Thibaud S Boutin

List of Publications by Year
in descending order

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38 papers	4,570 citations	331670 21 h-index	315739 38 g-index
48 all docs	48 docs citations	48 times ranked	9660 citing authors

#	Article	IF	Citations
1	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
2	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
3	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
4	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
5	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	21.4	328
6	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. Nature Metabolism, 2020, 2, 1135-1148.	11.9	327
7	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
8	The struggle for life of the genome's selfish architects. Biology Direct, 2011, 6, 19.	4.6	198
9	Long-term evolution of transposable elements. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 19375-19380.	7.1	151
10	New insights into the genetics of primary open-angle glaucoma based on meta-analyses of intraocular pressure and optic disc characteristics.. Human Molecular Genetics, 2017, 26, ddw399.	2.9	120
11	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	12.8	118
12	An epigenome-wide association study of sex-specific chronological ageing. Genome Medicine, 2020, 12, 1.	8.2	117
13	Exploration of haplotype research consortium imputation for genome-wide association studies in 20,032 Generation Scotland participants. Genome Medicine, 2017, 9, 23.	8.2	110
14	Genome-wide meta-analyses of stratified depression in Generation Scotland and UK Biobank. Translational Psychiatry, 2018, 8, 9.	4.8	66
15	Cross-ancestry genome-wide association analysis of corneal thickness strengthens link between complex and Mendelian eye diseases. Nature Communications, 2018, 9, 1864.	12.8	63
16	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
17	How does selfing affect the dynamics of selfish transposable elements?. Mobile DNA, 2012, 3, 5.	3.6	44
18	Characterisation of an inflammation-related epigenetic score and its association with cognitive ability. Clinical Epigenetics, 2020, 12, 113.	4.1	38

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19	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. Nature Communications, 2019, 10, 1383.	12.8	37
20	When do myopia genes have their effect? Comparison of genetic risks between children and adults. Genetic Epidemiology, 2016, 40, 756-766.	1.3	34
21	Linking protein to phenotype with Mendelian Randomization detects 38 proteins with causal roles in human diseases and traits. PLoS Genetics, 2020, 16, e1008785.	3.5	29
22	Genome-wide Regional Heritability Mapping Identifies a Locus Within the TOX2 Gene Associated With Major Depressive Disorder. Biological Psychiatry, 2017, 82, 312-321.	1.3	26
23	Insights into the genetic basis of retinal detachment. Human Molecular Genetics, 2020, 29, 689-702.	2.9	26
24	Multi-trait genome-wide association study identifies new loci associated with optic disc parameters. Communications Biology, 2019, 2, 435.	4.4	22
25	Genetic Landscape of the ACE2 Coronavirus Receptor. Circulation, 2022, 145, 1398-1411.	1.6	20
26	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	3.6	19
27	An actionable KCNH2 Long QT Syndrome variant detected by sequence and haplotype analysis in a population research cohort. Scientific Reports, 2019, 9, 10964.	3.3	17
28	Genome-wide meta-analysis identifies novel gender specific loci associated with thyroid antibodies level in Croatians. Genomics, 2019, 111, 737-743.	2.9	11
29	Genome-wide meta-analysis identifies novel loci associated with parathyroid hormone level. Molecular Medicine, 2018, 24, 15.	4.4	8
30	Genome-Wide Analysis Identifies Two Susceptibility Loci for Positive Thyroid Peroxidase and Thyroglobulin Antibodies. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 944-951.	3.6	6
31	Fine-mapping and cell-specific enrichment at corneal resistance factor loci prioritize candidate causal regulatory variants. Communications Biology, 2020, 3, 762.	4.4	6
32	Genome-wide association meta-analysis for total thyroid hormone levels in Croatian population. Journal of Human Genetics, 2019, 64, 473-480.	2.3	5
33	Genetic Variants in the ST6GAL1 Gene Are Associated with Thyroglobulin Plasma Level in Healthy Individuals. Thyroid, 2019, 29, 886-893.	4.5	5
34	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	4
35	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	3
36	SNP and Haplotype Regional Heritability Mapping (SNHap-RHM): Joint Mapping of Common and Rare Variation Affecting Complex Traits. Frontiers in Genetics, 2021, 12, 791712.	2.3	2

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37	Genome-Wide Association Analysis and Genomic Prediction of Thyroglobulin Plasma Levels. International Journal of Molecular Sciences, 2022, 23, 2173.	4.1	1
38	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. Obstetrical and Gynecological Survey, 2015, 70, 758-762.	0.4	0