

Jens S Andersen

List of Publications by Year in descending order

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118
papers

18,538
citations

20797

60
h-index

18633

119
g-index

126
all docs

126
docs citations

126
times ranked

26183
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteomic characterization of the human centrosome by protein correlation profiling. <i>Nature</i> , 2003, 426, 570-574.	13.7	1,204
2	Nucleolar proteome dynamics. <i>Nature</i> , 2005, 433, 77-83.	13.7	1,061
3	Directed Proteomic Analysis of the Human Nucleolus. <i>Current Biology</i> , 2002, 12, 1-11.	1.8	962
4	Identification of the receptor component of the E3 ubiquitin ligase. <i>Nature</i> , 1998, 396, 590-594.	13.7	650
5	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.	3.3	642
6	Axin-mediated CKI phosphorylation of beta -catenin at Ser 45: a molecular switch for the Wnt pathway. <i>Genes and Development</i> , 2002, 16, 1066-1076.	2.7	621
7	Analysis of the Plasmodium falciparum proteome by high-accuracy mass spectrometry. <i>Nature</i> , 2002, 419, 537-542.	13.7	596
8	Trans-complex formation by proteolipid channels in the terminal phase of membrane fusion. <i>Nature</i> , 2001, 409, 581-588.	13.7	487
9	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, 9666-9670.	3.3	487
10	Paraspeckles. <i>Current Biology</i> , 2002, 12, 13-25.	1.8	455
11	Matrix Protein 2 of Influenza A Virus Blocks Autophagosome Fusion with Lysosomes. <i>Cell Host and Microbe</i> , 2009, 6, 367-380.	5.1	454
12	Spermidine and resveratrol induce autophagy by distinct pathways converging on the acetylproteome. <i>Journal of Cell Biology</i> , 2011, 192, 615-629.	2.3	439
13	Regulation of Autophagy by Cytosolic Acetyl-Coenzyme A. <i>Molecular Cell</i> , 2014, 53, 710-725.	4.5	412
14	Interaction Profiling Identifies the Human Nuclear Exosome Targeting Complex. <i>Molecular Cell</i> , 2011, 43, 624-637.	4.5	355
15	A Mass Spectrometry-based Proteomic Approach for Identification of Serine/Threonine-phosphorylated Proteins by Enrichment with Phospho-specific Antibodies. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 517-527.	2.5	353
16	Proteomic Analysis of the Arabidopsis Nucleolus Suggests Novel Nucleolar Functions. <i>Molecular Biology of the Cell</i> , 2005, 16, 260-269.	0.9	352
17	Exome Capture Reveals ZNF423 and CEP164 Mutations, Linking Renal Ciliopathies to DNA Damage Response Signaling. <i>Cell</i> , 2012, 150, 533-548.	13.5	347
18	Microcolumns with self-assembled particle frits for proteomics. <i>Journal of Chromatography A</i> , 2002, 979, 233-239.	1.8	327

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19	Analysis of Nucleolar Protein Dynamics Reveals the Nuclear Degradation of Ribosomal Proteins. <i>Current Biology</i> , 2007, 17, 749-760.	1.8	314
20	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.	2.7	314
21	Novel asymmetrically localizing components of human centrosomes identified by complementary proteomics methods. <i>EMBO Journal</i> , 2011, 30, 1520-1535.	3.5	278
22	Distinct and Overlapping Sets of SUMO-1 and SUMO-2 Target Proteins Revealed by Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 2298-2310.	2.5	274
23	RGM is a repulsive guidance molecule for retinal axons. <i>Nature</i> , 2002, 419, 392-395.	13.7	272
24	Repo-Man recruits PP1 ³ to chromatin and is essential for cell viability. <i>Journal of Cell Biology</i> , 2006, 172, 679-692.	2.3	240
25	The human core exosome interacts with differentially localized processive RNases: hDIS3 and hDIS3L. <i>EMBO Journal</i> , 2010, 29, 2342-2357.	3.5	237
26	MSQuant, an Open Source Platform for Mass Spectrometry-Based Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 393-403.	1.8	237
27	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, 213-222.	2.5	227
28	Site-specific Phosphorylation Dynamics of the Nuclear Proteome during the DNA Damage Response. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1314-1323.	2.5	225
29	Identification of a Nuclear Exosome Decay Pathway for Processed Transcripts. <i>Molecular Cell</i> , 2016, 64, 520-533.	4.5	209
30	The chromatin-remodeling factor CHD4 coordinates signaling and repair after DNA damage. <i>Journal of Cell Biology</i> , 2010, 190, 731-740.	2.3	199
31	The human cap-binding complex is functionally connected to the nuclear RNA exosome. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1367-1376.	3.6	199
32	A Proteomic Study of SUMO-2 Target Proteins. <i>Journal of Biological Chemistry</i> , 2004, 279, 33791-33798.	1.6	197
33	Identification of Let-7 ⁴ -Regulated Oncofetal Genes. <i>Cancer Research</i> , 2008, 68, 2587-2591.	0.4	195
34	Organelle proteomics: turning inventories into insights. <i>EMBO Reports</i> , 2006, 7, 874-879.	2.0	185
35	Protein Kinase CK2 Is Coassembled with Small Conductance Ca ²⁺ -Activated K ⁺ Channels and Regulates Channel Gating. <i>Neuron</i> , 2004, 43, 847-858.	3.8	176
36	Regulated assembly of a supramolecular centrosome scaffold in vitro. <i>Science</i> , 2015, 348, 808-812.	6.0	170

