

Jens S Andersen

List of Publications by Year in descending order

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118
papers

18,538
citations

20817
60
h-index

18647
119
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126
all docs

126
docs citations

126
times ranked

26183
citing authors

#	ARTICLE	IF	CITATIONS
1	Transient accumulation and bidirectional movement of KIF13B in primary cilia. <i>Journal of Cell Science</i> , 2023, 136, .	2.0	10
2	Rapid factor depletion highlights intricacies of nucleoplasmic RNA degradation. <i>Nucleic Acids Research</i> , 2022, 50, 1583-1600.	14.5	15
3	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.	5.2	7
4	The long non-coding RNA MIR31HG regulates the senescence associated secretory phenotype. <i>Nature Communications</i> , 2021, 12, 2459.	12.8	27
5	CEP78 functions downstream of CEP350 to control biogenesis of primary cilia by negatively regulating CP110 levels. <i>ELife</i> , 2021, 10, .	6.0	29
6	Spatial Characterization of the Human Centrosome Proteome Opens Up New Horizons for a Small but Versatile Organelle. <i>Proteomics</i> , 2020, 20, e1900361.	2.2	6
7	Human RTEL1 associates with Poldip3 to facilitate responses to replication stress and R-loop resolution. <i>Genes and Development</i> , 2020, 34, 1065-1074.	5.9	27
8	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.	7.1	41
9	The human ZC3H3 and RBM26/27 proteins are critical for PAXT-mediated nuclear RNA decay. <i>Nucleic Acids Research</i> , 2020, 48, 2518-2530.	14.5	50
10	Rab35 controls cilium length, function and membrane composition. <i>EMBO Reports</i> , 2019, 20, e47625.	4.5	35
11	Selective autophagy maintains centrosome integrity and accurate mitosis by turnover of centriolar satellites. <i>Nature Communications</i> , 2019, 10, 4176.	12.8	61
12	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.	6.4	59
13	Characterizing ZC3H18, a Multi-domain Protein at the Interface of RNA Production and Destruction Decisions. <i>Cell Reports</i> , 2018, 22, 44-58.	6.4	33
14	<scp>eIF</scp> 5A is required for autophagy by mediating <scp>ATG</scp> 3 translation. <i>EMBO Reports</i> , 2018, 19, .	4.5	63
15	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.	2.6	9
16	Degradation of protein translation machinery by amino acid starvation-induced macroautophagy. <i>Autophagy</i> , 2017, 13, 1064-1075.	9.1	29
17	Mutually Exclusive CBC-Containing Complexes Contribute to RNA Fate. <i>Cell Reports</i> , 2017, 18, 2635-2650.	6.4	73
18	Identification of a Nuclear Exosome Decay Pathway for Processed Transcripts. <i>Molecular Cell</i> , 2016, 64, 520-533.	9.7	209

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19	SDCCAG8 Interacts with RAB Effector Proteins RABEP2 and ERC1 and Is Required for Hedgehog Signaling. PLoS ONE, 2016, 11, e0156081.	2.5	19
20	Regulated assembly of a supramolecular centrosome scaffold in vitro. Science, 2015, 348, 808-812.	12.6	170
21	Inducing autophagy. Autophagy, 2014, 10, 339-355.	9.1	65
22	ANCHR mediates Aurora-B-dependent abscission checkpoint control through retention of VPS4. Nature Cell Biology, 2014, 16, 547-557.	10.3	100
23	Regulation of Autophagy by Cytosolic Acetyl-Coenzyme A. Molecular Cell, 2014, 53, 710-725.	9.7	412
24	A divergent calponin homology (NNâ€“CH) domain defines a novel family: implications for evolution of ciliary IFT complex B proteins. Bioinformatics, 2014, 30, 899-902.	4.1	48
25	Characterization of early autophagy signaling by quantitative phosphoproteomics. Autophagy, 2014, 10, 356-371.	9.1	35
26	Renal-Retinal Ciliopathy Gene Sdccag8 Regulates DNA Damage Response Signaling. Journal of the American Society of Nephrology: JASN, 2014, 25, 2573-2583.	6.1	63
27	The <i>Caenorhabditis elegans</i> pericentriolar material components SPD-2 and SPD-5 are monomeric in the cytoplasm before incorporation into the PCM matrix. Molecular Biology of the Cell, 2014, 25, 2984-2992.	2.1	31
28	Quantitative proteomics identifies unanticipated regulators of nitrogen- and glucose starvation. Molecular BioSystems, 2014, 10, 2176-2188.	2.9	8
29	The human cap-binding complex is functionally connected to the nuclear RNA exosome. Nature Structural and Molecular Biology, 2013, 20, 1367-1376.	8.2	199
30	Centrosome Isolation and Analysis by Mass Spectrometry-Based Proteomics. Methods in Enzymology, 2013, 525, 371-393.	1.0	12
31	Protein tyrosine phosphatase SHP2/PTPN11 mistargeting as a consequence of SH2-domain point mutations associated with Noonan Syndrome and leukemia. Journal of Proteomics, 2013, 84, 132-147.	2.4	18
32	Acetylation dynamics of human nuclear proteins during the ionizing radiation-induced DNA damage response. Cell Cycle, 2013, 12, 1688-1695.	2.6	27
33	Friend or food. Autophagy, 2012, 8, 995-996.	9.1	4
34	Identification of Autophagosome-associated Proteins and Regulators by Quantitative Proteomic Analysis and Genetic Screens. Molecular and Cellular Proteomics, 2012, 11, M111.014035.	3.8	118
35	Taperin (c9orf75), a mutated gene in nonsyndromic deafness, encodes a vertebrate specific, nuclear localized protein phosphatase one alpha (PP1Î±) docking protein. Biology Open, 2012, 1, 128-139.	1.2	17
36	Exome Capture Reveals ZNF423 and CEP164 Mutations, Linking Renal Ciliopathies to DNA Damage Response Signaling. Cell, 2012, 150, 533-548.	28.9	347

