Modeling tissue contamination to improve molecular identification of the primary tumor site of metastases

Bioinformatics

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Citation Report

#	Article	IF	Citations
1	Development and validation of a microRNA based diagnostic assay for primary tumor site classification of liver core biopsies. Molecular Oncology, 2015, 9, 68-77.	2.1	10
2	Precision oncology in the age of integrative genomics. Nature Biotechnology, 2018, 36, 46-60.	9.4	104
3	Prediction of tumor metastasis from sequencing data in the era of genome sequencing. Briefings in Functional Genomics, 2019, 18, 412-418.	1.3	19
4	Assessment of Clinical Benefit of Integrative Genomic Profiling in Advanced Solid Tumors. JAMA Oncology, 2021, 7, 525-533.	3.4	65
5	Degrees of freedom for piecewise Lipschitz estimators. Annales De L'institut Henri Poincare (B) Probability and Statistics, 2018, 54, .	0.7	6