

Jens S Andersen

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

117
papers

15,817
citations

57
h-index

124
g-index

124
ext. papers

17,292
ext. citations

12
avg. IF

5.93
L-index

#	Paper	IF	Citations
117	Rapid factor depletion highlights intricacies of nucleoplasmic RNA degradation.. <i>Nucleic Acids Research</i> , 2022 ,	20.1	1
116	The long non-coding RNA MIR31HG regulates the senescence associated secretory phenotype. <i>Nature Communications</i> , 2021 , 12, 2459	17.4	6
115	MCM3 upregulation confers endocrine resistance in breast cancer and is a predictive marker of diminished tamoxifen benefit. <i>Npj Breast Cancer</i> , 2021 , 7, 2	7.8	3
114	CEP78 functions downstream of CEP350 to control biogenesis of primary cilia by negatively regulating CP110 levels. <i>ELife</i> , 2021 , 10,	8.9	11
113	Spatial Characterization of the Human Centrosome Proteome Opens Up New Horizons for a Small but Versatile Organelle. <i>Proteomics</i> , 2020 , 20, e1900361	4.8	2
112	Human RTEL1 associates with Poldip3 to facilitate responses to replication stress and R-loop resolution. <i>Genes and Development</i> , 2020 , 34, 1065-1074	12.6	8
111	A systems approach delivers a functional microRNA catalog and expanded targets for seizure suppression in temporal lobe epilepsy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 15977-15988	11.5	19
110	The human ZC3H3 and RBM26/27 proteins are critical for PAXT-mediated nuclear RNA decay. <i>Nucleic Acids Research</i> , 2020 , 48, 2518-2530	20.1	18
109	Selective autophagy maintains centrosome integrity and accurate mitosis by turnover of centriolar satellites. <i>Nature Communications</i> , 2019 , 10, 4176	17.4	32
108	Rab35 controls cilium length, function and membrane composition. <i>EMBO Reports</i> , 2019 , 20, e47625	6.5	16
107	CEP128 Localizes to the Subdistal Appendages of the Mother Centriole and Regulates TGF- β /BMP Signaling at the Primary Cilium. <i>Cell Reports</i> , 2018 , 22, 2584-2592	10.6	36
106	Characterizing ZC3H18, a Multi-domain Protein at the Interface of RNA Production and Destruction Decisions. <i>Cell Reports</i> , 2018 , 22, 44-58	10.6	19
105	eIF5A is required for autophagy by mediating ATG3 translation. <i>EMBO Reports</i> , 2018 , 19,	6.5	44
104	DNA damage-induced dynamic changes in abundance and cytosol-nuclear translocation of proteins involved in translational processes, metabolism, and autophagy. <i>Cell Cycle</i> , 2018 , 17, 2146-2163	4.7	4
103	Degradation of protein translation machinery by amino acid starvation-induced macroautophagy. <i>Autophagy</i> , 2017 , 13, 1064-1075	10.2	20
102	Mutually Exclusive CBC-Containing Complexes Contribute to RNA Fate. <i>Cell Reports</i> , 2017 , 18, 2635-2650	10.6	45
101	Identification of a Nuclear Exosome Decay Pathway for Processed Transcripts. <i>Molecular Cell</i> , 2016 , 64, 520-533	17.6	133

