

Thibaud S Boutin

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

4,570
citations

331259

21
h-index

315357

38
g-index

48
all docs

48
docs citations

48
times ranked

9660
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Wide Association Analysis and Genomic Prediction of Thyroglobulin Plasma Levels. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2173.	1.8	1
2	Genetic Landscape of the ACE2 Coronavirus Receptor. <i>Circulation</i> , 2022, 145, 1398-1411.	1.6	20
3	SNP and Haplotype Regional Heritability Mapping (SNHap-RHM): Joint Mapping of Common and Rare Variation Affecting Complex Traits. <i>Frontiers in Genetics</i> , 2021, 12, 791712.	1.1	2
4	An epigenome-wide association study of sex-specific chronological ageing. <i>Genome Medicine</i> , 2020, 12, 1.	3.6	117
5	Genome-Wide Analysis Identifies Two Susceptibility Loci for Positive Thyroid Peroxidase and Thyroglobulin Antibodies. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, 944-951.	1.8	6
6	Insights into the genetic basis of retinal detachment. <i>Human Molecular Genetics</i> , 2020, 29, 689-702.	1.4	26
7	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , 2020, 2, 1135-1148.	5.1	327
8	Characterisation of an inflammation-related epigenetic score and its association with cognitive ability. <i>Clinical Epigenetics</i> , 2020, 12, 113.	1.8	38
9	Fine-mapping and cell-specific enrichment at corneal resistance factor loci prioritize candidate causal regulatory variants. <i>Communications Biology</i> , 2020, 3, 762.	2.0	6
10	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, 2542.	5.8	59
11	Linking protein to phenotype with Mendelian Randomization detects 38 proteins with causal roles in human diseases and traits. <i>PLoS Genetics</i> , 2020, 16, e1008785.	1.5	29
12	Variants associated with HHIP expression have sex-differential effects on lung function. <i>Wellcome Open Research</i> , 2020, 5, 111.	0.9	3
13	Variants associated with HHIP expression have sex-differential effects on lung function. <i>Wellcome Open Research</i> , 2020, 5, 111.	0.9	4
14	An actionable KCNH2 Long QT Syndrome variant detected by sequence and haplotype analysis in a population research cohort. <i>Scientific Reports</i> , 2019, 9, 10964.	1.6	17
15	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	9.4	251
16	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	9.4	549
17	Genome-wide association meta-analysis for total thyroid hormone levels in Croatian population. <i>Journal of Human Genetics</i> , 2019, 64, 473-480.	1.1	5
18	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. <i>Nature Communications</i> , 2019, 10, 1383.	5.8	37

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19	Genetic Variants in the ST6GAL1 Gene Are Associated with Thyroglobulin Plasma Level in Healthy Individuals. <i>Thyroid</i> , 2019, 29, 886-893.	2.4	5
20	Multi-trait genome-wide association study identifies new loci associated with optic disc parameters. <i>Communications Biology</i> , 2019, 2, 435.	2.0	22
21	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. <i>Nature Genetics</i> , 2019, 51, 51-62.	9.4	328
22	Genome-wide meta-analysis identifies novel gender specific loci associated with thyroid antibodies level in Croatians. <i>Genomics</i> , 2019, 111, 737-743.	1.3	11
23	Genome-wide meta-analyses of stratified depression in Generation Scotland and UK Biobank. <i>Translational Psychiatry</i> , 2018, 8, 9.	2.4	66
24	Genome-wide meta-analysis identifies novel loci associated with parathyroid hormone level. <i>Molecular Medicine</i> , 2018, 24, 15.	1.9	8
25	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	9.4	924
26	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002037.	1.6	19
27	Cross-ancestry genome-wide association analysis of corneal thickness strengthens link between complex and Mendelian eye diseases. <i>Nature Communications</i> , 2018, 9, 1864.	5.8	63
28	New insights into the genetics of primary open-angle glaucoma based on meta-analyses of intraocular pressure and optic disc characteristics.. <i>Human Molecular Genetics</i> , 2017, 26, ddw399.	1.4	120
29	Exploration of haplotype research consortium imputation for genome-wide association studies in 20,032 Generation Scotland participants. <i>Genome Medicine</i> , 2017, 9, 23.	3.6	110
30	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	9.4	426
31	Genome-wide Regional Heritability Mapping Identifies a Locus Within the TOX2 Gene Associated With Major Depressive Disorder. <i>Biological Psychiatry</i> , 2017, 82, 312-321.	0.7	26
32	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. <i>Nature Communications</i> , 2017, 8, 910.	5.8	118
33	When do myopia genes have their effect? Comparison of genetic risks between children and adults. <i>Genetic Epidemiology</i> , 2016, 40, 756-766.	0.6	34
34	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. <i>Obstetrical and Gynecological Survey</i> , 2015, 70, 758-762.	0.2	0
35	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	9.4	357
36	How does selfing affect the dynamics of selfish transposable elements?. <i>Mobile DNA</i> , 2012, 3, 5.	1.3	44

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37	The struggle for life of the genome's selfish architects. <i>Biology Direct</i> , 2011, 6, 19.	1.9	198
38	Long-term evolution of transposable elements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 19375-19380.	3.3	151