Hilary C Martin

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4528450/publications.pdf

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25 papers	3,256 citations	361388 20 h-index	610883 24 g-index
40 all docs	40 docs citations	40 times ranked	6994 citing authors

#	Article	IF	Citations
1	Genome-wide association studies. Nature Reviews Methods Primers, 2021, 1, .	21.2	529
2	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
3	Evidence for 28 genetic disorders discovered by combining healthcare and research data. Nature, 2020, 586, 757-762.	27.8	343
4	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. Nature Genetics, 2015, 47, 717-726.	21.4	310
5	Common genetic variants contribute to risk of rare severe neurodevelopmental disorders. Nature, 2018, 562, 268-271.	27.8	246
6	Clinical whole-genome sequencing in severe early-onset epilepsy reveals new genes and improves molecular diagnosis. Human Molecular Genetics, 2014, 23, 3200-3211.	2.9	222
7	Point Mutations in Exon 1B of APC Reveal Gastric Adenocarcinoma and Proximal Polyposis of the Stomach as a Familial Adenomatous Polyposis Variant. American Journal of Human Genetics, 2016, 98, 830-842.	6.2	201
8	Quantifying the contribution of recessive coding variation to developmental disorders. Science, 2018, 362, 1161-1164.	12.6	158
9	Evaluating drug targets through human loss-of-function genetic variation. Nature, 2020, 581, 459-464.	27.8	115
10	Application of whole genome and RNA sequencing to investigate the genomic landscape of common variable immunodeficiency disorders. Clinical Immunology, 2015, 160, 301-314.	3.2	100
11	Human Slack Potassium Channel Mutations Increase Positive Cooperativity between Individual Channels. Cell Reports, 2014, 9, 1661-1672.	6.4	97
12	Identification of Common Genetic Variants Influencing Spontaneous Dizygotic Twinning and Female Fertility. American Journal of Human Genetics, 2016, 98, 898-908.	6.2	89
13	Cohort Profile: East London Genes & Health (ELGH), a community-based population genomics and health study in British Bangladeshi and British Pakistani people. International Journal of Epidemiology, 2020, 49, 20-21i.	1.9	71
14	MC3R links nutritional state to childhood growth and the timing of puberty. Nature, 2021, 599, 436-441.	27.8	59
15	Genetic correlates of phenotypic heterogeneity in autism. Nature Genetics, 2022, 54, 1293-1304.	21.4	51
16	Delineation of dominant and recessive forms of LZTR1â€associated Noonan syndrome. Clinical Genetics, 2019, 95, 693-703.	2.0	35
17	The contribution of X-linked coding variation to severe developmental disorders. Nature Communications, 2021, 12, 627.	12.8	33
18	Multicohort analysis of the maternal age effect on recombination. Nature Communications, 2015, 6, 7846.	12.8	29

#	Article	IF	Citations
19	Reduced reproductive success is associated with selective constraint on human genes. Nature, 2022, 603, 858-863.	27.8	29
20	Homozygous microdeletion of exon 5 in ZNF277 in a girl with specific language impairment. European Journal of Human Genetics, 2014, 22, 1165-1171.	2.8	27
21	Insights into Platypus Population Structure and History from Whole-Genome Sequencing. Molecular Biology and Evolution, 2018, 35, 1238-1252.	8.9	27
22	Integrating polygenic risk scores in the prediction of type 2 diabetes risk and subtypes in British Pakistanis and Bangladeshis: A population-based cohort study. PLoS Medicine, 2022, 19, e1003981.	8.4	24
23	Fine-scale population structure and demographic history of British Pakistanis. Nature Communications, 2021, 12, 7189.	12.8	21
24	Reply to Pembrey et al: â€˜ZNF277 microdeletions, specific language impairment and the meiotic mismatch methylation (3M) hypothesisâ€™. European Journal of Human Genetics, 2015, 23, 1113-1115.	2.8	2
25	Nature via Nurture, the Martin Way. Twin Research and Human Genetics, 2020, 23, 137-138.	0.6	0