Jan Ellenberg

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.

185	20,787	77	143
papers	citations	h-index	g-index
201	23,806 ext. citations	13.8	6.65
ext. papers		avg, IF	L-index

#	Paper	IF	Citations
185	REMBI: Recommended Metadata for Biological Images-enabling reuse of microscopy data in biology. <i>Nature Methods</i> , 2021 , 18, 1418-1422	21.6	16
184	Superaufgellite Erkennung rümlicher NBe mit Proximity-PAINT. Angewandte Chemie, 2021, 133, 726-73	313.6	
183	Super-Resolution Spatial Proximity Detection with Proximity-PAINT. <i>Angewandte Chemie - International Edition</i> , 2021 , 60, 716-720	16.4	3
182	Three-dimensional superresolution fluorescence microscopy maps the variable molecular architecture of the nuclear pore complex. <i>Molecular Biology of the Cell</i> , 2021 , 32, 1523-1533	3.5	7
181	Dual spindles assemble in bovine zygotes despite the presence of paternal centrosomes. <i>Journal of Cell Biology</i> , 2021 , 220,	7.3	5
180	Chemogenetic Control of Nanobodies. <i>Nature Methods</i> , 2020 , 17, 279-282	21.6	27
179	MINFLUX nanoscopy delivers 3D multicolor nanometer resolution in cells. <i>Nature Methods</i> , 2020 , 17, 217-224	21.6	204
178	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , 2020 , 587, 377-386	50.4	56
177	Direct Visualization of Single Nuclear Pore Complex Proteins Using Genetically-Encoded Probes for DNA-PAINT. <i>Angewandte Chemie</i> , 2019 , 131, 13138-13142	3.6	13
176	Nuclear pores as versatile reference standards for quantitative superresolution microscopy. <i>Nature Methods</i> , 2019 , 16, 1045-1053	21.6	105
175	Integrating Imaging and Omics: Computational Methods and Challenges. <i>Annual Review of Biomedical Data Science</i> , 2019 , 2, 175-197	5.6	17
174	Mysteries in embryonic development: How can errors arise so frequently at the beginning of mammalian life?. <i>PLoS Biology</i> , 2019 , 17, e3000173	9.7	10
173	Direct Visualization of Single Nuclear Pore Complex Proteins Using Genetically-Encoded Probes for DNA-PAINT. <i>Angewandte Chemie - International Edition</i> , 2019 , 58, 13004-13008	16.4	57
172	Photoactivation of silicon rhodamines via a light-induced protonation. <i>Nature Communications</i> , 2019 , 10, 4580	17.4	19
171	Determining cellular CTCF and cohesin abundances to constrain 3D genome models. <i>ELife</i> , 2019 , 8,	8.9	59
170	Absolute quantification of cohesin, CTCF and their regulators in human cells. <i>ELife</i> , 2019 , 8,	8.9	44
169	Real-time 3D single-molecule localization using experimental point spread functions. <i>Nature Methods</i> , 2018 , 15, 367-369	21.6	133

(2017-2018)

