

Jan Medenbach

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

22
papers

656
citations

13
h-index

25
g-index

25
ext. papers

848
ext. citations

11.3
avg, IF

3.92
L-index

#	Paper	IF	Citations
22	Translational control via protein-regulated upstream open reading frames. <i>Cell</i> , 2011 , 145, 902-13	56.2	98
21	CircRNA-protein complexes: IMP3 protein component defines subfamily of circRNPs. <i>Scientific Reports</i> , 2016 , 6, 31313	4.9	96
20	Purification of cross-linked RNA-protein complexes by phenol-toluol extraction. <i>Nature Communications</i> , 2019 , 10, 990	17.4	94
19	The expanding universe of ribonucleoproteins: of novel RNA-binding proteins and unconventional interactions. <i>Pflügers Archiv European Journal of Physiology</i> , 2016 , 468, 1029-40	4.6	60
18	Network of coregulated spliceosome components revealed by zebrafish mutant in recycling factor p110. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 6608-13	11.5	60
17	3cyclic phosphorylation of U6 snRNA leads to recruitment of recycling factor p110 through LSM proteins. <i>Rna</i> , 2008 , 14, 1532-8	5.8	39
16	RNA-Seq analysis in mutant zebrafish reveals role of U1C protein in alternative splicing regulation. <i>EMBO Journal</i> , 2011 , 30, 1965-76	13	34
15	Human U4/U6 snRNP recycling factor p110: mutational analysis reveals the function of the tetratricopeptide repeat domain in recycling. <i>Molecular and Cellular Biology</i> , 2004 , 24, 7392-401	4.8	34
14	Auto-regulatory feedback by RNA-binding proteins. <i>Journal of Molecular Cell Biology</i> , 2019 , 11, 930-939	6.3	33
13	Insights into the evolutionary conserved regulation of Rio ATPase activity. <i>Nucleic Acids Research</i> , 2018 , 46, 1441-1456	20.1	24
12	A multi-omics analysis reveals the unfolded protein response regulon and stress-induced resistance to folate-based antimetabolites. <i>Nature Communications</i> , 2020 , 11, 2936	17.4	19
11	Promiscuity in post-transcriptional control of gene expression: Drosophila sex-lethal and its regulatory partnerships. <i>FEBS Letters</i> , 2017 , 591, 1471-1488	3.8	18
10	A sensitive and simple targeted proteomics approach to quantify transcription factor and membrane proteins of the unfolded protein response pathway in glioblastoma cells. <i>Scientific Reports</i> , 2019 , 9, 8836	4.9	13
9	Human initiation factor eIF3 subunit b interacts with HCV IRES RNA through its N-terminal RNA recognition motif. <i>FEBS Letters</i> , 2009 , 583, 70-4	3.8	13
8	The zinc finger domains in U2AF26 and U2AF35 have diverse functionalities including a role in controlling translation. <i>RNA Biology</i> , 2020 , 17, 843-856	4.8	5
7	Sister-of-Sex-lethal is a repressor of translation. <i>Rna</i> , 2018 , 24, 149-158	5.8	5
6	Drosophila Sister-of-Sex-lethal reinforces a male-specific gene expression pattern by controlling Sex-lethal alternative splicing. <i>Nucleic Acids Research</i> , 2019 , 47, 2276-2288	20.1	5

- 5 Purification of Cross-linked RNA-Protein Complexes by Phenol-Toluol Extraction 3
- 4 RhoA regulates translation of the Nogo-A decoy SPARC in white matter-invading glioblastomas. *Acta Neuropathologica*, **2019**, 138, 275-293 14.3 2
- 3 Simple Targeted Assays for Metabolic Pathways and Signaling: A Powerful Tool for Targeted Proteomics. *Analytical Chemistry*, **2020**, 92, 13672-13676 7.8 1
- 2 Sedimentation Analysis of Ribonucleoprotein Complexes 428-437
- 1 Stress macht Zellen resistent gegen Folsäure-basierte Chemotherapeutika. *BioSpektrum*, **2020**, 26, 609-611 1