

# Defining the role of common variation in the genomic architecture of adult human height

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Mental health: Depression needs large human-genetics studies. <i>Nature</i> , 2014, 515, 189-191.	13.7	40
2	Compiling the Complement of Genes Implicated in Coronary Artery Disease. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 738-740.	5.1	4
3	High Time for Human Height. <i>Peritoneal Dialysis International</i> , 2014, 34, 685-686.	1.1	1
4	Daily variations in sleep: associated genes and effects on affect. <i>Journal of Sleep Research</i> , 2014, 23, 607-608.	1.7	1
5	All Humans, Great or Small, Short or Tall. <i>Molecular Syndromology</i> , 2014, 5, 257-258.	0.3	0
6	The CODATwins Project: The Cohort Description of Collaborative Project of Development of Anthropometrical Measures in Twins to Study Macro-Environmental Variation in Genetic and Environmental Effects on Anthropometric Traits. <i>Twin Research and Human Genetics</i> , 2015, 18, 348-360.	0.3	55
7	Polygenic Influence on Educational Attainment. <i>AERA Open</i> , 2015, 1, 233285841559997.	1.3	132
8	Editorial overview: Molecular and genetic bases of disease: Enter the post-GWAS era. <i>Current Opinion in Genetics and Development</i> , 2015, 33, 77-79.	1.5	5
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10	Schizophrenia. <i>Nature Reviews Disease Primers</i> , 2015, 1, 15067.	18.1	724
11	On improving the credibility of candidate gene studies: A review of candidate gene studies published in <i>Emotion</i> . <i>Emotion</i> , 2015, 15, 531-537.	1.5	12
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15	Genetic determination of height-mediated mate choice. <i>Genome Biology</i> , 2015, 16, 269.	3.8	33
16	De novo mutations in ARID1B associated with both syndromic and non-syndromic short stature. <i>BMC Genomics</i> , 2015, 16, 701.	1.2	27
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18	Explicit Modeling of Ancestry Improves Polygenic Risk Scores and BLUP Prediction. <i>Genetic Epidemiology</i> , 2015, 39, 427-438.	0.6	30

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22	Predictors of Pulmonary Infarction. <i>Medicine (United States)</i> , 2015, 94, e1488.	0.4	36
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31	Contrasting genetic architectures in different mouse reference populations used for studying complex traits. <i>Genome Research</i> , 2015, 25, 775-791.	2.4	56
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143	A prospective study of measured body size and height and risk of keratinocyte cancers and melanoma. <i>Cancer Epidemiology</i> , 2016, 40, 119-125.	0.8	27
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160	Detection of human adaptation during the past 2000 years. <i>Science</i> , 2016, 354, 760-764.	6.0	336
161	Genome-wide associations for birth weight and correlations with adult disease. <i>Nature</i> , 2016, 538, 248-252.	13.7	406
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164	Genome-wide association analysis identifies variation in vitamin D receptor and other host factors influencing the gut microbiota. <i>Nature Genetics</i> , 2016, 48, 1396-1406.	9.4	533
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171	Gene set analysis for interpreting genetic studies. <i>Human Molecular Genetics</i> , 2016, 25, R133-R140.	1.4	12
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526	Multi-polygenic score approach to trait prediction. <i>Molecular Psychiatry</i> , 2018, 23, 1368-1374.	4.1	167
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