

# Toyotaka Ishibashi

## List of Publications by Year in descending order

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62  
papers

2,556  
citations

147726

31  
h-index

206029

48  
g-index

64  
all docs

64  
docs citations

64  
times ranked

3098  
citing authors

#	ARTICLE	IF	CITATIONS
1	RECQL5 KIX domain splicing isoforms have distinct functions in transcription repression and DNA damage response. <i>DNA Repair</i> , 2021, 97, 103007.	1.3	1
2	The elevated transcription of ADAM19 by the oncohistone H2BE76K contributes to oncogenic properties in breast cancer. <i>Journal of Biological Chemistry</i> , 2021, 296, 100374.	1.6	17
3	Primate-specific histone variants. <i>Genome</i> , 2021, 64, 337-346.	0.9	13
4	Semisynthesis of site-specifically succinylated histone reveals that succinylation regulates nucleosome unwrapping rate and DNA accessibility. <i>Nucleic Acids Research</i> , 2020, 48, 9538-9549.	6.5	34
5	Histone H4 variant, H4G, drives ribosomal RNA transcription and breast cancer cell proliferation by loosening nucleolar chromatin structure. <i>Journal of Cellular Physiology</i> , 2020, 235, 9601-9608.	2.0	17
6	Cancer-associated histone mutation H2BG53D disrupts DNA-histone octamer interaction and promotes oncogenic phenotypes. <i>Signal Transduction and Targeted Therapy</i> , 2020, 5, 27.	7.1	17
7	The Characterization of Human Testis-Specific Histone Variant H2BFW on Nucleosome Stability and its Functional Role in Spermatogenesis. <i>Biophysical Journal</i> , 2020, 118, 378a.	0.2	0
8	The H2BG53D oncohistone directly upregulates ANXA3 transcription and enhances cell migration in pancreatic ductal adenocarcinoma. <i>Signal Transduction and Targeted Therapy</i> , 2020, 5, 106.	7.1	12
9	Screen identifies DYRK1B network as mediator of transcription repression on damaged chromatin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17019-17030.	3.3	12
10	Single cell transcriptomic landscapes of pattern formation, proliferation and growth in <i>Drosophila</i> wing imaginal discs. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	27
11	A novel histone H4 variant H4G regulates rDNA transcription in breast cancer. <i>Nucleic Acids Research</i> , 2019, 47, 8399-8409.	6.5	50
12	Site-Specific Installation of Succinyl Lysine Analog into Histones Reveals the Effect of H2BK34 Succinylation on Nucleosome Dynamics. <i>Cell Chemical Biology</i> , 2018, 25, 166-174.e7.	2.5	42
13	TEFM Enhances Transcription Elongation by Modifying mtRNAP Pausing Dynamics. <i>Biophysical Journal</i> , 2018, 115, 2295-2300.	0.2	9
14	Apical constriction is driven by a pulsatile apical myosin network in delaminating <i>Drosophila</i> neuroblasts. <i>Development (Cambridge)</i> , 2017, 144, 2153-2164.	1.2	47
15	Histone Variants and Posttranslational Modifications in Spermatogenesis and Infertility. , 2016, , 479-496.		2
16	Poly(ADP-ribosyl)ation-dependent Transient Chromatin Decondensation and Histone Displacement following Laser Microirradiation. <i>Journal of Biological Chemistry</i> , 2016, 291, 1789-1802.	1.6	80
17	Transcription factors IIS and IIF enhance transcription efficiency by differentially modifying RNA polymerase pausing dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 3419-3424.	3.3	49
18	Molecular Mechanisms of Transcription through Single-Molecule Experiments. <i>Chemical Reviews</i> , 2014, 114, 3203-3223.	23.0	74

