

Akihisa Osakabe

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

2,177
citations

257101

24
h-index

253896

43
g-index

49
all docs

49
docs citations

49
times ranked

2288
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structure of the human centromeric nucleosome containing CENP-A. <i>Nature</i> , 2011, 476, 232-235.	13.7	336
2	Structural basis of instability of the nucleosome containing a testis-specific histone variant, human H3T. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10454-10459.	3.3	195
3	Contribution of histone N-terminal tails to the structure and stability of nucleosomes. <i>FEBS Open Bio</i> , 2013, 3, 363-369.	1.0	105
4	Structures of human nucleosomes containing major histone H3 variants. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 578-583.	2.5	96
5	Testis-Specific Histone Variant H3t Gene Is Essential for Entry into Spermatogenesis. <i>Cell Reports</i> , 2017, 18, 593-600.	2.9	82
6	Nucleosome formation with the testis-specific histone H3 variant, H3t, by human nucleosome assembly proteins in vitro. <i>Nucleic Acids Research</i> , 2008, 36, 2208-2218.	6.5	78
7	Crystal structure of the overlapping dinucleosome composed of hexasome and octasome. <i>Science</i> , 2017, 356, 205-208.	6.0	77
8	The chromatin remodeler DDM1 prevents transposon mobility through deposition of histone variant H2A.W. <i>Nature Cell Biology</i> , 2021, 23, 391-400.	4.6	73
9	The centromeric nucleosome-like CENP α - τ -W α -X complex induces positive supercoils into DNA. <i>Nucleic Acids Research</i> , 2014, 42, 1644-1655.	6.5	72
10	Histone H2A variants confer specific properties to nucleosomes and impact on chromatin accessibility. <i>Nucleic Acids Research</i> , 2018, 46, 7675-7685.	6.5	65
11	N-terminal phosphorylation of HP1 \pm increases its nucleosome-binding specificity. <i>Nucleic Acids Research</i> , 2014, 42, 12498-12511.	6.5	63
12	Dynamic changes in CCAN organization through CENP-C during cell-cycle progression. <i>Molecular Biology of the Cell</i> , 2015, 26, 3768-3776.	0.9	62
13	Histone chaperone activity of Fanconi anemia proteins, FANCD2 and FANCI, is required for DNA crosslink repair. <i>EMBO Journal</i> , 2012, 31, 3524-3536.	3.5	61
14	Structural basis of a nucleosome containing histone H2A.B/H2A.Bbd that transiently associates with reorganized chromatin. <i>Scientific Reports</i> , 2013, 3, 3510.	1.6	61
15	Synthetic Posttranslational Modifications: Chemical Catalyst-Driven Regioselective Histone Acylation of Native Chromatin. <i>Journal of the American Chemical Society</i> , 2017, 139, 7568-7576.	6.6	60
16	Stable complex formation of CENP-B with the CENP-A nucleosome. <i>Nucleic Acids Research</i> , 2015, 43, 4909-4922.	6.5	59
17	Structural polymorphism in the L1 loop regions of human H2A.Z.1 and H2A.Z.2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2431-2439.	2.5	55
18	Nucleosome Formation Activity of Human Somatic Nuclear Autoantigenic Sperm Protein (sNASP). <i>Journal of Biological Chemistry</i> , 2010, 285, 11913-11921.	1.6	54

