

Karsten Rippe

List of Publications by Year in descending order

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Version: 2024-02-01

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	Liquidâ€“Liquid Phase Separation in Chromatin. Cold Spring Harbor Perspectives in Biology, 2022, 14, a040683.	5.5	80
2	KMT9 Controls Stemness and Growth of Colorectal Cancer. Cancer Research, 2022, 82, 210-220.	0.9	11
3	ALT-FISH quantifies alternative lengthening of telomeres activity by imaging of single-stranded repeats. Nucleic Acids Research, 2022, 50, e61-e61.	14.5	4
4	Functional organization of RNA polymerase II in nuclear subcompartments. Current Opinion in Cell Biology, 2022, 74, 88-96.	5.4	20
5	PITX1 Is a Regulator of TERT Expression in Prostate Cancer with Prognostic Power. Cancers, 2022, 14, 1267.	3.7	7
6	DNA sequence-dependent formation of heterochromatin nanodomains. Nature Communications, 2022, 13, 1861.	12.8	18
7	Transcription activation is enhanced by multivalent interactions independent of phase separation. Molecular Cell, 2022, 82, 1878-1893.e10.	9.7	88
8	Multiscale Fluorescence Imaging. , 2022, , 38-48.		0
9	Alternative lengthening of telomeres in childhood neuroblastoma from genome to proteome. Nature Communications, 2021, 12, 1269.	12.8	46
10	Is transcriptional regulation just going through a phase?. Molecular Cell, 2021, 81, 1579-1585.	9.7	27
11	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
12	Control of APOBEC3B induction and cccDNA decay by NF-Î³B and miR-138-5p. JHEP Reports, 2021, 3, 100354.	4.9	11
13	Transcriptional Activation of Heterochromatin by Recruitment of dCas9 Activators. Methods in Molecular Biology, 2021, 2351, 307-320.	0.9	2
14	Subclone-specific microenvironmental impact and drug response in refractory multiple myeloma revealed by singleâ€“cell transcriptomics. Nature Communications, 2021, 12, 6960.	12.8	53
15	Glioblastoma initiating cells are sensitive to histone demethylase inhibition due to epigenetic deregulation. International Journal of Cancer, 2020, 146, 1281-1292.	5.1	27
16	Expression of CCCTCâ€“binding factor (CTCF) is linked to poor prognosis in prostate cancer. Molecular Oncology, 2020, 14, 129-138.	4.6	19
17	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
18	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

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19	Mouse Heterochromatin Adopts Digital Compaction States without Showing Hallmarks of HP1-Driven Liquid-Liquid Phase Separation. <i>Molecular Cell</i> , 2020, 78, 236-249.e7.	9.7	214
20	Genomic footprints of activated telomere maintenance mechanisms in cancer. <i>Nature Communications</i> , 2020, 11, 733.	12.8	87
21	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	27.8	1,966
22	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , 2020, 52, 331-341.	21.4	431
23	Repetitive RNAs as Regulators of Chromatin-Associated Subcompartment Formation by Phase Separation. <i>Journal of Molecular Biology</i> , 2020, 432, 4270-4286.	4.2	53
24	Single-cell transcriptomes of the human skin reveal age-related loss of fibroblast priming. <i>Communications Biology</i> , 2020, 3, 188.	4.4	239
25	Tracing Reversible Light-Induced Binding with Near-infrared Fluorescent Proteins. <i>Methods in Molecular Biology</i> , 2020, 2173, 171-188.	0.9	1
26	Light-Induced Transcription Activation for Time-Lapse Microscopy Experiments in Living Cells. <i>Methods in Molecular Biology</i> , 2019, 2038, 251-270.	0.9	3
27	Pheno-seq $\hat{=}$ linking visual features and gene expression in 3D cell culture systems. <i>Scientific Reports</i> , 2019, 9, 12367.	3.3	16
28	Hyperparameter optimization for image analysis: application to prostate tissue images and live cell data of virus-infected cells. <i>International Journal of Computer Assisted Radiology and Surgery</i> , 2019, 14, 1847-1857.	2.8	6
29	TelomereHunter $\hat{=}$ in silico estimation of telomere content and composition from cancer genomes. <i>BMC Bioinformatics</i> , 2019, 20, 272.	2.6	56
30	GRUU-Net: Integrated convolutional and gated recurrent neural network for cell segmentation. <i>Medical Image Analysis</i> , 2019, 56, 68-79.	11.6	45
31	Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. <i>Molecular Systems Biology</i> , 2019, 15, e8339.	7.2	39
32	Identification of enhancer of mRNA decapping 4 as a novel fusion partner of MLL in acute myeloid leukemia. <i>Blood Advances</i> , 2019, 3, 761-765.	5.2	3
33	Black-Box Hyperparameter Optimization for Nuclei Segmentation in Prostate Tissue Images. <i>Informatik Aktuell</i> , 2019, , 345-350.	0.6	3
34	DNA (de)methylation in embryonic stem cells controls CTCF-dependent chromatin boundaries. <i>Genome Research</i> , 2019, 29, 750-761.	5.5	76
35	Modelling TERT regulation across 19 different cancer types based on the MIPRIIP 2.0 gene regulatory network approach. <i>BMC Bioinformatics</i> , 2019, 20, 737.	2.6	4
36	Loss of CCAAT $\hat{=}$ enhancer $\hat{=}$ binding protein alpha (CEBPA) is linked to poor prognosis in PTEN deleted and TMPRSS2:ERG fusion type prostate cancers. <i>Prostate</i> , 2019, 79, 302-311.	2.3	4

