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	The quantitative proteome of a human cell line. Molecular Systems Biology, 2011, 7, 549.	3.2	691
2	In situ structural analysis of the human nuclear pore complex. Nature, 2015, 526, 140-143.	13.7	361
3	Integrated Structural Analysis of the Human Nuclear Pore Complex Scaffold. Cell, 2013, 155, 1233-1243.	13.5	321
4	Cell type€specific nuclear pores: a case in point for context€dependent stoichiometry of molecular machines. Molecular Systems Biology, 2013, 9, 648.	3.2	277
5	NUFIP1 is a ribosome receptor for starvation-induced ribophagy. Science, 2018, 360, 751-758.	6.0	262
6	A Systems Biology Approach for the Investigation of the Heparin/Heparan Sulfate Interactome. Journal of Biological Chemistry, 2011, 286, 19892-19904.	1.6	203
7	Cellular and epigenetic drivers of stem cell ageing. Nature Reviews Molecular Cell Biology, 2018, 19, 594-610.	16.1	196
8	Integrated Transcriptome and Proteome Analyses Reveal Organ-Specific Proteome Deterioration in Old Rats. Cell Systems, 2015, 1, 224-237.	2.9	176
9	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
10	The heparanome and regulation of cell function: structures, functions and challenges. Frontiers in Bioscience - Landmark, 2008, Volume, 4309.	3.0	143
11	Metastatic-niche labelling reveals parenchymal cells with stem features. Nature, 2019, 572, 603-608.	13.7	139
12	Reduced proteasome activity in the aging brain results in ribosome stoichiometry loss and aggregation. Molecular Systems Biology, 2020, 16, e9596.	3.2	131
13	Spatiotemporal variation of mammalian protein complex stoichiometries. Genome Biology, 2016, 17, 47.	3.8	115
14	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
15	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
16	Landscape of nuclear transport receptor cargoÂspecificity. Molecular Systems Biology, 2017, 13, 962.	3.2	88
17	Architecture of the yeast Elongator complex. EMBO Reports, 2017, 18, 264-279.	2.0	75
18	Diversification of the Structural Determinants of Fibroblast Growth Factor-Heparin Interactions. Journal of Biological Chemistry, 2012, 287, 40061-40073.	1.6	69

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19	Identification of Heparin-binding Sites in Proteins by Selective Labeling. Molecular and Cellular Proteomics, 2009, 8, 2256-2265.	2.5	65
20	Spatial Tissue Proteomics Quantifies Inter- and Intratumor Heterogeneity in Hepatocellular Carcinoma (HCC). Molecular and Cellular Proteomics, 2018, 17, 810-825.	2.5	65
21	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
22	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
23	Loss of metabolic plasticity underlies metformin toxicity in aged Caenorhabditis elegans. Nature Metabolism, 2020, 2, 1316-1331.	5.1	61
24	TRPS1 shapes YAP/TEAD-dependent transcription in breast cancer cells. Nature Communications, 2018, 9, 3115.	5.8	58
25	Cohesin-mediated NF-κB signaling limits hematopoietic stem cell self-renewal in aging and inflammation. Journal of Experimental Medicine, 2019, 216, 152-175.	4.2	56
26	An integrated approach for genome annotation of the eukaryotic thermophile Chaetomium thermophilum. Nucleic Acids Research, 2014, 42, 13525-13533.	6.5	55
27	Species comparison of liver proteomes reveals links to naked mole-rat longevity and human aging. BMC Biology, 2018, 16, 82.	1.7	55
28	What have we learned on aging from omics studies?. Seminars in Cell and Developmental Biology, 2017, 70, 177-189.	2.3	54
29	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
30	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. IScience, 2019, 21, 664-680.	1.9	52
31	Region-Specific Proteome Changes of the Intestinal Epithelium during Aging and Dietary Restriction. Cell Reports, 2020, 31, 107565.	2.9	52
32	Symportin 1 chaperones 5S RNP assembly during ribosome biogenesis by occupying an essential rRNA-binding site. Nature Communications, 2015, 6, 6510.	5.8	51
33	The endosomal transcriptional regulator RNF11 integrates degradation and transport of EGFR. Journal of Cell Biology, 2016, 215, 543-558.	2.3	51
34	Automated structure modeling of large protein assemblies using crosslinks as distance restraints. Nature Methods, 2016, 13, 515-520.	9.0	49
35	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
36	Disentangling Genetic and Environmental Effects on the Proteotypes of Individuals. Cell, 2019, 177, 1308-1318.e10.	13.5	48

