Dalila Bensaddek

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5265433/publications.pdf

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