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37	Multi-channel Deep Transfer Learning for Nuclei Segmentation in Glioblastoma Cell Tissue Images. Informatik Aktuell, 2018, , 316-321.	0.6	3
38	Formation of Chromatin Subcompartments by APhase Separation. Biophysical Journal, 2018, 114, 2262-2270.	0.5	295
39	Integrative genomic and transcriptomic analysis of leiomyosarcoma. Nature Communications, 2018, 9, 144.	12.8	197
40	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
41	TelNet - a database for human and yeast genes involved in telomere maintenance. BMC Genetics, 2018, 19, 32.	2.7	36
42	Retrieving Chromatin Patterns from Deep Sequencing Data Using Correlation Functions. Biophysical Journal, 2017, 112, 473-490.	0.5	18
43	Tethering RNA to chromatin for fluorescence microscopy based analysis of nuclear organization. Methods, 2017, 123, 89-101.	3.8	8
44	Nucleosome repositioning during differentiation of a human myeloid leukemia cell line. Nucleus, 2017, 8, 188-204.	2.2	21
45	NucTools: analysis of chromatin feature occupancy profiles from high-throughput sequencing data. BMC Genomics, 2017, 18, 158.	2.8	39
46	DNMT and HDAC inhibitors induce cryptic transcription start sites encoded in long terminal repeats. Nature Genetics, 2017, 49, 1052-1060.	21.4	235
47	Real-time observation of light-controlled transcription in living cells. Journal of Cell Science, 2017, 130, 4213-4224.	2.0	19
48	Quantification of telomere features in tumor tissue sections by an automated 3D imaging-based workflow. Methods, 2017, 114, 60-73.	3.8	15
49	CHD3 and CHD4 form distinct NuRD complexes with different yet overlapping functionality. Nucleic Acids Research, 2017, 45, 10534-10554.	14.5	70
50	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
51	Telomere dysfunction and chromothripsis. International Journal of Cancer, 2016, 138, 2905-2914.	5.1	42
52	Environmentâ€induced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children. Molecular Systems Biology, 2016, 12, 861.	7.2	97
53	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
54	Regulation of nucleolus assembly by non-coding RNA polymerase II transcripts. Nucleus, 2016, 7, 308-318.	2.2	28

