

# Angus I Lamond

## List of Publications by Year in descending order

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239  
papers

28,719  
citations

4146

87  
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5988

160  
g-index

272  
all docs

272  
docs citations

272  
times ranked

27342  
citing authors

#	ARTICLE	IF	CITATIONS
1	The multifunctional nucleolus. <i>Nature Reviews Molecular Cell Biology</i> , 2007, 8, 574-585.	37.0	1,306
2	Nucleolar proteome dynamics. <i>Nature</i> , 2005, 433, 77-83.	27.8	1,061
3	Directed Proteomic Analysis of the Human Nucleolus. <i>Current Biology</i> , 2002, 12, 1-11.	3.9	962
4	Structure and Function in the Nucleus. <i>Science</i> , 1998, 280, 547-553.	12.6	884
5	The Nucleolus under Stress. <i>Molecular Cell</i> , 2010, 40, 216-227.	9.7	882
6	Nuclear speckles: a model for nuclear organelles. <i>Nature Reviews Molecular Cell Biology</i> , 2003, 4, 605-612.	37.0	870
7	Large-Scale Proteomic Analysis of the Human Spliceosome. <i>Genome Research</i> , 2002, 12, 1231-1245.	5.5	808
8	Retinoic acid regulates aberrant nuclear localization of PML-RAR $\alpha$ in acute promyelocytic leukemia cells. <i>Cell</i> , 1994, 76, 345-356.	28.9	691
9	Nuclear Speckles. <i>Cold Spring Harbor Perspectives in Biology</i> , 2011, 3, a000646-a000646.	5.5	664
10	Common genetic variation drives molecular heterogeneity in human iPSCs. <i>Nature</i> , 2017, 546, 370-375.	27.8	491
11	Mass spectrometry and EST-database searching allows characterization of the multi-protein spliceosome complex. <i>Nature Genetics</i> , 1998, 20, 46-50.	21.4	470
12	Paraspeckles. <i>Current Biology</i> , 2002, 12, 13-25.	3.9	455
13	Transcription-dependent colocalization of the U1, U2, U4/U6, and U5 snRNPs in coiled bodies. <i>Journal of Cell Biology</i> , 1992, 117, 1-14.	5.2	409
14	Identifying specific protein interaction partners using quantitative mass spectrometry and bead proteomes. <i>Journal of Cell Biology</i> , 2008, 183, 223-239.	5.2	404
15	Multidimensional proteomics for cell biology. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 269-280.	37.0	375
16	Proteomic Analysis of the Arabidopsis Nucleolus Suggests Novel Nucleolar Functions. <i>Molecular Biology of the Cell</i> , 2005, 16, 260-269.	2.1	352
17	CAJAL BODIES: A Long History of Discovery. <i>Annual Review of Cell and Developmental Biology</i> , 2005, 21, 105-131.	9.4	332
18	A Quantitative Spatial Proteomics Analysis of Proteome Turnover in Human Cells. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.011429.	3.8	332

