Pedro R Cutillas

List of Publications by Year
in descending order

83 papers	7,837 citations	159585 30 h-index	76900 74 g-index
88 all docs	88 docs citations	88 times ranked	18555 citing authors

#	Article	IF	Citations
1	Elucidating the role of the kinase activity of endothelial cell focal adhesion kinase in angiocrine signalling and tumour growth. Journal of Pathology, 2022, 256, 235-247.	4.5	7
2	Disruption of pancreatic stellate cell myofibroblast phenotype promotes pancreatic tumor invasion. Cell Reports, 2022, 38, 110227.	6.4	33
3	Suppression of Endothelial Cell FAK Expression Reduces Pancreatic Ductal Adenocarcinoma Metastasis after Gemcitabine Treatment. Cancer Research, 2022, 82, 1909-1925.	0.9	13
4	Implementation of Clinical Phosphoproteomics and Proteomics for Personalized Medicine. Methods in Molecular Biology, 2022, 2420, 87-106.	0.9	3
5	Targeting the lysine-specific demethylase 1 rewires kinase networks and primes leukemia cells for kinase inhibitor treatment. Science Signaling, 2022, 15, eabl7989.	3.6	15
6	The cytotoxic action of BCI is not dependent on its stated DUSP1 or DUSP6 targets in neuroblastoma cells. FEBS Open Bio, 2022, , .	2.3	4
7	eEF2K Activity Determines Synergy to Cotreatment of Cancer Cells With PI3K and MEK Inhibitors. Molecular and Cellular Proteomics, 2022, 21, 100240.	3.8	5
8	CKS1 inhibition depletes leukemic stem cells and protects healthy hematopoietic stem cells in acute myeloid leukemia. Science Translational Medicine, 2022, 14, .	12.4	8
9	Sequence and Structure-Based Analysis of Specificity Determinants in Eukaryotic Protein Kinases. Cell Reports, 2021, 34, 108602.	6.4	22
10	Rituximab and obinutuzumab differentially hijack the B cell receptor and NOTCH1 signaling pathways. IScience, 2021, 24, 102089.	4.1	14
11	His452Tyr polymorphism in the human 5-HT2A receptor affects clozapine-induced signaling networks revealed by quantitative phosphoproteomics. Biochemical Pharmacology, 2021, 185, 114440.	4.4	5
12	KDM5 inhibition offers a novel therapeutic strategy for the treatment of KMT2D mutant lymphomas. Blood, 2021, 138, 370-381.	1.4	33
13	Drug ranking using machine learning systematically predicts the efficacy of anti-cancer drugs. Nature Communications, 2021, 12, 1850.	12.8	68
14	ActivatingÂmutations in BRAFÂdisrupt the hypothalamo-pituitary axis leading to hypopituitarism in mice and humans. Nature Communications, 2021, 12, 2028.	12.8	12
15	Computational Analysis of Cholangiocarcinoma Phosphoproteomes Identifies Patient-Specific Drug Targets. Cancer Research, 2021, 81, 5765-5776.	0.9	9
16	TGFBI Production by Macrophages Contributes to an Immunosuppressive Microenvironment in Ovarian Cancer. Cancer Research, 2021, 81, 5706-5719.	0.9	64
17	Adipocytes disrupt the translational programme of acute lymphoblastic leukaemia to favour tumour survival and persistence. Nature Communications, 2021, 12, 5507.	12.8	15
18	Elucidation of the BMI1 interactome identifies novel regulatory roles in glioblastoma. NAR Cancer, 2021, 3, zcab009.	3.1	4