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37	Metabolic determination of cell fate through selective inheritance of mitochondria. Nature Cell Biology, 2022, 24, 148-154.	4.6	46
38	The GID ubiquitin ligase complex is a regulator of AMPK activity and organismal lifespan. Autophagy, 2020, 16, 1618-1634.	4.3	43
39	Characterization and quantification of proteins secreted by single human embryos prior to implantation. EMBO Molecular Medicine, 2015, 7, 1465-1479.	3.3	36
40	Spatially resolved analysis of FFPE tissue proteomes by quantitative mass spectrometry. Nature Protocols, 2020, 15, 2956-2979.	5.5	35
41	The Hematopoietic Bone Marrow Niche Ecosystem. Frontiers in Cell and Developmental Biology, 2021, 9, 705410.	1.8	34
42	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
43	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
44	Nucleoporin Nup155 is part of the p53 network in liver cancer. Nature Communications, 2019, 10, 2147.	5.8	29
45	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
46	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
47	Structure of the ribosome post-recycling complex probed by chemical cross-linking and mass spectrometry. Nature Communications, 2016, 7, 13248.	5.8	27
48	Proteomic Analysis Reveals GMP Synthetase as p53 Repression Target in Liver Cancer. American Journal of Pathology, 2017, 187, 228-235.	1.9	26
49	Histone Deacetylase Inhibitors (HDACi) Cause the Selective Depletion of Bromodomain Containing Proteins (BCPs). Molecular and Cellular Proteomics, 2015, 14, 1350-1360.	2.5	23
50	The Use of Targeted Proteomics to Determine the Stoichiometry of Large Macromolecular Assemblies. Methods in Cell Biology, 2014, 122, 117-146.	0.5	22
51	Protein lifetimes in aged brains reveal a proteostatic adaptation linking physiological aging to neurodegeneration. Science Advances, 2022, 8, .	4.7	22
52	Vulnerability of progeroid smooth muscle cells to biomechanical forces is mediated by MMP13. Nature Communications, 2020, 11, 4110.	5.8	20
53	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
54	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

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55	Quantitation of Reactive Acyl-CoA Species Mediated Protein Acylation by HPLC–MS/MS. Analytical Chemistry, 2019, 91, 12336-12343.	3.2	16
56	Stem cell aging: The upcoming era of proteins and metabolites. Mechanisms of Ageing and Development, 2020, 190, 111288.	2.2	16
57	PLCG1 is required for AML1-ETO leukemia stem cell self-renewal. Blood, 2022, 139, 1080-1097.	0.6	16
58	Quantifying compartment‐associated variations of protein abundance in proteomics data. Molecular Systems Biology, 2018, 14, e8131.	3.2	14
59	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
60	GMPPA defects cause a neuromuscular disorder with α-dystroglycan hyperglycosylation. Journal of Clinical Investigation, 2021, 131, .	3.9	13
61	Aging drives organ‐specific alterations of the inflammatory microenvironment guided by immunomodulatory mediators in mice. FASEB Journal, 2021, 35, e21558.	0.2	11
62	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
63	Mapping protein carboxymethylation sites provides insights into their role in proteostasis and cell proliferation. Nature Communications, 2021, 12, 6743.	5.8	11
64	Multifaceted Microcephaly-Related Gene MCPH1. Cells, 2022, 11, 275.	1.8	10
65	Glycation Alters the Fatty Acid Binding Capacity of Human Serum Albumin. Journal of Agricultural and Food Chemistry, 2022, 70, 3033-3046.	2.4	10
66	HAT cofactor TRRAP modulates microtubule dynamics via SP1 signaling to prevent neurodegeneration. ELife, 2021, 10, .	2.8	9
67	The N-terminal BRCT domain determines MCPH1 function in brain development and fertility. Cell Death and Disease, 2021, 12, 143.	2.7	9
68	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
69	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
70	ATR regulates neuronal activity by modulating presynaptic firing. Nature Communications, 2021, 12, 4067.	5.8	8
71	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
72	Following Protein–Glycosaminoglycan Polysaccharide Interactions with Differential Scanning Fluorimetry. Methods in Molecular Biology, 2012, 836, 171-182.	0.4	4

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73	Identifying Cell‑Type‑Specific Metabolic Signatures Using Transcriptome and Proteome Analyses. Current Protocols, 2021, 1, e245.	1.3	3
74	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
75	Conserved exchange of paralog proteins during neuronal differentiation. Life Science Alliance, 2022, 5, e202201397.	1.3	0
76	Veränderung der Bioaktivität von Proteinen durch Glykierung. Lebensmittelchemie, 2022, 76, .	0.0	0