

# Xavier Darzacq

## List of Publications by Year in descending order

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93  
papers

15,057  
citations

34016

52  
h-index

39575

94  
g-index

135  
all docs

135  
docs citations

135  
times ranked

15504  
citing authors

#	ARTICLE	IF	CITATIONS
1	Phase separation drives heterochromatin domain formation. <i>Nature</i> , 2017, 547, 241-245.	13.7	1,456
2	Imaging dynamic and selective low-complexity domain interactions that control gene transcription. <i>Science</i> , 2018, 361, .	6.0	750
3	In vivo dynamics of RNA polymerase II transcription. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 796-806.	3.6	603
4	Dynamics of Single mRNPs in Nuclei of Living Cells. <i>Science</i> , 2004, 304, 1797-1800.	6.0	476
5	CTCF and cohesin regulate chromatin loop stability with distinct dynamics. <i>ELife</i> , 2017, 6, .	2.8	476
6	RNA polymerase II clustering through carboxy-terminal domain phase separation. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 833-840.	3.6	456
7	Phase-separation mechanism for C-terminal hyperphosphorylation of RNA polymerase II. <i>Nature</i> , 2018, 558, 318-323.	13.7	428
8	Overcoming the bottleneck to widespread testing: a rapid review of nucleic acid testing approaches for COVID-19 detection. <i>Rna</i> , 2020, 26, 771-783.	1.6	426
9	Evaluating phase separation in live cells: diagnosis, caveats, and functional consequences. <i>Genes and Development</i> , 2019, 33, 1619-1634.	2.7	424
10	Cajal body-specific small nuclear RNAs: a novel class of 2'-O-methylation and pseudouridylation guide RNAs. <i>EMBO Journal</i> , 2002, 21, 2746-2756.	3.5	417
11	Real-Time Dynamics of RNA Polymerase II Clustering in Live Human Cells. <i>Science</i> , 2013, 341, 664-667.	6.0	417
12	Resolving the 3D Landscape of Transcription-Linked Mammalian Chromatin Folding. <i>Molecular Cell</i> , 2020, 78, 539-553.e8.	4.5	380
13	Fast multicolor 3D imaging using aberration-corrected multifocus microscopy. <i>Nature Methods</i> , 2013, 10, 60-63.	9.0	375
14	A transgenic mouse for in vivo detection of endogenous labeled mRNA. <i>Nature Methods</i> , 2011, 8, 165-170.	9.0	340
15	FISH-quant: automatic counting of transcripts in 3D FISH images. <i>Nature Methods</i> , 2013, 10, 277-278.	9.0	338
16	Gene Expression Is Circular: Factors for mRNA Degradation Also Foster mRNA Synthesis. <i>Cell</i> , 2013, 153, 1000-1011.	13.5	311
17	Dynamic Sorting of Nuclear Components into Distinct Nucleolar Caps during Transcriptional Inhibition. <i>Molecular Biology of the Cell</i> , 2005, 16, 2395-2413.	0.9	304
18	Single-molecule tracking in live cells reveals distinct target-search strategies of transcription factors in the nucleus. <i>ELife</i> , 2014, 3, .	2.8	273