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19	Live-cell imaging RNAi screen identifies PP2A <sup>B55</sup> and importin <sup>21</sup> as key mitotic exit regulators in human cells. <i>Nature Cell Biology</i> , 2010, 12, 886-893.	10.3	315
20	Analysis of Nucleolar Protein Dynamics Reveals the Nuclear Degradation of Ribosomal Proteins. <i>Current Biology</i> , 2007, 17, 749-760.	3.9	314
21	Highly efficient chemical synthesis of 2 <sup>â€²</sup> -O-methyloligoribonucleotides and tetrabiotinylated derivatives; novel probes that are resistant to degradation by RNA or DNA specific nucleases. <i>Nucleic Acids Research</i> , 1989, 17, 3373-3386.	14.5	286
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.	3.8	274
23	High-Resolution Whole-Genome Sequencing Reveals That Specific Chromatin Domains from Most Human Chromosomes Associate with Nucleoli. <i>Molecular Biology of the Cell</i> , 2010, 21, 3735-3748.	2.1	274
24	Cell fate decisions are specified by the dynamic ERK interactome. <i>Nature Cell Biology</i> , 2009, 11, 1458-1464.	10.3	264
25	Cajal Body dynamics and association with chromatin are ATP-dependent. <i>Nature Cell Biology</i> , 2002, 4, 502-508.	10.3	256
26	Paraspeckles. <i>Cold Spring Harbor Perspectives in Biology</i> , 2010, 2, a000687-a000687.	5.5	254
27	In Vivo Identification of Human Small Ubiquitin-like Modifier Polymerization Sites by High Accuracy Mass Spectrometry and an in Vitro to in Vivo Strategy. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 132-144.	3.8	251
28	HSP90 and Its R2TP/Prefoldin-like Cochaperone Are Involved in the Cytoplasmic Assembly of RNA Polymerase II. <i>Molecular Cell</i> , 2010, 39, 912-924.	9.7	246
29	NOPdb: Nucleolar Proteome Database–2008 update. <i>Nucleic Acids Research</i> , 2009, 37, D181-D184.	14.5	243
30	Repo-Man recruits PP1 <sup>3</sup> to chromatin and is essential for cell viability. <i>Journal of Cell Biology</i> , 2006, 172, 679-692.	5.2	240
31	In Vivo Analysis of Cajal Body Movement, Separation, and Joining in Live Human Cells. <i>Journal of Cell Biology</i> , 2000, 151, 1561-1574.	5.2	239
32	Amino acid-dependent cMyc expression is essential for NK cell metabolic and functional responses in mice. <i>Nature Communications</i> , 2018, 9, 2341.	12.8	238
33	Newly assembled snRNPs associate with coiled bodies before speckles, suggesting a nuclear snRNP maturation pathway. <i>Current Biology</i> , 1999, 9, 1065-1074.	3.9	227
34	Spatial Organization of Large-Scale Chromatin Domains in the Nucleus: A Magnified View of Single Chromosome Territories. <i>Journal of Cell Biology</i> , 1997, 139, 1597-1610.	5.2	220
35	Assembly of snRNP-containing coiled bodies is regulated in interphase and mitosis–evidence that the coiled body is a kinetic nuclear structure.. <i>Journal of Cell Biology</i> , 1993, 120, 841-852.	5.2	216
36	P54nrb Forms a Heterodimer with PSP1 That Localizes to Paraspeckles in an RNA-dependent Manner. <i>Molecular Biology of the Cell</i> , 2005, 16, 5304-5315.	2.1	207

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37	Ser/Thr-specific protein phosphatases are required for both catalytic steps of pre-mRNA splicing. <i>Nucleic Acids Research</i> , 1992, 20, 5263-5269.	14.5	200
38	A Proteomic Study of SUMO-2 Target Proteins. <i>Journal of Biological Chemistry</i> , 2004, 279, 33791-33798.	3.4	197
39	Condensin and Repo-Man co-operate in the regulation of chromosome architecture during mitosis. <i>Nature Cell Biology</i> , 2006, 8, 1133-1142.	10.3	195
40	The cytotoxic T cell proteome and its shaping by the kinase mTOR. <i>Nature Immunology</i> , 2016, 17, 104-112.	14.5	192
41	Requirement for an upstream element for optimal transcription of a bacterial tRNA gene. <i>Nature</i> , 1983, 305, 248-250.	27.8	182
42	Antisense probing of the human U4U6 snRNP with biotinylated 2'-OMe RNA oligonucleotides. <i>Cell</i> , 1989, 59, 531-539.	28.9	178
43	Condensed mitotic chromatin is accessible to transcription factors and chromatin structural proteins. <i>Journal of Cell Biology</i> , 2005, 168, 41-54.	5.2	177
44	A herpes simplex virus type 1 immediate-early gene product, IE63, regulates small nuclear ribonucleoprotein distribution.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 9056-9060.	7.1	172
45	hRRN3 is essential in the SL1-mediated recruitment of RNA Polymerase I to rRNA gene promoters. <i>EMBO Journal</i> , 2001, 20, 1373-1382.	7.8	168
46	Human miRNA Precursors with Box H/ACA snoRNA Features. <i>PLoS Computational Biology</i> , 2009, 5, e1000507.	3.2	167
47	Characterization and prediction of protein nucleolar localization sequences. <i>Nucleic Acids Research</i> , 2010, 38, 7388-7399.	14.5	167
48	A Quantitative Proteomics Analysis of Subcellular Proteome Localization and Changes Induced by DNA Damage. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 457-470.	3.8	164
49	The nucleolus. <i>Journal of Cell Science</i> , 2005, 118, 1335-1337.	2.0	161
50	Targeted snRNP depletion reveals an additional role for mammalian U1 snRNP in spliceosome assembly. <i>Cell</i> , 1990, 63, 293-302.	28.9	159
51	Cajal bodies and coilin moving towards function. <i>Journal of Cell Biology</i> , 2002, 159, 17-21.	5.2	159
52	Quantitative analysis of chromatin compaction in living cells using FLIM-FRET. <i>Journal of Cell Biology</i> , 2009, 187, 481-496.	5.2	153
53	Quantitative analysis of T cell proteomes and environmental sensors during T cell differentiation. <i>Nature Immunology</i> , 2019, 20, 1542-1554.	14.5	152
54	Quantitative kinetic analysis of nucleolar breakdown and reassembly during mitosis in live human cells. <i>Journal of Cell Biology</i> , 2004, 166, 787-800.	5.2	147

