

Michelle S Scott

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/589483/publications.pdf>

Version: 2024-02-01

60
papers

4,432
citations

117571

34
h-index

138417

58
g-index

69
all docs

69
docs citations

69
times ranked

6738
citing authors

#	ARTICLE	IF	CITATIONS
1	Global Survey of Organ and Organelle Protein Expression in Mouse: Combined Proteomic and Transcriptomic Profiling. <i>Cell</i> , 2006, 125, 173-186.	13.5	429
2	A Quantitative Spatial Proteomics Analysis of Proteome Turnover in Human Cells. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.011429.	2.5	332
3	From snoRNA to miRNA: Dual function regulatory non-coding RNAs. <i>Biochimie</i> , 2011, 93, 1987-1992.	1.3	207
4	PIPs: human protein-protein interaction prediction database. <i>Nucleic Acids Research</i> , 2009, 37, D651-D656.	6.5	206
5	The emerging landscape of small nucleolar <i>sno</i> RNAs in cell biology. <i>Wiley Interdisciplinary Reviews RNA</i> , 2015, 6, 381-397.	3.2	193
6	Human miRNA Precursors with Box H/ACA snoRNA Features. <i>PLoS Computational Biology</i> , 2009, 5, e1000507.	1.5	167
7	Characterization and prediction of protein nucleolar localization sequences. <i>Nucleic Acids Research</i> , 2010, 38, 7388-7399.	6.5	167
8	RNAcentral 2021: secondary structure integration, improved sequence search and new member databases. <i>Nucleic Acids Research</i> , 2021, 49, D212-D220.	6.5	160
9	Protection of p27Kip1 mRNA by quaking RNA binding proteins promotes oligodendrocyte differentiation. <i>Nature Neuroscience</i> , 2005, 8, 27-33.	7.1	151
10	NoD: a Nucleolar localization sequence detector for eukaryotic and viral proteins. <i>BMC Bioinformatics</i> , 2011, 12, 317.	1.2	149
11	UV-induced binding of ING1 to PCNA regulates the induction of apoptosis. <i>Journal of Cell Science</i> , 2001, 114, 3455-3462.	1.2	128
12	Identification of human miRNA precursors that resemble box C/D snoRNAs. <i>Nucleic Acids Research</i> , 2011, 39, 3879-3891.	6.5	123
13	Probabilistic prediction and ranking of human protein-protein interactions. <i>BMC Bioinformatics</i> , 2007, 8, 239.	1.2	115
14	A Polyadenylation-Dependent 3' End Maturation Pathway Is Required for the Synthesis of the Human Telomerase RNA. <i>Cell Reports</i> , 2015, 13, 2244-2257.	2.9	100
15	UV induces nucleolar translocation of ING1 through two distinct nucleolar targeting sequences. <i>Nucleic Acids Research</i> , 2001, 29, 2052-2058.	6.5	94
16	Deep transcriptome annotation enables the discovery and functional characterization of cryptic small proteins. <i>ELife</i> , 2017, 6, .	2.8	93
17	Predicting Subcellular Localization via Protein Motif Co-Occurrence. <i>Genome Research</i> , 2004, 14, 1957-1966.	2.4	92
18	Human ING1 Proteins Differentially Regulate Histone Acetylation. <i>Journal of Biological Chemistry</i> , 2002, 277, 29832-29839.	1.6	91

#	ARTICLE	IF	CITATIONS
19	Refining Protein Subcellular Localization. PLoS Computational Biology, 2005, 1, e66.	1.5	90
20	Tethering by lamin A stabilizes and targets the ING1 tumour suppressor. Nature Cell Biology, 2008, 10, 1333-1340.	4.6	86
21	snoDB: an interactive database of human snoRNA sequences, abundance and interactions. Nucleic Acids Research, 2020, 48, D220-D225.	6.5	83
22	Motif independent identification of potential RNA G-quadruplexes by G4RNA screener. Bioinformatics, 2017, 33, 3532-3537.	1.8	82
23	Human box C/D snoRNA processing conservation across multiple cell types. Nucleic Acids Research, 2012, 40, 3676-3688.	6.5	79
24	Chemogenomic profiling predicts antifungal synergies. Molecular Systems Biology, 2009, 5, 338.	3.2	71
25	OpenProt: a more comprehensive guide to explore eukaryotic coding potential and proteomes. Nucleic Acids Research, 2019, 47, D403-D410.	6.5	71
26	OpenProt 2021: deeper functional annotation of the coding potential of eukaryotic genomes. Nucleic Acids Research, 2021, 49, D380-D388.	6.5	71
27	Identifying Regulatory Subnetworks for a Set of Genes. Molecular and Cellular Proteomics, 2005, 4, 683-692.	2.5	61
28	Simultaneous sequencing of coding and noncoding RNA reveals a human transcriptome dominated by a small number of highly expressed noncoding genes. Rna, 2018, 24, 950-965.	1.6	61
29	Current RNA-seq methodology reporting limits reproducibility. Briefings in Bioinformatics, 2021, 22, 140-145.	3.2	55
30	Protein coding genes as hosts for noncoding RNA expression. Seminars in Cell and Developmental Biology, 2018, 29, 3-12.	2.3	52
31	Identification of discrete classes of small nucleolar RNA featuring different ends and RNA binding protein dependency. Nucleic Acids Research, 2014, 42, 10073-10085.	6.5	46
32	Handling multi-mapped reads in RNA-seq. Computational and Structural Biotechnology Journal, 2020, 18, 1569-1576.	1.9	44
33	G4RNA screener web server: User focused interface for RNA G-quadruplex prediction. Biochimie, 2018, 151, 115-118.	1.3	42
34	G4RNA: an RNA G-quadruplex database. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav059.	1.4	41
35	Analysis of Human Small Nucleolar RNAs (snoRNA) and the Development of snoRNA Modulator of Gene Expression Vectors. Molecular Biology of the Cell, 2010, 21, 1569-1584.	0.9	40
36	The cellular landscape of mid-size noncoding RNA. Wiley Interdisciplinary Reviews RNA, 2019, 10, e1530.	3.2	40

