A meta-analysis of 87,040 individuals identifies 23 new scancer

Nature Genetics 46, 1103-1109

DOI: 10.1038/ng.3094

Citation Report

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2	Trans-ethnic genome-wide association studies: advantages and challenges of mapping in diverse populations. Genome Medicine, 2014, 6, 91.	3.6	167
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4	Reevaluation of the BRCA2 truncating allele c.9976A > T (p.Lys3326Ter) in a familial breast cancer context. Scientific Reports, 2015, 5, 14800.	1.6	26
5	Functional annotation of HOT regions in the human genome: implications for human disease and cancer. Scientific Reports, 2015, 5, 11633.	1.6	24
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8	Systematic enrichment analysis of potentially functional regions for 103 prostate cancer risk-associated loci. Prostate, 2015, 75, 1264-1276.	1.2	37
9	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. Journal of the National Cancer Institute, 2015, 107, djv279.	3.0	152
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18	Vitamin D Receptor and RXR in the Postâ€Genomic Era. Journal of Cellular Physiology, 2015, 230, 758-766.	2.0	35
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