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19	Transcription Factors Modulate c-Fos Transcriptional Bursts. <i>Cell Reports</i> , 2014, 8, 75-83.	2.9	246
20	A single-molecule view of transcription reveals convoys of RNA polymerases and multi-scale bursting. <i>Nature Communications</i> , 2016, 7, 12248.	5.8	233
21	Mutations in the promoter of the telomerase gene <i>TERT</i> contribute to tumorigenesis by a two-step mechanism. <i>Science</i> , 2017, 357, 1416-1420.	6.0	224
22	Evidence for DNA-mediated nuclear compartmentalization distinct from phase separation. <i>ELife</i> , 2019, 8, .	2.8	222
23	A dynamic mode of mitotic bookmarking by transcription factors. <i>ELife</i> , 2016, 5, .	2.8	216
24	Modification of Sm small nuclear RNAs occurs in the nucleoplasmic Cajal body following import from the cytoplasm. <i>EMBO Journal</i> , 2003, 22, 1878-1888.	3.5	213
25	Robust model-based analysis of single-particle tracking experiments with Spot-On. <i>ELife</i> , 2018, 7, .	2.8	213
26	Live cell imaging of low- and non-repetitive chromosome loci using CRISPR-Cas9. <i>Nature Communications</i> , 2017, 8, 14725.	5.8	199
27	Quantitative Nanoscopy of Inhibitory Synapses: Counting Gephyrin Molecules and Receptor Binding Sites. <i>Neuron</i> , 2013, 79, 308-321.	3.8	190
28	Recent evidence that TADs and chromatin loops are dynamic structures. <i>Nucleus</i> , 2018, 9, 20-32.	0.6	188
29	A common sequence motif determines the Cajal body-specific localization of box H/ACA scaRNAs. <i>EMBO Journal</i> , 2003, 22, 4283-4293.	3.5	181
30	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
31	The In Vivo Kinetics of RNA Polymerase II Elongation during Co-Transcriptional Splicing. <i>PLoS Biology</i> , 2011, 9, e1000573.	2.6	171
32	Probing the target search of DNA-binding proteins in mammalian cells using TetR as model searcher. <i>Nature Communications</i> , 2015, 6, 7357.	5.8	171
33	Stepwise RNP assembly at the site of H/ACA RNA transcription in human cells. <i>Journal of Cell Biology</i> , 2006, 173, 207-218.	2.3	161
34	Dense Bicoid hubs accentuate binding along the morphogen gradient. <i>Genes and Development</i> , 2017, 31, 1784-1794.	2.7	161
35	Nucleolar Factors Direct the 2'-O-Ribose Methylation and Pseudouridylation of U6 Spliceosomal RNA. <i>Molecular and Cellular Biology</i> , 1999, 19, 6906-6917.	1.1	149
36	Dynamic multifactor hubs interact transiently with sites of active transcription in <i>Drosophila</i> embryos. <i>ELife</i> , 2018, 7, .	2.8	149

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37	PSF shaping using adaptive optics for three-dimensional single-molecule super-resolution imaging and tracking. <i>Optics Express</i> , 2012, 20, 4957.	1.7	140
38	Super-Resolution Dynamic Imaging of Dendritic Spines Using a Low-Affinity Photoconvertible Actin Probe. <i>PLoS ONE</i> , 2011, 6, e15611.	1.1	137
39	The SNARE Sec22b has a non-fusogenic function in plasma membrane expansion. <i>Nature Cell Biology</i> , 2014, 16, 434-444.	4.6	123
40	Guided nuclear exploration increases CTCF target search efficiency. <i>Nature Chemical Biology</i> , 2020, 16, 257-266.	3.9	113
41	Imaging Transcription in Living Cells. <i>Annual Review of Biophysics</i> , 2009, 38, 173-196.	4.5	112
42	Imaging gene expression in single living cells. <i>Nature Reviews Molecular Cell Biology</i> , 2004, 5, 855-862.	16.1	105
43	CTCF sites display cell cycle-dependent dynamics in factor binding and nucleosome positioning. <i>Genome Research</i> , 2019, 29, 236-249.	2.4	104
44	Determining cellular CTCF and cohesin abundances to constrain 3D genome models. <i>ELife</i> , 2019, 8, .	2.8	103
45	A Cajal body-specific pseudouridylation guide RNA is composed of two box H/ACA snoRNA-like domains. <i>Nucleic Acids Research</i> , 2002, 30, 4643-4649.	6.5	102
46	A stable mode of bookmarking by TBP recruits RNA polymerase II to mitotic chromosomes. <i>ELife</i> , 2018, 7, .	2.8	92
47	A new class of disordered elements controls DNA replication through initiator self-assembly. <i>ELife</i> , 2019, 8, .	2.8	92
48	Tuning levels of low-complexity domain interactions to modulate endogenous oncogenic transcription. <i>Molecular Cell</i> , 2022, 82, 2084-2097.e5.	4.5	89
49	The transcription factor activity gradient (TAG) model: contemplating a contact-independent mechanism for enhancer-promoter communication. <i>Genes and Development</i> , 2022, 36, 7-16.	2.7	80
50	Assessing the localization of centrosomal proteins by PALM/STORM nanoscopy. <i>Cytoskeleton</i> , 2011, 68, 619-627.	1.0	74
51	Cotranscriptional Recognition of Human Intronic Box H/ACA snoRNAs Occurs in a Splicing-Independent Manner. <i>Molecular and Cellular Biology</i> , 2006, 26, 2540-2549.	1.1	72
52	Multi-scale tracking reveals scale-dependent chromatin dynamics after DNA damage. <i>Molecular Biology of the Cell</i> , 2017, 28, 3323-3332.	0.9	71
53	Splicing-independent recruitment of U1 snRNP to a transcription unit in living cells. <i>Journal of Cell Science</i> , 2010, 123, 2085-2093.	1.2	59
54	Cohesin residency determines chromatin loop patterns. <i>ELife</i> , 2020, 9, .	2.8	59

