Karsten Rippe

List of Publications by Year
in descending order

164 papers	16,142 citations	19657 61 h-index	20358 116 g-index
188 all docs	188 docs citations	188 times ranked	21469 citing authors

#	Article	IF	Citations
1	Capturing Chromosome Conformation. Science, 2002, 295, 1306-1311.	12.6	3,210
2	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	27.8	1,966
3	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	21.4	431
4	Loss of the abundant nuclear non-coding RNAMALAT1is compatible with life and development. RNA Biology, 2012, 9, 1076-1087.	3.1	355
5	SIRT6 Recruits SNF2H to DNA Break Sites, Preventing Genomic Instability through Chromatin Remodeling. Molecular Cell, 2013, 51, 454-468.	9.7	324
6	Formation of Chromatin Subcompartments byÂPhase Separation. Biophysical Journal, 2018, 114, 2262-2270.	0.5	295
7	Action at a distance: DNA-looping and initiation of transcription. Trends in Biochemical Sciences, 1995, 20, 500-506.	7.5	271
8	Histone acetylation increases chromatin accessibility. Journal of Cell Science, 2005, 118, 5825-5834.	2.0	271
9	Genome-wide nucleosome positioning during embryonic stem cell development. Nature Structural and Molecular Biology, 2012, 19, 1185-1192.	8.2	245
10	Single-cell transcriptomes of the human skin reveal age-related loss of fibroblast priming. Communications Biology, 2020, 3, 188.	4.4	239
11	DNMT and HDAC inhibitors induce cryptic transcription start sites encoded in long terminal repeats. Nature Genetics, 2017, 49, 1052-1060.	21.4	235
12	Mouse Heterochromatin Adopts Digital Compaction States without Showing Hallmarks of HP1-Driven Liquid-Liquid Phase Separation. Molecular Cell, 2020, 78, 236-249.e7.	9.7	214
13	The 4D nucleome: Evidence for a dynamic nuclear landscape based on coâ€aligned active and inactive nuclear compartments. FEBS Letters, 2015, 589, 2931-2943.	2.8	211
14	Trichostatin A-induced histone acetylation causes decondensation of interphase chromatin. Journal of Cell Science, 2004, 117, 4277-4287.	2.0	207
15	Integrative genomic and transcriptomic analysis of leiomyosarcoma. Nature Communications, 2018, 9, 144.	12.8	197
16	HP1 Is Involved in Regulating the Global Impact of DNA Methylation on Alternative Splicing. Cell Reports, 2015, 10, 1122-1134.	6.4	179
17	Making contacts on a nucleic acid polymer. Trends in Biochemical Sciences, 2001, 26, 733-740.	7.5	166
18	HMGB2 Loss upon Senescence Entry Disrupts Genomic Organization and Induces CTCF Clustering across Cell Types. Molecular Cell, 2018, 70, 730-744.e6.	9.7	164

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19	Transcriptional activation via DNA-looping: visualization of intermediates in the activation pathway of E. coli RNA polymeraseÂ·Ïƒ54 holoenzyme by scanning force microscopy. Journal of Molecular Biology, 1997, 270, 125-138.	4.2	143
20	Epigenetic Upregulation of lncRNAs at 13q14.3 in Leukemia Is Linked to the In Cis Downregulation of a Gene Cluster That Targets NF-kB. PLoS Genetics, 2013, 9, e1003373.	3.5	134
21	Retrieving the intracellular topology from multi-scale protein mobility mapping in living cells. Nature Communications, 2014, 5, 4494.	12.8	133
22	Nucleosome repositioning links DNA (de)methylation and differential CTCF binding during stem cell development. Genome Research, 2014, 24, 1285-1295.	5.5	130
23	DNA sequence- and conformation-directed positioning of nucleosomes by chromatin-remodeling complexes. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15635-15640.	7.1	122
24	Alu elementâ€containing <scp>RNA</scp>s maintain nucleolar structure and function. EMBO Journal, 2015, 34, 2758-2774.	7.8	118
25	TERRA and the state of the telomere. Nature Structural and Molecular Biology, 2015, 22, 853-858.	8.2	114
26	Structure of a bacterial pyridoxal 5'-phosphate synthase complex. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 19284-19289.	7.1	110
27	Nucleosome Geometry and Internucleosomal Interactions Control the Chromatin Fiber Conformation. Biophysical Journal, 2008, 95, 3692-3705.	0.5	110
28	Nuclear body movement is determined by chromatin accessibility and dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13221-13226.	7.1	107
29	Three-dimensional organization of promyelocytic leukemia nuclear bodies. Journal of Cell Science, 2010, 123, 392-400.	2.0	106
30	Suv4-20h2 mediates chromatin compaction and is important for cohesin recruitment to heterochromatin. Genes and Development, 2013, 27, 859-872.	5.9	105
31	NUDT9, a Member of the Nudix Hydrolase Family, Is an Evolutionarily Conserved Mitochondrial ADP-ribose Pyrophosphatase. Journal of Biological Chemistry, 2003, 278, 1794-1801.	3.4	102
32	Environmentâ€induced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children. Molecular Systems Biology, 2016, 12, 861.	7.2	97
33	A 'loop recapture' mechanism for ACF-dependent nucleosome remodeling. Nature Structural and Molecular Biology, 2005, 12, 683-690.	8.2	94
34	Dynamics of Telomeres and Promyelocytic Leukemia Nuclear Bodies in a Telomerase-negative Human Cell Line. Molecular Biology of the Cell, 2009, 20, 2070-2082.	2.1	93
35	Dissecting intratumour heterogeneity of nodal B-cell lymphomas at the transcriptional, genetic and drug-response levels. Nature Cell Biology, 2020, 22, 896-906.	10.3	93
36	Structural insights into tail-anchored protein binding and membrane insertion by Get3. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21131-21136.	7.1	92

