Hanno Glimm

List of Publications by Year
in descending order

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Version: 2024-02-01

71	6,917	147801	98798
papers	citations	31 h-index	67 g-index

73	73	73	8879
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	<scp>MGMT</scp> inactivation as a new biomarker in patients with advanced biliary tract cancers. Molecular Oncology, 2022, 16, 2733-2746.	4.6	2
2	Ruxolitinib is effective in the treatment of a patient with refractory Tâ€ALL. EJHaem, 2021, 2, 139-142.	1.0	4
3	Functional States in Tumor-Initiating Cell Differentiation in Human Colorectal Cancer. Cancers, 2021, 13, 1097.	3.7	11
4	Response to Cabozantinib Following Acquired Entrectinib Resistance in a Patient WithETV6-NTRK3Fusion-Positive Carcinoma Harboring theNTRK3^{G623R}Solvent-Front Mutation. JCO Precision Oncology, 2021, 5, 687-694.	3.0	3
5	Comprehensive Genomic and Transcriptomic Analysis for Guiding Therapeutic Decisions in Patients with Rare Cancers. Cancer Discovery, 2021, 11, 2780-2795.	9.4	125
6	Degradation of CCNK/CDK12 is a druggable vulnerability of colorectal cancer. Cell Reports, 2021, 36, 109394.	6.4	41
7	High tumour mutational burden and EGFR/MAPK pathway activation are therapeutic targets in metastatic porocarcinoma. British Journal of Dermatology, 2021, , .	1.5	6
8	YAPâ€induced Ccl2 expression is associated with a switch in hepatic macrophage identity and vascular remodelling in liver cancer. Liver International, 2021, 41, 3011-3023.	3.9	17
9	Recurrent Germline Variant in the Cohesin Complex Gene RAD21 Predisposes Children to Lymphoblastic Leukemia and Lymphoma. Blood, 2021, 138, 3358-3358.	1.4	0
10	Rationale and design of the CRAFT (Continuous ReAssessment with Flexible ExTension in Rare) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382	4.5	6
11	Identification and characterization of a BRAF fusion oncoprotein with retained autoinhibitory domains. Oncogene, 2020, 39, 814-832.	5.9	19
12	Identification of BCL-XL as highly active survival factor and promising therapeutic target in colorectal cancer. Cell Death and Disease, 2020, 11, 875.	6.3	17
13	YAP Orchestrates Heterotypic Endothelial Cell Communication via HGF/c-MET Signaling in Liver Tumorigenesis. Cancer Research, 2020, 80, 5502-5514.	0.9	31
14	Detection of Structural Variants in Circulating Cell-Free DNA from Sarcoma Patients Using Next Generation Sequencing. Cancers, 2020, 12, 3627.	3.7	7
15	The landscape of chromothripsis across adult cancer types. Nature Communications, 2020, 11, 2320.	12.8	75
16	Conceptual framework for precision cancer medicine in Germany: Consensus statement of the Deutsche Krebshilfe working group â€˜Molecular Diagnostics and Therapyâ€™. European Journal of Cancer, 2020, 135, 1-7.	2.8	23
17	Harmonization and Standardization of Panel-Based Tumor Mutational Burden Measurement: Real-World Results and Recommendations ofÂtheÂQuality in Pathology Study. Journal of Thoracic Oncology, 2020, 15, 1177-1189.	1.1	81
18	A perivascular niche in the bone marrow hosts quiescent and proliferating tumorigenic colorectal cancer cells. International Journal of Cancer, 2020, 147, 519-531.	5.1	5

