

Eugen Rempel

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

1,737
citations

304368

22
h-index

454577

30
g-index

31
all docs

31
docs citations

31
times ranked

2316
citing authors

#	ARTICLE	IF	CITATIONS
1	Human embryonic stem cell-derived test systems for developmental neurotoxicity: a transcriptomics approach. Archives of Toxicology, 2013, 87, 123-143.	1.9	222
2	Implementing tumor mutational burden (TMB) analysis in routine diagnostics—a primer for molecular pathologists and clinicians. Translational Lung Cancer Research, 2018, 7, 703-715.	1.3	152
3	Toxicogenomics directory of chemically exposed human hepatocytes. Archives of Toxicology, 2014, 88, 2261-2287.	1.9	143
4	Size matters: Dissecting key parameters for panel-based tumor mutational burden analysis. International Journal of Cancer, 2019, 144, 848-858.	2.3	131
5	Design Principles of Concentration-Dependent Transcriptome Deviations in Drug-Exposed Differentiating Stem Cells. Chemical Research in Toxicology, 2014, 27, 408-420.	1.7	103
6	Measurement of tumor mutational burden (TMB) in routine molecular diagnostics: <i>in silico</i> and real-life analysis of three larger gene panels. International Journal of Cancer, 2019, 144, 2303-2312.	2.3	95
7	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.	2.3	85
8	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.	1.9	82
9	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.	0.5	81
10	Variant classification in precision oncology. International Journal of Cancer, 2019, 145, 2996-3010.	2.3	76
11	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.	0.5	69
12	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.	1.9	67
13	Glycerol-3-phosphate Acyltransferase 1 Promotes Tumor Cell Migration and Poor Survival in Ovarian Carcinoma. Cancer Research, 2017, 77, 4589-4601.	0.4	58
14	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.	1.9	53
15	Stem Cell Transcriptome Responses and Corresponding Biomarkers That Indicate the Transition from Adaptive Responses to Cytotoxicity. Chemical Research in Toxicology, 2017, 30, 905-922.	1.7	37
16	EDI3 links choline metabolism to integrin expression, cell adhesion and spreading. Cell Adhesion and Migration, 2014, 8, 499-508.	1.1	34
17	Immune cell recruitment in teratomas is impaired by increased Wnt secretion. Stem Cell Research, 2016, 17, 607-615.	0.3	32
18	RNA-Based Detection of Gene Fusions in Formalin-Fixed and Paraffin-Embedded Solid Cancer Samples. Cancers, 2019, 11, 1309.	1.7	32

#	ARTICLE	IF	CITATIONS
19	Hepatotoxicity of piperazine designer drugs: up-regulation of key enzymes of cholesterol and lipid biosynthesis. <i>Archives of Toxicology</i> , 2016, 90, 3045-3060.	1.9	31
20	YAP Orchestrates Heterotypic Endothelial Cell Communication via HGF/c-MET Signaling in Liver Tumorigenesis. <i>Cancer Research</i> , 2020, 80, 5502-5514.	0.4	31
21	<i>RSPO2</i> gene rearrangement: a powerful driver of β -catenin activation in liver tumours. <i>Gut</i> , 2019, 68, 1287-1296.	6.1	29
22	Quantifying potential confounders of panel-based tumor mutational burden (TMB) measurement. <i>Lung Cancer</i> , 2020, 142, 114-119.	0.9	28
23	Subclassification, survival prediction and drug target analyses of chemotherapy-naïve muscle-invasive bladder cancer with a molecular screening. <i>Oncotarget</i> , 2018, 9, 25935-25945.	0.8	22
24	The molecular signature of AML with increased ALDH activity suggests a stem cell origin. <i>Leukemia and Lymphoma</i> , 2018, 59, 2201-2210.	0.6	12
25	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. <i>Genes Chromosomes and Cancer</i> , 2020, 59, 406-416.	1.5	10
26	Targeting rare and non-canonical driver variants in NSCLC – An uncharted clinical field. <i>Lung Cancer</i> , 2021, 154, 131-141.	0.9	8
27	Conventional and semi-automatic histopathological analysis of tumor cell content for multigene sequencing of lung adenocarcinoma. <i>Translational Lung Cancer Research</i> , 2021, 10, 1666-1678.	1.3	6
28	Evaluation of TMB estimates for the prediction of response to immune checkpoint blockade. <i>Journal of Clinical Oncology</i> , 2019, 37, 2632-2632.	0.8	4
29	WEADE: A workflow for enrichment analysis and data exploration. <i>PLoS ONE</i> , 2018, 13, e0204016.	1.1	3
30	Subtype specific expression and survival prediction of pivotal lncRNAs in muscle invasive bladder cancer. <i>Scientific Reports</i> , 2020, 10, 20472.	1.6	1