

Marco Gerlinger

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/8483038/marco-gerlinger-publications-by-year.pdf>

Version: 2024-04-20

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

52
papers

9,718
citations

26
h-index

61
g-index

61
ext. papers

11,362
ext. citations

12.6
avg, IF

5.4
L-index

#	Paper	IF	Citations
52	Abstract PR012: Genetic and immune landscape evolution defines subtypes of MMR deficient colorectal cancer. <i>Cancer Research</i> , 2022 , 82, PR012-PR012	10.1	
51	Abstract A002: Genetic and immune landscape evolution defines subtypes of MMR deficient colorectal cancer. <i>Cancer Research</i> , 2022 , 82, A002-A002	10.1	
50	Mutational signatures impact the evolution of anti-EGFR antibody resistance in colorectal cancer. <i>Nature Ecology and Evolution</i> , 2021 , 5, 1024-1032	12.3	2
49	Computational Image Analysis of T-Cell Infiltrates in Resectable Gastric Cancer: Association with Survival and Molecular Subtypes. <i>Journal of the National Cancer Institute</i> , 2021 , 113, 88-98	9.7	8
48	Immunotherapy Sensitivity of Mismatch Repair-Deficient Cancer: Mutation Load Is Not Enough. <i>Cancer Cell</i> , 2021 , 39, 16-18	24.3	5
47	Identifying key questions in the ecology and evolution of cancer. <i>Evolutionary Applications</i> , 2021 , 14, 877-892	4.8	17
46	Extreme intratumour heterogeneity and driver evolution in mismatch repair deficient gastro-oesophageal cancer. <i>Nature Communications</i> , 2020 , 11, 139	17.4	22
45	Diagnostic Accuracy and Safety of Coaxial System in Oncology Patients Treated in a Specialist Cancer Center With Prospective Validation Within Clinical Trial Data. <i>Frontiers in Oncology</i> , 2020 , 10, 1634	5.3	1
44	Defining the true impact of coronavirus disease 2019 in the at-risk population of patients with cancer. <i>European Journal of Cancer</i> , 2020 , 136, 99-106	7.5	23
43	Circulating Tumour DNA Sequencing Identifies a Genetic Resistance-Gap in Colorectal Cancers with Acquired Resistance to EGFR-Antibodies and Chemotherapy. <i>Cancers</i> , 2020 , 12,	6.6	1
42	Detecting and Tracking Circulating Tumour DNA Copy Number Profiles during First Line Chemotherapy in Oesophagogastric Adenocarcinoma. <i>Cancers</i> , 2019 , 11,	6.6	9
41	CEA expression heterogeneity and plasticity confer resistance to the CEA-targeting bispecific immunotherapy antibody cibisatamab (CEA-TCB) in patient-derived colorectal cancer organoids 2019 , 7, 101		41
40	Genomic and Transcriptomic Determinants of Therapy Resistance and Immune Landscape Evolution during Anti-EGFR Treatment in Colorectal Cancer. <i>Cancer Cell</i> , 2019 , 36, 35-50.e9	24.3	94
39	Immunopeptidomics of colorectal cancer organoids reveals a sparse HLA class I neoantigen landscape and no increase in neoantigens with interferon or MEK-inhibitor treatment 2019 , 7, 309		46
38	Targeted drugs ramp up cancer mutability. <i>Science</i> , 2019 , 366, 1452-1453	33.3	7
37	Efficacy and Cardiotoxic Safety Profile of Raltitrexed in Fluoropyrimidines-Pretreated or High-Risk Cardiac Patients With GI Malignancies: Large Single-Center Experience. <i>Clinical Colorectal Cancer</i> , 2019 , 18, 64-71.e1	3.8	5
36	Metastasis Seeding Cells: Lone Invaders or Mass Migrators?. <i>Clinical Cancer Research</i> , 2018 , 24, 2032-2034.2	4.9	3