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37	Dissecting DNA-Histone Interactions in the Nucleosome by Molecular Dynamics Simulations of DNA Unwrapping. Biophysical Journal, 2011, 101, 1999-2008.	0.5	89
38	Transcription activation is enhanced by multivalent interactions independent of phase separation. Molecular Cell, 2022, 82, 1878-1893.e10.	9.7	88
39	Genomic footprints of activated telomere maintenance mechanisms in cancer. Nature Communications, 2020, 11, 733.	12.8	87
40	Analysis of Ligand Binding by Two-Colour Fluorescence Cross-Correlation Spectroscopy. Single Molecules, 2002, 3, 49-61.	0.9	85
41	Predicting nucleosome positions on the DNA: combining intrinsic sequence preferences and remodeler activities. Nucleic Acids Research, 2009, 37, 5641-5655.	14.5	85
42	Human ISWI chromatin-remodeling complexes sample nucleosomes via transient binding reactions and become immobilized at active sites. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 19873-19878.	7.1	85
43	On the Mechanism of Nucleosome Assembly by Histone Chaperone NAP1*. Journal of Biological Chemistry, 2006, 281, 16462-16472.	3.4	83
44	Dual color localization microscopy of cellular nanostructures. Biotechnology Journal, 2009, 4, 927-938.	3.5	83
45	PML body meets telomere. Nucleus, 2012, 3, 263-275.	2.2	80
46	Specificity, propagation, and memory of pericentric heterochromatin. Molecular Systems Biology, 2014, 10, 746.	7.2	80
47	Liquidâ€“Liquid Phase Separation in Chromatin. Cold Spring Harbor Perspectives in Biology, 2022, 14, a040683.	5.5	80
48	Genome organization: Balancing stability and plasticity. Biochimica Et Biophysica Acta - Molecular Cell Research, 2008, 1783, 2061-2079.	4.1	79
49	Chromatin remodelling in mammalian cells by ISWIâ€type complexes â€“ where, when and why?. FEBS Journal, 2011, 278, 3608-3618.	4.7	78
50	PML induces compaction, TRF2 depletion and DNA damage signaling at telomeres and promotes their alternative lengthening. Journal of Cell Science, 2015, 128, 1887-1900.	2.0	78
51	Structure and Function of the Hetero-oligomeric Cysteine Synthase Complex in Plants*. Journal of Biological Chemistry, 2010, 285, 32810-32817.	3.4	76
52	DNA (de)methylation in embryonic stem cells controls CTCF-dependent chromatin boundaries. Genome Research, 2019, 29, 750-761.	5.5	76
53	The Effect of Internucleosomal Interaction on Folding of the Chromatin Fiber. Biophysical Journal, 2008, 95, 3677-3691.	0.5	75
54	Multiscale Analysis of Dynamics and Interactions of Heterochromatin Protein 1 by Fluorescence Fluctuation Microscopy. Biophysical Journal, 2009, 97, 2876-2885.	0.5	74

