

Christopher S Hughes

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

2,641
citations

623574

14
h-index

752573

20
g-index

24
all docs

24
docs citations

24
times ranked

4549
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteomic analysis of archival breast cancer clinical specimens identifies biological subtypes with distinct survival outcomes. <i>Nature Communications</i> , 2022, 13, 896.	5.8	46
2	MEDB-18. Elongation control of mRNA translation supports Group 3 medulloblastoma adaptation to nutrient deprivation. <i>Neuro-Oncology</i> , 2022, 24, i108-i109.	0.6	0
3	HACE1 blocks HIF1 α accumulation under hypoxia in a RAC1 dependent manner. <i>Oncogene</i> , 2021, 40, 1988-2001.	2.6	5
4	Proteomic Screens for Suppressors of Anoikis Identify IL1RAP as a Promising Surface Target in Ewing Sarcoma. <i>Cancer Discovery</i> , 2021, 11, 2884-2903.	7.7	51
5	Not4 and Not5 modulate translation elongation by Rps7A ubiquitination, Rli1 moonlighting, and condensates that exclude eIF5A. <i>Cell Reports</i> , 2021, 36, 109633.	2.9	20
6	The FUS-DDIT3 Interactome in Myxoid Liposarcoma. <i>Neoplasia</i> , 2019, 21, 740-751.	2.3	26
7	A Standardized and Reproducible Proteomics Protocol for Bottom-Up Quantitative Analysis of Protein Samples Using SP3 and Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2019, 1959, 65-87.	0.4	25
8	Class I HDAC inhibitors enhance YB α acetylation and oxidative stress to block sarcoma metastasis. <i>EMBO Reports</i> , 2019, 20, e48375.	2.0	78
9	RawTools: Rapid and Dynamic Interrogation of Orbitrap Data Files for Mass Spectrometer System Management. <i>Journal of Proteome Research</i> , 2019, 18, 700-708.	1.8	20
10	Single-pot, solid-phase-enhanced sample preparation for proteomics experiments. <i>Nature Protocols</i> , 2019, 14, 68-85.	5.5	802
11	Parsing and Quantification of Raw Orbitrap Mass Spectrometer Data Using RawQuant. <i>Journal of Proteome Research</i> , 2018, 17, 2237-2247.	1.8	10
12	Extending the Compatibility of the SP3 Paramagnetic Bead Processing Approach for Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 1730-1740.	1.8	186
13	Using Public Data for Comparative Proteome Analysis in Precision Medicine Programs. <i>Proteomics - Clinical Applications</i> , 2018, 12, 1600179.	0.8	2
14	Investigating Acquisition Performance on the Orbitrap Fusion When Using Tandem MS/MS/MS Scanning with Isobaric Tags. <i>Journal of Proteome Research</i> , 2017, 16, 1839-1846.	1.8	20
15	Evaluating the Characteristics of Reporter Ion Signal Acquired in the Orbitrap Analyzer for Isobaric Mass Tag Proteome Quantification Experiments. <i>Journal of Proteome Research</i> , 2017, 16, 1831-1838.	1.8	8
16	CDK12 regulates alternative last exon mRNA splicing and promotes breast cancer cell invasion. <i>Nucleic Acids Research</i> , 2017, 45, 6698-6716.	6.5	114
17	CLK-dependent exon recognition and conjoined gene formation revealed with a novel small molecule inhibitor. <i>Nature Communications</i> , 2017, 8, 7.	5.8	108
18	Selective aggregation of the splicing factor Hsh155 suppresses splicing upon genotoxic stress. <i>Journal of Cell Biology</i> , 2017, 216, 4027-4040.	2.3	10

#	ARTICLE	IF	CITATIONS
19	Quantitative Profiling of Single Formalin Fixed Tumour Sections: proteomics for translational research. <i>Scientific Reports</i> , 2016, 6, 34949.	1.6	100
20	Identification of Maturation-Specific Proteins by Single-Cell Proteomics of Human Oocytes. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2616-2627.	2.5	173
21	Ultrasensitive proteome analysis using paramagnetic bead technology. <i>Molecular Systems Biology</i> , 2014, 10, 757.	3.2	835