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Publications (2)

Perola M, Vartiainen E, Jousilahti P, Rao D, Sarzynski M, Sørensen T, Astrup A, Kloppenburg M, Meulenbelt I, Zhang Y, Hofman A, Rivadeneira F, Jula A, Koskinen S, Knekt P, Heliövaara M, Eriksson J, Palotie A, Osmond C, Kajantie E, Uitterlinden A, Zeller T, Yao J, Sattar N, Ridker P, Brent Richards J, Rice T, Rathmann W, Rasmussen-Torvik L, Rankinen T, Pradhan A, Peters A, Savage D, Söderberg S, Wood A, Widén E, Wichmann H, Walker M, Vohli M, Uh H, van Heemst D, Vandenput L, Timpson N, Paternoster L, Loos R, Hansen T, Vestergaard H, Vollenweider P, Waeber G, Bergmann S, Waterworth D, Borecki I, Pramstaller P, Frayling T, Pedersen O, Hu F, Leibel R, Lindgren C, Franks P, Schadt E, Klein R, Jukema J, Spector T, Grallert H, Eline Slagboom P, Ferrucci L, Wareham N, März W, Bandinelli S, Casas J, Lorentzon M, Mellström D, Raitakari O, Lehtimäki T, Kähönen M, Viikari J, Isaacs A, van Dijk K, Langenberg C, Scott R, Lind L, Ohlsson C, Chasman D, Allison M, Bouchard C, Harris T, van Duijn C, Huupponen R, Nalls M, Buckley B, Liu Y, Guo X, Rose L, Mahajan A, Willems S, Renström F, Pasko D, Del Greco M F, Luan J, Kleber M, Pérusse L, Blangero J, Bellis C, Barroso I, Amuzu A, Amin N, Ramos Y, Ju Sung Y, Ahluwalia T, Gaunt T, Tanaka T, Lahti J, Zhao J, Hayes J, Drong A, Hedman Å, Feitosa M, Kriebel J, Sun Q, Skowronski A, Carli J, Pers T, Schick U, Henneman P, Eriksson J, Lyytikäinen L, Beekman M, Kristiansson K, Mangino M, Trompet S, Kutalik Z, Grarup N, Kilpeläinen T, Männistö S, Kraft P, Koenig W, Karlsson M, Jørgensen T, Jørgensen M, Jenny N, Jansson J, Ioan-Facsinay A, Ingelsson E, Kwekkeboom J, Laatikainen T, Myers R, Morris A, Menni C, Meisinger C, Marques-Vidal P, Lu Y, Lowe G, LeDuc C, Ladwig K, Illig T, Hunter D, Demirkan A, Delgado G, Deelen J, Day F, Dastani Z, Dale C, Crosslin D, de Craen A, I Chen Y, Finucane F, Ford I, Hicks A, Hernandez D, Herder C, Havulinna A, Hankinson S, Hallmans G, Gustafsson S, Gieger C, Garcia M, Böhringer S. Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. *Nat Commun* 2016; 7:10494.

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Defining the role of common variation in the genomic and biological architecture of adult human height. *Nat Genet* 2014; 46:1173-86.

Projects (0)

No results found.

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