Robert B Scharpf

List of Publications by Year
in descending order

41 papers	9,479 citations	318942 23 h-index	371746 37 g-index
42 all docs	42 docs citations	42 times ranked	21355 citing authors

#	Article	IF	Citations
1	Secondary analyses for genomeâ€wide association studies using expression quantitative trait loci. Genetic Epidemiology, 2022, , .	0.6	2
2	Cell-free DNA (cfDNA) fragmentomes predict tumor burden in metastatic colorectal cancer (mCRC).. Journal of Clinical Oncology, 2022, 40, 3541-3541.	0.8	0
3	Reply to: Limitations of molecular testing in combination with computerized tomographic for lung cancer screening. Nature Communications, 2022, 13, .	5.8	0
4	Early detection of lung cancer using cfDNA fragmentation.. Journal of Clinical Oncology, 2021, 39, 8519-8519.	0.8	3
5	Detection and characterization of lung cancer using cell-free DNA fragmentomes. Nature Communications, 2021, 12, 5060.	5.8	161
6	Multimodal genomic features predict outcome of immune checkpoint blockade in non-small-cell lung cancer. Nature Cancer, 2020, 1, 99-111.	5.7	141
7	Integrative Tumor and Immune Cell Multi-omic Analyses Predict Response to Immune Checkpoint Blockade in Melanoma. Cell Reports Medicine, 2020, 1, 100139.	3.3	45
8	Combining PARP with ATR inhibition overcomes PARP inhibitor and platinum resistance in ovarian cancer models. Nature Communications, 2020, 11, 3726.	5.8	169
9	Bayesian copy number detection and association in large-scale studies. BMC Cancer, 2020, 20, 856.	1.1	0
10	Genomic characterization of malignant progression in neoplastic pancreatic cysts. Nature Communications, 2020, 11, 4085.	5.8	77
11	White blood cell and cell-free DNA analyses for detection of residual disease in gastric cancer. Nature Communications, 2020, 11, 525.	5.8	158
12	Detection of de novo copy number deletions from targeted sequencing of trios. Bioinformatics, 2019, 35, 571-578.	1.8	2
13	Intraductal Papillary Mucinous Neoplasms Arise From Multiple Independent Clones, Each With Distinct Mutations. Gastroenterology, 2019, 157, 1123-1137.e22.	0.6	82
14	Genome-wide cell-free DNA fragmentation in patients with cancer. Nature, 2019, 570, 385-389.	13.7	764
15	Early Noninvasive Detection of Response to Targeted Therapy in Nonâ€“Small Cell Lung Cancer. Cancer Research, 2019, 79, 1204-1213.	0.4	75
16	Dynamics of Tumor and Immune Responses during Immune Checkpoint Blockade in Nonâ€“Small Cell Lung Cancer. Cancer Research, 2019, 79, 1214-1225.	0.4	226
17	Detection of rare disease variants in extended pedigrees using RVS. Bioinformatics, 2019, 35, 2509-2511.	1.8	6
18	Neoadjuvant PD-1 Blockade in Resectable Lung Cancer. New England Journal of Medicine, 2018, 378, 1976-1986.	13.9	1,495

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19	Integrated Genomic, Epigenomic, and Expression Analyses of Ovarian Cancer Cell Lines. Cell Reports, 2018, 25, 2617-2633.	2.9	74
20	Genome-Wide Association Study of Serum Fructosamine and Glycated Albumin in Adults Without Diagnosed Diabetes: Results From the Atherosclerosis Risk in Communities Study. Diabetes, 2018, 67, 1684-1696.	0.3	16
21	Whole exome association of rare deletions in multiplex oral cleft families. Genetic Epidemiology, 2017, 41, 61-69.	0.6	10
22	Evolution of Neoantigen Landscape during Immune Checkpoint Blockade in Nonâ€“Small Cell Lung Cancer. Cancer Discovery, 2017, 7, 264-276.	7.7	706
23	High grade serous ovarian carcinomas originate in the fallopian tube. Nature Communications, 2017, 8, 1093.	5.8	515
24	Direct detection of early-stage cancers using circulating tumor DNA. Science Translational Medicine, 2017, 9, .	5.8	808
25	Genome-Wide Association of Copy Number Polymorphisms and Kidney Function. PLoS ONE, 2017, 12, e0170815.	1.1	3
26	Identifying a Deletion Affecting Total Lung Capacity Among Subjects in the COPDGene Study Cohort. Genetic Epidemiology, 2016, 40, 81-88.	0.6	5
27	Hemizygous Deletion on Chromosome 3p26.1 Is Associated with Heavy Smoking among African American Subjects in the COPDGene Study. PLoS ONE, 2016, 11, e0164134.	1.1	4
28	The genomic landscape of response to EGFR blockade in colorectal cancer. Nature, 2015, 526, 263-267.	13.7	398
29	NDRG1 links p53 with proliferation-mediated centrosome homeostasis and genome stability. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11583-11588.	3.3	21
30	Copy number polymorphisms near SLC2A9 are associated with serum uric acid concentrations. BMC Genetics, 2014, 15, 81.	2.7	16
31	Fast detection of de novo copy number variants from SNP arrays for case-parent trios. BMC Bioinformatics, 2012, 13, 330.	1.2	13
32	A multilevel model to address batch effects in copy number estimation using SNP arrays. Biostatistics, 2011, 12, 33-50.	0.9	43
33	Using the R Package crlmm for Genotyping and Copy Number Estimation. Journal of Statistical Software, 2011, 40, 1-32.	1.8	1,136
34	Tackling the widespread and critical impact of batch effects in high-throughput data. Nature Reviews Genetics, 2010, 11, 733-739.	7.7	1,641
35	R Classes and Methods for SNP Array Data. Methods in Molecular Biology, 2010, 593, 67-79.	0.4	1
36	Rejoinder. Journal of the American Statistical Association, 2009, 104, 1318-1323.	1.8	0

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37	A Bayesian Model for Cross-Study Differential Gene Expression. Journal of the American Statistical Association, 2009, 104, 1295-1310.	1.8	29
38	Multiple loci associated with indices of renal function and chronic kidney disease. Nature Genetics, 2009, 41, 712-717.	9.4	553
39	Hidden Markov models for the assessment of chromosomal alterations using high-throughput SNP arrays. Annals of Applied Statistics, 2008, 2, 687-713.	0.5	45
40	SNPchip: R classes and methods for SNP array data. Bioinformatics, 2007, 23, 627-628.	1.8	13
41	When should one subtract background fluorescence in 2-color microarrays?. Biostatistics, 2006, 8, 695-707.	0.9	23