Alessandro Ori

List of Publications by Year
in descending order

76 papers	5,349 citations	109264 35 h-index	98753 67 g-index
87 all docs	87 docs citations	87 times ranked	9343 citing authors

#	Article	IF	Citations
1	PLCG1 is required for AML1-ETO leukemia stem cell self-renewal. Blood, 2022, 139, 1080-1097.	0.6	16
2	Multifaceted Microcephaly-Related Gene MCPH1. Cells, 2022, 11, 275.	1.8	10
3	Organelle dysfunction and its contribution to metabolic impairments in aging and age-related diseases. Current Opinion in Systems Biology, 2022, 30, 100416.	1.3	1
4	Metabolic determination of cell fate through selective inheritance of mitochondria. Nature Cell Biology, 2022, 24, 148-154.	4.6	46
5	Glycation Alters the Fatty Acid Binding Capacity of Human Serum Albumin. Journal of Agricultural and Food Chemistry, 2022, 70, 3033-3046.	2.4	10
6	Conserved exchange of paralog proteins during neuronal differentiation. Life Science Alliance, 2022, 5, e202201397.	1.3	0
7	VerÃnderung der BioaktivitÃt von Proteinen durch Glykierung. Lebensmittelchemie, 2022, 76, .	0.0	0
8	The natural compound atraric acid suppresses androgen-regulated neo-angiogenesis of castration-resistant prostate cancer through angiopoietin 2. Oncogene, 2022, 41, 3263-3277.	2.6	8
9	Protein lifetimes in aged brains reveal a proteostatic adaptation linking physiological aging to neurodegeneration. Science Advances, 2022, 8, .	4.7	22
10	HAT cofactor TRRAP modulates microtubule dynamics via SP1 signaling to prevent neurodegeneration. ELife, 2021, 10, .	2.8	9
11	The N-terminal BRCT domain determines MCPH1 function in brain development and fertility. Cell Death and Disease, 2021, 12, 143.	2.7	9
12	Aging drives organâ€specific alterations of the inflammatory microenvironment guided by immunomodulatory mediators in mice. FASEB Journal, 2021, 35, e21558.	0.2	11
13	GMPPA defects cause a neuromuscular disorder with Î±-dystroglycan hyperglycosylation. Journal of Clinical Investigation, 2021, 131, .	3.9	13
14	Extensive remodeling of the extracellular matrix during aging contributes to age-dependent impairments of muscle stem cell functionality. Cell Reports, 2021, 35, 109223.	2.9	49
15	ATR regulates neuronal activity by modulating presynaptic firing. Nature Communications, 2021, 12, 4067.	5.8	8
16	The Hematopoietic Bone Marrow Niche Ecosystem. Frontiers in Cell and Developmental Biology, 2021, 9, 705410.	1.8	34
17	Identifying Cellâ€Typeâ€Specific Metabolic Signatures Using Transcriptome and Proteome Analyses. Current Protocols, 2021, 1, e245.	1.3	3
18	Iron Oxide Nanoparticles Carrying 5-Fluorouracil in Combination with Magnetic Hyperthermia Induce Thrombogenic Collagen Fibers, Cellular Stress, and Immune Responses in Heterotopic Human Colon Cancer in Mice. Pharmaceutics, 2021, 13, 1625.	2.0	11