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37	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
38	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.	3.8	75
39	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.	2.1	20
40	Phosphoproteomic analysis of cells treated with longevity-related autophagy inducers. <i>Cell Cycle</i> , 2012, 11, 1827-1840.	2.6	33
41	Advancing Cell Biology Through Proteomics in Space and Time (PROSPECTS). <i>Molecular and Cellular Proteomics</i> , 2012, 11, O112.017731.	3.8	55
42	PhosphoSiteAnalyzer: A Bioinformatic Platform for Deciphering Phospho Proteomes Using Kinase Predictions Retrieved from NetworkIN. <i>Journal of Proteome Research</i> , 2012, 11, 3480-3486.	3.7	19
43	Interaction Profiling Identifies the Human Nuclear Exosome Targeting Complex. <i>Molecular Cell</i> , 2011, 43, 624-637.	9.7	355
44	Spermidine and resveratrol induce autophagy by distinct pathways converging on the acetylproteome. <i>Journal of Cell Biology</i> , 2011, 192, 615-629.	5.2	439
45	Decellularized Matrix from Tumorigenic Human Mesenchymal Stem Cells Promotes Neovascularization with Galectin-1 Dependent Endothelial Interaction. <i>PLoS ONE</i> , 2011, 6, e21888.	2.5	46
46	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.	3.8	38
47	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.	1.8	13
48	Novel asymmetrically localizing components of human centrosomes identified by complementary proteomics methods. <i>EMBO Journal</i> , 2011, 30, 1520-1535.	7.8	278
49	ErbB2-associated changes in the lysosomal proteome. <i>Proteomics</i> , 2011, 11, 2830-2838.	2.2	23
50	Quantitative proteomics identifies ferritin in the innate immune response of <i>C. elegans</i> . <i>Virulence</i> , 2011, 2, 120-130.	4.4	47
51	Longevity-relevant regulation of autophagy at the level of the acetylproteome. <i>Autophagy</i> , 2011, 7, 647-649.	9.1	34
52	The minotaur proteome: Avoiding cross-species identifications deriving from bovine serum in cell culture models. <i>Proteomics</i> , 2010, 10, 3040-3044.	2.2	42
53	The human core exosome interacts with differentially localized processive RNases: hDIS3 and hDIS3L. <i>EMBO Journal</i> , 2010, 29, 2342-2357.	7.8	237
54	Site-specific Phosphorylation Dynamics of the Nuclear Proteome during the DNA Damage Response. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1314-1323.	3.8	225