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55	Time-lapse Imaging Reveals Dynamic Relocalization of PP1 <sup>β</sup> throughout the Mammalian Cell Cycle. <i>Molecular Biology of the Cell</i> , 2003, 14, 107-117.	2.1	145
56	Mutational analysis of p80 coilin indicates a functional interaction between coiled bodies and the nucleolus. <i>Journal of Cell Biology</i> , 1995, 131, 817-831.	5.2	143
57	Splicing Regulation at the Second Catalytic Step by Sex-lethal Involves 3' Splice Site Recognition by SPF45. <i>Cell</i> , 2002, 109, 285-296.	28.9	140
58	snRNP protein expression enhances the formation of Cajal bodies containing p80-coilin and SMN. <i>Journal of Cell Science</i> , 2001, 114, 4407-4419.	2.0	137
59	Differential interaction of splicing snRNPs with coiled bodies and interchromatin granules during mitosis and assembly of daughter cell nuclei. <i>Journal of Cell Biology</i> , 1994, 126, 11-23.	5.2	134
60	Reversible Accumulation of PEGylated Single-Walled Carbon Nanotubes in the Mammalian Nucleus. <i>ACS Nano</i> , 2008, 2, 2085-2094.	14.6	134
61	Dynamic targeting of protein phosphatase 1 within the nuclei of living mammalian cells. <i>Journal of Cell Science</i> , 2001, 114, 4219-4228.	2.0	133
62	Characterization of Native Protein Complexes and Protein Isoform Variation Using Size-fractionation-based Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3851-3873.	3.8	132
63	Antigen receptor control of methionine metabolism in T cells. <i>ELife</i> , 2019, 8, .	6.0	132
64	Bioinformatic analysis of the nucleolus. <i>Biochemical Journal</i> , 2003, 376, 553-569.	3.7	130
65	Probing the structure and function of U2 snRNP with antisense oligonucleotides made of 2'-OMe RNA. <i>Cell</i> , 1989, 58, 383-390.	28.9	129
66	Two distinct arginine methyltransferases are required for biogenesis of Sm-class ribonucleoproteins. <i>Journal of Cell Biology</i> , 2007, 178, 733-740.	5.2	128
67	Multibatch TMT Reveals False Positives, Batch Effects and Missing Values. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1967-1980.	3.8	128
68	Identification of human miRNA precursors that resemble box C/D snoRNAs. <i>Nucleic Acids Research</i> , 2011, 39, 3879-3891.	14.5	123
69	Human <i>RIF1</i> and protein phosphatase 1 stimulate DNA replication origin licensing but suppress origin activation. <i>EMBO Reports</i> , 2017, 18, 403-419.	4.5	123
70	Global Subcellular Characterization of Protein Degradation Using Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 638-650.	3.8	121
71	A proteomic chronology of gene expression through the cell cycle in human myeloid leukemia cells. <i>ELife</i> , 2014, 3, e01630.	6.0	120
72	RNA polymerase interactions with the upstream region of the <i>E. coli</i> <i>tyrT</i> promoter. <i>Cell</i> , 1983, 35, 265-273.	28.9	113