35	Circulating tumour DNA, a promising biomarker for the management of colorectal cancer. <i>Critical Reviews in Oncology/Hematology</i> , 2018 , 122, 72-82	7	29
34	Ultra-Sensitive Mutation Detection and Genome-Wide DNA Copy Number Reconstruction by Error-Corrected Circulating Tumor DNA Sequencing. <i>Clinical Chemistry</i> , 2018 , 64, 1626-1635	5.5	31
33	Multiplexed single cell protein expression analysis in solid tumours using a miniaturised microfluidic assay. <i>Convergent Science Physical Oncology</i> , 2017 , 3, 024003		9
32	Classifying the evolutionary and ecological features of neoplasms. <i>Nature Reviews Cancer</i> , 2017 , 17, 605-619	3.19	208
31	Cancer (r)evolution. <i>Nature Ecology and Evolution</i> , 2017 , 1, 1051-1052	12.3	5
30	Heterogeneous response and progression patterns reveal phenotypic heterogeneity of tyrosine kinase inhibitor response in metastatic renal cell carcinoma. <i>BMC Medicine</i> , 2016 , 14, 185	11.4	21
29	Cancer Evolution and the Limits of Predictability in Precision Cancer Medicine. <i>Trends in Cancer</i> , 2016 , 2, 49-63	12.5	157
28	Genetic Intratumor Heterogeneity 2015 , 571-593		1
27	Dissecting cancer evolution at the macro-heterogeneity and micro-heterogeneity scale. <i>Current Opinion in Genetics and Development</i> , 2015 , 30, 1-6	4.9	52
26	Intratumour heterogeneity in urologic cancers: from molecular evidence to clinical implications. <i>European Urology</i> , 2015 , 67, 729-37	10.2	86
25	The promise of circulating tumor cell analysis in cancer management. <i>Genome Biology</i> , 2014 , 15, 448	18.3	38
24	Cancer: evolution within a lifetime. <i>Annual Review of Genetics</i> , 2014 , 48, 215-36	14.5	146
23	Spatial and temporal diversity in genomic instability processes defines lung cancer evolution. <i>Science</i> , 2014 , 346, 251-6	33.3	752
22	Development of synchronous VHL syndrome tumors reveals contingencies and constraints to tumor evolution. <i>Genome Biology</i> , 2014 , 15, 433	18.3	53
21	Systematic evaluation of the prognostic impact and intratumour heterogeneity of clear cell renal cell carcinoma biomarkers. <i>European Urology</i> , 2014 , 66, 936-48	10.2	109
20	Genomic architecture and evolution of clear cell renal cell carcinomas defined by multiregion sequencing. <i>Nature Genetics</i> , 2014 , 46, 225-233	36.3	866
19	Computational optimisation of targeted DNA sequencing for cancer detection. <i>Scientific Reports</i> , 2013 , 3, 3309	4.9	20
18	The effect of VEGF-targeted therapy on biomarker expression in sequential tissue from patients with metastatic clear cell renal cancer. <i>Clinical Cancer Research</i> , 2013 , 19, 6924-34	12.9	54

17	Parallel evolution of tumour subclones mimics diversity between tumours. <i>Journal of Pathology</i> , 2013 , 230, 356-64	9.4	70
16	Prognostic and predictive markers in metastatic renal cell carcinoma. <i>Journal of Clinical Oncology</i> , 2013 , 31, 971-2	2.2	5
15	Ultra-deep T cell receptor sequencing reveals the complexity and intratumour heterogeneity of T cell clones in renal cell carcinomas. <i>Journal of Pathology</i> , 2013 , 231, 424-32	9.4	83
14	Intratumor heterogeneity and branched evolution revealed by multiregion sequencing. <i>New England Journal of Medicine</i> , 2012 , 366, 883-892	59.2	5559
13	Genome-wide RNA interference analysis of renal carcinoma survival regulators identifies MCT4 as a Warburg effect metabolic target. <i>Journal of Pathology</i> , 2012 , 227, 146-56	9.4	79
12	Intratumor heterogeneity: seeing the wood for the trees. <i>Science Translational Medicine</i> , 2012 , 4, 127ps107.5	10.5	375
11	How Darwinian models inform therapeutic failure initiated by clonal heterogeneity in cancer medicine. <i>British Journal of Cancer</i> , 2010 , 103, 1139-43	8.7	312
10	Surveillance investigations after high-dose therapy with stem cell rescue for recurrent follicular lymphoma have no impact on management. <i>Haematologica</i> , 2010 , 95, 1130-5	6.6	8
9	Anti-cancer drug resistance: understanding the mechanisms through the use of integrative genomics and functional RNA interference. <i>European Journal of Cancer</i> , 2010 , 46, 2166-77	7.5	62
8	Elevated LDH predicts poor outcome of recurrent germ cell tumours treated with dose dense chemotherapy. <i>European Journal of Cancer</i> , 2010 , 46, 2913-8	7.5	13
7	Assessment of an RNA interference screen-derived mitotic and ceramide pathway metagene as a predictor of response to neoadjuvant paclitaxel for primary triple-negative breast cancer: a retrospective analysis of five clinical trials. <i>Lancet Oncology</i> , 2010 , 11, 358-65	21.7	97
6	Predictive biomarker discovery through the parallel integration of clinical trial and functional genomics datasets. <i>Genome Medicine</i> , 2010 , 2, 53	14.4	36
5	Active Surveillance Strategies Have Neither Clinical or Survival Benefit Following High-Dose Chemotherapy and Progenitor Cell Rescue in Follicular Lymphoma.. <i>Blood</i> , 2008 , 112, 3251-3251	2.2	
4	Spontaneous CD8 T cell responses against the melanocyte differentiation antigen RAB38/NY-MEL-1 in melanoma patients. <i>Journal of Immunology</i> , 2006 , 177, 8212-8	5.3	23
3	Egr-1 induces the expression of its corepressor nab2 by activation of the nab2 promoter thereby establishing a negative feedback loop. <i>Journal of Biological Chemistry</i> , 2005 , 280, 42785-93	5.4	72
2	Genomic and transcriptomic determinants of therapy resistance and immune landscape evolution during anti-EGFR treatment in colorectal cancer		1
1	Ultra-sensitive mutation detection and genome-wide DNA copy number reconstruction by error corrected circulating tumour DNA sequencing		1