

# Angus I Lamond

## List of Publications by Year in descending order

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239  
papers

28,719  
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4146

87  
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5988

160  
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272  
all docs

272  
docs citations

272  
times ranked

27342  
citing authors

#	ARTICLE	IF	CITATIONS
1	Nrf2 activation reprograms macrophage intermediary metabolism and suppresses the type I interferon response. <i>IScience</i> , 2022, 25, 103827.	4.1	51
2	Efficient and Rapid Analysis of Polysomes and Ribosomal Subunits in Cells and Tissues Using Ribo Mega-SEC. <i>Bio-protocol</i> , 2021, 11, e4106.	0.4	3
3	Erosion of human X chromosome inactivation causes major remodeling of the iPSC proteome. <i>Cell Reports</i> , 2021, 35, 109032.	6.4	23
4	Upregulation of RNA cap methyltransferase RNMT drives ribosome biogenesis during T cell activation. <i>Nucleic Acids Research</i> , 2021, 49, 6722-6738.	14.5	29
5	Tissue environment, not ontogeny, defines murine intestinal intraepithelial T lymphocytes. <i>ELife</i> , 2021, 10, .	6.0	14
6	DEPS-1 is required for piRNA-dependent silencing and PIWI condensate organisation in <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2020, 11, 4242.	12.8	16
7	Cyclin A triggers Mitosis either via the Greatwall kinase pathway or Cyclin B. <i>EMBO Journal</i> , 2020, 39, e104419.	7.8	52
8	Phosphoproteomics identifies a bimodal EPHA2 receptor switch that promotes embryonic stem cell differentiation. <i>Nature Communications</i> , 2020, 11, 1357.	12.8	12
9	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
10	Population-scale proteome variation in human induced pluripotent stem cells. <i>ELife</i> , 2020, 9, .	6.0	40
11	Multibatch TMT Reveals False Positives, Batch Effects and Missing Values. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1967-1980.	3.8	128
12	EMSY expression affects multiple components of the skin barrier with relevance to atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 470-481.	2.9	23
13	Quantitative analysis of T cell proteomes and environmental sensors during T cell differentiation. <i>Nature Immunology</i> , 2019, 20, 1542-1554.	14.5	152
14	Signal enhanced proteomics: a biological perspective on dissecting the functional organisation of cell proteomes. <i>Current Opinion in Chemical Biology</i> , 2019, 48, 114-122.	6.1	3
15	Composition of the Survival Motor Neuron (SMN) Complex in <i>Drosophila melanogaster</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 491-503.	1.8	16
16	The Encyclopedia of Proteome Dynamics: the KinoViewer. <i>Bioinformatics</i> , 2019, 35, 1441-1442.	4.1	9
17	Functional and proteomic analysis of a full thickness filaggrin-deficient skin organoid model. <i>Wellcome Open Research</i> , 2019, 4, 134.	1.8	13
18	Proteome turnover in the bloodstream and procyclic forms of <i>Trypanosoma brucei</i> measured by quantitative proteomics. <i>Wellcome Open Research</i> , 2019, 4, 152.	1.8	27