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73	Quantitative Proteomics and Dynamic Imaging of the Nucleolus Reveal Distinct Responses to UV and Ionizing Radiation. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.009241.	3.8	110
74	Inhibition of Protein Dephosphorylation Results in the Accumulation of Splicing snRNPs and Coiled Bodies within the Nucleolus. <i>Experimental Cell Research</i> , 1997, 230, 84-93.	2.6	108
75	Stable-isotope labeling with amino acids in nematodes. <i>Nature Methods</i> , 2011, 8, 849-851.	19.0	108
76	Antisense probes containing 2-aminoadenosine allow efficient depletion of U5 snRNP from HeLa splicing extracts. <i>Nucleic Acids Research</i> , 1991, 19, 3193-3198.	14.5	107
77	Mitotic phosphatases: no longer silent partners. <i>Current Opinion in Cell Biology</i> , 2006, 18, 623-631.	5.4	107
78	Proteomics Analysis of the Nucleolus in Adenovirus-infected Cells. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 117-130.	3.8	106
79	Antisense oligonucleotides made of 2'-O-alkylRNA: their properties and applications in RNA biochemistry. <i>FEBS Letters</i> , 1993, 325, 123-127.	2.8	105
80	Cloning and characterization of hSRP1A, a tissue-specific nuclear transport factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 582-587.	7.1	103
81	Cleaning up the masses: Exclusion lists to reduce contamination with HPLC-MS/MS. <i>Journal of Proteomics</i> , 2013, 88, 92-103.	2.4	102
82	Stringent control of bacterial transcription. <i>Cell</i> , 1985, 41, 6-8.	28.9	101
83	Dynamic Interactions Between Splicing snRNPs, Coiled Bodies and Nucleoli Revealed Using snRNP Protein Fusions to the Green Fluorescent Protein. <i>Experimental Cell Research</i> , 1998, 243, 290-304.	2.6	100
84	NOPdb: Nucleolar Proteome Database. <i>Nucleic Acids Research</i> , 2006, 34, D218-D220.	14.5	93
85	p72: a human nuclear DEAD box protein highly related to p68. <i>Nucleic Acids Research</i> , 1996, 24, 3739-3747.	14.5	92
86	Herpes Simplex Virus IE63 (ICP27) Protein Interacts with Spliceosome-Associated Protein 145 and Inhibits Splicing prior to the First Catalytic Step. <i>Journal of Virology</i> , 2001, 75, 4376-4385.	3.4	91
87	Cajal body proteins SMN and Coilin show differential dynamic behaviour in vivo. <i>Journal of Cell Science</i> , 2003, 116, 2039-2050.	2.0	91
88	Deep Proteome Analysis Identifies Age-Related Processes in <i>C.Âlegans</i> . <i>Cell Systems</i> , 2016, 3, 144-159.	6.2	90
89	The Spliceosome. <i>BioEssays</i> , 1993, 15, 595-603.	2.5	89
90	3D3/lyric: a novel transmembrane protein of the endoplasmic reticulum and nuclear envelope, which is also present in the nucleolus. <i>Experimental Cell Research</i> , 2004, 294, 94-105.	2.6	86