#	ARTICLE	IF	CITATIONS
37	Small nucleolar RNAs: continuing identification of novel members and increasing diversity of their molecular mechanisms of action. <i>Biochemical Society Transactions</i> , 2020, 48, 645-656.	1.6	37
38	UBB pseudogene 4 encodes functional ubiquitin variants. <i>Nature Communications</i> , 2020, 11, 1306.	5.8	34
39	Human Hepatocyte Nuclear Factor 4-1 \pm Encodes Isoforms with Distinct Transcriptional Functions. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 808-827.	2.5	31
40	Reducing the structure bias of RNA-Seq reveals a large number of non-annotated non-coding RNA. <i>Nucleic Acids Research</i> , 2020, 48, 2271-2286.	6.5	29
41	CoCo: RNA-seq read assignment correction for nested genes and multimapped reads. <i>Bioinformatics</i> , 2019, 35, 5039-5047.	1.8	28
42	Annotation of snoRNA abundance across human tissues reveals complex snoRNA-host gene relationships. <i>Genome Biology</i> , 2021, 22, 172.	3.8	28
43	RBFOX2 alters splicing outcome in distinct binding modes with multiple protein partners. <i>Nucleic Acids Research</i> , 2021, 49, 8370-8383.	6.5	20
44	Human plasma pregnancy-associated miRNAs and their temporal variation within the first trimester of pregnancy. <i>Reproductive Biology and Endocrinology</i> , 2022, 20, 14.	1.4	17
45	SnoRNA copy regulation affects family size, genomic location and family abundance levels. <i>BMC Genomics</i> , 2021, 22, 414.	1.2	12
46	Osteoclast signaling-targeting miR-146a-3p and miR-155-5p are downregulated in Paget's disease of bone. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2020, 1866, 165852.	1.8	11
47	High-grade ovarian cancer associated H/ACA snoRNAs promote cancer cell proliferation and survival. <i>NAR Cancer</i> , 2022, 4, zcab050.	1.6	10
48	Downregulation of KRAB zinc finger proteins in 5-fluorouracil resistant colorectal cancer cells. <i>BMC Cancer</i> , 2022, 22, 363.	1.1	9
49	PNAC: a protein nucleolar association classifier. <i>BMC Genomics</i> , 2011, 12, 74.	1.2	8
50	In silico analysis of RNA-seq requires a more complete description of methodology. <i>Nature Reviews Molecular Cell Biology</i> , 2019, 20, 451-452.	16.1	7
51	First trimester plasma microRNAs levels predict Matsuda Index-estimated insulin sensitivity between 24th and 29th week of pregnancy. <i>BMJ Open Diabetes Research and Care</i> , 2022, 10, e002703.	1.2	6
52	Extent of pre-translational regulation for the control of nucleocytoplasmic protein localization. <i>BMC Genomics</i> , 2016, 17, 472.	1.2	5
53	Factorial study of the RNA-seq computational workflow identifies biases as technical gene signatures. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa043.	1.5	4
54	miR profile in pagetic osteoclasts: from large-scale sequencing to gene expression study. <i>Journal of Molecular Medicine</i> , 2021, 99, 1771-1781.	1.7	4

#	ARTICLE	IF	CITATIONS
55	Human protein-protein interaction prediction. BMC Bioinformatics, 2010, 11, .	1.2	3
56	Widespread pre-translational regulation of the inclusion of signal peptides in human proteins. Genomics, 2017, 109, 113-122.	1.3	2
57	Enhanced snoMEN Vectors Facilitate Establishment of GFP ⁺ HIF-1 [±] Protein Replacement Human Cell Lines. PLoS ONE, 2016, 11, e0154759.	1.1	2
58	Cardiomyocyte-specific Srsf3 deletion reveals a mitochondrial regulatory role. FASEB Journal, 2021, 35, e21544.	0.2	1
59	Diversity, Overlap, and Relationships in the Small RNA Landscape. , 2012, , 23-48.		0
60	SAPFIR: A webserver for the identification of alternative protein features. BMC Bioinformatics, 2022, 23, .	1.2	0