168	A quantitative map of human Condensins provides new insights into mitotic chromosome architecture. <i>Journal of Cell Biology</i> , 2018 , 217, 2309-2328	7.3	89
167	Postmitotic nuclear pore assembly proceeds by radial dilation of small membrane openings. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 21-28	17.6	53
166	Correlative live and super-resolution imaging reveals the dynamic structure of replication domains. <i>Journal of Cell Biology</i> , 2018 , 217, 1973-1984	7.3	45
165	Live imaging of cell division in preimplantation mouse embryos using inverted light-sheet microscopy. <i>Methods in Cell Biology</i> , 2018 , 145, 279-292	1.8	6
164	Quantitative live and super-resolution microscopy of mitotic chromosomes. <i>Methods in Cell Biology</i> , 2018 , 145, 65-90	1.8	5
163	Dual-spindle formation in zygotes keeps parental genomes apart in early mammalian embryos. <i>Science</i> , 2018 , 361, 189-193	33.3	72
162	Modified aptamers enable quantitative sub-10-nm cellular DNA-PAINT imaging. <i>Nature Methods</i> , 2018 , 15, 685-688	21.6	98
161	The replicative helicase MCM recruits cohesin acetyltransferase ESCO2 to mediate centromeric sister chromatid cohesion. <i>EMBO Journal</i> , 2018 , 37,	13	26
160	ChromoTrace: Computational reconstruction of 3D chromosome configurations for super-resolution microscopy. <i>PLoS Computational Biology</i> , 2018 , 14, e1006002	5	1
159	Mechanisms of nuclear pore complex assembly - two different ways of building one molecular machine. <i>FEBS Letters</i> , 2018 , 592, 475-488	3.8	57
158	Gain of CTCF-Anchored Chromatin Loops Marks the Exit from Naive Pluripotency. <i>Cell Systems</i> , 2018 , 7, 482-495.e10	10.6	37
157	Multivariate Control of Transcript to Protein Variability in Single Mammalian Cells. <i>Cell Systems</i> , 2018 , 7, 398-411.e6	10.6	17
156	A call for public archives for biological image data. <i>Nature Methods</i> , 2018 , 15, 849-854	21.6	61
155	Experimental and computational framework for a dynamic protein atlas of human cell division. <i>Nature</i> , 2018 , 561, 411-415	50.4	65
154	Quantitative mapping of fluorescently tagged cellular proteins using FCS-calibrated four-dimensional imaging. <i>Nature Protocols</i> , 2018 , 13, 1445-1464	18.8	41
153	Generation and validation of homozygous fluorescent knock-in cells using CRISPR-Cas9 genome editing. <i>Nature Protocols</i> , 2018 , 13, 1465-1487	18.8	58
152	Real-Time Imaging of a Single Gene Reveals Transcription-Initiated Local Confinement. <i>Biophysical Journal</i> , 2017 , 113, 1383-1394	2.9	98
151	Topologically associating domains and chromatin loops depend on cohesin and are regulated by CTCF, WAPL, and PDS5 proteins. <i>EMBO Journal</i> , 2017 , 36, 3573-3599	13	360

