Benjamin Audit

List of Publications by Year
in descending order

91 papers	3,834 citations	101384 36 h-index	143772 57 g-index
102 all docs	102 docs citations	102 times ranked	3815 citing authors

#	Article	IF	Citations
1	FORK-seq: Single-Molecule Profiling of DNA Replication. Methods in Molecular Biology, 2022, 2477, 107-128.	0.4	0
2	Genome-wide mapping of individual replication fork velocities using nanopore sequencing. Nature Communications, 2022, 13, .	5.8	15
3	Human ORC/MCM density is low in active genes and correlates with replication time but does not delimit initiation zones. ELife, 2021, 10, .	2.8	23
4	Coupling between Sequence-Mediated Nucleosome Organization and Genome Evolution. Genes, 2021, 12, 851.	1.0	5
5	Organization of DNA Replication Origin Firing in Xenopus Egg Extracts: The Role of Intra-S Checkpoint. Genes, 2021, 12, 1224.	1.0	4
6	FORK-seq: replication landscape of the Saccharomyces cerevisiae genome by nanopore sequencing. Genome Biology, 2020, 21, 125.	3.8	39
7	Applications of Hybrid Nanoparticles in Biosensors. , 2019, , 431-455.		3
8	The Role of Nucleosome Positioning in Genome Function and Evolution. , 2018, , 41-79.		2
9	Evidence for DNA Sequence Encoding of an Accessible Nucleosomal Array across Vertebrates. Biophysical Journal, 2018, 114, 2308-2316.	0.2	8
10	Developmental and cancer-associated plasticity of DNA replication preferentially targets GC-poor, lowly expressed and late-replicating regions. Nucleic Acids Research, 2018, 46, 10157-10172.	6.5	30
11	Sensitive Hg^{2+} Ion Detection Using Metal Enhanced Fluorescence of Novel Polyvinyl Pyrrolidone (PVP)-Templated Gold Nanoparticles. Applied Spectroscopy, 2018, 72, 1645-1652.	1.2	12
12	The eukaryotic bell-shaped temporal rate of DNA replication origin firing emanates from a balance between origin activation and passivation. ELife, 2018, 7, .	2.8	14
13	Numerical Study of Novel Ratiometric Sensors Based on Plasmonâ€"Exciton Coupling. Applied Spectroscopy, 2017, 71, 2377-2384.	1.2	9
14	Multi-scale structural community organisation of the human genome. BMC Bioinformatics, 2017, 18, 209.	1.2	11
15	Evidence of selection for an accessible nucleosomal array in human. BMC Genomics, 2016, 17, 526.	1.2	25
16	Comparative Multifractal Analysis of Dynamic Infrared Thermograms and X-Ray Mammograms Enlightens Changes in the Environment of Malignant Tumors. Frontiers in Physiology, 2016, 7, 336.	1.3	18
17	From elasticity to inelasticity in cancer cell mechanics: A loss of scale-invariance. AIP Conference Proceedings, 2016, , .	0.3	8
18	Combining multifractal analyses of digital mammograms and infrared thermograms to assist in early breast cancer diagnosis. AIP Conference Proceedings, 2016, , .	0.3	11

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19	Deciphering DNA replication dynamics in eukaryotic cell populations in relation with their averaged chromatin conformations. Scientific Reports, 2016, 6, 22469.	1.6	9
20	Genome-wide alterations of the DNA replication program during tumor progression. AIP Conference Proceedings, 2016, , .	0.3	0
21	Ubiquitous human 'master' origins of replication are encoded in the DNA sequence via a local enrichment in nucleosome excluding energy barriers. Journal of Physics Condensed Matter, 2015, 27, 064102.	0.7	11
22	SWDreader: A wavelet-based algorithm using spectral phase to characterize spike-wave morphological variation in genetic models of absence epilepsy. Journal of Neuroscience Methods, 2015, 242, 127-140.	1.3	20
23	Embryonic Stem Cell Specific "Master" Replication Origins at the Heart of the Loss of Pluripotency. PLoS Computational Biology, 2015, 11, e1003969.	1.5	22
24	Structural organization of human replication timing domains. FEBS Letters, 2015, 589, 2944-2957.	1.3	28
25	The Spatiotemporal Program of DNA Replication Is Associated with Specific Combinations of Chromatin Marks in Human Cells. PLoS Genetics, 2014, 10, e1004282.	1.5	123
26	Wavelet-based multifractal analysis of dynamic infrared thermograms to assist in early breast cancer diagnosis. Frontiers in Physiology, 2014, 5, 176.	1.3	68
27	From the chromatin interaction network to the organization of the human genome into replication N/U-domains. New Journal of Physics, 2014, 16, 115014.	1.2	12
28	Large replication skew domains delimit GC-poor gene deserts in human. Computational Biology and Chemistry, 2014, 53, 153-165.	1.1	5
29	A Wavelet-Based Method for Multifractal Analysis of Medical Signals: Application to Dynamic Infrared Thermograms of Breast Cancer. Communications in Computer and Information Science, 2014, , 288-300.	0.4	5
30	From Simple Bacterial and Archaeal Replicons to Replication N/U-Domains. Journal of Molecular Biology, 2013, 425, 4673-4689.	2.0	32
31	Multifractal analysis of dynamic infrared imaging of breast cancer. Europhysics Letters, 2013, 104, 68001.	0.7	34
32	Revealing Long-Range Interconnected Hubs in Human Chromatin Interaction Data Using Graph Theory. Physical Review Letters, 2013, 111, 118102.	2.9	52
33	Multiscale analysis of genome-wide replication timing profiles using a wavelet-based signal-processing algorithm. Nature Protocols, 2013, 8, 98-110.	5.5	50
34	Megabase Replication Domains Along the Human Genome: Relation to Chromatin Structure and Genome Organisation. Sub-Cellular Biochemistry, 2013, 61, 57-80.	1.0	15
35	Human Genome Replication Proceeds through Four Chromatin States. PLoS Computational Biology, 2013, 9, e1003233.	1.5	54
36	Epigenetic regulation of the human genome: coherence between promoter activity and large-scale chromatin environment. Frontiers in Life Science: Frontiers of Interdisciplinary Research in the Life Sciences, 2013, 7, 44-62.	1.1	8

