

Tiffany Hung

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11378216/publications.pdf>

Version: 2024-02-01

11
papers

7,789
citations

933447

10
h-index

1281871

11
g-index

13
all docs

13
docs citations

13
times ranked

11898
citing authors

#	ARTICLE	IF	CITATIONS
1	Long non-coding RNA HOTAIR reprograms chromatin state to promote cancer metastasis. <i>Nature</i> , 2010, 464, 1071-1076.	27.8	4,648
2	Extensive and coordinated transcription of noncoding RNAs within cell-cycle promoters. <i>Nature Genetics</i> , 2011, 43, 621-629.	21.4	1,080
3	ING2 PHD domain links histone H3 lysine 4 methylation to active gene repression. <i>Nature</i> , 2006, 442, 96-99.	27.8	851
4	Long noncoding RNA in genome regulation. <i>RNA Biology</i> , 2010, 7, 582-585.	3.1	523
5	An inducible long noncoding RNA amplifies DNA damage signaling. <i>Nature Genetics</i> , 2016, 48, 1370-1376.	21.4	195
6	ING4 Mediates Crosstalk between Histone H3 K4 Trimethylation and H3 Acetylation to Attenuate Cellular Transformation. <i>Molecular Cell</i> , 2009, 33, 248-256.	9.7	191
7	HBO1 HAT Complexes Target Chromatin throughout Gene Coding Regions via Multiple PHD Finger Interactions with Histone H3 Tail. <i>Molecular Cell</i> , 2009, 33, 257-265.	9.7	163
8	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. <i>Nature Biotechnology</i> , 2021, 39, 1141-1150.	17.5	66
9	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. <i>Nature Biotechnology</i> , 2021, 39, 1151-1160.	17.5	39
10	Whole genome and exome sequencing reference datasets from a multi-center and cross-platform benchmark study. <i>Scientific Data</i> , 2021, 8, 296.	5.3	15
11	Pre- and post-treatment blood-based genomic landscape of patients with <i>ROS1</i> or <i>NTRK</i> fusion-positive solid tumours treated with entrectinib. <i>Molecular Oncology</i> , 2022, 16, 2000-2014.	4.6	10