100	SDCCAG8 Interacts with RAB Effector Proteins RABEP2 and ERC1 and Is Required for Hedgehog Signaling. <i>PLoS ONE</i> , 2016 , 11, e0156081	3.7	13
99	Centrosomes. Regulated assembly of a supramolecular centrosome scaffold in vitro. <i>Science</i> , 2015 , 348, 808-12	33.3	125
98	Regulation of autophagy by cytosolic acetyl-coenzyme A. <i>Molecular Cell</i> , 2014 , 53, 710-25	17.6	331
97	A divergent calponin homology (NN-CH) domain defines a novel family: implications for evolution of ciliary IFT complex B proteins. <i>Bioinformatics</i> , 2014 , 30, 899-902	7.2	28
96	Characterization of early autophagy signaling by quantitative phosphoproteomics. <i>Autophagy</i> , 2014 , 10, 356-71	10.2	26
95	Renal-retinal ciliopathy gene Sdccag8 regulates DNA damage response signaling. <i>Journal of the American Society of Nephrology: JASN</i> , 2014 , 25, 2573-83	12.7	46
94	The Caenorhabditis elegans pericentriolar material components SPD-2 and SPD-5 are monomeric in the cytoplasm before incorporation into the PCM matrix. <i>Molecular Biology of the Cell</i> , 2014 , 25, 2984-92 ^{3,5}		26
93	Quantitative proteomics identifies unanticipated regulators of nitrogen- and glucose starvation. <i>Molecular BioSystems</i> , 2014 , 10, 2176-88		3
92	Inducing autophagy: a comparative phosphoproteomic study of the cellular response to ammonia and rapamycin. <i>Autophagy</i> , 2014 , 10, 339-55	10.2	57
91	ANCHR mediates Aurora-B-dependent abscission checkpoint control through retention of VPS4. <i>Nature Cell Biology</i> , 2014 , 16, 550-60	23.4	78
90	The human cap-binding complex is functionally connected to the nuclear RNA exosome. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 1367-76	17.6	157
89	Centrosome isolation and analysis by mass spectrometry-based proteomics. <i>Methods in Enzymology</i> , 2013 , 525, 371-93	1.7	9
88	Protein tyrosine phosphatase SHP2/PTPN11 mistargeting as a consequence of SH2-domain point mutations associated with Noonan Syndrome and leukemia. <i>Journal of Proteomics</i> , 2013 , 84, 132-47	3.9	11
87	Acetylation dynamics of human nuclear proteins during the ionizing radiation-induced DNA damage response. <i>Cell Cycle</i> , 2013 , 12, 1688-95	4.7	24
86	Exome capture reveals ZNF423 and CEP164 mutations, linking renal ciliopathies to DNA damage response signaling. <i>Cell</i> , 2012 , 150, 533-48	56.2	266
85	Global mapping of protein phosphorylation events identifies Ste20, Sch9 and the cell-cycle regulatory kinases Cdc28/Pho85 as mediators of fatty acid starvation responses in Saccharomyces cerevisiae. <i>Molecular BioSystems</i> , 2012 , 8, 796-803		9
84	Temporal profiling and pulsed SILAC labeling identify novel secreted proteins during ex vivo osteoblast differentiation of human stromal stem cells. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 989-1007 ^{7,6}		64
83	Mass spectrometric identification of proteins that interact through specific domains of the poly(A) binding protein. <i>Molecular Genetics and Genomics</i> , 2012 , 287, 711-730	3.1	18

82	Phosphoproteomic analysis of cells treated with longevity-related autophagy inducers. <i>Cell Cycle</i> , 2012 , 11, 1827-40	4.7	28
81	Advancing cell biology through proteomics in space and time (PROSPECTS). <i>Molecular and Cellular Proteomics</i> , 2012 , 11, O112.017731	7.6	52
80	PhosphoSiteAnalyzer: a bioinformatic platform for deciphering phospho proteomes using kinase predictions retrieved from NetworKIN. <i>Journal of Proteome Research</i> , 2012 , 11, 3480-6	5.6	17
79	Friend or food: different cues to the autophagosomal proteome. <i>Autophagy</i> , 2012 , 8, 995-6	10.2	3
78	Identification of autophagosome-associated proteins and regulators by quantitative proteomic analysis and genetic screens. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M111.014035	7.6	99
77	Taperin (c9orf75), a mutated gene in nonsyndromic deafness, encodes a vertebrate specific, nuclear localized protein phosphatase one alpha (PP1) docking protein. <i>Biology Open</i> , 2012 , 1, 128-39	2.2	13
76	Interaction profiling identifies the human nuclear exosome targeting complex. <i>Molecular Cell</i> , 2011 , 43, 624-37	17.6	275
75	Spermidine and resveratrol induce autophagy by distinct pathways converging on the acetylproteome. <i>Journal of Cell Biology</i> , 2011 , 192, 615-29	7.3	362
74	Decellularized matrix from tumorigenic human mesenchymal stem cells promotes neovascularization with galectin-1 dependent endothelial interaction. <i>PLoS ONE</i> , 2011 , 6, e21888	3.7	38
73	Comparative proteomics and activity of a green sulfur bacterium through the water column of Lake Cadagno, Switzerland. <i>Environmental Microbiology</i> , 2011 , 13, 203-215	5.2	32
72	Quantitative proteomics of <i>Chlorobaculum tepidum</i> : insights into the sulfur metabolism of a phototrophic green sulfur bacterium. <i>FEMS Microbiology Letters</i> , 2011 , 323, 142-50	2.9	12
71	Novel asymmetrically localizing components of human centrosomes identified by complementary proteomics methods. <i>EMBO Journal</i> , 2011 , 30, 1520-35	13	235
70	ErbB2-associated changes in the lysosomal proteome. <i>Proteomics</i> , 2011 , 11, 2830-8	4.8	21
69	Quantitative proteomics identifies ferritin in the innate immune response of <i>C. elegans</i> . <i>Virulence</i> , 2011 , 2, 120-30	4.7	38
68	Longevity-relevant regulation of autophagy at the level of the acetylproteome. <i>Autophagy</i> , 2011 , 7, 647-60.2	10.2	30
67	The human core exosome interacts with differentially localized processive RNases: hDIS3 and hDIS3L. <i>EMBO Journal</i> , 2010 , 29, 2342-57	13	189
66	Site-specific phosphorylation dynamics of the nuclear proteome during the DNA damage response. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 1314-23	7.6	195
65	The chromatin-remodeling factor CHD4 coordinates signaling and repair after DNA damage. <i>Journal of Cell Biology</i> , 2010 , 190, 731-40	7.3	175