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19	Antigen receptor control of methionine metabolism in T cells. <i>ELife</i> , 2019, 8, .	6.0	132
20	Proteomic analysis of a filaggrin-deficient skin organoid model shows evidence of increased transcriptional-translational activity, keratinocyte-immune crosstalk and disordered axon guidance. <i>Wellcome Open Research</i> , 2019, 4, 134.	1.8	8
21	An evolutionarily conserved ribosome-rescue pathway maintains epidermal homeostasis. <i>Nature</i> , 2018, 556, 376-380.	27.8	47
22	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
23	Self-oligomerization regulates stability of survival motor neuron protein isoforms by sequestering an SCF <sup>Slmb</sup> degron. <i>Molecular Biology of the Cell</i> , 2018, 29, 96-110.	2.1	27
24	The Encyclopedia of Proteome Dynamics: a big data ecosystem for (prote)omics. <i>Nucleic Acids Research</i> , 2018, 46, D1202-D1209.	14.5	19
25	PIP30/FAM192A is a novel regulator of the nuclear proteasome activator PA28 <sup>̂3</sup> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6477-E6486.	7.1	29
26	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
27	Proteome-wide analysis of protein abundance and turnover remodelling during oncogenic transformation of human breast epithelial cells. <i>Wellcome Open Research</i> , 2018, 3, 51.	1.8	18
28	Efficient analysis of mammalian polysomes in cells and tissues using Ribo Mega-SEC. <i>ELife</i> , 2018, 7, .	6.0	40
29	Human <sup>scp</sup> RIF <sup>scp</sup> 1 and protein phosphatase 1 stimulate <sup>scp</sup> DNA <sup>scp</sup> replication origin licensing but suppress origin activation. <i>EMBO Reports</i> , 2017, 18, 403-419.	4.5	123
30	Common genetic variation drives molecular heterogeneity in human iPSCs. <i>Nature</i> , 2017, 546, 370-375.	27.8	491
31	Brd4 <sup>̂Brd2</sup> isoform switching coordinates pluripotent exit and Smad2 <sup>̂</sup> dependent lineage specification. <i>EMBO Reports</i> , 2017, 18, 1108-1122.	4.5	26
32	Multi-omics Analyses of Starvation Responses Reveal a Central Role for Lipoprotein Metabolism in Acute Starvation Survival in <i>C. elegans</i> . <i>Cell Systems</i> , 2017, 5, 38-52.e4.	6.2	52
33	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
34	Prediction of Protein Complexes in <i>Trypanosoma brucei</i> by Protein Correlation Profiling Mass Spectrometry and Machine Learning. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2254-2267.	3.8	24
35	Comparative genetic, proteomic and phosphoproteomic analysis of <i>C. elegans</i> embryos with a focus on ham-1/STOX and pig-1/MELK in dopaminergic neuron development. <i>Scientific Reports</i> , 2017, 7, 4314.	3.3	11
36	New Apex in Proteome Analysis. <i>Cell Systems</i> , 2017, 4, 581-582.	6.2	2

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37	The Chromatin Assembly Factor Complex 1 (CAF1) and 5-Azacytidine (5-AzaC) Affect Cell Motility in Src-transformed Human Epithelial Cells. <i>Journal of Biological Chemistry</i> , 2017, 292, 172-184.	3.4	12
38	A protein phosphatase network controls the temporal and spatial dynamics of differentiation commitment in human epidermis. <i>ELife</i> , 2017, 6, .	6.0	44
39	Proteomic analysis of cell cycle progression in asynchronous cultures, including mitotic subphases, using PRIMMUS. <i>ELife</i> , 2017, 6, .	6.0	53
40	Characterisation of the biflavonoid hinokiflavone as a pre-mRNA splicing modulator that inhibits SENP. <i>ELife</i> , 2017, 6, .	6.0	34
41	CDK dependent phosphorylation of PHD1 on Serine 130 determines specificity in substrate targeting in cells. <i>Journal of Cell Science</i> , 2016, 129, 191-205.	2.0	15
42	Unlocking the chromatin code by deciphering proteinâ€“DNA interactions. <i>Molecular Systems Biology</i> , 2016, 12, 887.	7.2	3
43	The histone chaperone Vps75 forms multiple oligomeric assemblies capable of mediating exchange between histone H3â€“H4 tetramers and Asf1â€“H3â€“H4 complexes. <i>Nucleic Acids Research</i> , 2016, 44, 6157-6172.	14.5	30
44	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
45	Analysis of Mass Spectrometry Data for Nucleolar Proteomics Experiments. <i>Methods in Molecular Biology</i> , 2016, 1455, 263-276.	0.9	0
46	Quantitative Proteomic Analysis of the Human Nucleolus. <i>Methods in Molecular Biology</i> , 2016, 1455, 249-262.	0.9	9
47	Deep Proteome Analysis Identifies Age-Related Processes in <i>C.Â elegans</i> . <i>Cell Systems</i> , 2016, 3, 144-159.	6.2	90
48	Microâ€“proteomics 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
49	The cytotoxic T cell proteome and its shaping by the kinase mTOR. <i>Nature Immunology</i> , 2016, 17, 104-112.	14.5	192
50	Enhanced snoMEN Vectors Facilitate Establishment of GFPâ€“HIF-1Î± Protein Replacement Human Cell Lines. <i>PLoS ONE</i> , 2016, 11, e0154759.	2.5	2
51	Global Proteomics Analysis of the Response to Starvation in <i>C. elegans</i> *. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1989-2001.	3.8	32
52	Evaluating the use of HILIC in large-scale, multi dimensional proteomics: Horses for courses?. <i>International Journal of Mass Spectrometry</i> , 2015, 391, 105-114.	1.5	10
53	Multidimensional proteomics for cell biology. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 269-280.	37.0	375
54	Time-Lapse Imaging of Nuclear Bodies. <i>Methods in Molecular Biology</i> , 2015, 1262, 55-67.	0.9	1