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37	Ordered Organelle Degradation during Starvation-induced Autophagy. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2419-2428.	2.5	166
38	The Ubiquitin-Proteasome System Is a Key Component of the SUMO-2/3 Cycle. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2107-2122.	2.5	143
39	The RNA-Binding Protein KSRP Promotes Decay of β -Catenin mRNA and Is Inactivated by PI3K-AKT Signaling. <i>PLoS Biology</i> , 2006, 5, e5.	2.6	132
40	Bioinformatic analysis of the nucleolus. <i>Biochemical Journal</i> , 2003, 376, 553-569.	1.7	130
41	The Vtc proteins in vacuole fusion: coupling NSF activity to V0trans-complex formation. <i>EMBO Journal</i> , 2002, 21, 259-269.	3.5	126
42	Mass spectrometry allows direct identification of proteins in large genomes. <i>Proteomics</i> , 2001, 1, 641-650.	1.3	124
43	BASP1 Is a Transcriptional Cosuppressor for the Wilms' Tumor Suppressor Protein WT1. <i>Molecular and Cellular Biology</i> , 2004, 24, 537-549.	1.1	120
44	p95-APP1 links membrane transport to Rac-mediated reorganization of actin. <i>Nature Cell Biology</i> , 2000, 2, 521-530.	4.6	119
45	Identification of Autophagosome-associated Proteins and Regulators by Quantitative Proteomic Analysis and Genetic Screens. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014035.	2.5	118
46	Identification of miRNA targets with stable isotope labeling by amino acids in cell culture. <i>Nucleic Acids Research</i> , 2006, 34, e107-e107.	6.5	112
47	Electrospray ionization and matrix assisted laser desorption/ionization mass spectrometry: Powerful analytical tools in recombinant protein chemistry. <i>Nature Biotechnology</i> , 1996, 14, 449-457.	9.4	110
48	Pseudosubstrate regulation of the SCF β -TrCP ubiquitin ligase by hnRNP-U. <i>Genes and Development</i> , 2002, 16, 439-451.	2.7	110
49	Quantitative proteomic assessment of very early cellular signaling events. <i>Nature Biotechnology</i> , 2007, 25, 566-568.	9.4	110
50	Functional genomics by mass spectrometry. <i>FEBS Letters</i> , 2000, 480, 25-31.	1.3	107
51	FACT facilitates chromatin transcription by RNA polymerases I and III. <i>EMBO Journal</i> , 2009, 28, 854-865.	3.5	106
52	ANCHR mediates Aurora-B-dependent abscission checkpoint control through retention of VPS4. <i>Nature Cell Biology</i> , 2014, 16, 547-557.	4.6	100
53	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.	1.1	98
54	NOPdb: Nucleolar Proteome Database. <i>Nucleic Acids Research</i> , 2006, 34, D218-D220.	6.5	93

