

Dalila Bensaddek

List of Publications by Year in descending order

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Version: 2024-02-01

16
papers

810
citations

1040056

9
h-index

996975

15
g-index

18
all docs

18
docs citations

18
times ranked

2132
citing authors

#	ARTICLE	IF	CITATIONS
1	Erosion of human X chromosome inactivation causes major remodeling of the iPSC proteome. <i>Cell Reports</i> , 2021, 35, 109032.	6.4	23
2	DEPS-1 is required for piRNA-dependent silencing and PIWI condensate organisation in <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2020, 11, 4242.	12.8	16
3	Population-scale proteome variation in human induced pluripotent stem cells. <i>ELife</i> , 2020, 9, .	6.0	40
4	Multibatch TMT Reveals False Positives, Batch Effects and Missing Values. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1967-1980.	3.8	128
5	Signal enhanced proteomics: a biological perspective on dissecting the functional organisation of cell proteomes. <i>Current Opinion in Chemical Biology</i> , 2019, 48, 114-122.	6.1	3
6	Common genetic variation drives molecular heterogeneity in human iPSCs. <i>Nature</i> , 2017, 546, 370-375.	27.8	491
7	Comparative genetic, proteomic and phosphoproteomic analysis of <i>C. elegans</i> embryos with a focus on ham-1/STOX and pig-1/MELK in dopaminergic neuron development. <i>Scientific Reports</i> , 2017, 7, 4314.	3.3	11
8	The Chromatin Assembly Factor Complex 1 (CAF1) and 5-Azacytidine (5-AzaC) Affect Cell Motility in Src-transformed Human Epithelial Cells. <i>Journal of Biological Chemistry</i> , 2017, 292, 172-184.	3.4	12
9	CDK dependent phosphorylation of PHD1 on Serine 130 determines specificity in substrate targeting in cells. <i>Journal of Cell Science</i> , 2016, 129, 191-205.	2.0	15
10	Unlocking the chromatin code by deciphering proteinâ€“DNA interactions. <i>Molecular Systems Biology</i> , 2016, 12, 887.	7.2	3
11	Analysis of Mass Spectrometry Data for Nucleolar Proteomics Experiments. <i>Methods in Molecular Biology</i> , 2016, 1455, 263-276.	0.9	0
12	Quantitative Proteomic Analysis of the Human Nucleolus. <i>Methods in Molecular Biology</i> , 2016, 1455, 249-262.	0.9	9
13	Microâ€“proteomics with iterative data analysis: Proteome analysis in <i>C. elegans</i> at the single worm level. <i>Proteomics</i> , 2016, 16, 381-392.	2.2	34
14	Enhanced snoMEN Vectors Facilitate Establishment of GFPâ€“HIF-1 β Protein Replacement Human Cell Lines. <i>PLoS ONE</i> , 2016, 11, e0154759.	2.5	2
15	Evaluating the use of HILIC in large-scale, multi dimensional proteomics: Horses for courses?. <i>International Journal of Mass Spectrometry</i> , 2015, 391, 105-114.	1.5	10
16	Targeted Knock-Down of miR21 Primary Transcripts Using snoMEN Vectors Induces Apoptosis in Human Cancer Cell Lines. <i>PLoS ONE</i> , 2015, 10, e0138668.	2.5	11