150	The cellular microscopy phenotype ontology. Journal of Biomedical Semantics, 2016, 7, 28	2.2	17
149	Ki-67 acts as a biological surfactant to disperse mitotic chromosomes. <i>Nature</i> , 2016 , 535, 308-12	50.4	269
148	Inverted light-sheet microscope for imaging mouse pre-implantation development. <i>Nature Methods</i> , 2016 , 13, 139-42	21.6	102
147	ARHGEF17 is an essential spindle assembly checkpoint factor that targets Mps1 to kinetochores. Journal of Cell Biology, 2016 , 212, 647-59	7.3	14
146	Nuclear pore assembly proceeds by an inside-out extrusion of the nuclear envelope. <i>ELife</i> , 2016 , 5,	8.9	107
145	Profiling DNA damage response following mitotic perturbations. <i>Nature Communications</i> , 2016 , 7, 1388	371 _{7.4}	33
144	A protocol for the systematic and quantitative measurement of protein-lipid interactions using the liposome-microarray-based assay. <i>Nature Protocols</i> , 2016 , 11, 1021-38	18.8	18
143	Sister chromatid resolution is an intrinsic part of chromosome organization in prophase. <i>Nature Cell Biology</i> , 2016 , 18, 692-9	23.4	59
142	A proposal for validation of antibodies. <i>Nature Methods</i> , 2016 , 13, 823-7	21.6	312
141	FUN-L: gene prioritization for RNAi screens. <i>Bioinformatics</i> , 2015 , 31, 2052-3	7.2	8
141	FUN-L: gene prioritization for RNAi screens. <i>Bioinformatics</i> , 2015 , 31, 2052-3 High-throughput fluorescence correlation spectroscopy enables analysis of proteome dynamics in living cells. <i>Nature Biotechnology</i> , 2015 , 33, 384-9	7.2	8
	High-throughput fluorescence correlation spectroscopy enables analysis of proteome dynamics in	,	112
140	High-throughput fluorescence correlation spectroscopy enables analysis of proteome dynamics in living cells. <i>Nature Biotechnology</i> , 2015 , 33, 384-9 An actin-dependent spindle position checkpoint ensures the asymmetric division in mouse oocytes.	44.5	112
140	High-throughput fluorescence correlation spectroscopy enables analysis of proteome dynamics in living cells. <i>Nature Biotechnology</i> , 2015 , 33, 384-9 An actin-dependent spindle position checkpoint ensures the asymmetric division in mouse oocytes. <i>Nature Communications</i> , 2015 , 6, 7784 Lipid Cooperativity as a General Membrane-Recruitment Principle for PH Domains. <i>Cell Reports</i> ,	44.5	112
140 139 138	High-throughput fluorescence correlation spectroscopy enables analysis of proteome dynamics in living cells. <i>Nature Biotechnology</i> , 2015 , 33, 384-9 An actin-dependent spindle position checkpoint ensures the asymmetric division in mouse oocytes. <i>Nature Communications</i> , 2015 , 6, 7784 Lipid Cooperativity as a General Membrane-Recruitment Principle for PH Domains. <i>Cell Reports</i> , 2015 , 12, 1519-30 A cell-based model system links chromothripsis with hyperploidy. <i>Molecular Systems Biology</i> , 2015 ,	44·5 17·4 10.6	112744
140 139 138	High-throughput fluorescence correlation spectroscopy enables analysis of proteome dynamics in living cells. <i>Nature Biotechnology</i> , 2015 , 33, 384-9 An actin-dependent spindle position checkpoint ensures the asymmetric division in mouse oocytes. <i>Nature Communications</i> , 2015 , 6, 7784 Lipid Cooperativity as a General Membrane-Recruitment Principle for PH Domains. <i>Cell Reports</i> , 2015 , 12, 1519-30 A cell-based model system links chromothripsis with hyperploidy. <i>Molecular Systems Biology</i> , 2015 , 11, 828	44.5 17.4 10.6	11274488
140 139 138 137	High-throughput fluorescence correlation spectroscopy enables analysis of proteome dynamics in living cells. <i>Nature Biotechnology</i> , 2015 , 33, 384-9 An actin-dependent spindle position checkpoint ensures the asymmetric division in mouse oocytes. <i>Nature Communications</i> , 2015 , 6, 7784 Lipid Cooperativity as a General Membrane-Recruitment Principle for PH Domains. <i>Cell Reports</i> , 2015 , 12, 1519-30 A cell-based model system links chromothripsis with hyperploidy. <i>Molecular Systems Biology</i> , 2015 , 11, 828 Multiple requirements of PLK1 during mouse oocyte maturation. <i>PLoS ONE</i> , 2015 , 10, e0116783 Live imaging and modeling of inner nuclear membrane targeting reveals its molecular	44.5 17.4 10.6 12.2	1127448855

(2011-2014)

132	MAP1S controls microtubule stability throughout the cell cycle in human cells. <i>Journal of Cell Science</i> , 2014 , 127, 5007-13	5.3	11
131	Comparative assessment of fluorescent transgene methods for quantitative imaging in human cells. <i>Molecular Biology of the Cell</i> , 2014 , 25, 3610-8	3.5	38
130	Imaging the assembly, structure, and function of the nuclear pore inside cells. <i>Methods in Cell Biology</i> , 2014 , 122, 219-38	1.8	11
129	Integration of biological data by kernels on graph nodes allows prediction of new genes involved in mitotic chromosome condensation. <i>Molecular Biology of the Cell</i> , 2014 , 25, 2522-36	3.5	36
128	Myo19 ensures symmetric partitioning of mitochondria and coupling of mitochondrial segregation to cell division. <i>Current Biology</i> , 2014 , 24, 2598-605	6.3	56
127	SNW1 enables sister chromatid cohesion by mediating the splicing of sororin and APC2 pre-mRNAs. <i>EMBO Journal</i> , 2014 , 33, 2643-58	13	39
126	Crowded chromatin is not sufficient for heterochromatin formation and not required for its maintenance. <i>Journal of Structural Biology</i> , 2013 , 184, 445-53	3.4	26
125	Wapl is an essential regulator of chromatin structure and chromosome segregation. <i>Nature</i> , 2013 , 501, 564-8	50.4	211
124	EGF-induced centrosome separation promotes mitotic progression and cell survival. <i>Developmental Cell</i> , 2013 , 25, 229-40	10.2	54
123	Dynamical modelling of phenotypes in a genome-wide RNAi live-cell imaging assay. <i>BMC Bioinformatics</i> , 2013 , 14, 308	3.6	10
122	Nuclear pore scaffold structure analyzed by super-resolution microscopy and particle averaging. <i>Science</i> , 2013 , 341, 655-8	33.3	307
121	Mitotic lamin disassembly is triggered by lipid-mediated signaling. <i>Journal of Cell Biology</i> , 2012 , 198, 981-90	7.3	50
120	The transition from meiotic to mitotic spindle assembly is gradual during early mammalian development. <i>Journal of Cell Biology</i> , 2012 , 198, 357-70	7.3	152
119	GTSE1 is a microtubule plus-end tracking protein that regulates EB1-dependent cell migration. <i>PLoS ONE</i> , 2012 , 7, e51259	3.7	40
118	Genome-wide RNAi screening identifies human proteins with a regulatory function in the early secretory pathway. <i>Nature Cell Biology</i> , 2012 , 14, 764-74	23.4	141
117	Nucleoporin NUP153 guards genome integrity by promoting nuclear import of 53BP1. <i>Cell Death and Differentiation</i> , 2012 , 19, 798-807	12.7	54
116	A fractal model for nuclear organization: current evidence and biological implications. <i>Nucleic Acids Research</i> , 2012 , 40, 8783-92	20.1	82
115	Complete kinetochore tracking reveals error-prone homologous chromosome biorientation in mammalian oocytes. <i>Cell</i> , 2011 , 146, 568-81	56.2	231