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55	Histone H2A C-Terminus Regulates Chromatin Dynamics, Remodeling, and Histone H1 Binding. PLoS Genetics, 2010, 6, e1001234.	3.5	73
56	De novo assembly of a PML nuclear subcompartment occurs through multiple pathways and induces telomere elongation. Journal of Cell Science, 2011, 124, 3603-3618.	2.0	72
57	Superhelix dimensions of a 1868 base pair plasmid determined by scanning force microscopy in air and in aqueous solution. Nucleic Acids Research, 1997, 25, 1736-1744.	14.5	70
58	CHD3 and CHD4 form distinct NuRD complexes with different yet overlapping functionality. Nucleic Acids Research, 2017, 45, 10534-10554.	14.5	70
59	Simultaneous Binding of Two DNA Duplexes to the NtrCâ^'Enhancer Complex Studied by Two-Color Fluorescence Cross-Correlation Spectroscopyâ€. Biochemistry, 2000, 39, 2131-2139.	2.5	69
60	High-precision structural analysis of subnuclear complexes in fixed and live cells via spatially modulated illumination (SMI) microscopy. Chromosome Research, 2008, 16, 367-382.	2.2	67
61	Nuclear architecture by RNA. Current Opinion in Genetics and Development, 2012, 22, 179-187.	3.3	67
62	Hypermutation of the Inactive X Chromosome Is a Frequent Event in Cancer. Cell, 2013, 155, 567-581.	28.9	67
63	Looping Dynamics of Linear DNA Molecules and the Effect of DNA Curvature: A Study by Brownian Dynamics Simulation. Biophysical Journal, 1998, 74, 773-779.	0.5	66
64	Dynamic organization of the cell nucleus. Current Opinion in Genetics and Development, 2007, 17, 373-380.	3.3	66
65	Structure and Drug interaction of parellel-stranded DNA studies by infrared spectroscope and fluorence. Nucleic Acids Research, 1993, 21, 5085-5091.	14.5	63
66	NAP1 Modulates Binding of Linker Histone H1 to Chromatin and Induces an Extended Chromatin Fiber Conformation. Journal of Biological Chemistry, 2005, 280, 34063-34072.	3.4	61
67	Mobility of multi-subunit complexes in the nucleus: accessibility and dynamics of chromatin subcompartments. Histochemistry and Cell Biology, 2005, 123, 217-228.	1.7	59
68	[11] Parallel-stranded duplex DNA. Methods in Enzymology, 1992, 211, 199-220.	1.0	58
69	Helix-coil transition of parallel-stranded DNA. Thermodynamics of hairpin and linear duplex oligonucleotides. Biochemistry, 1989, 28, 9528-9535.	2.5	57
70	Parallel-stranded duplex DNA containing blocks of trans purine-purine and purine-pyrimidine base pairs. Nucleic Acids Research, 1994, 22, 3293-3303.	14.5	57
71	TelomereHunter â€“ in silico estimation of telomere content and composition from cancer genomes. BMC Bioinformatics, 2019, 20, 272.	2.6	56
72	Association states of the transcription activator protein NtrC from E. coli determined by analytical ultracentrifugation 1 1Edited by K. Yamamoto. Journal of Molecular Biology, 1998, 278, 915-933.	4.2	55