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19	Proteomics and Phospho-Proteomics Reveal Predictive Signatures of Response and Mechanisms of Resistance to Midostaurin Plus Chemotherapy in FLT3 Mutant Positive Acute Myeloid Leukemia. Blood, 2021, 138, 3462-3462.	1.4	0
20	Targeted therapy for LIMD1-deficient non-small cell lung cancer subtypes. Cell Death and Disease, 2021, 12, 1075.	6.3	3
21	Liver Activation of Hepatocellular Nuclear Factor-4Î± by Small Activating RNA Rescues Dyslipidemia and Improves Metabolic Profile. Molecular Therapy - Nucleic Acids, 2020, 19, 361-370.	5.1	47
22	Transition to naÃ¯ve human pluripotency mirrors pan-cancer DNA hypermethylation. Nature Communications, 2020, 11, 3671.	12.8	17
23	Characterization of four subtypes in morphologically normal tissue excised proximal and distal to breast cancer. Npj Breast Cancer, 2020, 6, 38.	5.2	12
24	Withanolide Metabolites Inhibit PI3K/AKT and MAPK Pro-Survival Pathways and Induce Apoptosis in Acute Myeloid Leukemia Cells. Biomedicines, 2020, 8, 333.	3.2	10
25	Cancer Burden Is Controlled by Mural Cell-Î²3-Integrin Regulated Crosstalk with Tumor Cells. Cell, 2020, 181, 1346-1363.e21.	28.9	53
26	Prediction of Signed Protein Kinase Regulatory Circuits. Cell Systems, 2020, 10, 384-396.e9.	6.2	23
27	Cancer associated fibroblast FAK regulates malignant cell metabolism. Nature Communications, 2020, 11, 1290.	12.8	95
28	Bespoken Nanoceria: An Effective Treatment in Experimental Hepatocellular Carcinoma. Hepatology, 2020, 72, 1267-1282.	7.3	37
29	Reconstructing kinase network topologies from phosphoproteomics data reveals cancer-associated rewiring. Nature Biotechnology, 2020, 38, 493-502.	17.5	72
30	A systematic molecular and pharmacologic evaluation of AKT inhibitors reveals new insight into their biological activity. British Journal of Cancer, 2020, 123, 542-555.	6.4	22
31	PARP-1 activation after oxidative insult promotes energy stress-dependent phosphorylation of YAP1 and reduces cell viability. Biochemical Journal, 2020, 477, 4491-4513.	3.7	9
32	Integration of Deep Multi-Omics Profiling Veals New Insights into the Biology of Poor-Risk Acute Myeloid Leukemia. Blood, 2020, 136, 39-40.	1.4	0
33	Poly(ADP-Ribose) Polymerase-1 inhibition potentiates cell death and phosphorylation of DNA damage response proteins in oxidative stressed retinal cells. Experimental Eye Research, 2019, 188, 107790.	2.6	6
34	Perineural invasion in pancreatic cancer: proteomic analysis and inÂvitro modelling. Molecular Oncology, 2019, 13, 1075-1091.	4.6	38
35	Cerium Oxide Nanoparticles Protect against Oxidant Injury and Interfere with Oxidative Mediated Kinase Signaling in Human-Derived Hepatocytes. International Journal of Molecular Sciences, 2019, 20, 5959.	4.1	28
36	Dynamic trafficking and turnover of JAM-C is essential for endothelial cell migration. PLoS Biology, 2019, 17, e3000554.	5.6	13

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37	Dynamic trafficking and turnover of JAM-C is essential for endothelial cell migration. , 2019, 17, e3000554.		0
38	Dynamic trafficking and turnover of JAM-C is essential for endothelial cell migration. , 2019, 17, e3000554.		0
39	Dynamic trafficking and turnover of JAM-C is essential for endothelial cell migration. , 2019, 17, e3000554.		0
40	Dynamic trafficking and turnover of JAM-C is essential for endothelial cell migration. , 2019, 17, e3000554.		0
41	Dynamic trafficking and turnover of JAM-C is essential for endothelial cell migration. , 2019, 17, e3000554.		0
42	Dynamic trafficking and turnover of JAM-C is essential for endothelial cell migration. , 2019, 17, e3000554.		0
43	Gene activation of CEBPA using saRNA: preclinical studies of the first in human saRNA drug candidate for liver cancer. Oncogene, 2018, 37, 3216-3228.	5.9	60
44	PHLDA1 Mediates Drug Resistance in Receptor Tyrosine Kinase-Driven Cancer. Cell Reports, 2018, 22, 2469-2481.	6.4	34
45	Proteomic and genomic integration identifies kinase and differentiation determinants of kinase inhibitor sensitivity in leukemia cells. Leukemia, 2018, 32, 1818-1822.	7.2	36
46	Phosphoproteomics-Based Profiling of Kinase Activities in Cancer Cells. Methods in Molecular Biology, 2018, 1711, 103-132.	0.9	24
47	Deconstruction of a Metastatic Tumor Microenvironment Reveals a Common Matrix Response in Human Cancers. Cancer Discovery, 2018, 8, 304-319.	9.4	255
48	Endothelial cell rearrangements during vascular patterning require PI3-kinase-mediated inhibition of actomyosin contractility. Nature Communications, 2018, 9, 4826.	12.8	53
49	Factors Secreted by Cancer-Associated Fibroblasts that Sustain Cancer Stem Properties in Head and Neck Squamous Carcinoma Cells as Potential Therapeutic Targets. Cancers, 2018, 10, 334.	3.7	41
50	Anti-CD20 Monoclonal Antibodies Hijack the B-Cell Receptor Signaling Cascade Thereby Activating the NOTCH1 Signaling Pathway. Blood, 2018, 132, 588-588.	1.4	0
51	Approaches to identify kinase dependencies in cancer signalling networks. FEBS Letters, 2017, 591, 2577-2592.	2.8	11
52	Proteomic and genomic integration identifies kinase and differentiation determinants of kinase inhibitor sensitivity in leukemia cells. Leukemia, 2017, , .	7.2	0
53	Kinase activity ranking using phosphoproteomics data (KARP) quantifies the contribution of protein kinases to the regulation of cell viability. Molecular and Cellular Proteomics, 2017, 16, 1694-1704.	3.8	18
54	Characterisation of preproendothelin-1 derived peptides identifies Endothelin-Like Domain Peptide as a modulator of Endothelin-1. Scientific Reports, 2017, 7, 4956.	3.3	6

