

# 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	A Protocol for Studying Transcription Factor Dynamics Using Fast Single-Particle Tracking and Spot-On Model-Based Analysis. <i>Methods in Molecular Biology</i> , 2022, 2458, 151-174.	0.4	3
2	Dynamics of CTCF- and cohesin-mediated chromatin looping revealed by live-cell imaging. <i>Science</i> , 2022, 376, 496-501.	6.0	190
3	Reeling it in: how DNA topology drives loop extrusion by condensin. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 623-625.	3.6	1
4	The macro and micro of chromosome conformation capture. <i>Wiley Interdisciplinary Reviews: Developmental Biology</i> , 2021, 10, e395.	5.9	24
5	Tracking and interpreting long-range chromatin interactions with super-resolution live-cell imaging. <i>Current Opinion in Cell Biology</i> , 2021, 70, 18-26.	2.6	50
6	Promoters adopt distinct dynamic manifestations depending on transcription factor context. <i>Molecular Systems Biology</i> , 2021, 17, e9821.	3.2	6
7	Guided nuclear exploration increases CTCF target search efficiency. <i>Nature Chemical Biology</i> , 2020, 16, 257-266.	3.9	113
8	CTCF as a boundary factor for cohesin-mediated loop extrusion: evidence for a multi-step mechanism. <i>Nucleus</i> , 2020, 11, 132-148.	0.6	73
9	Advances in Chromatin and Chromosome Research: Perspectives from Multiple Fields. <i>Molecular Cell</i> , 2020, 79, 881-901.	4.5	42
10	3D ATAC-PALM: super-resolution imaging of the accessible genome. <i>Nature Methods</i> , 2020, 17, 430-436.	9.0	62
11	Resolving the 3D Landscape of Transcription-Linked Mammalian Chromatin Folding. <i>Molecular Cell</i> , 2020, 78, 539-553.e8.	4.5	380
12	Assessing Self-interaction of Mammalian Nuclear Proteins by Co-immunoprecipitation. <i>Bio-protocol</i> , 2020, 10, e3526.	0.2	3
13	Estimating Cellular Abundances of Halo-tagged Proteins in Live Mammalian Cells by Flow Cytometry. <i>Bio-protocol</i> , 2020, 10, e3527.	0.2	4
14	Distinct Classes of Chromatin Loops Revealed by Deletion of an RNA-Binding Region in CTCF. <i>Molecular Cell</i> , 2019, 76, 395-411.e13.	4.5	172
15	CTCF sites display cell cycle-dependent dynamics in factor binding and nucleosome positioning. <i>Genome Research</i> , 2019, 29, 236-249.	2.4	104
16	Determining cellular CTCF and cohesin abundances to constrain 3D genome models. <i>ELife</i> , 2019, 8, .	2.8	103
17	Evidence for DNA-mediated nuclear compartmentalization distinct from phase separation. <i>ELife</i> , 2019, 8, .	2.8	222
18	Recent evidence that TADs and chromatin loops are dynamic structures. <i>Nucleus</i> , 2018, 9, 20-32.	0.6	188

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19	Phase-separation mechanism for C-terminal hyperphosphorylation of RNA polymerase II. <i>Nature</i> , 2018, 558, 318-323.	13.7	428
20	Robust model-based analysis of single-particle tracking experiments with Spot-On. <i>ELife</i> , 2018, 7, .	2.8	213
21	Single Molecule Imaging in Live Embryos Using Lattice Light-Sheet Microscopy. <i>Methods in Molecular Biology</i> , 2018, 1814, 541-559.	0.4	24
22	RNA polymerase II clustering through carboxy-terminal domain phase separation. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 833-840.	3.6	456
23	CTCF and cohesin regulate chromatin loop stability with distinct dynamics. <i>ELife</i> , 2017, 6, .	2.8	476
24	Encoding four gene expression programs in the activation dynamics of a single transcription factor. <i>Current Biology</i> , 2016, 26, R269-R271.	1.8	44
25	Reconstructing dynamic molecular states from single-cell time series. <i>Journal of the Royal Society Interface</i> , 2016, 13, 20160533.	1.5	11
26	A dynamic mode of mitotic bookmarking by transcription factors. <i>ELife</i> , 2016, 5, .	2.8	216
27	cis Determinants of Promoter Threshold and Activation Timescale. <i>Cell Reports</i> , 2015, 12, 1226-1233.	2.9	39
28	High-throughput microfluidics to control and measure signaling dynamics in single yeast cells. <i>Nature Protocols</i> , 2015, 10, 1181-1197.	5.5	84
29	Limits on information transduction through amplitude and frequency regulation of transcription factor activity. <i>ELife</i> , 2015, 4, .	2.8	106
30	Promoter decoding of transcription factor dynamics involves a trade-off between noise and control of gene expression. <i>Molecular Systems Biology</i> , 2013, 9, 704.	3.2	138
31	Hydroxylation of methylated CpG dinucleotides reverses stabilisation of DNA duplexes by cytosine 5-methylation. <i>Chemical Communications</i> , 2011, 47, 5325.	2.2	65
32	Control of Olefin Geometry in Macrocyclic Ring-Closing Metathesis Using a Removable Silyl Group. <i>Journal of the American Chemical Society</i> , 2011, 133, 9196-9199.	6.6	65
33	Improved synthesis of 5-hydroxymethyl-2'-deoxycytidine phosphoramidite using a 2'-deoxyuridine to 2'-deoxycytidine conversion without temporary protecting groups. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2011, 21, 1181-1184.	1.0	28