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73	Heterochromatin Protein 1Î² (HP1Î²) has distinct functions and distinct nuclear distribution in pluripotent versus differentiated cells. Genome Biology, 2015, 16, 213.	8.8	55
74	Cancer Cells with Alternative Lengthening of Telomeres Do Not Display a General Hypersensitivity to ATR Inhibition. Frontiers in Oncology, 2016, 6, 186.	2.8	54
75	Repetitive RNAs as Regulators of Chromatin-Associated Subcompartment Formation by Phase Separation. Journal of Molecular Biology, 2020, 432, 4270-4286.	4.2	53
76	Subclone-specific microenvironmental impact and drug response in refractory multiple myeloma revealed by singleâ€cell transcriptomics. Nature Communications, 2021, 12, 6960.	12.8	53
77	The GTPase Cycle of the Chloroplast Import ReceptorsÂToc33/Toc34: Implications from MonomericÂand Dimeric Structures. Structure, 2008, 16, 585-596.	3.3	52
78	DNA binding and oligomerization of NtrC studied by fluorescence anisotropy and fluorescence correlation spectroscopy. Nucleic Acids Research, 1998, 26, 1373-1381.	14.5	48
79	Spectroscopic properties and helical stabilities of 25-nt parallel-stranded linear DNA duplexes. Biochemistry, 1989, 28, 9536-9541.	2.5	46
80	Alternative lengthening of telomeres in childhood neuroblastoma from genome to proteome. Nature Communications, 2021, 12, 1269.	12.8	46
81	GRUU-Net: Integrated convolutional and gated recurrent neural network for cell segmentation. Medical Image Analysis, 2019, 56, 68-79.	11.6	45
82	Association States of Nucleosome Assembly Protein 1 and Its Complexes with Histones. Journal of Biological Chemistry, 2005, 280, 15690-15699.	3.4	44
83	Coding RNAs with a non-coding function: Maintenance of open chromatin structure. Nucleus, 2011, 2, 410-424.	2.2	44
84	Increased vitamin D levels at birth and in early infancy increase offspring allergy riskâ€"evidence for involvement of epigenetic mechanisms. Journal of Allergy and Clinical Immunology, 2016, 137, 610-613.	2.9	43
85	A Parallel Stranded Linear DNA Duplex Incorporating dG Â· dC Base Pairs. Journal of Biomolecular Structure and Dynamics, 1990, 7, 1199-1209.	3.5	42
86	Telomere dysfunction and chromothripsis. International Journal of Cancer, 2016, 138, 2905-2914.	5.1	42
87	Scanning force microscopy of Escherichia coli RNA polymeraseÂ·Ïƒ 54 holoenzyme complexes with DNA in buffer and in air 1 1Edited by W. Baumeister. Journal of Molecular Biology, 1998, 283, 821-836.	4.2	41
88	Exploring the Conformational Space of Chromatin Fibers and Their Stability by Numerical Dynamic Phase Diagrams. Biophysical Journal, 2010, 98, 1028-1037.	0.5	41
89	Dynamic properties of independent chromatin domains measured by correlation spectroscopy in living cells. Epigenetics and Chromatin, 2016, 9, 57.	3.9	41
90	Calorimetric characterization of parallel-stranded DNA: stability, conformational flexibility, and ion binding. Journal of the American Chemical Society, 1992, 114, 5926-5928.	13.7	40

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91	Statisticalâ€“mechanical lattice models for proteinâ€“DNA binding in chromatin. Journal of Physics Condensed Matter, 2010, 22, 414105.	1.8	40
92	Dissecting chromatin interactions in living cells from protein mobility maps. Chromosome Research, 2011, 19, 99-115.	2.2	39
93	Changing Chromatin Fiber Conformation by Nucleosome Repositioning. Biophysical Journal, 2014, 107, 2141-2150.	0.5	39
94	NucTools: analysis of chromatin feature occupancy profiles from high-throughput sequencing data. BMC Genomics, 2017, 18, 158.	2.8	39
95	Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. Molecular Systems Biology, 2019, 15, e8339.	7.2	39
96	Assembly and mobility of exon-exon junction complexes in living cells. Rna, 2009, 15, 862-876.	3.5	38
97	Biochemical Characterization and Mass Spectrometric Disulfide Bond Mapping of Periplasmic Î±-Amylase MalS of Escherichia coli. Journal of Biological Chemistry, 1997, 272, 22125-22133.	3.4	37
98	Specificity mechanisms in the control of transcription. Biophysical Chemistry, 1996, 59, 231-246.	2.8	36
99	TelNet - a database for human and yeast genes involved in telomere maintenance. BMC Genetics, 2018, 19, 32.	2.7	36
100	A Lattice Model for Transcription Factor Access to Nucleosomal DNA. Biophysical Journal, 2010, 99, 2597-2607.	0.5	35
101	Force spectroscopy of chromatin fibers: Extracting energetics and structural information from Monte Carlo simulations. Biopolymers, 2011, 95, 435-447.	2.4	35
102	Binding kinetics of human ISWI chromatin-remodelers to DNA repair sites elucidate their target location mechanism. Nucleus, 2011, 2, 105-112.	2.2	35
103	Modeling nucleosome position distributions from experimental nucleosome positioning maps. Bioinformatics, 2013, 29, 2380-2386.	4.1	35
104	The viscoelastic properties of chromatin and the nucleoplasm revealed by scale-dependent protein mobility. Journal of Physics Condensed Matter, 2015, 27, 064115.	1.8	34
105	Targeting chromatin remodelers: Signals and search mechanisms. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2011, 1809, 497-508.	1.9	33
106	Conformation of Reconstituted Mononucleosomes and Effect of Linker Histone H1 Binding Studied by Scanning Force Microscopy. Biophysical Journal, 2003, 85, 4012-4022.	0.5	32
107	Aurora Kinase B Regulates Telomerase Activity via a Centromeric RNA in Stem Cells. Cell Reports, 2015, 11, 1667-1678.	6.4	31
108	Substrate properties of 25-nt parallel-stranded linear DNA duplexes. Biochemistry, 1989, 28, 9542-9549.	2.5	28