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55	Dynamic properties of independent chromatin domains measured by correlation spectroscopy in living cells. <i>Epigenetics and Chromatin</i> , 2016, 9, 57.	3.9	41
56	Increased vitamin D levels at birth and in early infancy increase offspring allergy risk—evidence for involvement of epigenetic mechanisms. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 137, 610-613.	2.9	43
57	Isolation of the protein and RNA content of active sites of transcription from mammalian cells. <i>Nature Protocols</i> , 2016, 11, 553-565.	12.0	20
58	<i>Alu</i> element-containing RNAs maintain nucleolar structure and function. <i>EMBO Journal</i> , 2015, 34, 2758-2774.	7.8	118
59	The 4D nucleome: Evidence for a dynamic nuclear landscape based on co-aligned active and inactive nuclear compartments. <i>FEBS Letters</i> , 2015, 589, 2931-2943.	2.8	211
60	Dissecting the nascent human transcriptome by analysing the RNA content of transcription factories. <i>Nucleic Acids Research</i> , 2015, 43, e95-e95.	14.5	28
61	Heterochromatin Protein 1 ² (HP1 ²) has distinct functions and distinct nuclear distribution in pluripotent versus differentiated cells. <i>Genome Biology</i> , 2015, 16, 213.	8.8	55
62	Affinity, stoichiometry and cooperativity of heterochromatin protein 1 (HP1) binding to nucleosomal arrays. <i>Journal of Physics Condensed Matter</i> , 2015, 27, 064110.	1.8	21
63	The viscoelastic properties of chromatin and the nucleoplasm revealed by scale-dependent protein mobility. <i>Journal of Physics Condensed Matter</i> , 2015, 27, 064115.	1.8	34
64	Aurora Kinase B Regulates Telomerase Activity via a Centromeric RNA in Stem Cells. <i>Cell Reports</i> , 2015, 11, 1667-1678.	6.4	31
65	PML induces compaction, TRF2 depletion and DNA damage signaling at telomeres and promotes their alternative lengthening. <i>Journal of Cell Science</i> , 2015, 128, 1887-1900.	2.0	78
66	HP1 Is Involved in Regulating the Global Impact of DNA Methylation on Alternative Splicing. <i>Cell Reports</i> , 2015, 10, 1122-1134.	6.4	179
67	TERRA and the state of the telomere. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 853-858.	8.2	114
68	Loss of cooperativity of secreted CD40L and increased dose-response to IL4 on CLL cell viability correlates with enhanced activation of NF- κ B and STAT6. <i>International Journal of Cancer</i> , 2015, 136, 65-73.	5.1	11
69	3D shape analysis of heterochromatin foci based on a 3D spherical harmonics intensity model. <i>Proceedings of SPIE</i> , 2014, , .	0.8	1
70	Specificity, propagation, and memory of pericentric heterochromatin. <i>Molecular Systems Biology</i> , 2014, 10, 746.	7.2	80
71	Nucleosome repositioning links DNA (de)methylation and differential CTCF binding during stem cell development. <i>Genome Research</i> , 2014, 24, 1285-1295.	5.5	130
72	Changing Chromatin Fiber Conformation by Nucleosome Repositioning. <i>Biophysical Journal</i> , 2014, 107, 2141-2150.	0.5	39

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73	Retrieving the intracellular topology from multi-scale protein mobility mapping in living cells. Nature Communications, 2014, 5, 4494.	12.8	133
74	Modeling Effects of Nucleosome Positioning in Short and Long Chromatin Fibers. Biophysical Journal, 2014, 106, 76a.	0.5	0
75	SIRT6 Recruits SNF2H to DNA Break Sites, Preventing Genomic Instability through Chromatin Remodeling. Molecular Cell, 2013, 51, 454-468.	9.7	324
76	Hypermethylation of the Inactive X Chromosome Is a Frequent Event in Cancer. Cell, 2013, 155, 567-581.	28.9	67
77	Epigenetic Upregulation of lncRNAs at 13q14.3 in Leukemia Is Linked to the In Cis Downregulation of a Gene Cluster That Targets NF- κ B. PLoS Genetics, 2013, 9, e1003373.	3.5	134
78	Evolutionary dynamics and information hierarchies in biological systems. Annals of the New York Academy of Sciences, 2013, 1305, 1-17.	3.8	6
79	Taking into account nucleosomes for predicting gene expression. Methods, 2013, 62, 26-38.	3.8	23
80	Modeling nucleosome position distributions from experimental nucleosome positioning maps. Bioinformatics, 2013, 29, 2380-2386.	4.1	35
81	Suv4-20h2 mediates chromatin compaction and is important for cohesin recruitment to heterochromatin. Genes and Development, 2013, 27, 859-872.	5.9	105
82	Establishing epigenetic domains via chromatin-bound histone modifiers. Annals of the New York Academy of Sciences, 2013, 1305, 29-43.	3.8	24
83	Segmentation of Heterochromatin Foci Using a 3D Spherical Harmonics Intensity Model. Informatik Aktuell, 2013, , 308-313.	0.6	1
84	PML body meets telomere. Nucleus, 2012, 3, 263-275.	2.2	80
85	Loss of the abundant nuclear non-coding RNA MALAT1 is compatible with life and development. RNA Biology, 2012, 9, 1076-1087.	3.1	355
86	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
87	Nuclear architecture by RNA. Current Opinion in Genetics and Development, 2012, 22, 179-187.	3.3	67
88	Genome-wide nucleosome positioning during embryonic stem cell development. Nature Structural and Molecular Biology, 2012, 19, 1185-1192.	8.2	245
89	Monte Carlo Simulations of Nucleosome Chains to Identify Factors that Control DNA Compaction and Access. RSC Biomolecular Sciences, 2012, , 198-235.	0.4	3
90	Calculating transcription factor binding maps for chromatin. Briefings in Bioinformatics, 2012, 13, 187-201.	6.5	21

