Mohamad Saad

List of Publications by Year
in descending order

13 papers	322 citations	1163117 8 h-index	1199594 12 g-index
14 all docs	14 docs citations	14 times ranked	569 citing authors

#	Article	IF	Citations
1	Genetic predisposition to cancer across people of different ancestries in Qatar: a population-based, cohort study. Lancet Oncology, The, 2022, 23, 341-352.	10.7	14
2	Untargeted Metabolomics Profiling Reveals Perturbations in Arginine-NO Metabolism in Middle Eastern Patients with Coronary Heart Disease. Metabolites, 2022, 12, 517.	2.9	5
3	Including diverse and admixed populations in genetic epidemiology research. Genetic Epidemiology, 2022, 46, 347-371.	1.3	11
4	Germline genetic contribution to the immune landscape of cancer. Immunity, 2021, 54, 367-386.e8.	14.3	95
5	Network-based identification of key master regulators associated with an immune-silent cancer phenotype. Briefings in Bioinformatics, 2021, 22, .	6.5	11
6	Distribution of Primary Brain Tumor Subtypes in Lebanon: A Multicenter Eleven-Year Study of 695 Patients. Cureus, 2021, 13, e17918.	0.5	2
7	Oncogenic states dictate the prognostic and predictive connotations of intratumoral immune response. , 2020, 8, e000617.		57
8	Prognostic impact of adenylyl cyclase-associated protein 2 (CAP2) in glioma: A clinicopathological study. Heliyon, 2020, 6, e03236.	3.2	5
9	Quality control and integration of genotypes from two calling pipelines for whole genome sequence data in the Alzheimer's disease sequencing project. Genomics, 2019, 111, 808-818.	2.9	26
10	Post-traumatic stress disorder in adult victims of cluster munitions in Lebanon: a 10-year longitudinal study. BMJ Open, 2017, 7, e017214.	1.9	34
11	Identity-by-descent estimation with population- and pedigree-based imputation in admixed family data. BMC Proceedings, 2016, 10, 295-301.	1.6	4
12	Power of Family‐Based Association Designs to Detect Rare Variants in Large Pedigrees Using Imputed Genotypes. Genetic Epidemiology, 2014, 38, 1-9.	1.3	27
13	Combining Family‐and Population‐Based Imputation Data for Association Analysis of Rare and Common Variants in Large Pedigrees. Genetic Epidemiology, 2014, 38, 579-590.	1.3	28