114	Micropilot: automation of fluorescence microscopy-based imaging for systems biology. <i>Nature Methods</i> , 2011 , 8, 246-9	21.6	107
113	Intracellular transport by an anchored homogeneously contracting F-actin meshwork. <i>Current Biology</i> , 2011 , 21, 606-11	6.3	55
112	Automatic quantification of microtubule dynamics enables RNAi-screening of new mitotic spindle regulators. <i>Cytoskeleton</i> , 2011 , 68, 266-78	2.4	33
111	A Nup133-dependent NPC-anchored network tethers centrosomes to the nuclear envelope in prophase. <i>Journal of Cell Biology</i> , 2011 , 192, 855-71	7-3	138
110	Phenotypic profiling of the human genome reveals gene products involved in plasma membrane targeting of SRC kinases. <i>Genome Research</i> , 2011 , 21, 1955-68	9.7	9
109	A system for imaging the regulatory noncoding Xist RNA in living mouse embryonic stem cells. <i>Molecular Biology of the Cell</i> , 2011 , 22, 2634-45	3.5	39
108	The quantitative proteome of a human cell line. <i>Molecular Systems Biology</i> , 2011 , 7, 549	12.2	586
107	The protein phosphatase 1 regulator PNUTS is a new component of the DNA damage response. <i>EMBO Reports</i> , 2010 , 11, 868-75	6.5	52
106	Phenotypic profiling of the human genome by time-lapse microscopy reveals cell division genes. <i>Nature</i> , 2010 , 464, 721-7	50.4	668
105	Visualization of image data from cells to organisms. <i>Nature Methods</i> , 2010 , 7, S26-41	21.6	189
104	CellCognition: time-resolved phenotype annotation in high-throughput live cell imaging. <i>Nature Methods</i> , 2010 , 7, 747-54	21.6	256
103	Live imaging of single nuclear pores reveals unique assembly kinetics and mechanism in interphase. <i>Journal of Cell Biology</i> , 2010 , 191, 15-22	7.3	110
102	High-throughput microscopy using live mammalian cells. Cold Spring Harbor Protocols, 2010, 2010, pdb.t	: o p⊵84	5
101	Automatic identification and clustering of chromosome phenotypes in a genome wide RNAi screen by time-lapse imaging. <i>Journal of Structural Biology</i> , 2010 , 170, 1-9	3.4	42
100	Systematic analysis of human protein complexes identifies chromosome segregation proteins. <i>Science</i> , 2010 , 328, 593-9	33.3	419
99	Nuclear import and assembly of influenza A virus RNA polymerase studied in live cells by fluorescence cross-correlation spectroscopy. <i>Journal of Virology</i> , 2010 , 84, 1254-64	6.6	66
98	Fluorescence perturbation techniques to study mobility and molecular dynamics of proteins in live cells: FRAP, photoactivation, photoconversion, and FLIP. <i>Cold Spring Harbor Protocols</i> , 2010 , 2010, pdb.t	^{1,2} op90	70
97	Automatic analysis of dividing cells in live cell movies to detect mitotic delays and correlate phenotypes in time. <i>Genome Research</i> , 2009 , 19, 2113-24	9.7	49

