## Diptasri Mandal

## 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<br/>papers1,037<br/>citations9<br/>h-index18<br/>g-index18<br/>ext. papers1,574<br/>ext. citations5.7<br/>avg, IF2.54<br/>L-index

#	Paper	IF	Citations
16	Genome-wide interaction analysis identified low-frequency variants with sex disparity in lung cancer risk <i>Human Molecular Genetics</i> , <b>2022</b> ,	5.6	1
15	Two-stage Study of Familial Prostate Cancer by Whole-exome Sequencing and Custom Capture Identifies 10 Novel Genes Associated with the Risk of Prostate Cancer. <i>European Urology</i> , <b>2021</b> , 79, 353-	- <del>3</del> 61 <sup>2</sup>	9
14	Rare deleterious germline variants and risk of lung cancer. <i>Npj Precision Oncology</i> , <b>2021</b> , 5, 12	9.8	O
13	A Germline Variant at 8q24 Contributes to Familial Clustering of Prostate Cancer in Men of African Ancestry. <i>European Urology</i> , <b>2020</b> , 78, 316-320	10.2	13
12	Whole Exome Sequencing of Highly Aggregated Lung Cancer Families Reveals Linked Loci for Increased Cancer Risk on Chromosomes 12q, 7p, and 4q. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2020</b> , 29, 434-442	4	6
11	Rare Variants in Known Susceptibility Loci and Their Contribution to Risk of Lung Cancer. <i>Journal of Thoracic Oncology</i> , <b>2018</b> , 13, 1483-1495	8.9	12
10	Genome-wide association study of familial lung cancer. <i>Carcinogenesis</i> , <b>2018</b> , 39, 1135-1140	4.6	24
9	gsSKAT: Rapid gene set analysis and multiple testing correction for rare-variant association studies using weighted linear kernels. <i>Genetic Epidemiology</i> , <b>2017</b> , 41, 297-308	2.6	5
8	Familial Lung Cancer: A Brief History from the Earliest Work to the Most Recent Studies. <i>Genes</i> , <b>2017</b> , 8,	4.2	16
7	Genome-wide association of familial prostate cancer cases identifies evidence for a rare segregating haplotype at 8q24.21. <i>Human Genetics</i> , <b>2016</b> , 135, 923-38	6.3	27
6	Focused Analysis of Exome Sequencing Data for Rare Germline Mutations in Familial and Sporadic Lung Cancer. <i>Journal of Thoracic Oncology</i> , <b>2016</b> , 11, 52-61	8.9	18
5	Post hoc Analysis for Detecting Individual Rare Variant Risk Associations Using Probit Regression Bayesian Variable Selection Methods in Case-Control Sequencing Studies. <i>Genetic Epidemiology</i> , <b>2016</b> , 40, 461-9	2.6	3
4	REVEL: An Ensemble Method for Predicting the Pathogenicity of Rare Missense Variants. <i>American Journal of Human Genetics</i> , <b>2016</b> , 99, 877-885	11	722
3	A recurrent mutation in PARK2 is associated with familial lung cancer. <i>American Journal of Human Genetics</i> , <b>2015</b> , 96, 301-8	11	47
2	Situs Inversus Totalis: From Anatomical Variation to Clinical Studies. <i>FASEB Journal</i> , <b>2015</b> , 29, 552.11	0.9	
1	HOXB13 is a susceptibility gene for prostate cancer: results from the International Consortium for Prostate Cancer Genetics (ICPCG). <i>Human Genetics</i> , <b>2013</b> , 132, 5-14	6.3	134