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91	A three-dimensional colocalization RNA interference screening platform to elucidate the alternative lengthening of telomeres pathway. <i>Biotechnology Journal</i> , 2012, 7, 103-116.	3.5	14
92	Dissecting DNA-Histone Interactions in the Nucleosome by Molecular Dynamics Simulations of DNA Unwrapping. <i>Biophysical Journal</i> , 2011, 101, 1999-2008.	0.5	89
93	Targeting chromatin remodelers: Signals and search mechanisms. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2011, 1809, 497-508.	1.9	33
94	Chromatin remodelling in mammalian cells by ISWI-type complexes – where, when and why?. <i>FEBS Journal</i> , 2011, 278, 3608-3618.	4.7	78
95	Nucleosome mediated crosstalk between transcription factors at eukaryotic enhancers. <i>Physical Biology</i> , 2011, 8, 044001.	1.8	23
96	Dissecting chromatin interactions in living cells from protein mobility maps. <i>Chromosome Research</i> , 2011, 19, 99-115.	2.2	39
97	Force spectroscopy of chromatin fibers: Extracting energetics and structural information from Monte Carlo simulations. <i>Biopolymers</i> , 2011, 95, 435-447.	2.4	35
98	Coding RNAs with a non-coding function: Maintenance of open chromatin structure. <i>Nucleus</i> , 2011, 2, 410-424.	2.2	44
99	De novo assembly of a PML nuclear subcompartment occurs through multiple pathways and induces telomere elongation. <i>Journal of Cell Science</i> , 2011, 124, 3603-3618.	2.0	72
100	Binding kinetics of human ISWI chromatin-remodelers to DNA repair sites elucidate their target location mechanism. <i>Nucleus</i> , 2011, 2, 105-112.	2.2	35
101	Defining the structural requirements for ribose 5-phosphate binding and intersubunit cross-talk of the malarial pyridoxal 5-phosphate synthase. <i>FEBS Letters</i> , 2010, 584, 4169-4174.	2.8	7
102	Human ISWI chromatin-remodeling complexes sample nucleosomes via transient binding reactions and become immobilized at active sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19873-19878.	7.1	85
103	Histone H2A C-Terminus Regulates Chromatin Dynamics, Remodeling, and Histone H1 Binding. <i>PLoS Genetics</i> , 2010, 6, e1001234.	3.5	73
104	Exploring the Conformational Space of Chromatin Fibers and Their Stability by Numerical Dynamic Phase Diagrams. <i>Biophysical Journal</i> , 2010, 98, 1028-1037.	0.5	41
105	A Lattice Model for Transcription Factor Access to Nucleosomal DNA. <i>Biophysical Journal</i> , 2010, 99, 2597-2607.	0.5	35
106	Statistical mechanical lattice models for protein-DNA binding in chromatin. <i>Journal of Physics Condensed Matter</i> , 2010, 22, 414105.	1.8	40
107	Structure and Function of the Hetero-oligomeric Cysteine Synthase Complex in Plants*. <i>Journal of Biological Chemistry</i> , 2010, 285, 32810-32817.	3.4	76
108	Three-dimensional organization of promyelocytic leukemia nuclear bodies. <i>Journal of Cell Science</i> , 2010, 123, 392-400.	2.0	106