(2007-2009)

96	Molecular crowding affects diffusion and binding of nuclear proteins in heterochromatin and reveals the fractal organization of chromatin. <i>EMBO Journal</i> , 2009 , 28, 3785-98	13	320
95	RNF168 binds and amplifies ubiquitin conjugates on damaged chromosomes to allow accumulation of repair proteins. <i>Cell</i> , 2009 , 136, 435-46	56.2	683
94	Formation of the nuclear envelope permeability barrier studied by sequential photoswitching and flux analysis. <i>Biophysical Journal</i> , 2009 , 97, 1891-7	2.9	21
93	Chromophore-assisted laser inactivation of alpha- and gamma-tubulin SNAP-tag fusion proteins inside living cells. <i>ACS Chemical Biology</i> , 2009 , 4, 127-38	4.9	36
92	Nuclear pore complex assembly through the cell cycle: regulation and membrane organization. <i>FEBS Letters</i> , 2008 , 582, 2004-16	3.8	105
91	Sun1 forms immobile macromolecular assemblies at the nuclear envelope. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2008 , 1783, 2415-26	4.9	69
90	A new model for asymmetric spindle positioning in mouse oocytes. <i>Current Biology</i> , 2008 , 18, 1986-92	6.3	239
89	EML3 is a nuclear microtubule-binding protein required for the correct alignment of chromosomes in metaphase. <i>Journal of Cell Science</i> , 2008 , 121, 1718-26	5.3	35
88	Systematic kinetic analysis of mitotic dis- and reassembly of the nuclear pore in living cells. <i>Journal of Cell Biology</i> , 2008 , 180, 857-65	7.3	197
87	Work flow for multiplexing siRNA assays by solid-phase reverse transfection in multiwell plates. Journal of Biomolecular Screening, 2008, 13, 575-80		67
87		23.4	146
	Journal of Biomolecular Screening, 2008, 13, 575-80 Maximal chromosome compaction occurs by axial shortening in anaphase and depends on Aurora	23.4	146
86	Maximal chromosome compaction occurs by axial shortening in anaphase and depends on Aurora kinase. <i>Nature Cell Biology</i> , 2007 , 9, 822-31		146
86 85	Maximal chromosome compaction occurs by axial shortening in anaphase and depends on Aurora kinase. <i>Nature Cell Biology</i> , 2007 , 9, 822-31 LambdaN-GFP: an RNA reporter system for live-cell imaging. <i>Nature Methods</i> , 2007 , 4, 633-6 Reverse transfection on cell arrays for high content screening microscopy. <i>Nature Protocols</i> , 2007 ,	21.6	146 178 162
86 85 84	Maximal chromosome compaction occurs by axial shortening in anaphase and depends on Aurora kinase. Nature Cell Biology, 2007, 9, 822-31 LambdaN-GFP: an RNA reporter system for live-cell imaging. Nature Methods, 2007, 4, 633-6 Reverse transfection on cell arrays for high content screening microscopy. Nature Protocols, 2007, 2, 392-9 Structure and nuclear import function of the C-terminal domain of influenza virus polymerase PB2	21.6	146 178 162
86 85 84 83	Maximal chromosome compaction occurs by axial shortening in anaphase and depends on Aurora kinase. Nature Cell Biology, 2007, 9, 822-31 LambdaN-GFP: an RNA reporter system for live-cell imaging. Nature Methods, 2007, 4, 633-6 Reverse transfection on cell arrays for high content screening microscopy. Nature Protocols, 2007, 2, 392-9 Structure and nuclear import function of the C-terminal domain of influenza virus polymerase PB2 subunit. Nature Structural and Molecular Biology, 2007, 14, 229-33	21.6 18.8 17.6	146 178 162 245
86 85 84 83 82	Maximal chromosome compaction occurs by axial shortening in anaphase and depends on Aurora kinase. Nature Cell Biology, 2007, 9, 822-31 LambdaN-GFP: an RNA reporter system for live-cell imaging. Nature Methods, 2007, 4, 633-6 Reverse transfection on cell arrays for high content screening microscopy. Nature Protocols, 2007, 2, 392-9 Structure and nuclear import function of the C-terminal domain of influenza virus polymerase PB2 subunit. Nature Structural and Molecular Biology, 2007, 14, 229-33 Nuclear envelope. Current Biology, 2007, 17, R154-6 Measuring structural dynamics of chromosomes in living cells by fluorescence microscopy. Methods,	21.6 18.8 17.6 6.3	146 178 162 245

