically-predicted phenotype. ***Plos Genet***. 19(9):e1010934

Baronas J.M. et al. (2023) Genome-wide CRISPR screening of chondrocyte maturation newly implicates genes in skeletal growth and height-associated GWAS loci. ***Cell Genomics***. Apr 14;3(5):100299.

Abellaloui A., Yengo L., Verweij K.J.H. & Visscher P.M. (2023) 15 years of GWAS discovery: Realizing the promise. ***AJHG*** 110(2): 179-194.

Visscher P.M. & Yengo L. (2023) The Effect of the Scale of Grant Scoring on Ranking Accuracy. ***F1000*** 11(1197).

Mbarek H. et al. (2023) Genome-wide association study meta-analysis of dizygotic twinning illuminates genetic regulation of female fecundity. ***Human Reproduction***. 39(1):240 - 257

Wang X. et al. (2023) Cross-ancestry analyses identify new genetic loci associated with 25-hydroxyvitamin D. ***Plos Genetic***. 19(11,e1011033

### 2022

Okbay et al. (2022) Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. ***Nat. Genet.*** 54(4): 437-449.

Mahajan et al. (2022) Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. ***Nat. Genet.*** 54(5): 560-572.

Pang S. Yengo L. et al. (2022) Genetic and Modifiable Risk Factors Combine Multiplicatively in Common Disease. ***Clin. Res. Card.*** 112: 247-257.

Wainschtein et al. (2022) Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. ***Nat. Genet***. 54(3): 263-273.

Gomez et al. (2022) Phenotypic and genetic factors associated with donation of DNA and consent to record linkage for prescription history in the Australian Genetics of Depression Study. ***Eur. Arch. of Psych and Clin. Neurosci***. 1-10

Huang et al. (2022) Genomics and Phenomics of Body Mass Index Reveals a Complex Disease Network. ***Nat. Comm***. 13 (1), 7973.

Yamamoto et al. (2022) Genetic footprints of assortative mating in the Japanese population. ***Nat Hum. Behav***. 7(1): 65-73.

Border et al. (2022) Assortative mating biases marker-based heritability estimators. ***Nat. Comm***. 13(1), 1- 10.

## 2021

Niemi M.E.K. et al. (2021) Mapping the human genetic architecture of COVID-19. ***Nature*** 600, 472 – 477.

Visscher P.M, Yengo L., Cox N.J., Wray N.R. (2021) Discovery and implications of polygenicity of common diseases. ***Science*** 373 (6562) 1468 – 1473.

Pathak et al. (2021). Integrative genomic analyses identify susceptibility genes underlying COVID-19 hospitalization. ***Nat. Comm.*** 12 (1):1-11.

Chen et al. (2021) The trans-ancestral genomic architecture of glycemic traits. ***Nat. Genet.*** 53(6):840-860.

Porcu E. et al. (2021). *Triangulating evidence from longitudinal and Mendelian randomization studies of metabolomic biomarkers for type 2 diabetes* ***Scientific Reports*** 11(1), 1-10.

Guo J. et al (2021) *Quantifying genetic heterogeneity between continental populations for human height and body mass index*. ***Scientific Reports*** 11(1), 1-9.

Zeng J. et al. (2021) *Widespread signatures of natural selection across human complex traits and functional genomic categories*. ***Nat. Comm.*** 12:1164.

Kemper K., Yengo L. et al. Phenotypic covariance across the entire spectrum of relatedness for 86 billion pairs of individuals. ***Nat. Comm*** 12:1050.

Lagou V. et al. *Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability*. ***Nat. Comm*** 12:24.

Volgelezang S. *Novel loci for childhood body mass index and shared heritability with adult cardiometabolic traits*. ***Plos Genetics***. 16(10), e1008718.

Bonnefond et al. *Pathogenic variants in actionable MODY genes are associated with type 2 diabetes*. ***Nat. Metab.*** 2(10):1126-1134.

## 2020

Zhang Q. et al. (2020). *Risk prediction of late-onset Alzheimer's disease implies an oligogenic architecture.* ***Nat. Comm***. 11(1), 1-11.

Couvy-Duschene B. et al. (2020). *A unified framework for association and prediction from vertex-wise grey-matter structure* ***Hum. Brain. Map***. 41(14), 4062-4076.

