Marie Verbanck

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3194652/publications.pdf

Version: 2024-02-01

22 papers 5,584 citations

16 h-index 17 g-index

25 all docs

25 docs citations

25 times ranked 8476 citing authors

#	Article	IF	CITATIONS
1	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. Genome Biology, 2021, 22, 49.	3.8	150
2	The expression of genes in top obesity-associated loci is enriched in insula and substantia nigra brain regions involved in addiction and reward. International Journal of Obesity, 2020, 44, 539-543.	1.6	38
3	Tissue-specific genetic features inform prediction of drug side effects in clinical trials. Science Advances, 2020, 6, .	4.7	33
4	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study. PLoS Genetics, 2020, 16, e1008684.	1.5	17
5	Title is missing!. , 2020, 16, e1008684.		O
6	Title is missing!. , 2020, 16, e1008684.		0
7	Title is missing!. , 2020, 16, e1008684.		O
8	Title is missing!. , 2020, 16, e1008684.		0
9	Title is missing!. , 2020, 16, e1008684.		O
10	Title is missing!. , 2020, 16, e1008684.		0
10	Title is missing!., 2020, 16, e1008684. HOPS: a quantitative score reveals pervasive horizontal pleiotropy in human genetic variation is driven by extreme polygenicity of human traits and diseases. Genome Biology, 2019, 20, 222.	3.8	0 47
	HOPS: a quantitative score reveals pervasive horizontal pleiotropy in human genetic variation is	3.8	
11	HOPS: a quantitative score reveals pervasive horizontal pleiotropy in human genetic variation is driven by extreme polygenicity of human traits and diseases. Genome Biology, 2019, 20, 222. Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570,		47
11 12	HOPS: a quantitative score reveals pervasive horizontal pleiotropy in human genetic variation is driven by extreme polygenicity of human traits and diseases. Genome Biology, 2019, 20, 222. Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518. No causal effects of serum urate levels on the risk of chronic kidney disease: A Mendelian	13.7	47 679
11 12 13	HOPS: a quantitative score reveals pervasive horizontal pleiotropy in human genetic variation is driven by extreme polygenicity of human traits and diseases. Genome Biology, 2019, 20, 222. Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518. No causal effects of serum urate levels on the risk of chronic kidney disease: A Mendelian randomization study. PLoS Medicine, 2019, 16, e1002725. Detection of widespread horizontal pleiotropy in causal relationships inferred from Mendelian	13.7 3.9	47 679 97
11 12 13	HOPS: a quantitative score reveals pervasive horizontal pleiotropy in human genetic variation is driven by extreme polygenicity of human traits and diseases. Genome Biology, 2019, 20, 222. Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518. No causal effects of serum urate levels on the risk of chronic kidney disease: A Mendelian randomization study. PLoS Medicine, 2019, 16, e1002725. Detection of widespread horizontal pleiotropy in causal relationships inferred from Mendelian randomization between complex traits and diseases. Nature Genetics, 2018, 50, 693-698. 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, 2018,	13.7 3.9 9.4	47 679 97 3,593
11 12 13 14	HOPS: a quantitative score reveals pervasive horizontal pleiotropy in human genetic variation is driven by extreme polygenicity of human traits and diseases. Genome Biology, 2019, 20, 222. Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518. No causal effects of serum urate levels on the risk of chronic kidney disease: A Mendelian randomization study. PLoS Medicine, 2019, 16, e1002725. Detection of widespread horizontal pleiotropy in causal relationships inferred from Mendelian randomization between complex traits and diseases. Nature Genetics, 2018, 50, 693-698. 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, 2018, 103, 691-706. Expression and functional assessment of candidate type 2 diabetes susceptibility genes identify four	13.7 3.9 9.4 2.6	47 679 97 3,593

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19	DNA Damage and the Activation of the p53 Pathway Mediate Alterations in Metabolic and Secretory Functions of Adipocytes. Diabetes, 2016, 65, 3062-3074.	0.3	92
20	The kynurenine pathway is activated in human obesity and shifted toward kynurenine monooxygenase activation. Obesity, 2015, 23, 2066-2074.	1.5	196
21	Regularised PCA to denoise and visualise data. Statistics and Computing, 2015, 25, 471-486.	0.8	23
22	A new unsupervised gene clustering algorithm based on the integration of biological knowledge into expression data. BMC Bioinformatics, 2013, 14, 42.	1.2	20