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55	The chromatin-remodeling factor CHD4 coordinates signaling and repair after DNA damage. <i>Journal of Cell Biology</i> , 2010, 190, 731-740.	5.2	199
56	MSQuant, an Open Source Platform for Mass Spectrometry-Based Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 393-403.	3.7	237
57	Organelle Proteomics by Label-Free and SILAC-Based Protein Correlation Profiling. <i>Methods in Molecular Biology</i> , 2010, 658, 255-265.	0.9	10
58	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.	2.5	98
59	FACT facilitates chromatin transcription by RNA polymerases I and III. <i>EMBO Journal</i> , 2009, 28, 854-865.	7.8	106
60	Matrix Protein 2 of Influenza A Virus Blocks Autophagosome Fusion with Lysosomes. <i>Cell Host and Microbe</i> , 2009, 6, 367-380.	11.0	454
61	Identification of SUMO Target Proteins by Quantitative Proteomics. <i>Methods in Molecular Biology</i> , 2009, 497, 19-31.	0.9	27
62	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.	0.7	26
63	Temporal Profiling of the Chromatin Proteome Reveals System-wide Responses to Replication Inhibition. <i>Current Biology</i> , 2008, 18, 838-843.	3.9	36
64	Identification of a membrane proteomic signature for human embryonic stem cells independent of culture conditions. <i>Stem Cell Research</i> , 2008, 1, 219-227.	0.7	34
65	Ordered Organelle Degradation during Starvation-induced Autophagy. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2419-2428.	3.8	166
66	Identification of Let-7 α -Regulated Oncofetal Genes. <i>Cancer Research</i> , 2008, 68, 2587-2591.	0.9	195
67	The Ubiquitin-Proteasome System Is a Key Component of the SUMO-2/3 Cycle. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2107-2122.	3.8	143
68	Ordered bulk degradation via autophagy. <i>Autophagy</i> , 2008, 4, 1057-1059.	9.1	32
69	Signal Transduction by Growth Factor Receptors: Signaling in an Instant. <i>Cell Cycle</i> , 2007, 6, 2913-2916.	2.6	9
70	Bod1, a novel kinetochore protein required for chromosome biorientation. <i>Journal of Cell Biology</i> , 2007, 179, 187-197.	5.2	49
71	Quantitative proteomic assessment of very early cellular signaling events. <i>Nature Biotechnology</i> , 2007, 25, 566-568.	17.5	110
72	A mass spectrometry α -friendly database for cSNP identification. <i>Nature Methods</i> , 2007, 4, 465-466.	19.0	72

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73	Analysis of Nucleolar Protein Dynamics Reveals the Nuclear Degradation of Ribosomal Proteins. <i>Current Biology</i> , 2007, 17, 749-760.	3.9	314
74	Identification of miRNA targets with stable isotope labeling by amino acids in cell culture. <i>Nucleic Acids Research</i> , 2006, 34, e107-e107.	14.5	112
75	A Wiring of the Human Nucleolus. <i>Molecular Cell</i> , 2006, 22, 285-295.	9.7	56
76	Organellar proteomics: turning inventories into insights. <i>EMBO Reports</i> , 2006, 7, 874-879.	4.5	185
77	NOPdb: Nucleolar Proteome Database. <i>Nucleic Acids Research</i> , 2006, 34, D218-D220.	14.5	93
78	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.	5.6	132
79	Repo-Man recruits PP1 β to chromatin and is essential for cell viability. <i>Journal of Cell Biology</i> , 2006, 172, 679-692.	5.2	240
80	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.	7.1	642
81	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.	3.8	274
82	A Proteomic Approach to the Inventory of the Human Centrosome. , 2005, , 123-142.		6
83	Rapid desalting of protein samples for on-line microflow electrospray ionization mass spectrometry. <i>Analytical Biochemistry</i> , 2005, 342, 160-162.	2.4	27
84	Nucleolar proteome dynamics. <i>Nature</i> , 2005, 433, 77-83.	27.8	1,061
85	Proteomic Analysis of the Arabidopsis Nucleolus Suggests Novel Nucleolar Functions. <i>Molecular Biology of the Cell</i> , 2005, 16, 260-269.	2.1	352
86	BASP1 Is a Transcriptional Cosuppressor for the Wilms' Tumor Suppressor Protein WT1. <i>Molecular and Cellular Biology</i> , 2004, 24, 537-549.	2.3	120
87	A Proteomic Study of SUMO-2 Target Proteins. <i>Journal of Biological Chemistry</i> , 2004, 279, 33791-33798.	3.4	197
88	Protein Kinase CK2 Is Coassembled with Small Conductance Ca ²⁺ -Activated K ⁺ Channels and Regulates Channel Gating. <i>Neuron</i> , 2004, 43, 847-858.	8.1	176
89	Proteomic characterization of the human centrosome by protein correlation profiling. <i>Nature</i> , 2003, 426, 570-574.	27.8	1,204
90	Bioinformatic analysis of the nucleolus. <i>Biochemical Journal</i> , 2003, 376, 553-569.	3.7	130

