Anders Sejr Hansen

List of Publications by Year
in descending order

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33 papers	4,289 citations	236612 25 h-index	395343 33 g-index
57 all docs	57 docs citations	57 times ranked	4555 citing authors

#	Article	IF	Citations
1	CTCF and cohesin regulate chromatin loop stability with distinct dynamics. ELife, 2017, 6, .	2.8	476
2	RNA polymerase II clustering through carboxy-terminal domain phase separation. Nature Structural and Molecular Biology, 2018, 25, 833-840.	3.6	456
3	Phase-separation mechanism forÂC-terminal hyperphosphorylation of RNA polymerase II. Nature, 2018, 558, 318-323.	13.7	428
4	Resolving the 3D Landscape of Transcription-Linked Mammalian Chromatin Folding. Molecular Cell, 2020, 78, 539-553.e8.	4.5	380
5	Evidence for DNA-mediated nuclear compartmentalization distinct from phase separation. ELife, 2019, 8, .	2.8	222
6	A dynamic mode of mitotic bookmarking by transcription factors. ELife, 2016, 5, .	2.8	216
7	Robust model-based analysis of single-particle tracking experiments with Spot-On. ELife, 2018, 7, .	2.8	213
8	Dynamics of CTCF- and cohesin-mediated chromatin looping revealed by live-cell imaging. Science, 2022, 376, 496-501.	6.0	190
9	Recent evidence that TADs and chromatin loops are dynamic structures. Nucleus, 2018, 9, 20-32.	0.6	188
10	Distinct Classes of Chromatin Loops Revealed by Deletion of an RNA-Binding Region in CTCF. Molecular Cell, 2019, 76, 395-411.e13.	4.5	172
11	Promoter decoding of transcription factor dynamics involves a tradeâ€off between noise and control of gene expression. Molecular Systems Biology, 2013, 9, 704.	3.2	138
12	Guided nuclear exploration increases CTCF target search efficiency. Nature Chemical Biology, 2020, 16, 257-266.	3.9	113
13	Limits on information transduction through amplitude and frequency regulation of transcription factor activity. ELife, 2015, 4, .	2.8	106
14	CTCF sites display cell cycleâ€“dependent dynamics in factor binding and nucleosome positioning. Genome Research, 2019, 29, 236-249.	2.4	104
15	Determining cellular CTCF and cohesin abundances to constrain 3D genome models. ELife, 2019, 8, .	2.8	103
16	High-throughput microfluidics to control and measure signaling dynamics in single yeast cells. Nature Protocols, 2015, 10, 1181-1197.	5.5	84
17	CTCF as a boundary factor for cohesin-mediated loop extrusion: evidence for a multi-step mechanism. Nucleus, 2020, 11, 132-148.	0.6	73
18	Hydroxylation of methylated CpG dinucleotides reverses stabilisation of DNA duplexes by cytosine 5-methylation. Chemical Communications, 2011, 47, 5325.	2.2	65

#	Article	IF	Citations
19	Control of Olefin Geometry in Macrocyclic Ring-Closing Metathesis Using a Removable Silyl Group. Journal of the American Chemical Society, 2011, 133, 9196-9199.	6.6	65
20	3D ATAC-PALM: super-resolution imaging of the accessible genome. Nature Methods, 2020, 17, 430-436.	9.0	62
21	Tracking and interpreting long-range chromatin interactions with super-resolution live-cell imaging. Current Opinion in Cell Biology, 2021, 70, 18-26.	2.6	50
22	Encoding four gene expression programs in the activation dynamics of a single transcription factor. Current Biology, 2016, 26, R269-R271.	1.8	44
23	Advances in Chromatin and Chromosome Research: Perspectives from Multiple Fields. Molecular Cell, 2020, 79, 881-901.	4.5	42
24	cis Determinants of Promoter Threshold and Activation Timescale. Cell Reports, 2015, 12, 1226-1233.	2.9	39
25	Improved synthesis of 5-hydroxymethyl-2â€²-deoxycytidine phosphoramidite using a 2â€²-deoxyuridine to 2â€²-deoxycytidine conversion without temporary protecting groups. Bioorganic and Medicinal Chemistry Letters, 2011, 21, 1181-1184.	1.0	28
26	Single Molecule Imaging in Live Embryos Using Lattice Light-Sheet Microscopy. Methods in Molecular Biology, 2018, 1814, 541-559.	0.4	24
27	The macro and micro of chromosome conformation capture. Wiley Interdisciplinary Reviews: Developmental Biology, 2021, 10, e395.	5.9	24
28	Reconstructing dynamic molecular states from single-cell time series. Journal of the Royal Society Interface, 2016, 13, 20160533.	1.5	11
29	Promoters adopt distinct dynamic manifestations depending on transcription factor context. Molecular Systems Biology, 2021, 17, e9821.	3.2	6
30	Estimating Cellular Abundances of Halo-tagged Proteins in Live Mammalian Cells by Flow Cytometry. Bio-protocol, 2020, 10, e3527.	0.2	4
31	Assessing Self-interaction of Mammalian Nuclear Proteins by Co-immunoprecipitation. Bio-protocol, 2020, 10, e3526.	0.2	3
32	A Protocol for Studying Transcription Factor Dynamics Using Fast Single-Particle Tracking and Spot-On Model-Based Analysis. Methods in Molecular Biology, 2022, 2458, 151-174.	0.4	3
33	Reeling it in: how DNA topology drives loop extrusion by condensin. Nature Structural and Molecular Biology, 2022, 29, 623-625.	3.6	1