Baselmans B.M.L., Yengo L., van Rheenen W., Wray N.R. (2020) *Risk in Relatives, Heritability, SNP-Based Heritability, and Genetic Correlations in Psychiatric Disorders: A Review*. ***Biol. Psychiatry*** 89(1):11-19.

Raymond B., Yengo L., et al. (2020) Using prior information from humans to prioritize genes and gene-associated variants for complex traits in livestock. ***Plos Genetics***. 16(9), e1008780.

Muto V. et al. Alzheimer's disease genetic risk and sleep phenotypes: association with more slow waves and daytime sleepiness. ***Sleep*** 44(1):zsaa137.

## 2019

Lloyd-Jones L. et al. (2019) *Improved polygenic prediction by Bayesian multiple regression on summary statistics*. ***Nat. Comm***. 10:5086.

Wu Y. et al. (2019) *Genome-wide association study of medication-use and associated disease in the UK Biobank*. ***Nat. Comm***. 10:1891.

Yengo L. et al. (2019) *No evidence for social genetic effects or genetic similarity among friends beyond that due to population stratification: a reappraisal of Domingue et al (2018)*. ***Behavior Genetics***. 50:67–71.

Liu C.T. et al. (2019) *Genome-wide Association study of Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals*. ***Scientific Report***. 9:9439.

Wray N. & Yengo L. et al. (2019) *Assortative mating in autism spectrum disorder: toward an evidence base from DNA data, but not there yet*. ***Biol. Psychiatry***. 86(4): 250–252.

Abdellaoui A. et al. (2019) *Genetic correlates of social stratification in Great Britain***. *Nat. Hum. Behav*. 3**:1332–1342

## 2018

Yengo L. & Visscher P.M. (2018) *Assortative Mating on Complex Traits Revisited: Double first cousins and the X-chromosome*. ***Theor. Popul. Biol***. 124:51-60.

Yengo L. et al. *Reply to Kardos et al.: Estimation of inbreeding depression from SNP data*. ***PNAS*** 115:E2494-E2495 (2018).

Zeng J. et al. (2018) *Signatures of negative selection in the genetic architecture of human complex traits.* ***Nat. Genet***. 50(5): 747-753.

Xue A. et al. *Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes*. ***Nat. Comm***. Jul 27; 9(1):2941 (2018).

Yap C.X. Sirodenko J., Marioni R.E., Yengo L., Wray N.R. & Visscher P.M. *Misestimation of heritability and prediction accuracy of male-pattern baldness*. ***Nat. Comm***. Jul 29; 9(1):2537 (2018).

Lee J.J. et al. et al. *Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals*. ***Nat. Genet***. 50(8): 1112-1121 (2018).

Colodro-Conde L. et al. *Association between population density and genetic risk for schizophrenia*. ***JAMA Psychiatry*** 75 (9): 901-910 (2018).

## 2017

Wheeler E. et al. *Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: a transethnic genome-wide association study*. ***Plos Medicine*** 14(9) (2017).

Verbanck M. et al. *Low-dose exposure to bisphenols A, F and S of human primary adipocyte impacts coding and non-coding RNA profiles*. ***Plos One*** 12(6) (2017).

Gopal P., Cobb J., Yengo L., et al. *Early metabolic markers identify potential targets for the prevention of type 2 diabetes*. ***Diabetologia*** 60(9):1740-1750 (2017).

Scott R et al. *An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans*. ***Diabetes*** 66(11):2888-2902 (2017).

## 2016

Field Y., Boyle E.A., Telis N., Gao Z., Gaulton K.J., Golan D., Yengo L., Rocheleau G., Froguel P., McCarthy M. & Pritchard J.K. (2016) *Detection of human adaptation during the past 2000 years*. ***Science*** 354(6313):760-764.

Lazaridis I. et al., Yengo L., Hovhannisyan N.A., Patterson N., Pinhasi R. & Reich D. (2016) *Genomic insights into the origin of farming in the ancient Near East*. ***Nature*** 536:419-424.

Justice A.E. et al. *Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits*. ***Nat. Comm***. 8:14977 (2016).

Graff M. et al *Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults*. ***Plos Genet***. 13(8): e1006972 (2016).

Schumann G. et al. *KLB is associated with alcohol drinking, and its gene product β-Klotho is necessary for FGF21 regulation of alcohol preference*. ***PNAS*** 113 (50): 14372-14377 (2016).

Barban N. et al. *Genome-wide analysis identifies 12 loci influencing human reproductive behavior*. ***Nat. Genet***. 48(12):1462-1472 (2016).