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19	Metastatic adult pancreatoblastoma: Multimodal treatment and molecular characterization of a very rare disease. Pancreatology, 2020, 20, 425-432.	1.1	11
20	Targetable ERBB2 mutations identified in neurofibroma/schwannoma hybrid nerve sheath tumors. Journal of Clinical Investigation, 2020, 130, 2488-2495.	8.2	23
21	KIT-Dependent and KIT-Independent Genomic Heterogeneity of Resistance in Gastrointestinal Stromal Tumors â€" TORC1/2 Inhibition as Salvage Strategy. Molecular Cancer Therapeutics, 2019, 18, 1985-1996.	4.1	22
22	Pheno-seq â€" linking visual features and gene expression in 3D cell culture systems. Scientific Reports, 2019, 9, 12367.	3.3	16
23	Salinomycin: Anti-tumor activity in a pre-clinical colorectal cancer model. PLoS ONE, 2019, 14, e0211916.	2.5	27
24	Systematic Generation of Patient-Derived Tumor Models in Pancreatic Cancer. Cells, 2019, 8, 142.	4.1	9
25	Integrative genomic and transcriptomic analysis of leiomyosarcoma. Nature Communications, 2018, 9, 144.	12.8	197
26	Stk33 is required for spermatid differentiation and male fertility in mice. Developmental Biology, 2018, 433, 84-93.	2.0	13
27	Validating Comprehensive Next-Generation Sequencing Results for Precision Oncology: The NCT/DKTK Molecularly Aided Stratification for Tumor Eradication Research Experience. JCO Precision Oncology, 2018, 2, 1-13.	3.0	20
28	NRG1 Fusions in KRAS Wild-Type Pancreatic Cancer. Cancer Discovery, 2018, 8, 1087-1095.	9.4	189
29	Mapping Active Gene-Regulatory Regions in Human Repopulating Long-Term HSCs. Cell Stem Cell, 2018, 23, 132-146.e9.	11.1	14
30	Cell-of-Origin DNA Methylation Signatures Are Maintained during Colorectal Carcinogenesis. Cell Reports, 2018, 23, 3407-3418.	6.4	66
31	PD-L1 (CD274) copy number gain, expression, and immune cell infiltration as candidate predictors for response to immune checkpoint inhibitors in soft-tissue sarcoma. OncoImmunology, 2017, 6, e1279777.	4.6	50
32	Precision oncology based on omics data: The NCT Heidelberg experience. International Journal of Cancer, 2017, 141, 877-886.	5.1	133
33	Succession of transiently active tumorâ€initiating cell clones in human pancreatic cancer xenografts. EMBO Molecular Medicine, 2017, 9, 918-932.	6.9	36
34	Genetic subclone architecture of tumor clone-initiating cells in colorectal cancer. Journal of Experimental Medicine, 2017, 214, 2073-2088.	8.5	30
35	Genome-wide Specificity of Highly Efficient TALENs and CRISPR/Cas9 for T Cell Receptor Modification. Molecular Therapy - Methods and Clinical Development, 2017, 4, 213-224.	4.1	32
36	Patient-derived xenografts of gastrointestinal cancers are susceptible to rapid and delayed B-lymphoproliferation. International Journal of Cancer, 2017, 140, 1356-1363.	5.1	26

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37	Genomics of Immunotherapy-Associated Hyperprogressorsâ€"Letter. Clinical Cancer Research, 2017, 23, 6374-6375.	7.0	11
38	Asymmetric Centriole Numbers at Spindle Poles Cause Chromosome Missegregation in Cancer. Cell Reports, 2017, 20, 1906-1920.	6.4	49
39	Targeting Fibroblast Growth Factor Receptor 1 for Treatment of Soft-Tissue Sarcoma. Clinical Cancer Research, 2017, 23, 962-973.	7.0	29
40	Mutant KIT as imatinib-sensitive target in metastatic sinonasal carcinoma. Annals of Oncology, 2017, 28, 142-148.	1.2	30
41	The AP-1 transcription factor JunB is essential for multiple myeloma cell proliferation and drug resistance in the bone marrow microenvironment. Leukemia, 2017, 31, 1570-1581.	7.2	60
42	Colorectal cancerâ€initiating cells caught in the act. EMBO Molecular Medicine, 2017, 9, 856-858.	6.9	12
43	Integrating next-generation sequencing into clinical oncology: strategies, promises and pitfalls. ESMO Open, 2016, 1, e000094.	4.5	126
44	Integration of genomics and histology revises diagnosis and enables effective therapy of refractory cancer of unknown primary with PDL1 amplification. Journal of Physical Education and Sports Management, 2016, 2, a001180.	1.2	57
45	Phenotypic differentiation does not affect tumorigenicity of primary human colon cancer initiating cells. Cancer Letters, 2016, 371, 326-333.	7.2	11
46	Cooperation of BRAFF595L and mutant HRAS in histiocytic sarcoma provides new insights into oncogenic BRAF signaling. Leukemia, 2016, 30, 937-946.	7.2	52
47	Induction of the proapoptotic tumor suppressor gene Cell Adhesion Molecule 1 by chemotherapeutic agents is repressed in therapy resistant acute myeloid leukemia. Molecular Carcinogenesis, 2015, 54, 1815-1819.	2.7	9
48	The <scp>tRNA</scp> methyltransferase Dnmt2 is required forÂaccurate polypeptide synthesis duringÂhaematopoiesis. EMBO Journal, 2015, 34, 2350-2362.	7.8	154
49	So rare we need to hunt for them: reframing the ethical debate on incidental findings. Genome Medicine, 2015, 7, 83.	8.2	19
50	High-throughput monitoring of integration site clonality in preclinical and clinical gene therapy studies. Molecular Therapy - Methods and Clinical Development, 2015, 2, 14061.	4.1	8
51	Recurrent CDKN1B (p27) mutations in hairy cell leukemia. Blood, 2015, 126, 1005-1008.	1.4	88
52	High-resolution analysis of the human T-cell receptor repertoire. Nature Communications, 2015, 6, 8081.	12.8	123
53	Gene Therapy for Wiskott-Aldrich Syndromeâ€"Long-Term Efficacy and Genotoxicity. Science Translational Medicine, 2014, 6, 227ra33.	12.4	460
54	Stable Long-Term Blood Formation by Stem Cells in Murine Steady-State Hematopoiesis. Stem Cells, 2012, 30, 1961-1970.	3.2	11