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55	Targeted Knock-Down of miR21 Primary Transcripts Using snoMEN Vectors Induces Apoptosis in Human Cancer Cell Lines. PLoS ONE, 2015, 10, e0138668.	2.5	11
56	Proteomic analysis of the response to cell cycle arrests in human myeloid leukemia cells. ELife, 2015, 4, .	6.0	46
57	FMDV replicons encoding green fluorescent protein are replication competent. Journal of Virological Methods, 2014, 209, 35-40.	2.1	31
58	Identification of Small Molecule Inhibitors of Pre-mRNA Splicing. Journal of Biological Chemistry, 2014, 289, 34683-34698.	3.4	62
59	A perspective on proteomics in cell biology. Trends in Cell Biology, 2014, 24, 257-264.	7.9	50
60	Proteomic and 3D structure analyses highlight the C/D box snoRNP assembly mechanism and its control. Journal of Cell Biology, 2014, 207, 463-480.	5.2	57
61	A role for the CB-associated SUMO isopeptidase USPL1 in RNAPII-mediated snRNA transcription. Journal of Cell Science, 2014, 127, 1065-78.	2.0	48
62	A proteomic chronology of gene expression through the cell cycle in human myeloid leukemia cells. ELife, 2014, 3, e01630.	6.0	120
63	Cleaning up the masses: Exclusion lists to reduce contamination with HPLC-MS/MS. Journal of Proteomics, 2013, 88, 92-103.	2.4	102
64	Identification and Functional Characterization of FMN2, a Regulator of the Cyclin-Dependent Kinase Inhibitor p21. Molecular Cell, 2013, 49, 922-933.	9.7	39
65	PHD1 Links Cell-Cycle Progression to Oxygen Sensing through Hydroxylation of the Centrosomal Protein Cep192. Developmental Cell, 2013, 26, 381-392.	7.0	74
66	RNA-binding protein GLD-1/quaking genetically interacts with the <i>mir-35</i> and the <i>let-7</i> miRNA pathways in <i>Caenorhabditis elegans</i> . Open Biology, 2013, 3, 130151.	3.6	22
67	Characterization of Native Protein Complexes and Protein Isoform Variation Using Size-fractionation-based Quantitative Proteomics. Molecular and Cellular Proteomics, 2013, 12, 3851-3873.	3.8	132
68	Global Subcellular Characterization of Protein Degradation Using Quantitative Proteomics. Molecular and Cellular Proteomics, 2013, 12, 638-650.	3.8	121
69	FMN2 is a novel regulator of the cyclin-dependent kinase inhibitor p21. Cell Cycle, 2013, 12, 2348-2354.	2.6	11
70	Modulation of Higher Order Chromatin Conformation in Mammalian Cell Nuclei Can Be Mediated by Polyamines and Divalent Cations. PLoS ONE, 2013, 8, e67689.	2.5	65
71	Analysis of Human Protein Replacement Stable Cell Lines Established using snoMEN-PR Vector. PLoS ONE, 2013, 8, e62305.	2.5	6
72	Plant SILAC: Stable-Isotope Labelling with Amino Acids of Arabidopsis Seedlings for Quantitative Proteomics. PLoS ONE, 2013, 8, e72207.	2.5	39

