# Eugen Rempel

List of Publications by Year
in descending order

| | | | |
|---|---|---|---|
| 30 papers | 1,737 citations | 304743 <br> 22 h-index | 454955 <br> 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. | 4.2 | 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. | 2.8 | 152 |
| 3 | Toxicogenomics directory of chemically exposed human hepatocytes. Archives of Toxicology, 2014, 88, 2261-2287. | 4.2 | 143 |
| 4 | Size matters: Dissecting key parameters for panel-based tumor mutational burden analysis. International Journal of Cancer, 2019, 144, 848-858. | 5.1 | 131 |
| 5 | Design Principles of Concentration-Dependent Transcriptome Deviations in Drug-Exposed Differentiating Stem Cells. Chemical Research in Toxicology, 2014, 27, 408-420. | 3.3 | 103 |
| 6 | Measurement of tumor mutational burden (TMB) in routine molecular diagnostics: *in silico* and real-life analysis of three larger gene panels. International Journal of Cancer, 2019, 144, 2303-2312. | 5.1 | 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. | 5.1 | 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. | 4.2 | 82 |
| 9 | 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 |
| 10 | Variant classification in precision oncology. International Journal of Cancer, 2019, 145, 2996-3010. | 5.1 | 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. | 1.1 | 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. | 4.2 | 67 |
| 13 | Glycerol-3-phosphate Acyltransferase 1 Promotes Tumor Cell Migration and Poor Survival in Ovarian Carcinoma. Cancer Research, 2017, 77, 4589-4601. | 0.9 | 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. | 4.2 | 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. | 3.3 | 37 |
| 16 | EDI3 links choline metabolism to integrin expression, cell adhesion and spreading. Cell Adhesion and Migration, 2014, 8, 499-508. | 2.7 | 34 |
| 17 | Immune cell recruitment in teratomas is impaired by increased Wnt secretion. Stem Cell Research, 2016, 17, 607-615. | 0.7 | 32 |
| 18 | RNA-Based Detection of Gene Fusions in Formalin-Fixed and Paraffin-Embedded Solid Cancer Samples. Cancers, 2019, 11, 1309. | 3.7 | 32 |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 19 | 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 |
| 20 | YAP Orchestrates Heterotypic Endothelial Cell Communication via HGF/c-MET Signaling in Liver Tumorigenesis. Cancer Research, 2020, 80, 5502-5514. | 0.9 | 31 |
| 21 | *RSPO2* gene rearrangement: a powerful driver of Î²-catenin activation in liver tumours. Gut, 2019, 68, 1287-1296. | 12.1 | 29 |
| 22 | Quantifying potential confounders of panel-based tumor mutational burden (TMB) measurement. Lung Cancer, 2020, 142, 114-119. | 2.0 | 28 |
| 23 | Subclassification, survival prediction and drug target analyses of chemotherapy-naÃ¯ve muscle-invasive bladder cancer with a molecular screening. Oncotarget, 2018, 9, 25935-25945. | 1.8 | 22 |
| 24 | The molecular signature of AML with increased ALDH activity suggests a stem cell origin. Leukemia and Lymphoma, 2018, 59, 2201-2210. | 1.3 | 12 |
| 25 | Immunoâ€oncology gene expression profiling of formalinâ€fixed and paraffinâ€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 |
| 26 | Targeting rare and non-canonical driver variants in NSCLC â€" An uncharted clinical field. Lung Cancer, 2021, 154, 131-141. | 2.0 | 8 |
| 27 | 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 |
| 28 | Evaluation of TMB estimates for the prediction of response to immune checkpoint blockage.. Journal of Clinical Oncology, 2019, 37, 2632-2632. | 1.6 | 4 |
| 29 | WEADE: A workflow for enrichment analysis and data exploration. PLoS ONE, 2018, 13, e0204016. | 2.5 | 3 |
| 30 | Subtype specific expression and survival prediction of pivotal lncRNAs in muscle invasive bladder cancer. Scientific Reports, 2020, 10, 20472. | 3.3 | 1 |