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55	Overexpression, Purification, and Characterization of Recombinant Barley α -Amylases 1 and 2 Secreted by the Methylothrophic Yeast <i>Pichia pastoris</i> . <i>Protein Expression and Purification</i> , 1996, 8, 204-214.	0.6	79
56	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.	2.5	75
57	Mutually Exclusive CBC-Containing Complexes Contribute to RNA Fate. <i>Cell Reports</i> , 2017, 18, 2635-2650.	2.9	73
58	A mass spectrometry-friendly database for cSNP identification. <i>Nature Methods</i> , 2007, 4, 465-466.	9.0	72
59	Inducing autophagy. <i>Autophagy</i> , 2014, 10, 339-355.	4.3	65
60	Renal-Retinal Ciliopathy Gene <i>Sdccag8</i> Regulates DNA Damage Response Signaling. <i>Journal of the American Society of Nephrology: JASN</i> , 2014, 25, 2573-2583.	3.0	63
61	eIF5A is required for autophagy by mediating ATG3 translation. <i>EMBO Reports</i> , 2018, 19, .	2.0	63
62	Inhibition of Adipocyte Differentiation by Resistin-like Molecule β . <i>Journal of Biological Chemistry</i> , 2002, 277, 42011-42016.	1.6	61
63	Selective autophagy maintains centrosome integrity and accurate mitosis by turnover of centriolar satellites. <i>Nature Communications</i> , 2019, 10, 4176.	5.8	61
64	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.	2.9	59
65	A Wiring of the Human Nucleolus. <i>Molecular Cell</i> , 2006, 22, 285-295.	4.5	56
66	Advancing Cell Biology Through Proteomics in Space and Time (PROSPECTS). <i>Molecular and Cellular Proteomics</i> , 2012, 11, O112.017731.	2.5	55
67	The human ZC3H3 and RBM26/27 proteins are critical for PAXT-mediated nuclear RNA decay. <i>Nucleic Acids Research</i> , 2020, 48, 2518-2530.	6.5	50
68	Bod1, a novel kinetochore protein required for chromosome biorientation. <i>Journal of Cell Biology</i> , 2007, 179, 187-197.	2.3	49
69	A divergent calponin homology (NCH) domain defines a novel family: implications for evolution of ciliary IFT complex B proteins. <i>Bioinformatics</i> , 2014, 30, 899-902.	1.8	48
70	Quantitative proteomics identifies ferritin in the innate immune response of <i>C. elegans</i> . <i>Virulence</i> , 2011, 2, 120-130.	1.8	47
71	Decellularized Matrix from Tumorigenic Human Mesenchymal Stem Cells Promotes Neovascularization with Galectin-1 Dependent Endothelial Interaction. <i>PLoS ONE</i> , 2011, 6, e21888.	1.1	46
72	The minotaur proteome: Avoiding cross-species identifications deriving from bovine serum in cell culture models. <i>Proteomics</i> , 2010, 10, 3040-3044.	1.3	42

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73	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.	3.3	41
74	Analysis of Tyrosine Phosphorylation Sites in Signaling Molecules by a Phosphotyrosine-Specific Immonium Ion Scanning Method. <i>Science Signaling</i> , 2002, 2002, pl16-pl16.	1.6	38
75	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.	1.8	38
76	Temporal Profiling of the Chromatin Proteome Reveals System-wide Responses to Replication Inhibition. <i>Current Biology</i> , 2008, 18, 838-843.	1.8	36
77	Characterization of early autophagy signaling by quantitative phosphoproteomics. <i>Autophagy</i> , 2014, 10, 356-371.	4.3	35
78	Rab35 controls cilium length, function and membrane composition. <i>EMBO Reports</i> , 2019, 20, e47625.	2.0	35
79	Identification of a membrane proteomic signature for human embryonic stem cells independent of culture conditions. <i>Stem Cell Research</i> , 2008, 1, 219-227.	0.3	34
80	Longevity-relevant regulation of autophagy at the level of the acetylproteome. <i>Autophagy</i> , 2011, 7, 647-649.	4.3	34
81	Phosphoproteomic analysis of cells treated with longevity-related autophagy inducers. <i>Cell Cycle</i> , 2012, 11, 1827-1840.	1.3	33
82	Characterizing ZC3H18, a Multi-domain Protein at the Interface of RNA Production and Destruction Decisions. <i>Cell Reports</i> , 2018, 22, 44-58.	2.9	33
83	Ordered bulk degradation via autophagy. <i>Autophagy</i> , 2008, 4, 1057-1059.	4.3	32
84	The <i>Caenorhabditis elegans</i> 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, 2984-2992.	0.9	31
85	Degradation of protein translation machinery by amino acid starvation-induced macroautophagy. <i>Autophagy</i> , 2017, 13, 1064-1075.	4.3	29
86	CEP78 functions downstream of CEP350 to control biogenesis of primary cilia by negatively regulating CP110 levels. <i>ELife</i> , 2021, 10, .	2.8	29
87	Rapid desalting of protein samples for on-line microflow electrospray ionization mass spectrometry. <i>Analytical Biochemistry</i> , 2005, 342, 160-162.	1.1	27
88	Identification of SUMO Target Proteins by Quantitative Proteomics. <i>Methods in Molecular Biology</i> , 2009, 497, 19-31.	0.4	27
89	Acetylation dynamics of human nuclear proteins during the ionizing radiation-induced DNA damage response. <i>Cell Cycle</i> , 2013, 12, 1688-1695.	1.3	27
90	Human RTEL1 associates with Poldip3 to facilitate responses to replication stress and R-loop resolution. <i>Genes and Development</i> , 2020, 34, 1065-1074.	2.7	27