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55	Protein motion in the nucleus: from anomalous diffusion to weak interactions. <i>Biochemical Society Transactions</i> , 2018, 46, 945-956.	1.6	56
56	A dynamic interplay of enhancer elements regulates <i>Klf4</i> expression in naïve pluripotency. <i>Genes and Development</i> , 2017, 31, 1795-1808.	2.7	49
57	TRIM8 modulates the EWS/FLI oncoprotein to promote survival in Ewing sarcoma. <i>Cancer Cell</i> , 2021, 39, 1262-1278.e7.	7.7	49
58	Geometry of the nucleus: a perspective on gene expression regulation. <i>Current Opinion in Chemical Biology</i> , 2014, 20, 112-119.	2.8	48
59	Multifocus microscopy with precise color multi-phase diffractive optics applied in functional neuronal imaging. <i>Biomedical Optics Express</i> , 2016, 7, 855.	1.5	47
60	Covalent Protein Labeling and Improved Single-Molecule Optical Properties of Aqueous CdSe/CdS Quantum Dots. <i>ACS Nano</i> , 2017, 11, 6773-6781.	7.3	47
61	Switch-like Arp2/3 activation upon WASP and WIP recruitment to an apparent threshold level by multivalent linker proteins in vivo. <i>ELife</i> , 2017, 6, .	2.8	47
62	RNA asymmetric distribution and daughter/mother differentiation in yeast. <i>Current Opinion in Microbiology</i> , 2003, 6, 614-620.	2.3	46
63	Dynamics of transcription and mRNA export. <i>Current Opinion in Cell Biology</i> , 2005, 17, 332-339.	2.6	45
64	Processing of Intron-Encoded Box C/D Small Nucleolar RNAs Lacking a 5'-Terminal Stem Structure. <i>Molecular and Cellular Biology</i> , 2000, 20, 4522-4531.	1.1	44
65	Imaging Transcription: Past, Present, and Future. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2015, 80, 1-8.	2.0	41
66	Single cell correlation fractal dimension of chromatin. <i>Nucleus</i> , 2014, 5, 75-84.	0.6	40
67	Intra-nuclear mobility and target search mechanisms of transcription factors: A single-molecule perspective on gene expression. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 482-493.	0.9	39
68	Accessing the third dimension in localization-based super-resolution microscopy. <i>Physical Chemistry Chemical Physics</i> , 2014, 16, 16340-16348.	1.3	38
69	Stable assembly of HIV-1 export complexes occurs cotranscriptionally. <i>Rna</i> , 2014, 20, 1-8.	1.6	33
70	Single-molecule diffusometry reveals no catalysis-induced diffusion enhancement of alkaline phosphatase as proposed by FCS experiments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21328-21335.	3.3	32
71	Gene expression within a dynamic nuclear landscape. <i>EMBO Journal</i> , 2006, 25, 3469-3479.	3.5	30
72	The Histone Chaperone FACT Induces Cas9 Multi-turnover Behavior and Modifies Genome Manipulation in Human Cells. <i>Molecular Cell</i> , 2020, 79, 221-233.e5.	4.5	28