78	Compensation of global movement for improved tracking of cells in time-lapse confocal microscopy image sequences 2007 ,		2
77	Condensin I stabilizes chromosomes mechanically through a dynamic interaction in live cells. <i>Current Biology</i> , 2006 , 16, 333-44	6.3	249
76	Nuclear actin: a lack of export allows formation of filaments. Current Biology, 2006, 16, R321-3	6.3	4
75	Live-cell imaging reveals a stable cohesin-chromatin interaction after but not before DNA replication. <i>Current Biology</i> , 2006 , 16, 1571-8	6.3	245
74	Automated analysis of the mitotic phases of human cells in 3D fluorescence microscopy image sequences. <i>Lecture Notes in Computer Science</i> , 2006 , 9, 840-8	0.9	21
73	NuSAP, a mitotic RanGTP target that stabilizes and cross-links microtubules. <i>Molecular Biology of the Cell</i> , 2006 , 17, 2646-60	3.5	93
72	Resolution of chiasmata in oocytes requires separase-mediated proteolysis. <i>Cell</i> , 2006 , 126, 135-46	56.2	186
71	Monitoring the permeability of the nuclear envelope during the cell cycle. <i>Methods</i> , 2006 , 38, 17-24	4.6	35
70	Fluorophores for live cell imaging of AGT fusion proteins across the visible spectrum. <i>BioTechniques</i> , 2006 , 41, 167-70, 172, 174-5	2.5	65
69	Minimizing the risk of reporting false positives in large-scale RNAi screens. <i>Nature Methods</i> , 2006 , 3, 77	7 2 91.6	362
68	High-throughput RNAi screening by time-lapse imaging of live human cells. <i>Nature Methods</i> , 2006 , 3, 385-90	21.6	320
67	High-throughput fluorescence microscopy for systems biology. <i>Nature Reviews Molecular Cell Biology</i> , 2006 , 7, 690-6	48.7	324
66	Dissecting the contribution of diffusion and interactions to the mobility of nuclear proteins. <i>Biophysical Journal</i> , 2006 , 90, 1878-94	2.9	149
65	Automated Analysis of Mitotic Phenotypes in Fluorescence Microscopy Images of Human Cells 2006 , 374-378		1
64	A contractile nuclear actin network drives chromosome congression in oocytes. <i>Nature</i> , 2005 , 436, 812-	· 8 50.4	186
63	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, 1201-14	5.8	37
62	Distinct functions of condensin I and II in mitotic chromosome assembly. <i>Journal of Cell Science</i> , 2004 , 117, 6435-45	5.3	272
61	RanBP2/Nup358 provides a major binding site for NXF1-p15 dimers at the nuclear pore complex and functions in nuclear mRNA export. <i>Molecular and Cellular Biology</i> , 2004 , 24, 1155-67	4.8	79

(2003-2004)