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19	Mapping protein carboxymethylation sites provides insights into their role in proteostasis and cell proliferation. Nature Communications, 2021, 12, 6743.	5.8	11
20	The GID ubiquitin ligase complex is a regulator of AMPK activity and organismal lifespan. Autophagy, 2020, 16, 1618-1634.	4.3	43
21	Spatially resolved analysis of FFPE tissue proteomes by quantitative mass spectrometry. Nature Protocols, 2020, 15, 2956-2979.	5.5	35
22	Reduced proteasome activity in the aging brain results in ribosome stoichiometry loss and aggregation. Molecular Systems Biology, 2020, 16, e9596.	3.2	131
23	Loss of metabolic plasticity underlies metformin toxicity in aged Caenorhabditis elegans. Nature Metabolism, 2020, 2, 1316-1331.	5.1	61
24	Vulnerability of progeroid smooth muscle cells to biomechanical forces is mediated by MMP13. Nature Communications, 2020, 11, 4110.	5.8	20
25	Stem cell aging: The upcoming era of proteins and metabolites. Mechanisms of Ageing and Development, 2020, 190, 111288.	2.2	16
26	Region-Specific Proteome Changes of the Intestinal Epithelium during Aging and Dietary Restriction. Cell Reports, 2020, 31, 107565.	2.9	52
27	Metastatic-niche labelling reveals parenchymal cells with stem features. Nature, 2019, 572, 603-608.	13.7	139
28	Quantitation of Reactive Acyl-CoA Species Mediated Protein Acylation by HPLCâ€"MS/MS. Analytical Chemistry, 2019, 91, 12336-12343.	3.2	16
29	Nucleoporin Nup155 is part of the p53 network in liver cancer. Nature Communications, 2019, 10, 2147.	5.8	29
30	Disentangling Genetic and Environmental Effects on the Proteotypes of Individuals. Cell, 2019, 177, 1308-1318.e10.	13.5	48
31	Profiling of gallbladder carcinoma reveals distinct miRNA profiles and activation of STAT1 by the tumor suppressive miRNA-145-5p. Scientific Reports, 2019, 9, 4796.	1.6	29
32	Comparison of Protein Quantification in a Complex Background by DIA and TMT Workflows with Fixed Instrument Time. Journal of Proteome Research, 2019, 18, 1340-1351.	1.8	107
33	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. IScience, 2019, 21, 664-680.	1.9	52
34	Karyopherin Î±2-dependent import of E2F1 and TFDP1 maintains protumorigenic stathmin expression in liver cancer. Cell Communication and Signaling, 2019, 17, 159.	2.7	29
35	Increased Expression of Immature Mannose-Containing Glycoproteins and Sialic Acid in Aged Mouse Brains. International Journal of Molecular Sciences, 2019, 20, 6118.	1.8	8
36	Cohesin-mediated NF-Î°B signaling limits hematopoietic stem cell self-renewal in aging and inflammation. Journal of Experimental Medicine, 2019, 216, 152-175.	4.2	56

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37	Spatial Tissue Proteomics Quantifies Inter- and Intratumor Heterogeneity in Hepatocellular Carcinoma (HCC). Molecular and Cellular Proteomics, 2018, 17, 810-825.	2.5	65
38	NUFIP1 is a ribosome receptor for starvation-induced ribophagy. Science, 2018, 360, 751-758.	6.0	262
39	Cellular and epigenetic drivers of stem cell ageing. Nature Reviews Molecular Cell Biology, 2018, 19, 594-610.	16.1	196
40	Quantifying compartmentâ€associated variations ofÂprotein abundance in proteomics data. Molecular Systems Biology, 2018, 14, e8131.	3.2	14
41	Species comparison of liver proteomes reveals links to naked mole-rat longevity and human aging. BMC Biology, 2018, 16, 82.	1.7	55
42	TRPS1 shapes YAP/TEAD-dependent transcription in breast cancer cells. Nature Communications, 2018, 9, 3115.	5.8	58
43	Architecture of the yeast Elongator complex. EMBO Reports, 2017, 18, 264-279.	2.0	75
44	What have we learned on aging from omics studies?. Seminars in Cell and Developmental Biology, 2017, 70, 177-189.	2.3	54
45	Proteomic Analysis Reveals GMP Synthetase as p53 Repression Target in Liver Cancer. American Journal of Pathology, 2017, 187, 228-235.	1.9	26
46	Landscape of nuclear transport receptor cargoÂspecificity. Molecular Systems Biology, 2017, 13, 962.	3.2	88
47	Automated structure modeling of large protein assemblies using crosslinks as distance restraints. Nature Methods, 2016, 13, 515-520.	9.0	49
48	Structure of the ribosome post-recycling complex probed by chemical cross-linking and mass spectrometry. Nature Communications, 2016, 7, 13248.	5.8	27
49	The endosomal transcriptional regulator RNF11 integrates degradation and transport of EGFR. Journal of Cell Biology, 2016, 215, 543-558.	2.3	51
50	Spatiotemporal variation of mammalian protein complex stoichiometries. Genome Biology, 2016, 17, 47.	3.8	115
51	Cellular apoptosis susceptibility (CAS) is linked to integrin Î²1 and required for tumor cell migration and invasion in hepatocellular carcinoma (HCC). Oncotarget, 2016, 7, 22883-22892.	0.8	18
52	Characterization and quantification of proteins secreted by single human embryos prior to implantation. EMBO Molecular Medicine, 2015, 7, 1465-1479.	3.3	36
53	Xlink Analyzer: Software for analysis and visualization of cross-linking data in the context of three-dimensional structures. Journal of Structural Biology, 2015, 189, 177-183.	1.3	156
54	Structural basis for assembly and function of the Nup82 complex in the nuclear pore scaffold. Journal of Cell Biology, 2015, 208, 283-297.	2.3	64