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37	Replication Fork Polarity Gradients Revealed by Megabase-Sized U-Shaped Replication Timing Domains in Human Cell Lines. PLoS Computational Biology, 2012, 8, e1002443.	1.5	70
38	Publisher's Note: Inferring Where and When Replication Initiates from Genome-Wide Replication Timing Data [Phys. Rev. Lett.108, 268101 (2012)]. Physical Review Letters, 2012, 109, .	2.9	0
39	Inferring Where and When Replication Initiates from Genome-Wide Replication Timing Data. Physical Review Letters, 2012, 108, 268101.	2.9	25
40	3D chromatin conformation correlates with replication timing and is conserved in resting cells. Nucleic Acids Research, 2012, 40, 9470-9481.	6.5	76
41	Gene organization inside replication domains in mammalian genomes. Comptes Rendus - Mecanique, 2012, 340, 745-757.	2.1	12
42	Linking the DNA strand asymmetry to the spatio-temporal replication program. European Physical Journal E, 2012, 35, 92.	0.7	16
43	Linking the DNA strand asymmetry to the spatio-temporal replication program. European Physical Journal E, 2012, 35, 123.	0.7	13
44	FractalsFractal and WaveletsWavelets : What Can We Learn on Transcription and Replication from Wavelet-Based Multifractal AnalysisMultifractal analysis of DNA SequencesDNA sequence ?. , 2012, , 606-636.		0
45	Revisiting polymer statistical physics to account for the presence of long-range-correlated structural disorder in 2D DNA chains. European Physical Journal E, 2011, 34, 119.	0.7	2
46	Multi-scale coding of genomic information: From DNA sequence to genome structure and function. Physics Reports, 2011, 498, 45-188.	10.3	108
47	Replication-Associated Mutational Asymmetry in the Human Genome. Molecular Biology and Evolution, 2011, 28, 2327-2337.	3.5	66
48	Evidence for Sequential and Increasing Activation of Replication Origins along Replication Timing Gradients in the Human Genome. PLoS Computational Biology, 2011, 7, e1002322.	1.5	124
49	Revealing intermittency in experimental data with steep power spectra. Europhysics Letters, 2010, 90, 50007.	0.7	13
50	Wavelet-based method to disentangle transcription- and replication-associated strand asymmetries in mammalian genomes. Applied and Computational Harmonic Analysis, 2010, 28, 150-170.	1.1	22
51	A novel strategy of transcription regulation by intragenic nucleosome ordering. Genome Research, 2010, 20, 59-67.	2.4	64
52	Impact of replication timing on non-CpG and CpG substitution rates in mammalian genomes. Genome Research, 2010, 20, 447-457.	2.4	187
53	Effect of Genomic Long-Range Correlations on DNA Persistence Length: From Theory to Single Molecule Experiments. Journal of Physical Chemistry B, 2010, 114, 5125-5143.	1.2	33
54	Nucleosome positioning by genomic excluding-energy barriers. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 22257-22262.	3.3	54