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109	Reactivity of parallel-stranded DNA to chemical modification reagents. Biochemistry, 1990, 29, 9831-9839.	2.5	28
110	Dissecting the nascent human transcriptome by analysing the RNA content of transcription factories. Nucleic Acids Research, 2015, 43, e95-e95.	14.5	28
111	Regulation of nucleolus assembly by non-coding RNA polymerase II transcripts. Nucleus, 2016, 7, 308-318.	2.2	28
112	Xâ€ray crystal structure of Saccharomyces cerevisiae Pdx1 provides insights into the oligomeric nature of PLP synthases. FEBS Letters, 2009, 583, 2179-2186.	2.8	27
113	Glioblastoma initiating cells are sensitive to histone demethylase inhibition due to epigenetic deregulation. International Journal of Cancer, 2020, 146, 1281-1292.	5.1	27
114	Is transcriptional regulation just going through a phase?. Molecular Cell, 2021, 81, 1579-1585.	9.7	27
115	On the Significance of Toc-GTPase Homodimers. Journal of Biological Chemistry, 2008, 283, 23104-23112.	3.4	26
116	Dimerization of signalling modules of the EvgAS and BvgAS phosphorelay systems. BBA - Proteins and Proteomics, 2000, 1478, 341-354.	2.1	25
117	The Effect of the DNA Conformation on the Rate of NtrC activated Transcription of Escherichia coli RNA PolymeraseÂ·Ïƒ54 Holoenzyme. Journal of Molecular Biology, 2000, 300, 709-725.	4.2	25
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127	Functional organization of RNA polymerase II in nuclear subcompartments. Current Opinion in Cell Biology, 2022, 74, 88-96.	5.4	20
128	Real-time observation of light-controlled transcription in living cells. Journal of Cell Science, 2017, 130, 4213-4224.	2.0	19
129	Expression of CCCTCâ€binding factor (CTCF) is linked to poor prognosis in prostate cancer. Molecular Oncology, 2020, 14, 129-138.	4.6	19
130	Retrieving Chromatin Patterns from Deep Sequencing Data Using Correlation Functions. Biophysical Journal, 2017, 112, 473-490.	0.5	18
131	DNA sequence-dependent formation of heterochromatin nanodomains. Nature Communications, 2022, 13, 1861.	12.8	18
132	A spherical harmonics intensity model for 3D segmentation and 3D shape analysis of heterochromatin foci. Medical Image Analysis, 2016, 32, 18-31.	11.6	17
133	Pheno-seq â€“ linking visual features and gene expression in 3D cell culture systems. Scientific Reports, 2019, 9, 12367.	3.3	16
134	Binding affinity of Escherichia coli RNA polymerasemiddle dotsigma54 holoenzyme for the glnAp2, nifH and nifL promoters. Nucleic Acids Research, 2002, 30, 4094-4101.	14.5	15
135	Quantification of telomere features in tumor tissue sections by an automated 3D imaging-based workflow. Methods, 2017, 114, 60-73.	3.8	15
136	Methylome-based cell-of-origin modeling (Methyl-COOM) identifies aberrant expression of immune regulatory molecules in CLL. Genome Medicine, 2020, 12, 29.	8.2	15
137	RNA polymerase II transcription compartments: from multivalent chromatin binding to liquid droplet formation?. Nature Reviews Molecular Cell Biology, 2021, 22, 645-646.	37.0	15
138	A threeâ€dimensional colocalization RNA interference screening platform to elucidate the alternative lengthening of telomeres pathway. Biotechnology Journal, 2012, 7, 103-116.	3.5	14
139	Quantifying transient binding of ISWI chromatin remodelers in living cells by pixel-wise photobleaching profile evolution analysis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E3221-30.	7.1	13
140	Interactions of Histones with DNA: Nucleosome Assembly, Stability, Dynamics, and Higher Order Structure. , 0, , 135-172.		12
141	Loss of cooperativity of secreted CD40L and increased dose-response to IL4 on CLL cell viability correlates with enhanced activation of NF-ĸB and STAT6. International Journal of Cancer, 2015, 136, 65-73.	5.1	11
142	Control of APOBEC3B induction and cccDNA decay by NF-Î²B and miR-138-5p. JHEP Reports, 2021, 3, 100354.	4.9	11
143	KMT9 Controls Stemness and Growth of Colorectal Cancer. Cancer Research, 2022, 82, 210-220.	0.9	11
144	Rational design and molecular characterization of a chimaeric response regulator protein. Journal of Molecular Biology, 2001, 310, 283-290.	4.2	10