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91	Nuclear organization of pre-mRNA splicing factors. <i>Current Opinion in Cell Biology</i> , 1999, 11, 372-377.	5.4	85
92	Molecular analysis of the coiled body. <i>Journal of Cell Science</i> , 1995, 1995, 107-113.	2.0	84
93	UV-induced fragmentation of Cajal bodies. <i>Journal of Cell Biology</i> , 2006, 175, 401-413.	5.2	83
94	The Dynamics of the Nucleolus. <i>Critical Reviews in Eukaryotic Gene Expression</i> , 2003, 13, 39-54.	0.9	82
95	Nuclear substructure and dynamics. <i>Current Biology</i> , 2003, 13, R825-R828.	3.9	81
96	Human box C/D snoRNA processing conservation across multiple cell types. <i>Nucleic Acids Research</i> , 2012, 40, 3676-3688.	14.5	79
97	Purification and characterisation of p99, a nuclear modulator of protein phosphatase 1 activity. <i>FEBS Letters</i> , 1997, 420, 57-62.	2.8	78
98	Site-directed ribose methylation identifies 2'-OH groups in polyadenylation substrates critical for AAUAAA recognition and poly(A) addition. <i>Cell</i> , 1991, 65, 125-133.	28.9	76
99	Non-snRNP protein splicing factors. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1993, 1173, 247-265.	2.4	76
100	Mass spectrometry-based immuno-precipitation proteomics – The user's guide. <i>Proteomics</i> , 2011, 11, 1153-1159.	2.2	76
101	PHD1 Links Cell-Cycle Progression to Oxygen Sensing through Hydroxylation of the Centrosomal Protein Cep192. <i>Developmental Cell</i> , 2013, 26, 381-392.	7.0	74
102	A Proteomic Screen for Nucleolar SUMO Targets Shows SUMOylation Modulates the Function of Nop5/Nop58. <i>Molecular Cell</i> , 2010, 39, 618-631.	9.7	72
103	Large-Scale Isolation of Cajal Bodies from HeLa Cells. <i>Molecular Biology of the Cell</i> , 2002, 13, 2461-2473.	2.1	68
104	Localisation of splicing snRNPs in mammalian cells. <i>Molecular Biology Reports</i> , 1993, 18, 127-133.	2.3	66
105	Cell biology and the genome projects a concerted strategy for characterizing multiprotein complexes by using mass spectrometry. <i>Trends in Cell Biology</i> , 1997, 7, 139-142.	7.9	65
106	Yeast Pescadillo is required for multiple activities during 60S ribosomal subunit synthesis. <i>Rna</i> , 2002, 8, 626-636.	3.5	65
107	Displacement affinity chromatography of protein phosphatase one (PP1) complexes. <i>BMC Biochemistry</i> , 2008, 9, 28.	4.4	65
108	Modulation of Higher Order Chromatin Conformation in Mammalian Cell Nuclei Can Be Mediated by Polyamines and Divalent Cations. <i>PLoS ONE</i> , 2013, 8, e67689.	2.5	65

