

Eugen Rempel

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

1,737
citations

304743

22
h-index

454955

30
g-index

31
all docs

31
docs citations

31
times ranked

2316
citing authors

#	ARTICLE	IF	CITATIONS
1	Targeting rare and non-canonical driver variants in NSCLC – An uncharted clinical field. Lung Cancer, 2021, 154, 131-141.	2.0	8
2	Conventional and semi-automatic histopathological analysis of tumor cell content for multigene sequencing of lung adenocarcinoma. Translational Lung Cancer Research, 2021, 10, 1666-1678.	2.8	6
3	YAP Orchestrates Heterotypic Endothelial Cell Communication via HGF/c-MET Signaling in Liver Tumorigenesis. Cancer Research, 2020, 80, 5502-5514.	0.9	31
4	Subtype specific expression and survival prediction of pivotal lncRNAs in muscle invasive bladder cancer. Scientific Reports, 2020, 10, 20472.	3.3	1
5	Immuno-oncology gene expression profiling of formalin-fixed and paraffin-embedded clear cell renal cell carcinoma: Performance comparison of the NanoString nCounter technology with targeted RNA sequencing. Genes Chromosomes and Cancer, 2020, 59, 406-416.	2.8	10
6	Harmonization and Standardization of Panel-Based Tumor Mutational Burden Measurement: Real-World Results and Recommendations of the Quality in Pathology Study. Journal of Thoracic Oncology, 2020, 15, 1177-1189.	1.1	81
7	Quantifying potential confounders of panel-based tumor mutational burden (TMB) measurement. Lung Cancer, 2020, 142, 114-119.	2.0	28
8	RNA-Based Detection of Gene Fusions in Formalin-Fixed and Paraffin-Embedded Solid Cancer Samples. Cancers, 2019, 11, 1309.	3.7	32
9	Spatial and Temporal Heterogeneity of Panel-Based Tumor Mutational Burden in Pulmonary Adenocarcinoma: Separating Biology From Technical Artifacts. Journal of Thoracic Oncology, 2019, 14, 1935-1947.	1.1	69
10	Variant classification in precision oncology. International Journal of Cancer, 2019, 145, 2996-3010.	5.1	76
11	Measurement of tumor mutational burden (TMB) in routine molecular diagnostics: <i>in silico</i> and <i>real-life</i> analysis of three larger gene panels. International Journal of Cancer, 2019, 144, 2303-2312.	5.1	95
12	Combined targeted DNA and RNA sequencing of advanced NSCLC in routine molecular diagnostics: Analysis of the first 3,000 Heidelberg cases. International Journal of Cancer, 2019, 145, 649-661.	5.1	85
13	Size matters: Dissecting key parameters for panel-based tumor mutational burden analysis. International Journal of Cancer, 2019, 144, 848-858.	5.1	131
14	<i>RSPO2</i> gene rearrangement: a powerful driver of β -catenin activation in liver tumours. Gut, 2019, 68, 1287-1296.	12.1	29
15	Evaluation of TMB estimates for the prediction of response to immune checkpoint blockage.. Journal of Clinical Oncology, 2019, 37, 2632-2632.	1.6	4
16	The molecular signature of AML with increased ALDH activity suggests a stem cell origin. Leukemia and Lymphoma, 2018, 59, 2201-2210.	1.3	12
17	Implementing tumor mutational burden (TMB) analysis in routine diagnostics – a primer for molecular pathologists and clinicians. Translational Lung Cancer Research, 2018, 7, 703-715.	2.8	152
18	Subclassification, survival prediction and drug target analyses of chemotherapy-naïve muscle-invasive bladder cancer with a molecular screening. Oncotarget, 2018, 9, 25935-25945.	1.8	22

#	ARTICLE	IF	CITATIONS
19	WEADE: A workflow for enrichment analysis and data exploration. PLoS ONE, 2018, 13, e0204016.	2.5	3
20	Definition of transcriptome-based indices for quantitative characterization of chemically disturbed stem cell development: introduction of the STOP-Toxukn and STOP-Toxukk tests. Archives of Toxicology, 2017, 91, 839-864.	4.2	53
21	Stem Cell Transcriptome Responses and Corresponding Biomarkers That Indicate the Transition from Adaptive Responses to Cytotoxicity. Chemical Research in Toxicology, 2017, 30, 905-922.	3.3	37
22	Glycerol-3-phosphate Acyltransferase 1 Promotes Tumor Cell Migration and Poor Survival in Ovarian Carcinoma. Cancer Research, 2017, 77, 4589-4601.	0.9	58
23	Immune cell recruitment in teratomas is impaired by increased Wnt secretion. Stem Cell Research, 2016, 17, 607-615.	0.7	32
24	Hepatotoxicity of piperazine designer drugs: up-regulation of key enzymes of cholesterol and lipid biosynthesis. Archives of Toxicology, 2016, 90, 3045-3060.	4.2	31
25	A transcriptome-based classifier to identify developmental toxicants by stem cell testing: design, validation and optimization for histone deacetylase inhibitors. Archives of Toxicology, 2015, 89, 1599-1618.	4.2	82
26	Toxicogenomics directory of chemically exposed human hepatocytes. Archives of Toxicology, 2014, 88, 2261-2287.	4.2	143
27	ED13 links choline metabolism to integrin expression, cell adhesion and spreading. Cell Adhesion and Migration, 2014, 8, 499-508.	2.7	34
28	Design Principles of Concentration-Dependent Transcriptome Deviations in Drug-Exposed Differentiating Stem Cells. Chemical Research in Toxicology, 2014, 27, 408-420.	3.3	103
29	From transient transcriptome responses to disturbed neurodevelopment: role of histone acetylation and methylation as epigenetic switch between reversible and irreversible drug effects. Archives of Toxicology, 2014, 88, 1451-1468.	4.2	67
30	Human embryonic stem cell-derived test systems for developmental neurotoxicity: a transcriptomics approach. Archives of Toxicology, 2013, 87, 123-143.	4.2	222