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109	Dynamics of Telomeres and Promyelocytic Leukemia Nuclear Bodies in a Telomerase-negative Human Cell Line. <i>Molecular Biology of the Cell</i> , 2009, 20, 2070-2082.	2.1	93
110	Assembly and mobility of exon-exon junction complexes in living cells. <i>Rna</i> , 2009, 15, 862-876.	3.5	38
111	Predicting nucleosome positions on the DNA: combining intrinsic sequence preferences and remodeler activities. <i>Nucleic Acids Research</i> , 2009, 37, 5641-5655.	14.5	85
112	X-ray crystal structure of <i>Saccharomyces cerevisiae</i> Pdx1 provides insights into the oligomeric nature of PLP synthases. <i>FEBS Letters</i> , 2009, 583, 2179-2186.	2.8	27
113	Analysis of protein mobilities and interactions in living cells by multifocal fluorescence fluctuation microscopy. <i>European Biophysics Journal</i> , 2009, 38, 813-828.	2.2	22
114	Dual color localization microscopy of cellular nanostructures. <i>Biotechnology Journal</i> , 2009, 4, 927-938.	3.5	83
115	Multiscale Analysis of Dynamics and Interactions of Heterochromatin Protein 1 by Fluorescence Fluctuation Microscopy. <i>Biophysical Journal</i> , 2009, 97, 2876-2885.	0.5	74
116	Structural insights into tail-anchored protein binding and membrane insertion by Get3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21131-21136.	7.1	92
117	High-precision structural analysis of subnuclear complexes in fixed and live cells via spatially modulated illumination (SMI) microscopy. <i>Chromosome Research</i> , 2008, 16, 367-382.	2.2	67
118	Genome organization: Balancing stability and plasticity. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2008, 1783, 2061-2079.	4.1	79
119	The GTPase Cycle of the Chloroplast Import Receptors Toc33/Toc34: Implications from Monomeric and Dimeric Structures. <i>Structure</i> , 2008, 16, 585-596.	3.3	52
120	The Effect of Internucleosomal Interaction on Folding of the Chromatin Fiber. <i>Biophysical Journal</i> , 2008, 95, 3677-3691.	0.5	75
121	Nucleosome Geometry and Internucleosomal Interactions Control the Chromatin Fiber Conformation. <i>Biophysical Journal</i> , 2008, 95, 3692-3705.	0.5	110
122	On the Significance of Toc-GTPase Homodimers. <i>Journal of Biological Chemistry</i> , 2008, 283, 23104-23112.	3.4	26
123	DNA sequence- and conformation-directed positioning of nucleosomes by chromatin-remodeling complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 15635-15640.	7.1	122
124	Dynamic organization of the cell nucleus. <i>Current Opinion in Genetics and Development</i> , 2007, 17, 373-380.	3.3	66
125	Structure of a bacterial pyridoxal 5'-phosphate synthase complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 19284-19289.	7.1	110
126	On the Mechanism of Nucleosome Assembly by Histone Chaperone NAP1*. <i>Journal of Biological Chemistry</i> , 2006, 281, 16462-16472.	3.4	83