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73	A Quantitative Spatial Proteomics Analysis of Proteome Turnover in Human Cells. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.011429.	3.8	332
74	Characterization of MRFAP1 Turnover and Interactions Downstream of the NEDD8 Pathway. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014407.	3.8	23
75	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
76	Human box C/D snoRNA processing conservation across multiple cell types. <i>Nucleic Acids Research</i> , 2012, 40, 3676-3688.	14.5	79
77	The Adenomatous Polyposis Coli Protein Contributes to Normal Compaction of Mitotic Chromatin. <i>PLoS ONE</i> , 2012, 7, e38102.	2.5	13
78	Inhibition of Pre-mRNA Splicing by a Synthetic Blom7Î±-Interacting Small RNA. <i>PLoS ONE</i> , 2012, 7, e47497.	2.5	1
79	Perturbation of Chromatin Structure Globally Affects Localization and Recruitment of Splicing Factors. <i>PLoS ONE</i> , 2012, 7, e48084.	2.5	44
80	hCINAP is an atypical mammalian nuclear adenylate kinase with an ATPase motif: Structural and functional studies. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 206-220.	2.6	27
81	Advancing Cell Biology Through Proteomics in Space and Time (PROSPECTS). <i>Molecular and Cellular Proteomics</i> , 2012, 11, O112.017731.	3.8	55
82	The Dynamic Proteome of the Nucleolus. , 2011, , 29-42.		0
83	Nuclear Speckles. <i>Cold Spring Harbor Perspectives in Biology</i> , 2011, 3, a000646-a000646.	5.5	664
84	Exo70, a subunit of the exocyst complex, interacts with SNEVhPrp19/hPso4 and is involved in pre-mRNA splicing. <i>Biochemical Journal</i> , 2011, 438, 81-91.	3.7	19
85	Stable-isotope labeling with amino acids in nematodes. <i>Nature Methods</i> , 2011, 8, 849-851.	19.0	108
86	An intranucleolar body associated with rDNA. <i>Chromosoma</i> , 2011, 120, 481-499.	2.2	30
87	PNAC: a protein nucleolar association classifier. <i>BMC Genomics</i> , 2011, 12, 74.	2.8	8
88	Mass spectrometry-based immuno-precipitation proteomics - The user's guide. <i>Proteomics</i> , 2011, 11, 1153-1159.	2.2	76
89	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
90	A role for SUMOylation in snoRNP biogenesis revealed by quantitative proteomics. <i>Nucleus</i> , 2011, 2, 30-37.	2.2	21

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91	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
92	Identification of human miRNA precursors that resemble box C/D snoRNAs. <i>Nucleic Acids Research</i> , 2011, 39, 3879-3891.	14.5	123
93	A role for SUMOylation in snoRNP biogenesis revealed by quantitative proteomics. <i>Nucleus</i> , 2011, 2, 30-37.	2.2	17
94	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
95	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
96	The nuclear ATPase/adenylate kinase hCINAP is recruited to perinucleolar caps generated upon RNA pol.II inhibition. <i>FEBS Letters</i> , 2010, 584, 4559-4564.	2.8	7
97	p53-Dependent subcellular proteome localization following DNA damage. <i>Proteomics</i> , 2010, 10, 4087-4097.	2.2	51
98	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
99	Live-cell imaging RNAi screen identifies PP2A <sup>B55</sup> and importin- $\beta$ 1 as key mitotic exit regulators in human cells. <i>Nature Cell Biology</i> , 2010, 12, 886-893.	10.3	315
100	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
101	Characterization and prediction of protein nucleolar localization sequences. <i>Nucleic Acids Research</i> , 2010, 38, 7388-7399.	14.5	167
102	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
103	Paraspeckles. <i>Cold Spring Harbor Perspectives in Biology</i> , 2010, 2, a000687-a000687.	5.5	254
104	Proteomics Analysis of the Nucleolus in Adenovirus-infected Cells. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 117-130.	3.8	106
105	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
106	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
107	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
108	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