60	Hypophosphorylated SR splicing factors transiently localize around active nucleolar organizing regions in telophase daughter nuclei. <i>Journal of Cell Biology</i> , 2004 , 167, 51-63	7.3	50
59	LAP2alpha and BAF transiently localize to telomeres and specific regions on chromatin during nuclear assembly. <i>Journal of Cell Science</i> , 2004 , 117, 6117-28	5.3	151
58	Calcium rises locally trigger focal adhesion disassembly and enhance residency of focal adhesion kinase at focal adhesions. <i>Journal of Biological Chemistry</i> , 2004 , 279, 28715-23	5.4	108
57	Quantitative kinetic analysis of nucleolar breakdown and reassembly during mitosis in live human cells. <i>Journal of Cell Biology</i> , 2004 , 166, 787-800	7.3	130
56	Automatic identification of subcellular phenotypes on human cell arrays. <i>Genome Research</i> , 2004 , 14, 1130-6	9.7	166
55	The entire Nup107-160 complex, including three new members, is targeted as one entity to kinetochores in mitosis. <i>Molecular Biology of the Cell</i> , 2004 , 15, 3333-44	3.5	218
54	Light microscopy of echinoderm embryos. <i>Methods in Cell Biology</i> , 2004 , 74, 371-409	1.8	37
53	Automatic real-time three-dimensional cell tracking by fluorescence microscopy. <i>Journal of Microscopy</i> , 2004 , 216, 131-7	1.9	123
52	Mapping the dynamic organization of the nuclear pore complex inside single living cells. <i>Nature Cell Biology</i> , 2004 , 6, 1114-21	23.4	364
51	Regulation of sister chromatid cohesion between chromosome arms. Current Biology, 2004, 14, 1187-9.	3 6.3	188
50	Roles of polo-like kinase 1 in the assembly of functional mitotic spindles. Current Biology, 2004, 14, 171	2 <i>6</i> 232	289
49	Dynamics of nuclear pore complex organization through the cell cycle. <i>Current Opinion in Cell Biology</i> , 2004 , 16, 314-21	9	81
48	Nuclear envelope dynamics in oocytes: from germinal vesicle breakdown to mitosis. <i>Current Opinion in Cell Biology</i> , 2003 , 15, 88-95	9	39
47	Dynamics of chromosome positioning during the cell cycle. Current Opinion in Cell Biology, 2003, 15, 66	4-31	24
46	Global chromosome positions are transmitted through mitosis in mammalian cells. <i>Cell</i> , 2003 , 112, 751-	- 65 6.2	237
45	Cyclic, proteasome-mediated turnover of unliganded and liganded ERalpha on responsive promoters is an integral feature of estrogen signaling. <i>Molecular Cell</i> , 2003 , 11, 695-707	17.6	625
44	NuSAP, a novel microtubule-associated protein involved in mitotic spindle organization. <i>Journal of Cell Biology</i> , 2003 , 162, 1017-29	7.3	149
43	Nuclear envelope breakdown in starfish oocytes proceeds by partial NPC disassembly followed by a rapidly spreading fenestration of nuclear membranes. <i>Journal of Cell Biology</i> , 2003 , 160, 1055-68	7.3	126

42	4D imaging to assay complex dynamics in live specimens. <i>Nature Cell Biology</i> , 2003 , Suppl, S14-9	23.4	22
41	Remodelling the walls of the nucleus. <i>Nature Reviews Molecular Cell Biology</i> , 2002 , 3, 487-97	48.7	184
40	Ribonucleoprotein-dependent localization of the yeast class V myosin Myo4p. <i>Journal of Cell Biology</i> , 2002 , 159, 971-82	7.3	61
39	Chromosomal association of Ran during meiotic and mitotic divisions. <i>Journal of Cell Science</i> , 2002 , 115, 4685-93	5.3	19
38	Nuclear envelope breakdown proceeds by microtubule-induced tearing of the lamina. <i>Cell</i> , 2002 , 108, 83-96	56.2	371
37	Histone H3 phosphorylation during Xenopus oocyte maturation: regulation by the MAP kinase/p90Rsk pathway and uncoupling from DNA condensation. <i>FEBS Letters</i> , 2002 , 518, 23-8	3.8	22
36	Dynamics of Nuclear Envelope Proteins During the Cell Cycle in Mammalian Cells 2002 , 15-28		1
35	Four-dimensional imaging and quantitative reconstruction to analyse complex spatiotemporal processes in live cells. <i>Nature Cell Biology</i> , 2001 , 3, 852-5	23.4	89
34	Nucleocytoplasmic transport: diffusion channel or phase transition?. Current Biology, 2001, 11, R551-4	6.3	21
33	An evolutionarily conserved NPC subcomplex, which redistributes in part to kinetochores in mammalian cells. <i>Journal of Cell Biology</i> , 2001 , 154, 1147-60	7-3	276
32	Nuclear pore complexes form immobile networks and have a very low turnover in live mammalian cells. <i>Journal of Cell Biology</i> , 2001 , 154, 71-84	7.3	340
31	A new model for nuclear envelope breakdown. <i>Molecular Biology of the Cell</i> , 2001 , 12, 503-10	3.5	81
30	A bromodomain protein, MCAP, associates with mitotic chromosomes and affects G(2)-to-M transition. <i>Molecular and Cellular Biology</i> , 2000 , 20, 6537-49	4.8	233
29	Dynamics and retention of misfolded proteins in native ER membranes. <i>Nature Cell Biology</i> , 2000 , 2, 28	8 <i>-2</i> 354	232
28	A Bromodomain Protein, MCAP, Associates with Mitotic Chromosomes and Affects G2-to-M Transition. <i>Molecular and Cellular Biology</i> , 2000 , 20, 6537-6549	4.8	3
27	Dual-colour imaging with GFP variants. <i>Trends in Cell Biology</i> , 1999 , 9, 52-6	18.3	148
26	Golgi membranes are absorbed into and reemerge from the ER during mitosis. <i>Cell</i> , 1999 , 99, 589-601	56.2	295
25	Dynamics and mobility of nuclear envelope proteins in interphase and mitotic cells revealed by green fluorescent protein chimeras. <i>Methods</i> , 1999 , 19, 362-72	4.6	53