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127	A 'loop recapture' mechanism for ACF-dependent nucleosome remodeling. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 683-690.	8.2	94
128	Mobility of multi-subunit complexes in the nucleus: accessibility and dynamics of chromatin subcompartments. <i>Histochemistry and Cell Biology</i> , 2005, 123, 217-228.	1.7	59
129	Association States of Nucleosome Assembly Protein 1 and Its Complexes with Histones. <i>Journal of Biological Chemistry</i> , 2005, 280, 15690-15699.	3.4	44
130	NAP1 Modulates Binding of Linker Histone H1 to Chromatin and Induces an Extended Chromatin Fiber Conformation. <i>Journal of Biological Chemistry</i> , 2005, 280, 34063-34072.	3.4	61
131	Histone acetylation increases chromatin accessibility. <i>Journal of Cell Science</i> , 2005, 118, 5825-5834.	2.0	271
132	Trichostatin A-induced histone acetylation causes decondensation of interphase chromatin. <i>Journal of Cell Science</i> , 2004, 117, 4277-4287.	2.0	207
133	Nuclear body movement is determined by chromatin accessibility and dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13221-13226.	7.1	107
134	Conformation of Reconstituted Mononucleosomes and Effect of Linker Histone H1 Binding Studied by Scanning Force Microscopy. <i>Biophysical Journal</i> , 2003, 85, 4012-4022.	0.5	32
135	NUDT9, a Member of the Nudix Hydrolase Family, Is an Evolutionarily Conserved Mitochondrial ADP-ribose Pyrophosphatase. <i>Journal of Biological Chemistry</i> , 2003, 278, 1794-1801.	3.4	102
136	Binding affinity of Escherichia coli RNA polymerase middle domain sigma54 holoenzyme for the glnAp2, nifH and nifL promoters. <i>Nucleic Acids Research</i> , 2002, 30, 4094-4101.	14.5	15
137	Capturing Chromosome Conformation. <i>Science</i> , 2002, 295, 1306-1311.	12.6	3,210
138	Analysis of Ligand Binding by Two-Colour Fluorescence Cross-Correlation Spectroscopy. <i>Single Molecules</i> , 2002, 3, 49-61.	0.9	85
139	Analysis of Ligand Binding by Two-Colour Fluorescence Cross-Correlation Spectroscopy. <i>Single Molecules</i> , 2002, 3, 49-61.	0.9	5
140	Rational design and molecular characterization of a chimaeric response regulator protein. <i>Journal of Molecular Biology</i> , 2001, 310, 283-290.	4.2	10
141	Making contacts on a nucleic acid polymer. <i>Trends in Biochemical Sciences</i> , 2001, 26, 733-740.	7.5	166
142	Dimerization of signalling modules of the EvgAS and BvgAS phosphorelay systems. <i>BBA - Proteins and Proteomics</i> , 2000, 1478, 341-354.	2.1	25
143	The Effect of the DNA Conformation on the Rate of NtrC activated Transcription of Escherichia coli RNA Polymerase sigma54 Holoenzyme. <i>Journal of Molecular Biology</i> , 2000, 300, 709-725.	4.2	25
144	Simultaneous Binding of Two DNA Duplexes to the NtrC~Enhancer Complex Studied by Two-Color Fluorescence Cross-Correlation Spectroscopy. <i>Biochemistry</i> , 2000, 39, 2131-2139.	2.5	69

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145	Scanning force microscopy of Escherichia coli RNA polymerase σ 54 holoenzyme complexes with DNA in buffer and in air 1 Edited by W. Baumeister. Journal of Molecular Biology, 1998, 283, 821-836.	4.2	41
146	Association states of the transcription activator protein NtrC from E. coli determined by analytical ultracentrifugation 1 Edited by K. Yamamoto. Journal of Molecular Biology, 1998, 278, 915-933.	4.2	55
147	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
148	DNA binding and oligomerization of NtrC studied by fluorescence anisotropy and fluorescence correlation spectroscopy. Nucleic Acids Research, 1998, 26, 1373-1381.	14.5	48
149	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
150	Biochemical Characterization and Mass Spectrometric Disulfide Bond Mapping of Periplasmic α -Amylase MaS of Escherichia coli. Journal of Biological Chemistry, 1997, 272, 22125-22133.	3.4	37
151	Transcriptional activation via DNA-looping: visualization of intermediates in the activation pathway of E. coli RNA polymerase σ 54 holoenzyme by scanning force microscopy. Journal of Molecular Biology, 1997, 270, 125-138.	4.2	143
152	Specificity mechanisms in the control of transcription. Biophysical Chemistry, 1996, 59, 231-246.	2.8	36
153	Action at a distance: DNA-looping and initiation of transcription. Trends in Biochemical Sciences, 1995, 20, 500-506.	7.5	271
154	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
155	Structure and Drug interaction of parallel-stranded DNA studies by infrared spectroscopy and fluorescence. Nucleic Acids Research, 1993, 21, 5085-5091.	14.5	63
156	[11] Parallel-stranded duplex DNA. Methods in Enzymology, 1992, 211, 199-220.	1.0	58
157	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
158			

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163	Substrate properties of 25-nt parallel-stranded linear DNA duplexes. <i>Biochemistry</i> , 1989, 28, 9542-9549.	2.5	28
164	Interactions of Histones with DNA: Nucleosome Assembly, Stability, Dynamics, and Higher Order Structure. , 0, , 135-172.		12