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109	Toward a High-Resolution View of Nuclear Dynamics. <i>Science</i> , 2007, 318, 1402-1407.	12.6	63
110	Establishment of a Protein Frequency Library and Its Application in the Reliable Identification of Specific Protein Interaction Partners. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 861-879.	3.8	63
111	Identification of Small Molecule Inhibitors of Pre-mRNA Splicing. <i>Journal of Biological Chemistry</i> , 2014, 289, 34683-34698.	3.4	62
112	Guidelines for reporting the use of gel electrophoresis in proteomics. <i>Nature Biotechnology</i> , 2008, 26, 863-864.	17.5	61
113	Global Membrane Protein Interactome Analysis using In vivo Crosslinking and Mass Spectrometry-based Protein Correlation Profiling. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2476-2490.	3.8	61
114	The Helicase Aquarius/EMB-4 Is Required to Overcome Intronic Barriers to Allow Nuclear RNAi Pathways to Heritably Silence Transcription. <i>Developmental Cell</i> , 2017, 42, 241-255.e6.	7.0	61
115	Detecting Protein-Protein Interactions In Vivo with FRET using Multiphoton Fluorescence Lifetime Imaging Microscopy (FLIM). <i>Current Protocols in Cytometry</i> , 2007, 42, Unit12.10.	3.7	60
116	Quantitative Proteomic Analysis of Chromatin Reveals that Ctf18 Acts in the DNA Replication Checkpoint. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.005561.	3.8	60
117	Synthesis and applications of oligoribonucleotides with selected 2'-O-methylation using the 2'-O-[1-(2-fluorophenyl)-4-methoxypiperidin-4-yl] protecting group. <i>Nucleic Acids Research</i> , 1990, 18, 5143-5151.	14.5	59
118	Nuclear organization of splicing snRNPs during differentiation of murine erythroleukemia cells in vitro. <i>Journal of Cell Biology</i> , 1993, 123, 1055-1068.	5.2	58
119	Direct interaction between hnRNP M and CDC5L/PLRG1 proteins affects alternative splice site choice. <i>EMBO Reports</i> , 2010, 11, 445-451.	4.5	57
120	Proteomic and 3D structure analyses highlight the C/D box snoRNP assembly mechanism and its control. <i>Journal of Cell Biology</i> , 2014, 207, 463-480.	5.2	57
121	Protein phosphatase 4 interacts with the Survival of Motor Neurons complex and enhances the temporal localisation of snRNPs. <i>Journal of Cell Science</i> , 2003, 116, 1905-1913.	2.0	55
122	Advancing Cell Biology Through Proteomics in Space and Time (PROSPECTS). <i>Molecular and Cellular Proteomics</i> , 2012, 11, O112.017731.	3.8	55
123	Interaction of U-box E3 ligase SNEV with PSMB4, the $\beta 7$ subunit of the 20S proteasome. <i>Biochemical Journal</i> , 2005, 388, 593-603.	3.7	54
124	The serine/arginine-rich protein SF2/ASF regulates protein sumoylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 16119-16124.	7.1	54
125	Metabolic complexity in the RNA world and implications for the origin of protein synthesis. <i>Journal of Molecular Evolution</i> , 1990, 30, 7-15.	1.8	53
126	Spatial mapping of splicing factor complexes involved in exon and intron definition. <i>Journal of Cell Biology</i> , 2008, 181, 921-934.	5.2	53



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127	Proteomic analysis of cell cycle progression in asynchronous cultures, including mitotic subphases, using PRIMMUS. <i>ELife</i> , 2017, 6, .	6.0	53
128	Multi-omics Analyses of Starvation Responses Reveal a Central Role for Lipoprotein Metabolism in Acute Starvation Survival in <i>C.Ælegans</i> . <i>Cell Systems</i> , 2017, 5, 38-52.e4.	6.2	52
129	Cyclin A triggers Mitosis either via the Greatwall kinase pathway or Cyclin B. <i>EMBO Journal</i> , 2020, 39, e104419.	7.8	52
130	p53-Dependent subcellular proteome localization following DNA damage. <i>Proteomics</i> , 2010, 10, 4087-4097.	2.2	51
131	Nrf2 activation reprograms macrophage intermediary metabolism and suppresses the type I interferon response. <i>IScience</i> , 2022, 25, 103827.	4.1	51
132	In vivo analysis of NHPX reveals a novel nucleolar localization pathway involving a transient accumulation in splicing speckles. <i>Journal of Cell Biology</i> , 2002, 157, 615-629.	5.2	50
133	A perspective on proteomics in cell biology. <i>Trends in Cell Biology</i> , 2014, 24, 257-264.	7.9	50
134	Protein phosphatase 1 can modulate alternative 5' splice site selection in a HeLa splicing extract. <i>FEBS Letters</i> , 1994, 352, 276-280.	2.8	49
135	Systematic Analysis of Protein Pools, Isoforms, and Modifications Affecting Turnover and Subcellular Localization. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013680.	3.8	48
136	A role for the CB-associated SUMO isopeptidase USPL1 in RNAPII-mediated snRNA transcription. <i>Journal of Cell Science</i> , 2014, 127, 1065-78.	2.0	48
137	A Direct Interaction between the Carboxyl-terminal Region of CDC5L and the WD40 Domain of PLRG1 Is Essential for Pre-mRNA Splicing. <i>Journal of Biological Chemistry</i> , 2001, 276, 42370-42381.	3.4	47
138	An evolutionarily conserved ribosome-rescue pathway maintains epidermal homeostasis. <i>Nature</i> , 2018, 556, 376-380.	27.8	47
139	SNEV is an evolutionarily conserved splicing factor whose oligomerization is necessary for spliceosome assembly. <i>Nucleic Acids Research</i> , 2005, 33, 6868-6883.	14.5	46
140	Proteomic analysis of the response to cell cycle arrests in human myeloid leukemia cells. <i>ELife</i> , 2015, 4, .	6.0	46
141	Perturbation of Chromatin Structure Globally Affects Localization and Recruitment of Splicing Factors. <i>PLoS ONE</i> , 2012, 7, e48084.	2.5	44
142	A protein phosphatase network controls the temporal and spatial dynamics of differentiation commitment in human epidermis. <i>ELife</i> , 2017, 6, .	6.0	44
143	SPF30 Is an Essential Human Splicing Factor Required for Assembly of the U4/U5/U6 Tri-small Nuclear Ribonucleoprotein into the Spliceosome. <i>Journal of Biological Chemistry</i> , 2001, 276, 31142-31150.	3.4	43
144	FRET analyses of the U2AF complex localize the U2AF35/U2AF65 interaction in vivo and reveal a novel self-interaction of U2AF35. <i>Rna</i> , 2005, 11, 1201-1214.	3.5	43

