Maya Ghoussaini

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3551939/publications.pdf

Version: 2024-02-01

25 papers 3,895 citations

331670 21 h-index 25 g-index

25 all docs

25 docs citations

25 times ranked 8373 citing authors

| # | Article | IF | CITATIONS |
|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 1 | Open Targets Platform: supporting systematic drug–target identification and prioritisation. Nucleic Acids Research, 2021, 49, D1302-D1310. | 14.5 | 265 |
| 2 | 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 |
| 3 | A proteome-wide genetic investigation identifies several SARS-CoV-2-exploited host targets of clinical relevance. ELife, 2021, 10, . | 6.0 | 23 |
| 4 | 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 |
| 5 | Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73. | 21.4 | 120 |
| 6 | Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. Science, 2020, 370, . | 12.6 | 508 |
| 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 | Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94. | 27.8 | 1,099 |
| 9 | 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 |
| 10 | Identification 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 |
| 11 | 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 |
| 12 | Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375. | 12.8 | 93 |
| 13 | Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast–ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675. | 12.8 | 78 |
| 14 | 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 |
| 15 | 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 |
| 16 | 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 |
| 17 | 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 |
| 18 | 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 |

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|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 19 | Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999. | 12.8 | 105 |
| 20 | Inherited Genetic Susceptibility to Breast Cancer. American Journal of Pathology, 2013, 183, 1038-1051. | 3.8 | 82 |
| 21 | Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318. | 21.4 | 256 |
| 22 | Analysis of the SIM1 Contribution to Polygenic Obesity in the French Population. Obesity, 2010, 18, 1670-1675. | 3.0 | 13 |
| 23 | Polygenic susceptibility to breast cancer: current state-of-the-art. Future Oncology, 2009, 5, 689-701. | 2.4 | 35 |
| 24 | Multiple Loci With Different Cancer Specificities Within the 8q24 Gene Desert. Journal of the National Cancer Institute, 2008, 100, 962-966. | 6.3 | 306 |
| 25 | 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 |