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55	Impact of phosphoproteomics in the translation of kinaseâ€targeted therapies. Proteomics, 2017, 17, 1600235.	2.2	28
56	Label-Free Phosphoproteomic Approach for Kinase Signaling Analysis. Methods in Molecular Biology, 2017, 1636, 199-217.	0.9	10
57	Integrated transcriptomic and proteomic analysis identifies protein kinase CK2 as a key signaling node in an inflammatory cytokine network in ovarian cancer cells. Oncotarget, 2016, 7, 15648-15661.	1.8	13
58	NCK Associated Protein 1 Modulated by miRNAâ€214 Determines Vascular Smooth Muscle Cell Migration, Proliferation, and Neointima Hyperplasia. Journal of the American Heart Association, 2016, 5, .	3.7	50
59	Fumarate is an epigenetic modifier that elicits epithelial-to-mesenchymal transition. Nature, 2016, 537, 544-547.	27.8	443
60	Disulfide-activated protein kinase G Iî± regulates cardiac diastolic relaxation and fine-tunes the Frankâ€“Starling response. Nature Communications, 2016, 7, 13187.	12.8	46
61	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	9.1	4,701
62	Application of Proteomics in Cancer Biomarker Discovery: GeLC-MS/MS. Methods in Molecular Biology, 2016, 1381, 201-209.	0.9	1
63	The MAP kinase pathway coordinates crossover designation with disassembly of synaptonemal complex proteins during meiosis. ELife, 2016, 5, e12039.	6.0	36
64	Empirical inference of circuitry and plasticity in a kinase signaling network. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7719-7724.	7.1	69
65	Large-scale models of signal propagation in human cells derived from discovery phosphoproteomic data. Nature Communications, 2015, 6, 8033.	12.8	79
66	ERK and RSK are necessary for TRH-induced inhibition of r-ERG potassium currents in rat pituitary GH 3 cells. Cellular Signalling, 2015, 27, 1720-1730.	3.6	5
67	Role of phosphoproteomics in the development of personalized cancer therapies. Proteomics - Clinical Applications, 2015, 9, 383-395.	1.6	40
68	The urinary proteome and metabonome differ from normal in adults with mitochondrial disease. Kidney International, 2015, 87, 610-622.	5.2	41
69	Cross-species Proteomics Reveals Specific Modulation of Signaling in Cancer and Stromal Cells by Phosphoinositide 3-kinase (PI3K) Inhibitors. Molecular and Cellular Proteomics, 2014, 13, 1457-1470.	3.8	24
70	Environmental Stress Affects the Activity of Metabolic and Growth Factor Signaling Networks and Induces Autophagy Markers in MCF7 Breast Cancer Cells. Molecular and Cellular Proteomics, 2014, 13, 836-848.	3.8	33
71	Approaches for measuring signalling plasticity in the context of resistance to targeted cancer therapies. Biochemical Society Transactions, 2014, 42, 791-797.	3.4	5
72	Phosphoproteomics data classify hematological cancer cell lines according to tumor type and sensitivity to kinase inhibitors. Genome Biology, 2013, 14, R37.	9.6	60

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73	Polyamine production is downstream and upstream of oncogenic PI3K signalling and contributes to tumour cell growth. Biochemical Journal, 2013, 450, 619-628.	3.7	21
74	Kinase-Substrate Enrichment Analysis Provides Insights into the Heterogeneity of Signaling Pathway Activation in Leukemia Cells. Science Signaling, 2013, 6, rs6.	3.6	298
75	Phosphoproteomic Analysis of Leukemia Cells under Basal and Drug-treated Conditions Identifies Markers of Kinase Pathway Activation and Mechanisms of Resistance. Molecular and Cellular Proteomics, 2012, 11, 453-466.	3.8	62
76	Global profiling of protein kinase activities in cancer cells by mass spectrometry. Journal of Proteomics, 2012, 77, 492-503.	2.4	12
77	Advances in phosphopeptide enrichment techniques for phosphoproteomics. Amino Acids, 2012, 43, 1009-1024.	2.7	100
78	Characterization of a TiO2 enrichment method for label-free quantitative phosphoproteomics. Methods, 2011, 54, 370-378.	3.8	101
79	A Self-validating Quantitative Mass Spectrometry Method for Assessing the Accuracy of High-content Phosphoproteomic Experiments. Molecular and Cellular Proteomics, 2011, 10, M110.003079.	3.8	49
80	Biological signalling activity measurements using mass spectrometry. Biochemical Journal, 2011, 434, 189-199.	3.7	31
81	Approaches and Applications of Quantitative LC-MS for Proteomics and Activitomics. Methods in Molecular Biology, 2010, 658, 3-17.	0.9	10
82	Analysis of Peptides in Biological Fluids by LC-MS/MS. Methods in Molecular Biology, 2010, 658, 311-321.	0.9	4
83	Quantitative Profile of Five Murine Core Proteomes Using Label-free Functional Proteomics. Molecular and Cellular Proteomics, 2007, 6, 1560-1573.	3.8	105