64	MSQuant, an open source platform for mass spectrometry-based quantitative proteomics. <i>Journal of Proteome Research</i> , 2010 , 9, 393-403	5.6	225
63	The minotaur proteome: avoiding cross-species identifications deriving from bovine serum in cell culture models. <i>Proteomics</i> , 2010 , 10, 3040-4	4.8	36
62	Organelle proteomics by label-free and SILAC-based protein correlation profiling. <i>Methods in Molecular Biology</i> , 2010 , 658, 255-65	1.4	9
61	Depletion of kinesin 5B affects lysosomal distribution and stability and induces peri-nuclear accumulation of autophagosomes in cancer cells. <i>PLoS ONE</i> , 2009 , 4, e4424	3.7	82
60	FACT facilitates chromatin transcription by RNA polymerases I and III. <i>EMBO Journal</i> , 2009 , 28, 854-65	13	93
59	Matrix protein 2 of influenza A virus blocks autophagosome fusion with lysosomes. <i>Cell Host and Microbe</i> , 2009 , 6, 367-80	23.4	387
58	Identification of SUMO target proteins by quantitative proteomics. <i>Methods in Molecular Biology</i> , 2009 , 497, 19-31	1.4	25
57	HDAC activity is required for p65/RelA-dependent repression of PPARdelta-mediated transactivation in human keratinocytes. <i>Journal of Investigative Dermatology</i> , 2008 , 128, 1095-106	4.3	18
56	Temporal profiling of the chromatin proteome reveals system-wide responses to replication inhibition. <i>Current Biology</i> , 2008 , 18, 838-43	6.3	32
55	Identification of a membrane proteomic signature for human embryonic stem cells independent of culture conditions. <i>Stem Cell Research</i> , 2008 , 1, 219-27	1.6	31
54	Ordered organelle degradation during starvation-induced autophagy. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 2419-28	7.6	145
53	Identification of let-7-regulated oncofetal genes. <i>Cancer Research</i> , 2008 , 68, 2587-91	10.1	177
52	The ubiquitin-proteasome system is a key component of the SUMO-2/3 cycle. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 2107-22	7.6	124
51	Ordered bulk degradation via autophagy. <i>Autophagy</i> , 2008 , 4, 1057-9	10.2	31
50	Quantitative proteomic assessment of very early cellular signaling events. <i>Nature Biotechnology</i> , 2007 , 25, 566-8	44.5	103
49	A mass spectrometry-friendly database for cSNP identification. <i>Nature Methods</i> , 2007 , 4, 465-6	21.6	57
48	Analysis of nucleolar protein dynamics reveals the nuclear degradation of ribosomal proteins. <i>Current Biology</i> , 2007 , 17, 749-60	6.3	279
47	Signal transduction by growth factor receptors: signaling in an instant. <i>Cell Cycle</i> , 2007 , 6, 2913-6	4.7	9