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91	Inhibition of Adipocyte Differentiation by Resistin-like Molecule $\hat{\pm}$. Journal of Biological Chemistry, 2002, 277, 42011-42016.	3.4	61
92	Pseudosubstrate regulation of the SCF β -TrCP ubiquitin ligase by hnRNP-U. Genes and Development, 2002, 16, 439-451.	5.9	110
93	A Proteomic Approach for Identification of Secreted Proteins during the Differentiation of 3T3-L1 Preadipocytes to Adipocytes. Molecular and Cellular Proteomics, 2002, 1, 213-222.	3.8	227
94	Analysis of Tyrosine Phosphorylation Sites in Signaling Molecules by a Phosphotyrosine-Specific Immonium Ion Scanning Method. Science Signaling, 2002, 2002, pl16-pl16.	3.6	38
95	Axin-mediated CKI phosphorylation of β -catenin at Ser 45: a molecular switch for the Wnt pathway. Genes and Development, 2002, 16, 1066-1076.	5.9	621
96	A Mass Spectrometry-based Proteomic Approach for Identification of Serine/Threonine-phosphorylated Proteins by Enrichment with Phospho-specific Antibodies. Molecular and Cellular Proteomics, 2002, 1, 517-527.	3.8	353
97	Multi-Protein Complexes Studied by Mass Spectrometry. Scientific World Journal, The, 2002, 2, 91-92.	2.1	1
98	Paraspeckles. Current Biology, 2002, 12, 13-25.	3.9	455
99	Directed Proteomic Analysis of the Human Nucleolus. Current Biology, 2002, 12, 1-11.	3.9	962
100	RGM is a repulsive guidance molecule for retinal axons. Nature, 2002, 419, 392-395.	27.8	272
101	Analysis of the Plasmodium falciparum proteome by high-accuracy mass spectrometry. Nature, 2002, 419, 537-542.	27.8	596
102	Microcolumns with self-assembled particle frits for proteomics. Journal of Chromatography A, 2002, 979, 233-239.	3.7	327
103	The Vtc proteins in vacuole fusion: coupling NSF activity to V0trans-complex formation. EMBO Journal, 2002, 21, 259-269.	7.8	126
104	Mass spectrometry allows direct identification of proteins in large genomes. Proteomics, 2001, 1, 641-650.	2.2	124
105	Trans-complex formation by proteolipid channels in the terminal phase of membrane fusion. Nature, 2001, 409, 581-588.	27.8	487
106	p70S6 kinase signals cell survival as well as growth, inactivating the pro-apoptotic molecule BAD. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 9666-9670.	7.1	487
107	p95-APP1 links membrane transport to Rac-mediated reorganization of actin. Nature Cell Biology, 2000, 2, 521-530.	10.3	119
108	Functional genomics by mass spectrometry. FEBS Letters, 2000, 480, 25-31.	2.8	107

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109	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.	5.9	314
110	Identification of the receptor component of the ϵ -ubiquitin ligase. <i>Nature</i> , 1998, 396, 590-594.	27.8	650
111	Overexpression, Purification, and Characterization of Recombinant Barley α -Amylases 1 and 2 Secreted by the Methylophilic Yeast <i>Pichia pastoris</i> . <i>Protein Expression and Purification</i> , 1996, 8, 204-214.	1.3	79
112	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.	17.5	110
113	Evaluation of mass spectrometric techniques for characterization of engineered proteins. <i>Molecular Biotechnology</i> , 1995, 4, 1-12.	2.4	16
114	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. <i>Journal of Biological Chemistry</i> , 1995, 270, 6000-6005.	3.4	15
115	Characterization of the different spectral forms of glutamate 1-semialdehyde aminotransferase by mass spectrometry. <i>Biochemistry</i> , 1995, 34, 15918-15924.	2.5	17
116	Localization of an O-glycosylated site in the recombinant barley α -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
117	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
118	Electrospray Mass Spectrometry Characterization of Post-Translational Modifications of Barley α -Amylase 1 Produced in Yeast. <i>Nature Biotechnology</i> , 1993, 11, 1162-1165.	17.5	23