Ehret G.B. et al. *The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals*. ***Nat. Genet***. 48(10):1171-1184 (2016).

Morandi A., Bonnefond A. Lobbens S. Yengo L. et al. *Associations between type 2 diabetes-related genetic scores and metabolic traits, in obese and normal-weight youths*. ***JCEM*** 101(11):4244-4250 (2016).

Fuchsberger C. et al. *The genetic architecture of type 2 diabetes*. ***Nature*** 536(7614):41-47 (2016)

Favennec M. et al. *Post-Bariatric Surgery Changes in Quinolinic and Xanthurenic Acid Concentrations Are Associated with Glucose Homeostasis*. ***PLoS One*** 11(6):e0158051 (2016)

Rabhi N et al. *KAT2B Is Required for Pancreatic Beta Cell Adaptation to Metabolic Stress by Controlling the Unfolded Protein Response*. ***Cell Reports*** 15(5):1051-1061 (2016)

Horikoshi M. et al. *Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms*. ***Hum. Mol. Genet***. 25(10):2070-2081 (2016)

Lu Y. et al. *New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk*. ***Nat. Comm***. 7(10495) (2016).

Pattaro C. et al. *Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function*. ***Nat. Comm***. 7:10023. (2016)

Felix J.F. et al. *Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index*. ***Hum. Mol. Genet***. 25(2):389-403 (2016)

## 2015

Gaulton K.J. et al. *Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci*. ***Nat. Genet***. 47(12):1415-1425 (2015)

Winkler T.W. et al. *The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study*. ***PLoS Genet***. 11(10)e1005378 (2015)

Favennec M., Hennart B., Caiazzo R., Leloire A., Yengo L. et al. *The Kynurenine Pathway is Activated in Human Obesity and Shifted Toward Kynurenine Monooxygenase Activation*. ***Obesity*** 23(10):2066-74 (2015)

Joshi P.K. et al. *Directional dominance on stature and cognition in diverse human populations*. ***Nature*** 523(7561):459-462 (2015)

Chambers J.C. et al. *Epigenome-wide association of DNA methylation markers in peripheral blood from Indian Asians and Europeans with incident type 2 diabetes: A nested case-control study*. ***Lancet. Endocrin***. 3(7):526-534 (2015)

Bonnefond A, Yengo L. et al. *The loss-of-function PCSK9 p.R46L genetic variant does not alter glucose homeostasis*. ***Diabetologia*** 58(9):2051-2055 (2015)

Al-Sinani S et al. Yengo L., Froguel P. & Bayoumi R. *Association of gene variants with susceptibility to type 2 diabetes among Omanis*. ***WJD*** 6(2):358-66 (2015)

Shungin D. et al. *New genetic loci link adipose and insulin biology to body fat distribution.* ***Nature*** 518 (7538):187-196 (2015).

Locke et al. *Genetic studies of body mass index yield new insights for obesity biology*. ***Nature*** 518(7538):197-206 (2015).

Mejía-Benítez M.A., Bonnefond A., Yengo L. et al. *Beneficial effect of a high number of copies of salivary amylase AMY1 gene on obesity risk in Mexican children*. ***Diabetologia*** 11/2014; 58(2):290-294 (2015)

## 2014

Wood A.R. et al. *Defining the role of common variation in the genomic and biological architecture of adult human height*. ***Nat. Genet.*** 46(11):11731186 (2014)

Rouskas K., Cauchi S., Raverdy V., Yengo L., Froguel P. & Pattou F. *Weight loss independent association of TCF7L2 gene polymorphism with fasting blood glucose after Roux-en-Y Gastric Bypass in type 2 diabetic patients*. ***Surgery for Obesity and Related Diseases*** 10(4):679-683 (2014)

Vaxillaire M., Yengo L. et al. *Type 2 diabetes-related genetic risk scores associated with variations in fasting plasma glucose and development of impaired glucose homeostasis in the prospective DESIR study*. ***Diabetologia*** 57(8):1601-1610 (2014)

Yengo L., Jacques J. & Biernacki C. et al. *Variable clustering in high dimensional linear regression models*. ***Journal de la Société de Statistique de Paris (SFdS)***. 155(2):38-56 (2014).

