

Reuven Agami

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

3,528
citations

471061

17
h-index

552369

26
g-index

27
all docs

27
docs citations

27
times ranked

6200
citing authors

#	ARTICLE	IF	CITATIONS
1	A Genetic Screen Implicates miRNA-372 and miRNA-373 As Oncogenes in Testicular Germ Cell Tumors. <i>Cell</i> , 2006, 124, 1169-1181.	13.5	1,186
2	eRNAs Are Required for p53-Dependent Enhancer Activity and Gene Transcription. <i>Molecular Cell</i> , 2013, 49, 524-535.	4.5	484
3	Transcription Impacts the Efficiency of mRNA Translation via Co-transcriptional N6-adenosine Methylation. <i>Cell</i> , 2017, 169, 326-337.e12.	13.5	372
4	Functional genetic screens for enhancer elements in the human genome using CRISPR-Cas9. <i>Nature Biotechnology</i> , 2016, 34, 192-198.	9.4	352
5	Tumour-specific proline vulnerability uncovered by differential ribosome codon reading. <i>Nature</i> , 2016, 530, 490-494.	13.7	202
6	BRD7 is a candidate tumour suppressor gene required for p53 function. <i>Nature Cell Biology</i> , 2010, 12, 380-389.	4.6	194
7	The tumor-suppressive functions of the human INK4A locus. <i>Cancer Cell</i> , 2003, 4, 311-319.	7.7	181
8	p53 induces transcriptional and translational programs to suppress cell proliferation and growth. <i>Genome Biology</i> , 2013, 14, R32.	13.9	97
9	Anti-tumour immunity induces aberrant peptide presentation in melanoma. <i>Nature</i> , 2021, 590, 332-337.	13.7	81
10	Applying CRISPR-Cas9 tools to identify and characterize transcriptional enhancers. <i>Nature Reviews Molecular Cell Biology</i> , 2016, 17, 597-604.	16.1	54
11	Tryptophan depletion results in tryptophan-to-phenylalanine substituents. <i>Nature</i> , 2022, 603, 721-727.	13.7	47
12	Translatome analysis reveals altered serine and glycine metabolism in T-cell acute lymphoblastic leukemia cells. <i>Nature Communications</i> , 2019, 10, 2542.	5.8	43
13	<scp>SLC</scp> 1A3 contributes to Lâ€asparaginase resistance in solid tumors. <i>EMBO Journal</i> , 2019, 38, e102147.	3.5	41
14	Proteomic patterns associated with response to breast cancer neoadjuvant treatment. <i>Molecular Systems Biology</i> , 2020, 16, e9443.	3.2	41
15	Functional CRISPR screen identifies AP1-associated enhancer regulating FOXF1 to modulate oncogene-induced senescence. <i>Genome Biology</i> , 2018, 19, 118.	3.8	38
16	A fragment-like approach to PYCR1 inhibition. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2019, 29, 2626-2631.	1.0	28
17	A CRISPR-Cas9 screen identifies essential CTCF anchor sites for estrogen receptor-driven breast cancer cell proliferation. <i>Nucleic Acids Research</i> , 2019, 47, 9557-9572.	6.5	21
18	Oncogene-dependent sloppiness in mRNA translation. <i>Molecular Cell</i> , 2021, 81, 4709-4721.e9.	4.5	21

#	ARTICLE	IF	CITATIONS
19	A comprehensive enhancer screen identifies TRAM2 as a key and novel mediator of YAP oncogenesis. <i>Genome Biology</i> , 2021, 22, 54.	3.8	16
20	TGF β 1-induced leucine limitation uncovered by differential ribosome codon reading. <i>EMBO Reports</i> , 2017, 18, 549-557.	2.0	8
21	CUEDC1 is a primary target of ER α essential for the growth of breast cancer cells. <i>Cancer Letters</i> , 2018, 436, 87-95.	3.2	7
22	Queuing up the ribosome: nutrition and the microbiome control protein synthesis. <i>EMBO Journal</i> , 2018, 37, .	3.5	4
23	Suppression of heparan sulfation re-sensitizes YAP1-driven melanoma to MAPK pathway inhibitors. <i>Oncogene</i> , 2022, 41, 3953-3968.	2.6	4
24	The methylated way to translation. <i>Oncotarget</i> , 2017, 8, 93313-93314.	0.8	2
25	Slippy-Sloppy translation: a tale of programmed and induced-ribosomal frameshifting. <i>Trends in Genetics</i> , 2022, 38, 1123-1133.	2.9	2
26	More or less "the same"? mRNA fluctuations are balanced during translation. <i>EMBO Journal</i> , 2019, 38, e103651.	3.5	0