

Etienne Becht

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

24 papers	3,559 citations	16 h-index	25 g-index
25 ext. papers	5,790 ext. citations	15.9 avg, IF	5.35 L-index

#	Paper	IF	Citations
24	Non-terminally exhausted tumor-resident memory HBV-specific T _H 1 cell responses correlate with relapse-free survival in hepatocellular carcinoma. <i>Immunity</i> , 2021 , 54, 1825-1840.e7	32.3	14
23	Spatial UMAP and Image Cytometry for Topographic Immuno-oncology Biomarker Discovery. <i>Cancer Immunology Research</i> , 2021 , 9, 1262-1269	12.5	1
22	High-throughput single-cell quantification of hundreds of proteins using conventional flow cytometry and machine learning. <i>Science Advances</i> , 2021 , 7, eabg0505	14.3	11
21	Aggregating transcript-level analyses for single-cell differential gene expression. <i>Nature Methods</i> , 2020 , 17, 583-585	21.6	1
20	Combinatorial Single-Cell Analyses of Granulocyte-Monocyte Progenitor Heterogeneity Reveals an Early Uni-potent Neutrophil Progenitor. <i>Immunity</i> , 2020 , 53, 303-318.e5	32.3	51
19	The murine Microenvironment Cell Population counter method to estimate abundance of tissue-infiltrating immune and stromal cell populations in murine samples using gene expression. <i>Genome Medicine</i> , 2020 , 12, 86	14.4	17
18	Single-Cell Analysis of Human Mononuclear Phagocytes Reveals Subset-Defining Markers and Identifies Circulating Inflammatory Dendritic Cells. <i>Immunity</i> , 2019 , 51, 573-589.e8	32.3	174
17	Reverse-engineering flow-cytometry gating strategies for phenotypic labelling and high-performance cell sorting. <i>Bioinformatics</i> , 2019 , 35, 301-308	7.2	14
16	Large-Scale HLA Tetramer Tracking of T Cells during Dengue Infection Reveals Broad Acute Activation and Differentiation into Two Memory Cell Fates. <i>Immunity</i> , 2019 , 51, 1119-1135.e5	32.3	17
15	The clinical role of the TME in solid cancer. <i>British Journal of Cancer</i> , 2019 , 120, 45-53	8.7	155
14	Transcriptomic analysis of the tumor microenvironment to guide prognosis and immunotherapies. <i>Cancer Immunology, Immunotherapy</i> , 2018 , 67, 981-988	7.4	58
13	Dimensionality reduction for visualizing single-cell data using UMAP. <i>Nature Biotechnology</i> , 2018 ,	44.5	1432
12	Cancer immune contexture and immunotherapy. <i>Current Opinion in Immunology</i> , 2016 , 39, 7-13	7.8	93
11	Immune Contexture, Immunoscore, and Malignant Cell Molecular Subgroups for Prognostic and Theranostic Classifications of Cancers. <i>Advances in Immunology</i> , 2016 , 130, 95-190	5.6	120
10	Estimating the population abundance of tissue-infiltrating immune and stromal cell populations using gene expression. <i>Genome Biology</i> , 2016 , 17, 218	18.3	791
9	Orchestration and Prognostic Significance of Immune Checkpoints in the Microenvironment of Primary and Metastatic Renal Cell Cancer. <i>Clinical Cancer Research</i> , 2015 , 21, 3031-40	12.9	249
8	The immune response in cancer: from immunology to pathology to immunotherapy. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2015 , 467, 127-35	5.1	42

7	Molecular subtypes of clear cell renal cell carcinoma are associated with sunitinib response in the metastatic setting. <i>Clinical Cancer Research</i> , 2015 , 21, 1329-39	12.9	172
6	Prognostic and theranostic impact of molecular subtypes and immune classifications in renal cell cancer (RCC) and colorectal cancer (CRC). <i>OncolImmunology</i> , 2015 , 4, e1049804	7.2	34
5	The immune contexture of primary and metastatic human tumours. <i>Current Opinion in Immunology</i> , 2014 , 27, 8-15	7.8	85
4	Shaping of an effective immune microenvironment to and by cancer cells. <i>Cancer Immunology, Immunotherapy</i> , 2014 , 63, 991-7	7.4	25
3	The murine Microenvironment Cell Population counter method to estimate abundance of tissue-infiltrating immune and stromal cell populations in murine samples using gene expression		1
2	Infinity Flow: High-throughput single-cell quantification of 100s of proteins using conventional flow cytometry and machine learning		1
1	webMCP-counter: a web interface for transcriptomics-based quantification of immune and stromal cells in heterogeneous human or murine samples		1