24	Kinetic analysis of secretory protein traffic and characterization of golgi to plasma membrane transport intermediates in living cells. <i>Journal of Cell Biology</i> , 1998 , 143, 1485-503	7.3	510
23	ZAP-70 association with T cell receptor zeta (TCRzeta): fluorescence imaging of dynamic changes upon cellular stimulation. <i>Journal of Cell Biology</i> , 1998 , 143, 613-24	7.3	52
22	Retrograde transport of Golgi-localized proteins to the ER. Journal of Cell Biology, 1998, 140, 1-15	7.3	213
21	Two-color green fluorescent protein time-lapse imaging. <i>BioTechniques</i> , 1998 , 25, 838-42, 844-6	2.5	58
20	The transmembrane domain of a carboxyl-terminal anchored protein determines localization to the endoplasmic reticulum. <i>Journal of Biological Chemistry</i> , 1997 , 272, 1970-5	5.4	112
19	Nuclear membrane dynamics and reassembly in living cells: targeting of an inner nuclear membrane protein in interphase and mitosis. <i>Journal of Cell Biology</i> , 1997 , 138, 1193-206	7.3	667
18	Molecular basis for the interaction of [Nle4,D-Phe7]melanocyte stimulating hormone with the human melanocortin-1 receptor. <i>Journal of Biological Chemistry</i> , 1997 , 272, 23000-10	5.4	113
17	A quantitative map of human Condensins provides new insights into mitotic chromosome architecture		2
16	Real-time chromatin dynamics at the single gene level during transcription activation		2
15	ChromoTrace: Computational Reconstruction of 3D Chromosome Configurations for Super-Resolution Microscopy		1
14	Fast, robust and precise 3D localization for arbitrary point spread functions		1
13	CTCF, WAPL and PDS5 proteins control the formation of TADs and loops by cohesin		8
12	Generation and validation of homozygous fluorescent knock-in cells using CRISPR/Cas9 genome editing	g	4
11	Quantitative mapping of fluorescently tagged cellular proteins using FCS-calibrated four dimensional imaging		4
10	Non-rodent mammalian zygotes assemble dual spindles despite the presence of paternal centrosomes		3
9	3D super-resolution fluorescence microscopy maps the variable molecular architecture of the Nuclear Pore Complex		1
8	Experimental and computational framework for a dynamic protein atlas of human cell division		3
7	Nuclear pores as versatile reference standards for quantitative superresolution microscopy		4

6	Chemogenetic Control of Nanobodies	3
5	MINFLUX nanoscopy delivers multicolor nanometer 3D-resolution in (living) cells	4
4	Dual spindle formation in zygotes keeps parental genomes apart in early mammalian embryos	1
3	Visualization of loop extrusion by DNA nanoscale tracing in single human cells	4
2	A quantitative map of nuclear pore assembly reveals two distinct mechanisms	2
1	Rapid generation of homozygous fluorescent knock-in human cells using CRISPR/Cas9 genome editing and validation by automated imaging and digital PCR screening	1