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55	Distinct Types of Tumor-Initiating Cells Form Human Colon Cancer Tumors and Metastases. Cell Stem Cell, 2011, 9, 357-365.	11.1	276
56	You Can Count on This: Barcoded Hematopoietic Stem Cells. Cell Stem Cell, 2011, 9, 390-392.	11.1	10
57	An unbiased genome-wide analysis of zinc-finger nuclease specificity. Nature Biotechnology, 2011, 29, 816-823.	17.5	488
58	Deregulated EVI1 Expression Leads to Genomic Instability and G1 Cell Cycle Arrest. Blood, 2011, 118, 2431-2431.	1.4	0
59	Genomic instability and myelodysplasia with monosomy 7 consequent to EVI1 activation after gene therapy for chronic granulomatous disease. Nature Medicine, 2010, 16, 198-204.	30.7	727
60	Genome-wide high-throughput integrome analyses by nrLAM-PCR and next-generation sequencing. Nature Protocols, 2010, 5, 1379-1395.	12.0	161
61	Stem-Cell Gene Therapy for the Wiskottâ€“Aldrich Syndrome. New England Journal of Medicine, 2010, 363, 1918-1927.	27.0	505
62	Comprehensive genomic access to vector integration in clinical gene therapy. Nature Medicine, 2009, 15, 1431-1436.	30.7	173
63	High-resolution insertion-site analysis by linear amplificationâ€“mediated PCR (LAM-PCR). Nature Methods, 2007, 4, 1051-1057.	19.0	281
64	Vector integration is nonrandom and clustered and influences the fate of lymphopoiesis in SCID-X1 gene therapy. Journal of Clinical Investigation, 2007, 117, 2225-2232.	8.2	221
65	Gammaretrovirus-mediated correction of SCID-X1 is associated with skewed vector integration site distribution in vivo. Journal of Clinical Investigation, 2007, 117, 2241-2249.	8.2	185
66	Correction of X-linked chronic granulomatous disease by gene therapy, augmented by insertional activation of MDS1-EVI1, PRDM16 or SETBP1. Nature Medicine, 2006, 12, 401-409.	30.7	1,129
67	Insertional Activation of MDS1/EVI1, PRDM16 and SETBP1 in a Successful Chronic Granulomatous Disease (CGD) Gene Therapy Trial.. Blood, 2006, 108, 3274-3274.	1.4	0
68	Efficient marking of human cells with rapid but transient repopulating activity in autografted recipients. Blood, 2005, 106, 893-898.	1.4	33
69	Sustained Polyclonal Hematopoietic Repopulation after Successful SCID-X1 Gene Therapy by Means of a Non Random Integrating Pseudotyped Gammaretrovector.. Blood, 2004, 104, 290-290.	1.4	7
70	Persistence of eGFP Marked Bone Marrow Cells in Long-Term Hematopoiesis.. Blood, 2004, 104, 2111-2111.	1.4	0
71	A Model for the Detection of Clonality in Marked Hematopoietic Stem Cells. Annals of the New York Academy of Sciences, 2001, 938, 146-156.	3.8	25