

# Jasper Anckaert

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1506521/publications.pdf>

Version: 2024-02-01

16  
papers

1,670  
citations

840728

11  
h-index

996954

15  
g-index

28  
all docs

28  
docs citations

28  
times ranked

4003  
citing authors

#	ARTICLE	IF	CITATIONS
1	The long non-coding RNA SAMMSON is essential for uveal melanoma cell survival. <i>Oncogene</i> , 2022, 41, 15-25.	5.9	15
2	RNA biomarkers from proximal liquid biopsy for diagnosis of ovarian cancer. <i>Neoplasia</i> , 2022, 24, 155-164.	5.3	4
3	CiLiQuant: Quantification of RNA Junction Reads Based on Their Circular or Linear Transcript Origin. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	2.1	1
4	Comprehensive RNA dataset of tissue and plasma from patients with esophageal cancer or precursor lesions. <i>Scientific Data</i> , 2022, 9, 86.	5.3	1
5	The RNA Atlas expands the catalog of human non-coding RNAs. <i>Nature Biotechnology</i> , 2021, 39, 1453-1465.	17.5	75
6	The MicroRNA Landscape of Acute Beta Cell Destruction in Type 1 Diabetic Recipients of Intraportal Islet Grafts. <i>Cells</i> , 2021, 10, 1693.	4.1	4
7	Charting Extracellular Transcriptomes in The Human Biofluid RNA Atlas. <i>Cell Reports</i> , 2020, 33, 108552.	6.4	50
8	SMARTer single cell total RNA sequencing. <i>Nucleic Acids Research</i> , 2019, 47, e93-e93.	14.5	38
9	Performance assessment of total RNA sequencing of human biofluids and extracellular vesicles. <i>Scientific Reports</i> , 2019, 9, 17574.	3.3	46
10	LNCipedia 5: towards a reference set of human long non-coding RNAs. <i>Nucleic Acids Research</i> , 2019, 47, D135-D139.	14.5	403
11	EV-TRACK: transparent reporting and centralizing knowledge in extracellular vesicle research. <i>Nature Methods</i> , 2017, 14, 228-232.	19.0	886
12	decodeRNAâ€” predicting non-coding RNA functions using guilt-by-association. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	16
13	Zipper plot: visualizing transcriptional activity of genomic regions. <i>BMC Bioinformatics</i> , 2017, 18, 231.	2.6	5
14	miSTAR: miRNA target prediction through modeling quantitative and qualitative miRNA binding site information in a stacked model structure. <i>Nucleic Acids Research</i> , 2016, 45, gkw1260.	14.5	18
15	RDML-Ninja and RDMLdb for standardized exchange of qPCR data. <i>BMC Bioinformatics</i> , 2015, 16, 197.	2.6	12
16	miRBase Tracker: keeping track of microRNA annotation changes. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, .	3.0	73