46	Bod1, a novel kinetochore protein required for chromosome biorientation. <i>Journal of Cell Biology</i> , 2007 , 179, 187-97	7.3	44
45	NOPdb: Nucleolar Proteome Database. <i>Nucleic Acids Research</i> , 2006 , 34, D218-20	20.1	85
44	The RNA-binding protein KSRP promotes decay of beta-catenin mRNA and is inactivated by PI3K-AKT signaling. <i>PLoS Biology</i> , 2006 , 5, e5	9.7	123
43	Repo-Man recruits PP1 gamma to chromatin and is essential for cell viability. <i>Journal of Cell Biology</i> , 2006 , 172, 679-92	7.3	218
42	Reversible lysine acetylation controls the activity of the mitochondrial enzyme acetyl-CoA synthetase 2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 10224-10229	11.5	564
41	Distinct and overlapping sets of SUMO-1 and SUMO-2 target proteins revealed by quantitative proteomics. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 2298-310	7.6	236
40	Identification of miRNA targets with stable isotope labeling by amino acids in cell culture. <i>Nucleic Acids Research</i> , 2006 , 34, e107	20.1	108
39	A wiring of the human nucleolus. <i>Molecular Cell</i> , 2006 , 22, 285-95	17.6	52
38	Organellar proteomics: turning inventories into insights. <i>EMBO Reports</i> , 2006 , 7, 874-9	6.5	175
37	A Proteomic Approach to the Inventory of the Human Centrosome 2005 , 123-142		3
36	Rapid desalting of protein samples for on-line microflow electrospray ionization mass spectrometry. <i>Analytical Biochemistry</i> , 2005 , 342, 160-2	3.1	26
35	Nucleolar proteome dynamics. <i>Nature</i> , 2005 , 433, 77-83	50.4	946
34	Proteomic analysis of the Arabidopsis nucleolus suggests novel nucleolar functions. <i>Molecular Biology of the Cell</i> , 2005 , 16, 260-9	3.5	313
33	BASP1 is a transcriptional cosuppressor for the WilmsTumor suppressor protein WT1. <i>Molecular and Cellular Biology</i> , 2004 , 24, 537-49	4.8	102
32	A proteomic study of SUMO-2 target proteins. <i>Journal of Biological Chemistry</i> , 2004 , 279, 33791-8	5.4	181
31	Protein kinase CK2 is coassembled with small conductance Ca(2+)-activated K+ channels and regulates channel gating. <i>Neuron</i> , 2004 , 43, 847-58	13.9	155
30	Bioinformatic analysis of the nucleolus. <i>Biochemical Journal</i> , 2003 , 376, 553-69	3.8	114
29	Proteomic characterization of the human centrosome by protein correlation profiling. <i>Nature</i> , 2003 , 426, 570-4	50.4	1077