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145	Tethering RNA to chromatin for fluorescence microscopy based analysis of nuclear organization. Methods, 2017, 123, 89-101.	3.8	8
146	Defining the structural requirements for ribose 5â€phosphateâ€binding and intersubunit crossâ€talk of the malarial pyridoxal 5â€phosphate synthase. FEBS Letters, 2010, 584, 4169-4174.	2.8	7
147	PITX1 Is a Regulator of TERT Expression in Prostate Cancer with Prognostic Power. Cancers, 2022, 14, 1267.	3.7	7
148	Evolutionary dynamics and information hierarchies in biological systems. Annals of the New York Academy of Sciences, 2013, 1305, 1-17.	3.8	6
149	Hyperparameter optimization for image analysis: application to prostate tissue images and live cell data of virus-infected cells. International Journal of Computer Assisted Radiology and Surgery, 2019, 14, 1847-1857.	2.8	6
150	Analysis of Ligand Binding by Two-Colour Fluorescence Cross-Correlation Spectroscopy. Single Molecules, 2002, 3, 49-61.	0.9	5
151	Modelling TERT regulation across 19 different cancer types based on the MIPRIP 2.0 gene regulatory network approach. BMC Bioinformatics, 2019, 20, 737.	2.6	4
152	Loss of CCAATâ€enhancerâ€binding protein alpha (CEBPA) is linked to poor prognosis in PTEN deleted and TMPRSS2:ERG fusion type prostate cancers. Prostate, 2019, 79, 302-311.	2.3	4
153	ALT-FISH quantifies alternative lengthening of telomeres activity by imaging of single-stranded repeats. Nucleic Acids Research, 2022, 50, e61-e61.	14.5	4
154	Monte Carlo Simulations of Nucleosome Chains to Identify Factors that Control DNA Compaction and Access. RSC Biomolecular Sciences, 2012, , 198-235.	0.4	3
155	Multi-channel Deep Transfer Learning for Nuclei Segmentation in Glioblastoma Cell Tissue Images. Informatik Aktuell, 2018, , 316-321.	0.6	3
156	Light-Induced Transcription Activation for Time-Lapse Microscopy Experiments in Living Cells. Methods in Molecular Biology, 2019, 2038, 251-270.	0.9	3
157	Identification of enhancer of mRNA decapping 4 as a novel fusion partner of MLL in acute myeloid leukemia. Blood Advances, 2019, 3, 761-765.	5.2	3
158	Black-Box Hyperparameter Optimization for Nuclei Segmentation in Prostate Tissue Images. Informatik Aktuell, 2019, , 345-350.	0.6	3
159	Transcriptional Activation of Heterochromatin by Recruitment of dCas9 Activators. Methods in Molecular Biology, 2021, 2351, 307-320.	0.9	2
160	3D shape analysis of heterochromatin foci based on a 3D spherical harmonics intensity model. Proceedings of SPIE, 2014, , .	0.8	1
161	Segmentation of Heterochromatin Foci Using a 3D Spherical Harmonics Intensity Model. Informatik Aktuell, 2013, , 308-313.	0.6	1
162	Tracing Reversible Light-Induced Binding with Near-infrared Fluorescent Proteins. Methods in Molecular Biology, 2020, 2173, 171-188.	0.9	1

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163	Modeling Effects of Nucleosome Positioning in Short and Long Chromatin Fibers. Biophysical Journal, 2014, 106, 76a.	0.5	0
164	Multiscale Fluorescence Imaging. , 2022, , 38-48.		0