

# Stephen C Benz

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4343063/publications.pdf>

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14  
papers

2,053  
citations

933447

10  
h-index

1281871

11  
g-index

15  
all docs

15  
docs citations

15  
times ranked

5603  
citing authors

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