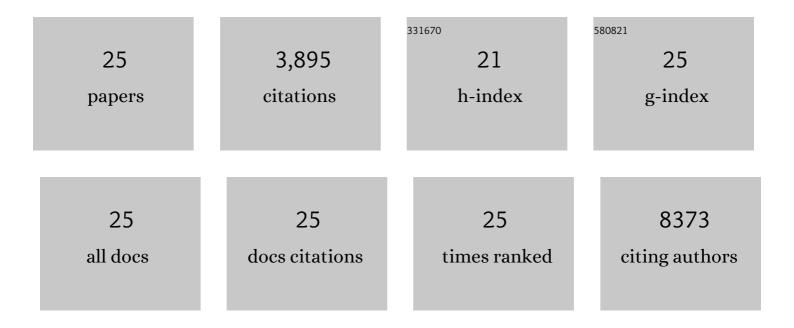
Maya Ghoussaini

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
2	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. Science, 2020, 370, .	12.6	508
3	Multiple Loci With Different Cancer Specificities Within the 8q24 Gene Desert. Journal of the National Cancer Institute, 2008, 100, 962-966.	6.3	306
4	Open Targets Platform: supporting systematic drug–target identification and prioritisation. Nucleic Acids Research, 2021, 49, D1302-D1310.	14.5	265
5	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	21.4	256
6	An open approach to systematically prioritize causal variants and genes at all published human GWAS trait-associated loci. Nature Genetics, 2021, 53, 1527-1533.	21.4	208
7	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	21.4	184
8	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	21.4	125
9	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
10	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	105
11	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
12	Implication of the Pro12Ala polymorphism of the PPAR-gamma 2gene in type 2 diabetes and obesity in the French population. BMC Medical Genetics, 2005, 6, 11.	2.1	92
13	Inherited Genetic Susceptibility to Breast Cancer. American Journal of Pathology, 2013, 183, 1038-1051.	3.8	82
14	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast–ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
15	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. American Journal of Human Genetics, 2015, 96, 5-20.	6.2	76
16	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. American Journal of Human Genetics, 2016, 99, 903-911.	6.2	59
17	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	5.1	51
18	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. American Journal of Human Genetics, 2015, 97, 22-34.	6.2	37

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#	Article	IF	CITATIONS
19	Polygenic susceptibility to breast cancer: current state-of-the-art. Future Oncology, 2009, 5, 689-701.	2.4	35
20	ldentification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. Breast Cancer Research, 2016, 18, 64.	5.0	31
21	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1680-1691.	2.5	24
22	A proteome-wide genetic investigation identifies several SARS-CoV-2-exploited host targets of clinical relevance. ELife, 2021, 10, .	6.0	23
23	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). Scientific Reports, 2016, 6, 32512.	3.3	19
24	Analysis of the SIM1 Contribution to Polygenic Obesity in the French Population. Obesity, 2010, 18, 1670-1675.	3.0	13
25	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203.	6.2	6