Stephen C Benz

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Safety, Feasibility, and Merits of Longitudinal Molecular Testing of Multiple Metastatic Sites to Inform mTNBC Patient Treatment in the Intensive Trial of Omics in Cancer. JCO Precision Oncology, 2022, 6, e2100280.	3.0	1
2	Identification and validation of expressed HLA-binding breast cancer neoepitopes for potential use in individualized cancer therapy. , 2021, 9, e002605.		7
3	Multiregion exome sequencing of ovarian immature teratomas reveals 2N near-diploid genomes, paucity of somatic mutations, and extensive allelic imbalances shared across mature, immature, and disseminated components. Modern Pathology, 2020, 33, 1193-1206.	5.5	25
4	A risk-associated Active transcriptome phenotype expressed by histologically normal human breast tissue and linked to a pro-tumorigenic adipocyte population. Breast Cancer Research, 2020, 22, 81.	5.0	12
5	Single-Cell Profiling Reveals Divergent, Globally Patterned Immune Responses in Murine Skin Inflammation. IScience, 2020, 23, 101582.	4.1	30
6	Overcoming hypoxia-induced functional suppression of NK cells. , 2020, 8, e000246.		44
7	A deep learning image-based intrinsic molecular subtype classifier of breast tumors reveals tumor heterogeneity that may affect survival. Breast Cancer Research, 2020, 22, 12.	5.0	69
8	Efficient Tumor Clearance and Diversified Immunity through Neoepitope Vaccines and Combinatorial Immunotherapy. Cancer Immunology Research, 2019, 7, 1359-1370.	3.4	22
9	A20 and ABIN1 Suppression of a Keratinocyte Inflammatory Program with a Shared Single-Cell Expression Signature in Diverse Human Rashes. Journal of Investigative Dermatology, 2019, 139, 1264-1273.	0.7	16
10	Transcriptional Programming of Normal and Inflamed Human Epidermis at Single-Cell Resolution. Cell Reports, 2018, 25, 871-883.	6.4	206
11	APOBEC mutation drives early-onset squamous cell carcinomas in recessive dystrophic epidermolysis bullosa. Science Translational Medicine, 2018, 10, .	12.4	91
12	Identification of an immune gene expression signature associated with favorable clinical features in Treg-enriched patient tumor samples. Npj Genomic Medicine, 2018, 3, 14.	3.8	33
13	Comprehensive genomic transcriptomic tumor-normal gene panel analysis for enhanced precision in patients with lung cancer. Oncotarget, 2018, 9, 19223-19232.	1.8	11
14	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	28.9	1,485