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19	Histone H3.5 forms an unstable nucleosome and accumulates around transcription start sites in human testis. <i>Epigenetics and Chromatin</i> , 2016, 9, 2.	1.8	53
20	The evolution and functional divergence of the histone H2B family in plants. <i>PLoS Genetics</i> , 2020, 16, e1008964.	1.5	51
21	Structure and function of human histone H3.Y nucleosome. <i>Nucleic Acids Research</i> , 2016, 44, 6127-6141.	6.5	44
22	Structural basis of pyrimidine-pyrimidone (6 ⁴) photoproduct recognition by UV-DDB in the nucleosome. <i>Scientific Reports</i> , 2015, 5, 16330.	1.6	39
23	Synthetic Chromatin Acylation by an Artificial Catalyst System. <i>CheM</i> , 2017, 2, 840-859.	5.8	29
24	Nap1 stimulates homologous recombination by RAD51 and RAD54 in higher-ordered chromatin containing histone H1. <i>Scientific Reports</i> , 2014, 4, 4863.	1.6	27
25	Vertebrate Spt2 is a novel nucleolar histone chaperone that assists in ribosomal DNA transcription. <i>Journal of Cell Science</i> , 2013, 126, 1323-32.	1.2	24
26	Influence of DNA methylation on positioning and DNA flexibility of nucleosomes with pericentric satellite DNA. <i>Open Biology</i> , 2015, 5, 150128.	1.5	22
27	C-terminal acidic domain of histone chaperone human <i>NAP1</i> is an efficient binding assistant for histone H2A ^{H2B} , but not H3 ^{H4} . <i>Genes To Cells</i> , 2016, 21, 252-263.	0.5	21
28	Crystal Structure and Characterization of Novel Human Histone H3 Variants, H3.6, H3.7, and H3.8. <i>Biochemistry</i> , 2017, 56, 2184-2196.	1.2	20
29	A Synthetic Approach to Reconstruct the Evolutionary and Functional Innovations of the Plant Histone Variant H2A.W. <i>Current Biology</i> , 2021, 31, 182-191.e5.	1.8	20
30	Nap1 regulates proper CENP-B binding to nucleosomes. <i>Nucleic Acids Research</i> , 2013, 41, 2869-2880.	6.5	19
31	Structure of human nucleosome containing the testis-specific histone variant TSH2B. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 444-449.	0.4	18
32	Crystal structure of the nucleosome containing ultraviolet light-induced cyclobutane pyrimidine dimer. <i>Biochemical and Biophysical Research Communications</i> , 2016, 471, 117-122.	1.0	17
33	DNA Binding Properties of the Actin-Related Protein Arp8 and Its Role in DNA Repair. <i>PLoS ONE</i> , 2014, 9, e108354.	1.1	16
34	Structural Diversity of Nucleosomes Characterized by Native Mass Spectrometry. <i>Analytical Chemistry</i> , 2018, 90, 8217-8226.	3.2	15
35	Structural Studies of Overlapping Dinucleosomes in Solution. <i>Biophysical Journal</i> , 2020, 118, 2209-2219.	0.2	15
36	Structural and biochemical analyses of the human PAD4 variant encoded by a functional haplotype gene. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 112-118.	2.5	14

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37	Human tNASP Promotes in Vitro Nucleosome Assembly with Histone H3.3. <i>Biochemistry</i> , 2015, 54, 1171-1179.	1.2	13
38	Histone renegades: Unusual H2A histone variants in plants and animals. <i>Seminars in Cell and Developmental Biology</i> , 2023, 135, 35-42.	2.3	13
39	Genome-Wide Profiling of Histone Modifications and Histone Variants in <i>Arabidopsis thaliana</i> and <i>Marchantia polymorpha</i> . <i>Methods in Molecular Biology</i> , 2017, 1610, 93-106.	0.4	9
40	Polymorphism of apyrimidinic DNA structures in the nucleosome. <i>Scientific Reports</i> , 2017, 7, 41783.	1.6	9
41	Influence of polynucleosome preparation methods on sedimentation velocity analysis of chromatin. <i>Journal of Biochemistry</i> , 2017, 161, 381-388.	0.9	5
42	The evolution and functional divergence of the histone H2B family in plants. , 2020, 16, e1008964.		1
43	The evolution and functional divergence of the histone H2B family in plants. , 2020, 16, e1008964.		0
44	The evolution and functional divergence of the histone H2B family in plants. , 2020, 16, e1008964.		0
45	The evolution and functional divergence of the histone H2B family in plants. , 2020, 16, e1008964.		0
46	The evolution and functional divergence of the histone H2B family in plants. , 2020, 16, e1008964.		0