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55	Histone Deacetylase Inhibitors (HDACi) Cause the Selective Depletion of Bromodomain Containing Proteins (BCPs). Molecular and Cellular Proteomics, 2015, 14, 1350-1360.	2.5	23
56	Integrated Transcriptome and Proteome Analyses Reveal Organ-Specific Proteome Deterioration in Old Rats. Cell Systems, 2015, 1, 224-237.	2.9	176
57	In situ structural analysis of the human nuclear pore complex. Nature, 2015, 526, 140-143.	13.7	361
58	Symportin 1 chaperones 5S RNP assembly during ribosome biogenesis by occupying an essential rRNA-binding site. Nature Communications, 2015, 6, 6510.	5.8	51
59	The Use of Targeted Proteomics to Determine the Stoichiometry of Large Macromolecular Assemblies. Methods in Cell Biology, 2014, 122, 117-146.	0.5	22
60	Proliferation and migration activities of fibroblast growth factor-2 in endothelial cells are modulated by its direct interaction with heparin affin regulatory peptide. Biochimie, 2014, 107, 350-357.	1.3	8
61	An integrated approach for genome annotation of the eukaryotic thermophile Chaetomium thermophilum. Nucleic Acids Research, 2014, 42, 13525-13533.	6.5	55
62	Prosurvival function of the cellular apoptosis susceptibility/importin-Î±1 transport cycle is repressed by p53 in liver cancer. Hepatology, 2014, 60, 884-895.	3.6	29
63	Association of condensin with chromosomes depends on DNA binding by its HEAT-repeat subunits. Nature Structural and Molecular Biology, 2014, 21, 560-568.	3.6	100
64	Characterisation of the interaction of neuropilin-1 with heparin and a heparan sulfate mimetic library of heparin-derived sugars. PeerJ, 2014, 2, e461.	0.9	14
65	Integrated Structural Analysis of the Human Nuclear Pore Complex Scaffold. Cell, 2013, 155, 1233-1243.	13.5	321
66	Cell typeâ€specific nuclear pores: a case in point for contextâ€dependent stoichiometry of molecular machines. Molecular Systems Biology, 2013, 9, 648.	3.2	277
67	Diversification of the Structural Determinants of Fibroblast Growth Factor-Heparin Interactions. Journal of Biological Chemistry, 2012, 287, 40061-40073.	1.6	69
68	Following Proteinâ€"Glycosaminoglycan Polysaccharide Interactions with Differential Scanning Fluorimetry. Methods in Molecular Biology, 2012, 836, 171-182.	0.4	4
69	A Systems Biology Approach for the Investigation of the Heparin/Heparan Sulfate Interactome. Journal of Biological Chemistry, 2011, 286, 19892-19904.	1.6	203
70	The quantitative proteome of a human cell line. Molecular Systems Biology, 2011, 7, 549.	3.2	691
71	Comparable stabilisation, structural changes and activities can be induced in FGF by a variety of HS and non-GAG analogues: implications for sequence-activity relationships. Organic and Biomolecular Chemistry, 2010, 8, 5390.	1.5	29
72	Differential Scanning Fluorimetry Measurement of Protein Stability Changes upon Binding to Glycosaminoglycans: A Screening Test for Binding Specificity. Analytical Chemistry, 2010, 82, 3796-3802.	3.2	53

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73	Cations Modulate Polysaccharide Structure To Determine FGFâˆ'FGFR Signaling: A Comparison of Signaling and Inhibitory Polysaccharide Interactions with FGF-1 in Solution. Biochemistry, 2009, 48, 4772-4779.	1.2	16
74	Identification of Heparin-binding Sites in Proteins by Selective Labeling. Molecular and Cellular Proteomics, 2009, 8, 2256-2265.	2.5	65
75	The heparanome and regulation of cell function: structures, functions and challenges. Frontiers in Bioscience - Landmark, 2008, Volume, 4309.	3.0	143
76	Antiproliferative activity of CCN3: Involvement of the C-terminal module and post-translational regulation. Journal of Cellular Biochemistry, 2007, 101, 1475-1491.	1.2	61