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109	The Nucleolus under Stress. <i>Molecular Cell</i> , 2010, 40, 216-227.	9.7	882
110	Blom71± Is a Novel Heterogeneous Nuclear Ribonucleoprotein K Homology Domain Protein Involved in Pre-mRNA Splicing That Interacts with SNEVPrp19-Pso4. <i>Journal of Biological Chemistry</i> , 2009, 284, 29193-29204.	3.4	12
111	Human miRNA Precursors with Box H/ACA snoRNA Features. <i>PLoS Computational Biology</i> , 2009, 5, e1000507.	3.2	167
112	Cell fate decisions are specified by the dynamic ERK interactome. <i>Nature Cell Biology</i> , 2009, 11, 1458-1464.	10.3	264
113	NOPdb: Nucleolar Proteome Database–2008 update. <i>Nucleic Acids Research</i> , 2009, 37, D181-D184.	14.5	243
114	Quantitative analysis of chromatin compaction in living cells using FLIMâ€FRET. <i>Journal of Cell Biology</i> , 2009, 187, 481-496.	5.2	153
115	Displacement affinity chromatography of protein phosphatase one (PP1) complexes. <i>BMC Biochemistry</i> , 2008, 9, 28.	4.4	65
116	Guidelines for reporting the use of gel electrophoresis in proteomics. <i>Nature Biotechnology</i> , 2008, 26, 863-864.	17.5	61
117	Nuclear functions in space and time: Gene expression in a dynamic, constrained environment. <i>FEBS Letters</i> , 2008, 582, 1960-1970.	2.8	23
118	Reversible Accumulation of PEGylated Single-Walled Carbon Nanotubes in the Mammalian Nucleus. <i>ACS Nano</i> , 2008, 2, 2085-2094.	14.6	134
119	Nuclear Organisation and Subnuclear Bodies. <i>Progress in Molecular and Subcellular Biology</i> , 2008, 35, 1-22.	1.6	17
120	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
121	Where in the cell is the minor spliceosome?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8485-8486.	7.1	20
122	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
123	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
124	Visualization of Intracellular PP1 Targeting Through Transiently and Stably Expressed Fluorescent Protein Fusions. , 2007, 365, 133-154.		14
125	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
126	Detecting Proteinâ€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



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127	Toward a High-Resolution View of Nuclear Dynamics. <i>Science</i> , 2007, 318, 1402-1407.	12.6	63
128	The nuclear PP1 interacting protein ZAP3 (ZAP) is a putative nucleoside kinase that complexes with SAM68, CIA, NF110/45, and HNRNP-G. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2007, 1774, 1339-1350.	2.3	29
129	The multifunctional nucleolus. <i>Nature Reviews Molecular Cell Biology</i> , 2007, 8, 574-585.	37.0	1,306
130	RNA polymerase II transcription in living color. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 788-790.	8.2	5
131	Analysis of Nucleolar Protein Dynamics Reveals the Nuclear Degradation of Ribosomal Proteins. <i>Current Biology</i> , 2007, 17, 749-760.	3.9	314
132	UV-induced fragmentation of Cajal bodies. <i>Journal of Cell Biology</i> , 2006, 175, 401-413.	5.2	83
133	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
134	Mitotic phosphatases: no longer silent partners. <i>Current Opinion in Cell Biology</i> , 2006, 18, 623-631.	5.4	107
135	NOPdb: Nucleolar Proteome Database. <i>Nucleic Acids Research</i> , 2006, 34, D218-D220.	14.5	93
136	Repo-Man recruits PP1 <sup>13</sup> to chromatin and is essential for cell viability. <i>Journal of Cell Biology</i> , 2006, 172, 679-692.	5.2	240
137	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
138	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
139	Nucleolar proteome dynamics. <i>Nature</i> , 2005, 433, 77-83.	27.8	1,061
140	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
141	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
142	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
143	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
144	The nucleolus. <i>Journal of Cell Science</i> , 2005, 118, 1335-1337.	2.0	161

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145	Proteomic Analysis of the Arabidopsis Nucleolus Suggests Novel Nucleolar Functions. <i>Molecular Biology of the Cell</i> , 2005, 16, 260-269.	2.1	352
146	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
147	CAJAL BODIES: A Long History of Discovery. <i>Annual Review of Cell and Developmental Biology</i> , 2005, 21, 105-131.	9.4	332
148	A Proteomic Study of SUMO-2 Target Proteins. <i>Journal of Biological Chemistry</i> , 2004, 279, 33791-33798.	3.4	197
149	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
150	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
151	Nuclear substructure and dynamics. <i>Current Biology</i> , 2003, 13, R825-R828.	3.9	81
152	Nuclear speckles: a model for nuclear organelles. <i>Nature Reviews Molecular Cell Biology</i> , 2003, 4, 605-612.	37.0	870
153	hLodestar/HuF2 interacts with CDC5L and is involved in pre-mRNA splicing. <i>Biochemical and Biophysical Research Communications</i> , 2003, 308, 793-801.	2.1	15
154	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
155	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
156	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
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158	Bioinformatic analysis of the nucleolus. <i>Biochemical Journal</i> , 2003, 376, 553-569.	3.7	130
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