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19	Complete Dissection of Transcription Elongation Reveals Slow Translocation of RNA Polymerase II in a Linear Ratchet Mechanism. <i>Biophysical Journal</i> , 2014, 106, 485a-486a.	0.2	1
20	A Quantitative Kinetic Model of Eukaryotic Transcription Elongation from Single-Molecule Experiments. <i>Biophysical Journal</i> , 2013, 104, 364a.	0.2	0
21	Complete dissection of transcription elongation reveals slow translocation of RNA polymerase II in a linear ratchet mechanism. <i>ELife</i> , 2013, 2, e00971.	2.8	111
22	Nucleosomal Elements that Control the Topography of the Barrier to Transcription. <i>Cell</i> , 2012, 151, 738-749.	13.5	162
23	Dissecting the Nucleosomal Barrier to Transcription. <i>Biophysical Journal</i> , 2012, 102, 284a.	0.2	0
24	Nascent RNA structure modulates the transcriptional dynamics of RNA polymerases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8948-8953.	3.3	95
25	Histone Variants. , 2010, , 2409-2425.		0
26	H2A.Bbd: an X-chromosome-encoded histone involved in mammalian spermiogenesis. <i>Nucleic Acids Research</i> , 2010, 38, 1780-1789.	6.5	71
27	Phosphorylation of Histone H2A.X by DNA-dependent Protein Kinase Is Not Affected by Core Histone Acetylation, but It Alters Nucleosome Stability and Histone H1 Binding. <i>Journal of Biological Chemistry</i> , 2010, 285, 17778-17788.	1.6	41
28	The evolutionary differentiation of two histone H2A.Z variants in chordates (H2A.Z-1 and H2A.Z-2) is mediated by a stepwise mutation process that affects three amino acid residues. <i>BMC Evolutionary Biology</i> , 2009, 9, 31.	3.2	72
29	Characterization of the histone H2A.Z-1 and H2A.Z-2 isoforms in vertebrates. <i>BMC Biology</i> , 2009, 7, 86.	1.7	89
30	The multi- $\epsilon$ replication protein ( $\epsilon$ RPA) system – a new perspective. <i>FEBS Journal</i> , 2009, 276, 943-963.	2.2	54
31	New developments in post-translational modifications and functions of histone H2A variants This paper is one of a selection of papers published in this Special Issue, entitled CSBMCB's 51st Annual Meeting – Epigenetics and Chromatin Dynamics, and has undergone the Journal's usual peer review process. <i>Biochemistry and Cell Biology</i> , 2009, 87, 7-17.	0.9	35
32	Acetylation of Vertebrate H2A.Z and Its Effect on the Structure of the Nucleosome. <i>Biochemistry</i> , 2009, 48, 5007-5017.	1.2	83
33	H2A.Z and H3.3 Histone Variants Affect Nucleosome Structure: Biochemical and Biophysical Studies. <i>Biochemistry</i> , 2009, 48, 10852-10857.	1.2	87
34	MeCP2 preferentially binds to methylated linker DNA in the absence of the terminal tail of histone H3 and independently of histone acetylation. <i>FEBS Letters</i> , 2008, 582, 1157-1162.	1.3	41
35	H2A.Bbd: a quickly evolving hypervariable mammalian histone that destabilizes nucleosomes in an acetylation-independent way. <i>FASEB Journal</i> , 2008, 22, 316-326.	0.2	49
36	MBD4-Mediated Glycosylase Activity on a Chromatin Template Is Enhanced by Acetylation. <i>Molecular and Cellular Biology</i> , 2008, 28, 4734-4744.	1.1	15

