Tatsuya Morisaki

List of Publications by Year
in descending order

32 papers	2,828 citations	471509 17 h-index	477307 29 g-index
43 all docs	43 docs citations	43 times ranked	3751 citing authors

#	Article	IF	Citations
1	Single-Molecule Imaging of mRNA Interactions with Stress Granules. Methods in Molecular Biology, 2022, 2428, 349-360.	0.9	1
2	Imaging translational control by Argonaute with single-molecule resolution in live cells. Nature Communications, 2022, 13, .	12.8	17
3	Live-cell imaging reveals the spatiotemporal organization of endogenous RNA polymerase II phosphorylation at a single gene. Nature Communications, 2021, 12, 3158.	12.8	36
4	A Multi-color Bicistronic Biosensor to Compare the Translation Dynamics of Different Open Reading Frames at Single-molecule Resolution in Live Cells. Bio-protocol, 2021, 11, e4096.	0.4	2
5	Quantifying the dynamics of IRES and cap translation with single-molecule resolution in live cells. Nature Structural and Molecular Biology, 2020, 27, 1095-1104.	8.2	30
6	Coupling of translation quality control and mRNA targeting to stress granules. Journal of Cell Biology, 2020, 219, .	5.2	40
7	A genetically encoded probe for imaging nascent and mature HA-tagged proteins in vivo. Nature Communications, 2019, 10, 2947.	12.8	72
8	Computational design and interpretation of single-RNA translation experiments. PLoS Computational Biology, 2019, 15, e1007425.	3.2	12
9	Multicolour single-molecule tracking of mRNA interactions with RNP granules. Nature Cell Biology, 2019, 21, 162-168.	10.3	168
10	Live-Cell Single RNA Imaging Reveals Bursts of Translational Frameshifting. Molecular Cell, 2019, 75, 172-183.e9.	9.7	40
11	Computational design and interpretation of single-RNA translation experiments. , 2019, 15, e1007425.		0
12	Computational design and interpretation of single-RNA translation experiments. , 2019, 15, e1007425.		0
13	Computational design and interpretation of single-RNA translation experiments. , 2019, 15, e1007425.		0
14	Computational design and interpretation of single-RNA translation experiments. , 2019, 15, e1007425.		0
15	Quantifying Single mRNA Translation Kinetics in Living Cells. Cold Spring Harbor Perspectives in Biology, 2018, 10, a032078.	5.5	37
16	Single-molecule analysis of steroid receptor and cofactor action in living cells. Nature Communications, 2017, 8, 15896.	12.8	111
17	Live-cell p53 single-molecule binding is modulated by C-terminal acetylation and correlates with transcriptional activity. Nature Communications, 2017, 8, 313.	12.8	104
18	She1 affects dynein through direct interactions with the microtubule and the dynein microtubule-binding domain. Nature Communications, 2017, 8, 2151.	12.8	25

#	Article	IF	Citations
19	Steroid Receptors Reprogram FoxA1 Occupancy through Dynamic Chromatin Transitions. Cell, 2016, 165, 593-605.	28.9	257
20	Real-time quantification of single RNA translation dynamics in living cells. Science, 2016, 352, 1425-1429.	12.6	317
21	Single molecule tracking of Ace1p in Saccharomyces cerevisiae defines a characteristic residence time for non-specific interactions of transcription factors with chromatin. Nucleic Acids Research, 2016, 44, e160-e160.	14.5	52
22	Single-molecule analysis of transcription factor binding at transcription sites in live cells. Nature Communications, 2014, 5, 4456.	12.8	152
23	Transcription Factors Modulate c-Fos Transcriptional Bursts. Cell Reports, 2014, 8, 75-83.	6.4	246
24	Photoswitching-Free FRAP Analysis with a Genetically Encoded Fluorescent Tag. PLoS ONE, 2014, 9, e107730.	2.5	18
25	A benchmark for chromatin binding measurements in live cells. Nucleic Acids Research, 2012, 40, e119-e119.	14.5	275
26	Minimizing the Impact of Photoswitching of Fluorescent Proteins on FRAP Analysis. Biophysical Journal, 2012, 102, 1656-1665.	0.5	50
27	Using Gene Expression Noise to Understand Gene Regulation. Science, 2012, 336, 183-187.	12.6	685
28	Metalâ€Stimulated Regulation of Transcription by an Artificial Zincâ€Finger Protein. ChemBioChem, 2010, 11, 1653-1655.	2.6	10
29	Positive and negative cooperativity of modularly assembled zinc fingers. Biochemical and Biophysical Research Communications, 2009, 387, 440-443.	2.1	13
30	Rapid Transcriptional Activity <i>in Vivo</i> and Slow DNA Binding <i>in Vitro</i> by an Artificial Multi-Zinc Finger Protein. Biochemistry, 2008, 47, 10171-10177.	2.5	12
31	An artificial six-zinc finger peptide with polyarginine linker: Selective binding to the discontinuous DNA sequences. Biochemical and Biophysical Research Communications, 2005, 333, 167-173.	2.1	9
32	Swapping of the Î²-Hairpin Region between Sp1 and GLI Zinc Fingers:Â Significant Role of the Î²-Hairpin Region in DNA Binding Properties of C2H2-type Zinc Finger Peptidesâ€. Biochemistry, 2005, 44, 2523-2528.	2.5	12