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91	The long non-coding RNA MIR31HG regulates the senescence associated secretory phenotype. <i>Nature Communications</i> , 2021, 12, 2459.	5.8	27
92	HDAC Activity Is Required for p65/RelA-Dependent Repression of PPAR γ -Mediated Transactivation in Human Keratinocytes. <i>Journal of Investigative Dermatology</i> , 2008, 128, 1095-1106.	0.3	26
93	The Complete Amino Acid Sequence and Disulphide Bond Arrangement of Oat Alcohol-soluble Avenin-3. <i>FEBS Journal</i> , 1994, 224, 631-638.	0.2	25
94	Electrospray Mass Spectrometry Characterization of Post-Translational Modifications of Barley β -Amylase 1 Produced in Yeast. <i>Nature Biotechnology</i> , 1993, 11, 1162-1165.	9.4	23
95	ErbB2-associated changes in the lysosomal proteome. <i>Proteomics</i> , 2011, 11, 2830-2838.	1.3	23
96	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.	1.0	20
97	PhosphoSiteAnalyzer: A Bioinformatic Platform for Deciphering Phospho Proteomes Using Kinase Predictions Retrieved from NetworkIN. <i>Journal of Proteome Research</i> , 2012, 11, 3480-3486.	1.8	19
98	SDCCAG8 Interacts with RAB Effector Proteins RABEP2 and ERC1 and Is Required for Hedgehog Signaling. <i>PLoS ONE</i> , 2016, 11, e0156081.	1.1	19
99	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, 132-147.	1.2	18
100	Characterization of the different spectral forms of glutamate 1-semialdehyde aminotransferase by mass spectrometry. <i>Biochemistry</i> , 1995, 34, 15918-15924.	1.2	17
101	Taperin (c9orf75), a mutated gene in nonsyndromic deafness, encodes a vertebrate specific, nuclear localized protein phosphatase one alpha (PP1 α) docking protein. <i>Biology Open</i> , 2012, 1, 128-139.	0.6	17
102	Localization of an O-glycosylated site in the recombinant barley β -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, 547-554.	0.5	16
103	Evaluation of mass spectrometric techniques for characterization of engineered proteins. <i>Molecular Biotechnology</i> , 1995, 4, 1-12.	1.3	16
104	The Phosphorylated Ribosomal Protein S7 in Tetrahymena Is Homologous with Mammalian S4 and the Phosphorylated Residues Are Located in the C-terminal Region. <i>Journal of Biological Chemistry</i> , 1995, 270, 6000-6005.	1.6	15
105	Rapid factor depletion highlights intricacies of nucleoplasmic RNA degradation. <i>Nucleic Acids Research</i> , 2022, 50, 1583-1600.	6.5	15
106	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, 142-150.	0.7	13
107	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 <i>Saccharomyces cerevisiae</i> . <i>Molecular BioSystems</i> , 2012, 8, 796.	2.9	12
108	Centrosome Isolation and Analysis by Mass Spectrometry-Based Proteomics. <i>Methods in Enzymology</i> , 2013, 525, 371-393.	0.4	12

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109	Organelle Proteomics by Label-Free and SILAC-Based Protein Correlation Profiling. <i>Methods in Molecular Biology</i> , 2010, 658, 255-265.	0.4	10
110	Transient accumulation and bidirectional movement of KIF13B in primary cilia. <i>Journal of Cell Science</i> , 2023, 136, .	1.2	10
111	Signal Transduction by Growth Factor Receptors: Signaling in an Instant. <i>Cell Cycle</i> , 2007, 6, 2913-2916.	1.3	9
112	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.	1.3	9
113	Quantitative proteomics identifies unanticipated regulators of nitrogen- and glucose starvation. <i>Molecular BioSystems</i> , 2014, 10, 2176-2188.	2.9	8
114	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.	2.3	7
115	A Proteomic Approach to the Inventory of the Human Centrosome. , 2005, , 123-142.		6
116	Spatial Characterization of the Human Centrosome Proteome Opens Up New Horizons for a Small but Versatile Organelle. <i>Proteomics</i> , 2020, 20, e1900361.	1.3	6
117	Friend or food. <i>Autophagy</i> , 2012, 8, 995-996.	4.3	4
118	Multi-Protein Complexes Studied by Mass Spectrometry. <i>Scientific World Journal, The</i> , 2002, 2, 91-92.	0.8	1