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List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

16 2,376 15 10 h-index g-index citations papers 16 18 4.53 3,972 L-index ext. citations avg, IF ext. papers

#	Paper	IF	Citations
15	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals <i>Nature Genetics</i> , 2022 ,	36.3	7
14	Probabilistic inference of the genetic architecture underlying functional enrichment of complex traits. <i>Nature Communications</i> , 2021 , 12, 6972	17.4	1
13	Polygenic burden could explain high rates of affective disorders in a community with restricted founder population. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2021 , 186, 367-375	3.5	
12	Estimation of non-additive genetic variance in human complex traits from a large sample of unrelated individuals. <i>American Journal of Human Genetics</i> , 2021 , 108, 786-798	11	19
11	GWAS of peptic ulcer disease implicates Helicobacter pylori infection, other gastrointestinal disorders and depression. <i>Nature Communications</i> , 2021 , 12, 1146	17.4	20
10	Genome-wide association study of dietary intake in the UK biobank study and its associations with schizophrenia and other traits. <i>Translational Psychiatry</i> , 2020 , 10, 51	8.6	10
9	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. <i>Nature Communications</i> , 2020 , 11, 1647	17.4	58
8	Risk prediction of late-onset Alzheimerks disease implies an oligogenic architecture. <i>Nature Communications</i> , 2020 , 11, 4799	17.4	41
7	Improved polygenic prediction by Bayesian multiple regression on summary statistics. <i>Nature Communications</i> , 2019 , 10, 5086	17.4	114
6	Signatures of negative selection in the genetic architecture of human complex traits. <i>Nature Genetics</i> , 2018 , 50, 746-753	36.3	178
5	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. <i>Nature Genetics</i> , 2018 , 50, 1112-1121	36.3	950
4	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. <i>Nature Communications</i> , 2018 , 9, 2941	17.4	262
3	Meta-analysis of genome-wide association studies for height and body mass index in ~700000 individuals of European ancestry. <i>Human Molecular Genetics</i> , 2018 , 27, 3641-3649	5.6	711
2	Estimation of non-additive genetic variance in human complex traits from a large sample of unrelated individuals		3
1	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration		2