28	Multi-Protein Complexes Studied by Mass Spectrometry. <i>Scientific World Journal, The</i> , 2002 , 2, 91-92	2.2	1
27	Paraspeckles: a novel nuclear domain. <i>Current Biology</i> , 2002 , 12, 13-25	6.3	383
26	Directed proteomic analysis of the human nucleolus. <i>Current Biology</i> , 2002 , 12, 1-11	6.3	883
25	RGM is a repulsive guidance molecule for retinal axons. <i>Nature</i> , 2002 , 419, 392-5	50.4	244
24	Analysis of the Plasmodium falciparum proteome by high-accuracy mass spectrometry. <i>Nature</i> , 2002 , 419, 537-42	50.4	538
23	Microcolumns with self-assembled particle frits for proteomics. <i>Journal of Chromatography A</i> , 2002 , 979, 233-9	4.5	260
22	The Vtc proteins in vacuole fusion: coupling NSF activity to V(0) trans-complex formation. <i>EMBO Journal</i> , 2002 , 21, 259-69	13	107
21	Inhibition of adipocyte differentiation by resistin-like molecule alpha. Biochemical characterization of its oligomeric nature. <i>Journal of Biological Chemistry</i> , 2002 , 277, 42011-6	5.4	51
20	Pseudosubstrate regulation of the SCF(beta-TrCP) ubiquitin ligase by hnRNP-U. <i>Genes and Development</i> , 2002 , 16, 439-51	12.6	101
19	A proteomic approach for identification of secreted proteins during the differentiation of 3T3-L1 preadipocytes to adipocytes. <i>Molecular and Cellular Proteomics</i> , 2002 , 1, 213-22	7.6	202
18	Analysis of tyrosine phosphorylation sites in signaling molecules by a phosphotyrosine-specific immonium ion scanning method. <i>Science Signaling</i> , 2002 , 2002, pl16	8.8	28
17	Axin-mediated CKI phosphorylation of beta-catenin at Ser 45: a molecular switch for the Wnt pathway. <i>Genes and Development</i> , 2002 , 16, 1066-76	12.6	548
16	A mass spectrometry-based proteomic approach for identification of serine/threonine-phosphorylated proteins by enrichment with phospho-specific antibodies: identification of a novel protein, Frigg, as a protein kinase A substrate. <i>Molecular and Cellular Proteomics</i> , 2002 , 1, 517-27	7.6	318
15	Mass spectrometry allows direct identification of proteins in large genomes. <i>Proteomics</i> , 2001 , 1, 641-50	4.8	115
14	Trans-complex formation by proteolipid channels in the terminal phase of membrane fusion. <i>Nature</i> , 2001 , 409, 581-8	50.4	440
13	p70S6 kinase signals cell survival as well as growth, inactivating the pro-apoptotic molecule BAD. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 9666-70	11.5	431
12	p95-APP1 links membrane transport to Rac-mediated reorganization of actin. <i>Nature Cell Biology</i> , 2000 , 2, 521-30	23.4	115
11	Functional genomics by mass spectrometry. <i>FEBS Letters</i> , 2000 , 480, 25-31	3.8	91

10	Nucleolin and YB-1 are required for JNK-mediated interleukin-2 mRNA stabilization during T-cell activation. <i>Genes and Development</i> , 2000 , 14, 1236-1248	12.6	202
9	Identification of the receptor component of the IkappaBalpha-ubiquitin ligase. <i>Nature</i> , 1998 , 396, 590-4	50.4	591
8	Overexpression, purification, and characterization of recombinant barley alpha-amylases 1 and 2 secreted by the methylotrophic yeast <i>Pichia pastoris</i> . <i>Protein Expression and Purification</i> , 1996 , 8, 204-14 ²		64
7	Electrospray ionization and matrix assisted laser desorption/ionization mass spectrometry: powerful analytical tools in recombinant protein chemistry. <i>Nature Biotechnology</i> , 1996 , 14, 449-57	44.5	99
6	Evaluation of mass spectrometric techniques for characterization of engineered proteins. <i>Molecular Biotechnology</i> , 1995 , 4, 1-12	3	14
5	The phosphorylated ribosomal protein S7 in <i>Tetrahymena</i> is homologous with mammalian S4 and the phosphorylated residues are located in the C-terminal region. Structural characterization of proteins separated by two-dimensional polyacrylamide gel electrophoresis. <i>Journal of Biological Chemistry</i> , 1995 , 270, 1000-5	5.4	14
4	Characterization of the different spectral forms of glutamate 1-semialdehyde aminotransferase by mass spectrometry. <i>Biochemistry</i> , 1995 , 34, 15918-24	3.2	14
3	Localization of an O-glycosylated site in the recombinant barley alpha-amylase 1 produced in yeast and correction of the amino acid sequence using matrix-assisted laser desorption/ionization mass spectrometry of peptide mixtures. <i>Biological Mass Spectrometry</i> , 1994 , 23, 547-54		16
2	The complete amino acid sequence and disulphide bond arrangement of oat alcohol-soluble avenin-3. <i>FEBS Journal</i> , 1994 , 224, 631-8		22
1	Electrospray mass spectrometry characterization of post-translational modifications of barley alpha-amylase 1 produced in yeast. <i>Nature Biotechnology</i> , 1993 , 11, 1162-5	44.5	18