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37	Probasin promoter assembles into a strongly positioned nucleosome that permits androgen receptor binding. <i>Molecular and Cellular Endocrinology</i> , 2007, 268, 10-19.	1.6	16
38	Higher plant RecA-like protein is homologous to RadA. <i>DNA Repair</i> , 2006, 5, 80-88.	1.3	11
39	A novel protein refolding method using a zeolite. <i>Analytical Biochemistry</i> , 2006, 348, 307-314.	1.1	23
40	Characterization of T-DNA Insertion Mutants and RNAi Silenced Plants of <i>Arabidopsis thaliana</i> UV-damaged DNA Binding Protein 2 (AtUV-DDB2). <i>Plant Molecular Biology</i> , 2006, 61, 227-240.	2.0	32
41	A Higher Plant Has Three Different Types of RPA Heterotrimeric Complex. <i>Journal of Biochemistry</i> , 2006, 139, 99-104.	0.9	45
42	H2A.Z Stabilizes Chromatin in a Way That Is Dependent on Core Histone Acetylation. <i>Journal of Biological Chemistry</i> , 2006, 281, 20036-20044.	1.6	63
43	DNA Repair Mechanisms in UV-B Tolerant Plants. <i>Japan Agricultural Research Quarterly</i> , 2006, 40, 107-113.	0.1	7
44	Two types of replication protein A in seed plants. <i>FEBS Journal</i> , 2005, 272, 3270-3281.	2.2	37
45	Interaction between proliferating cell nuclear antigen (PCNA) and a DnaJ induced by DNA damage. <i>Journal of Plant Research</i> , 2005, 118, 91-97.	1.2	29
46	Plastid DNA polymerases from higher plants, <i>Arabidopsis thaliana</i> . <i>Biochemical and Biophysical Research Communications</i> , 2005, 334, 43-50.	1.0	50
47	Characterization of the origin recognition complex (ORC) from a higher plant, rice ( <i>Oryza sativa</i> L.). <i>Gene</i> , 2005, 353, 23-30.	1.0	16
48	<i>Arabidopsis</i> COP10 forms a complex with DDB1 and DET1 in vivo and enhances the activity of ubiquitin conjugating enzymes. <i>Genes and Development</i> , 2004, 18, 2172-2181.	2.7	186
49	DNA repair in higher plants; photoreactivation is the major DNA repair pathway in non-proliferating cells while excision repair (nucleotide excision repair and base excision repair) is active in proliferating cells. <i>Nucleic Acids Research</i> , 2004, 32, 2760-2767.	6.5	91
50	Plant DNA polymerase $\hat{\mu}$ , a DNA repair enzyme that functions in plant meristematic and meiotic tissues. <i>FEBS Journal</i> , 2004, 271, 2799-2807.	0.2	92
51	Degradation of proliferating cell nuclear antigen by 26S proteasome in rice ( <i>Oryza sativa</i> L.). <i>Planta</i> , 2004, 218, 640-646.	1.6	14
52	Characterization of Rad6 from a higher plant, rice ( <i>Oryza sativa</i> L.) and its interaction with Sgt1, a subunit of the SCF ubiquitin ligase complex. <i>Biochemical and Biophysical Research Communications</i> , 2004, 314, 434-439.	1.0	22
53	Characterization of all the subunits of replication factor C from a higher plant, rice ( <i>Oryza sativa</i> L.), and their relation to development. <i>Plant Molecular Biology</i> , 2003, 53, 15-25.	2.0	43
54	OsSEND-1: a new RAD2 nuclease family member in higher plants. <i>Plant Molecular Biology</i> , 2003, 51, 59-70.	2.0	31

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55	Interaction between proliferating cell nuclear antigen and JUN-activation-domain-binding protein $\hat{A}$ 1 in the meristem of rice, <i>Oryza sativa</i> L.. <i>Planta</i> , 2003, 217, 175-183.	1.6	8
56	Plant-specific regulation of replication protein $\hat{i}$ $\frac{1}{2}$ A2 (OsRPA2) from rice during the cell cycle and in response to ultraviolet light exposure. <i>Planta</i> , 2003, 217, 457-465.	1.6	17
57	Rice UV-damaged DNA binding protein homologues are most abundant in proliferating tissues. <i>Gene</i> , 2003, 308, 79-87.	1.0	33
58	A novel DNA polymerase homologous to <i>Escherichia coli</i> DNA polymerase I from a higher plant, rice ( <i>Oryza sativa</i> L.). <i>Nucleic Acids Research</i> , 2002, 30, 1585-1592.	6.5	63
59	Characterization of DNA polymerase $\hat{I}$ from a higher plant, rice ( <i>Oryza sativa</i> L.). <i>Gene</i> , 2002, 295, 19-26.	1.0	27
60	Two types of replication protein A 70 kDa subunit in rice, <i>Oryza sativa</i> : molecular cloning, characterization, and cellular & tissue distribution. <i>Gene</i> , 2001, 272, 335-343.	1.0	53
61	A plant homologue of 36 kDa subunit of replication factor C: molecular cloning and characterization. <i>Plant Science</i> , 2001, 161, 99-106.	1.7	7
62	Molecular cloning and characterization of a plant homologue of the origin recognition complex 1 (ORC1). <i>Plant Science</i> , 2000, 158, 33-39.	1.7	26