Mahajan A. et al. *Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility*. ***Nat. Genet***. 46(3):234-244 (2014)

Dik V.K. et al. *Coffee and tea consumption, genotype- based CYP1A2 and NAT2 activity and colorectal cancer risk- Results from the EPIC cohort study*. ***Intern. J. Cancer***. 135(2):401-412 (2014)

## 2013

Bonnet F. et al. *Parental history of type 2 diabetes, TCF7L2 variant and lower insulin secretion are associated with incident hypertension. Data from the DESIR and RISC cohorts*. ***Diabetologia*** 56(11):2414-2423 (2013)

Bottolo L et al. *GUESS-ing Polygenic Associations with Multiple Phenotypes Using a GPU-Based Evolutionary Stochastic Search Algorithm*. ***PLoS Genet***. 9(8):e1003657 (2013)

Bonnefond A et al. Yengo L. & Froguel P. *Association between large detectable clonal mosaicism and type 2 diabetes with vascular complications*. ***Nat. Genet***. 45(9):1040-1043 (2013)

Robiou-du-Pont S, Yengo L. et al. *Common variants near BDNF and SH2B1 show nominal evidence of association with snacking behavior in European populations*. ***J Mol. Med***. 91(9):1109-1115 (2013).

den Hoed M. et al. *Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders*. ***Nat. Genet***. 45(6):621-631 (2013)

Bonnefond A. et al. *Transcription factor gene MNX1 is a novel cause of permanent neonatal diabetes in a consanguineous family*. ***Diabetes & Metabolism*** 39(3):276-280 (2013)

Mejía-Benítez M.A., Klünder-Klünder M., Yengo L. et al. *Analysis of the contribution of FTO, NPC1, ENPP1, NEGR1, GNPDA2 and MC4R genes to obesity in Mexican children*. ***BMC Med Genet*** 14(1):21 (2013)

Köttgen A. et al. *Genome-wide association analyses identify 18 new loci associated with serum urate concentrations*. ***Nat. Genet***. 45(2):145-154 (2013)

Bonnefond A., Yengo L. et al. *Reassessment of the putative role of BLK-p.A71T loss-of-function mutation in MODY and type 2 diabetes*. ***Diabetologia*** 56(3):492-496 (2013)

Albrechtsen A. et al. *Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes*. ***Diabetologia*** 56(2):298-310 (2013)

Robiou-du-Pont S., Bonnefond A., Yengo L. et al. *Contribution of 24 obesity-associated genetic variants to insulin resistance, pancreatic beta-cell function and type 2 diabetes risk in the French population*. ***IJO*** 37(7):980-985 (2013)

## 2012

Scott R.A. et al. *Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways*. ***Nat. Genet***. 44(9):991-1005 (2012)

Morris A.P. et al. *Large-scale association analysis provides insights into the genetic architecture and pathophysiology of Type 2 diabetes*. ***Nat. Genet***. 44(9):981-990 (2012)

Perry J.R.B, Voight B.F., Yengo L. et al. *Stratifying Type 2 Diabetes Cases by BMI Identifies Genetic Risk Variants in LAMA1 and Enrichment for Risk Variants in Lean Compared to Obese Cases*. ***PLoS Genet***; 8(5):e1002741 (2012)

Cauchi S. et al. *European genetic variants associated with type 2 diabetes in North African Arabs*. ***Diabetes & Metabolism*** 38(4):316-23 (2012)

Ichimura A. et al. *Dysfunction of lipid sensor GPR120 leads to obesity in both mouse and human*. ***Nature*** 483(7389):350-354 (2012)

Bonnefond A., Clement N., Fawcett K, Yengo L. et al. *Rare MTNR1B variants impairing melatonin receptor 1B function contribute to type 2 diabetes*. ***Nat. Genet***. 44(3):297-301 (2012)

Marquez M. et al. *Low-Frequency Variants in HMGA1 Are Not Associated With Type 2 Diabetes Risk*. ***Diabetes*** 61(2):524-30 (2012)

Creemers J.W.M. et al. *Heterozygous Mutations Causing Partial Prohormone Convertase 1 Deficiency Contribute to Human Obesity*. ***Diabetes*** 61(2):383-90 (2012)

## 2011

Bonnefond A. et al. *Disruption of a novel KLF-p300-regulated pathway for insulin biosynthesis revealed by studies of the c.-331 INS mutation found in neonatal diabetes mellitus*. ***J. Biol. Chem***. 286(32):28414-28424 (2011).

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## Pre-prints

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