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73	Open-source RNA extraction and RT-qPCR methods for SARS-CoV-2 detection. <i>PLoS ONE</i> , 2021, 16, e0246647.	1.1	27
74	Structure of the human SAGA coactivator complex. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 989-996.	3.6	27
75	Dynamic association and localization of human H/ACA RNP proteins. <i>Rna</i> , 2006, 12, 2057-2062.	1.6	25
76	Evidence for an Integrated Gene Repression Mechanism Based on mRNA Isoform Toggling in Human Cells. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1045-1053.	0.8	25
77	Single Molecule Imaging in Live Embryos Using Lattice Light-Sheet Microscopy. <i>Methods in Molecular Biology</i> , 2018, 1814, 541-559.	0.4	24
78	Faster and less phototoxic 3D fluorescence microscopy using a versatile compressed sensing scheme. <i>Optics Express</i> , 2017, 25, 13668.	1.7	18
79	Master regulators in primary skin fibroblast fate reprogramming in a human ex vivo model of chronic wounds. <i>Wound Repair and Regeneration</i> , 2016, 24, 247-262.	1.5	17
80	Weak multivalent biomolecular interactions: a strength versus numbers tug of war with implications for phase partitioning. <i>Rna</i> , 2022, 28, 48-51.	1.6	17
81	High-Frequency Promoter Firing Links THO Complex Function to Heavy Chromatin Formation. <i>Cell Reports</i> , 2013, 5, 1082-1094.	2.9	14
82	The Dynamic Range of Transcription. <i>Molecular Cell</i> , 2008, 30, 545-546.	4.5	12
83	Caffeine Prevents Transcription Inhibition and P-TEFb/7SK Dissociation Following UV-Induced DNA Damage. <i>PLoS ONE</i> , 2010, 5, e11245.	1.1	11
84	Transcription activation depends on the length of the RNA polymerase II C-terminal domain. <i>EMBO Journal</i> , 2021, 40, e107015.	3.5	11
85	Dual-color 3D PALM/dSTORM imaging of centrosomal proteins using MicAO 3DSR. <i>Proceedings of SPIE</i> , 2013, , .	0.8	7
86	Simple, Inexpensive RNA Isolation and One-Step RT-qPCR Methods for SARS-CoV-2 Detection and General Use. <i>Current Protocols</i> , 2021, 1, e130.	1.3	7
87	Short Exposure to the DNA Intercalator DRAQ5 Dislocates the Transcription Machinery and Induces Cell Death. <i>Photochemistry and Photobiology</i> , 2011, 87, 256-261.	1.3	6
88	Role of the DHH1 Gene in the Regulation of Monocarboxylic Acids Transporters Expression in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2014, 9, e111589.	1.1	4
89	Estimating Cellular Abundances of Halo-tagged Proteins in Live Mammalian Cells by Flow Cytometry. <i>Bio-protocol</i> , 2020, 10, e3527.	0.2	4
90	Assessing Self-interaction of Mammalian Nuclear Proteins by Co-immunoprecipitation. <i>Bio-protocol</i> , 2020, 10, e3526.	0.2	3

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91	Chromatin Dynamics upon DNA Damage. , 0, , .		2
92	A Bayesian nonparametric approach to super-resolution single-molecule localization. Annals of Applied Statistics, 2021, 15, .	0.5	2
93	Selective Activation of Alternative MYC Core Promoters by Wnt-Responsive Enhancers. Genes, 2018, 9, 270.	1.0	1