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List of Publications by Year
in descending order

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27 papers	4,487 citations	448610 19 h-index	466096 32 g-index
36 all docs	36 docs citations	36 times ranked	9417 citing authors

#	Article	IF	Citations
1	Computational Models for Clinical Applications in Personalized Medicineâ€"Guidelines and Recommendations for Data Integration and Model Validation. Journal of Personalized Medicine, 2022, 12, 166.	1.1	24
2	A Polygenic and Phenotypic Risk Prediction for Polycystic Ovary Syndrome Evaluated by Phenome-Wide Association Studies. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 1918-1936.	1.8	40
3	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.3	26
4	Host Genetics at the Intersection of Autoimmunity and COVID-19: A Potential Key for Heterogeneous COVID-19 Severity. Frontiers in Immunology, 2020, 11, 586111.	2.2	26
5	Genetic studies of abdominal MRI data identify genes regulating hepcidin as major determinants of liver iron concentration. Journal of Hepatology, 2019, 71, 594-602.	1.8	23
6	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	2.6	21
7	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
8	The severity of ankylosing spondylitis and responses to anti-tumour necrosis factor biologics are not influenced by the tumour necrosis factor receptor polymorphism incriminated in multiple sclerosis. Genes and Immunity, 2019, 20, 167-171.	2.2	6
9	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. PLoS Genetics, 2018, 14, e1007813.	1.5	341
10	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
11	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
12	Sexual dimorphisms in genetic loci linked to body fat distribution. Bioscience Reports, 2017, 37, .	1.1	58
13	Testing the role of predicted gene knockouts in human anthropometric trait variation. Human Molecular Genetics, 2016, 25, 2082-2092.	1.4	10
14	Insights into the Genetic Susceptibility to Type 2 Diabetes from Genome-Wide Association Studies of Obesity-Related Traits. Current Diabetes Reports, 2015, 15, 83.	1.7	47
15	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
16	Genome-wide association of polycystic ovary syndrome implicates alterations in gonadotropin secretion in European ancestry populations. Nature Communications, 2015, 6, 7502.	5.8	314
17	Ankylosing spondylitis is associated with the anthrax toxin receptor 2 gene (ANTXR2). Annals of the Rheumatic Diseases, 2014, 73, 2054-2058.	0.5	20
18	A CCR6 variant strongly associated with rheumatoid arthritis in two populations is not associated with ankylosing spondylitis. Rheumatology International, 2013, 33, 2443-2444.	1.5	5

#	Article	IF	Citations
19	Identification of multiple risk variants for ankylosing spondylitis through high-density genotyping of immune-related loci. Nature Genetics, 2013, 45, 730-738.	9.4	699
20	The histone demethylase JARID1A is associated with susceptibility to ankylosing spondylitis. Genes and Immunity, 2011, 12, 395-398.	2.2	16
21	Interaction between ERAP1 and HLA-B27 in ankylosing spondylitis implicates peptide handling in the mechanism for HLA-B27 in disease susceptibility. Nature Genetics, 2011, 43, 761-767.	9.4	778
22	A common functional variant of endoplasmic reticulum aminopeptidase 2 (ERAP2) that reduces major histocompatibility complex class I expression is not associated with ankylosing spondylitis. Rheumatology, 2011, 50, 1720-1721.	0.9	15
23	Genome-wide association study of ankylosing spondylitis identifies non-MHC susceptibility loci. Nature Genetics, 2010, 42, 123-127.	9.4	573
24	The chromosome 16q region associated with ankylosing spondylitis includes the candidate gene tumour necrosis factor receptor type 1-associated death domain (TRADD). Annals of the Rheumatic Diseases, 2010, 69, 1243-1246.	0.5	33
25	Elucidating the chromosome 9 association with AS; CARD9 is a candidate gene. Genes and Immunity, 2010, 11, 490-496.	2.2	67
26	Investigating the genetic association between ERAP1 and ankylosing spondylitis. Human Molecular Genetics, 2009, 18, 4204-4212.	1.4	123
27	Association between the interleukin 23 receptor and ankylosing spondylitis is confirmed by a new UK case-control study and meta-analysis of published series. Rheumatology, 2009, 48, 386-389.	0.9	91