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55	Open chromatin encoded in DNA sequence is the signature of â€˜masterâ€™ replication origins in human cells. Nucleic Acids Research, 2009, 37, 6064-6075.	6.5	52
56	Analysis of fine-scale mammalian evolutionary breakpoints provides new insight into their relation to genome organisation. BMC Genomics, 2009, 10, 335.	1.2	58
57	Atomic Force Microscopy In Solution Shows Nucleosome Positioning By Excluding Genomic Energy Barriers. Biophysical Journal, 2009, 96, 419a.	0.2	0
58	Generalized wormlike chain model for long-range correlated heteropolymers. Europhysics Letters, 2009, 86, 48001.	0.7	6
59	FractalsFractal and WaveletsWavelets : What Can We Learn on Transcription and Replication from Wavelet-Based Multifractal AnalysisMultifractal analysis of DNA SequencesDNA sequence ?. , 2009, , 3893-3924.		2
60	Spontaneous emergence of sequence-dependent rosettelike folding of chromatin fiber. Physical Review E, 2008, 77, 061923.	0.8	14
61	Wavelet-based multifractal analysis. Scholarpedia Journal, 2008, 3, 4103.	0.3	39
62	Bifractality of human DNA strand-asymmetry profiles results from transcription. Physical Review E, 2007, 75, 032902.	0.8	37
63	Experiments Confirm the Influence of Genome Long-Range Correlations on Nucleosome Positioning. Physical Review Letters, 2007, 99, 218103.	2.9	60
64	Human gene organization driven by the coordination of replication and transcription. Genome Research, 2007, 17, 1278-1285.	2.4	147
65	DNA Replication Timing Data Corroborate <i>In Silico</i> Human Replication Origin Predictions. Physical Review Letters, 2007, 99, 248102.	2.9	39
66	CORRIE: enzyme sequence annotation with confidence estimates. BMC Bioinformatics, 2007, 8, S3.	1.2	14
67	Formation and positioning of nucleosomes: Effect of sequence-dependent long-range correlated structural disorder. European Physical Journal E, 2006, 19, 263-277.	0.7	32
68	Probabilistic annotation of protein sequences based on functional classifications. BMC Bioinformatics, 2005, 6, 302.	1.2	24
69	An Exponential Core in the Heart of the Yeast Protein Interaction Network. Molecular Biology and Evolution, 2005, 22, 421-425.	3.5	50
70	CoGenT++: an extensive and extensible data environment for computational genomics. Bioinformatics, 2005, 21, 3806-3810.	1.8	22
71	Thermodynamics of DNA Loops with Long-Range Correlated Structural Disorder. Physical Review Letters, 2005, 95, 068101.	2.9	43
72	From DNA Sequence Analysis to Modeling Replication in the Human Genome. Physical Review Letters, 2005, 94, 248103.	2.9	52

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73	Replication-associated strand asymmetries in mammalian genomes: Toward detection of replication origins. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 9836-9841.	3.3	133
74	Percolation of annotation errors through hierarchically structured protein sequence databases. Mathematical Biosciences, 2005, 193, 223-234.	0.9	67
75	Are splicing mutations the most frequent cause of hereditary disease?. FEBS Letters, 2005, 579, 1900-1903.	1.3	327
76	Wavelet Analysis of DNA Bending Profiles reveals Structural Constraints on the Evolution of Genomic Sequences. Journal of Biological Physics, 2004, 30, 33-81.	0.7	30
77	From Genes to Genomes: Universal Scale-invariant Properties of Microbial Chromosome Organisation. Journal of Molecular Biology, 2003, 332, 617-633.	2.0	38
78	Beyond 100 genomes. Genome Biology, 2003, 4, 402.	13.9	23
79	Influence of the sequence on elastic properties of long DNA chains. Physical Review E, 2003, 67, 032901.	0.8	16
80	COmplete GENome Tracking (COGENT): a flexible data environment for computational genomics. Bioinformatics, 2003, 19, 1451-1452.	1.8	40
81	Modeling the percolation of annotation errors in a database of protein sequences. Bioinformatics, 2002, 18, 1641-1649.	1.8	153
82	Wavelet Based Multifractal Formalism: Applications to DNA Sequences, Satellite Images of the Cloud Structure, and Stock Market Data. , 2002, , 26-102.		65
83	Long-range Correlations between DNA Bending Sites: Relation to the Structure and Dynamics of Nucleosomes. Journal of Molecular Biology, 2002, 316, 903-918.	2.0	99
84	Wavelet-based estimators of scaling behavior. IEEE Transactions on Information Theory, 2002, 48, 2938-2954.	1.5	90
85	Strain-specific genes of Helicobacter pylori: distribution, function and dynamics. Nucleic Acids Research, 2001, 29, 4395-4404.	6.5	43
86	Long-Range Correlations in Genomic DNA: A Signature of the Nucleosomal Structure. Physical Review Letters, 2001, 86, 2471-2474.	2.9	127
87	Genome sequences and great expectations. Genome Biology, 2000, 2, interactions0001.1.	13.9	40
88	Thermodynamics of fractal signals based on wavelet analysis: application to fully developed turbulence data and DNA sequences. Physica A: Statistical Mechanics and Its Applications, 1998, 254, 24-45.	1.2	39
89	What can we learn with wavelets about DNA sequences?. Physica A: Statistical Mechanics and Its Applications, 1998, 249, 439-448.	1.2	81
90	Nucleotide composition effects on the long-range correlations in human genes. European Physical Journal B, 1998, 1, 259-263.	0.6	37

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91	Holographic study of a vibrating bell: An undergraduate laboratory experiment. American Journal of Physics, 1998, 66, 380-385.	0.3	4