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145	Alteration of the growth-rate-dependent regulation of <i>Escherichia coli</i> tyrT expression by promoter mutations. <i>Journal of Molecular Biology</i> , 1986, 189, 251-255.	4.2	41
146	Analysis of Human Small Nucleolar RNAs (snoRNA) and the Development of snoRNA Modulator of Gene Expression Vectors. <i>Molecular Biology of the Cell</i> , 2010, 21, 1569-1584.	2.1	40
147	Efficient analysis of mammalian polysomes in cells and tissues using Ribo Mega-SEC. <i>ELife</i> , 2018, 7, .	6.0	40
148	Population-scale proteome variation in human induced pluripotent stem cells. <i>ELife</i> , 2020, 9, .	6.0	40
149	Sequence-specific affinity selection of mammalian splicing complexes. <i>Nucleic Acids Research</i> , 1990, 18, 7373-7379.	14.5	39
150	RRP1B Targets PP1 to Mammalian Cell Nucleoli and Is Associated with Pre-60S Ribosomal Subunits. <i>Molecular Biology of the Cell</i> , 2010, 21, 4212-4226.	2.1	39
151	Identification and Functional Characterization of FMN2, a Regulator of the Cyclin-Dependent Kinase Inhibitor p21. <i>Molecular Cell</i> , 2013, 49, 922-933.	9.7	39
152	Quantitative Profiling of the Human Substantia Nigra Proteome from Laser-capture Microdissected FFPE Tissue. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 839-851.	3.8	39
153	Plant SILAC: Stable-Isotope Labelling with Amino Acids of Arabidopsis Seedlings for Quantitative Proteomics. <i>PLoS ONE</i> , 2013, 8, e72207.	2.5	39
154	Neuronal Differentiation in the Rat Hippocampus Involves a Stage-specific Reorganization of Subnuclear Structure both <i>In Vivo</i> and <i>In Vitro</i> . <i>European Journal of Neuroscience</i> , 1996, 8, 892-905.	2.6	37
155	Proteomic Analysis of the Cell Cycle of Procylic Form <i>Trypanosoma brucei</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1184-1195.	3.8	36
156	Nuclear RNA processing. <i>Current Opinion in Cell Biology</i> , 1991, 3, 493-501.	5.4	35
157	Characterization of hCINAP, a Novel Coilin-interacting Protein Encoded by a Transcript from the Transcription Factor TAFII32 Locus. <i>Journal of Biological Chemistry</i> , 2005, 280, 36429-36441.	3.4	35
158	Microproteomics with iterative data analysis: Proteome analysis in <i>C. elegans</i> at the single worm level. <i>Proteomics</i> , 2016, 16, 381-392.	2.2	34
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