Yasuo Tsunaka

List of Publications by Year
in descending order

24	975	566801 15	610482 24
papers	citations	h-index	g-index

25	25	25	1200
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Characteristic H3 N-tail dynamics in the nucleosome core particle, nucleosome, and chromatosome. IScience, 2022, 25, 103937.	1.9	5
2	Histone tail network and modulation in a nucleosome. Current Opinion in Structural Biology, 2022, 75, 102436.	2.6	8
3	The N-terminal Tails of Histones H2A and H2B Adopt Two Distinct Conformations in the Nucleosome with Contact and Reduced Contact to DNA. Journal of Molecular Biology, 2021, 433, 167110.	2.0	16
4	Partial Replacement of Nucleosomal DNA with Human FACT Induces Dynamic Exposure and Acetylation of Histone H3 N-Terminal Tails. IScience, 2020, 23, 101641.	1.9	15
5	Acetylated histone H4 tail enhances histone H3 tail acetylation by altering their mutual dynamics in the nucleosome. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19661-19663.	3.3	31
6	Structural visualization of key steps in nucleosome reorganization by human FACT. Scientific Reports, 2019, 9, 10183.	1.6	42
7	Significance of a histone-like protein with its native structure for the diagnosis of asymptomatic tuberculosis. PLoS ONE, 2018, 13, e0204160.	1.1	5
8	FACT Creates a Transiently Accessible Nucleosome Structure Through Integrated Reorganization Mechanism. Biochemistry & Molecular Biology Journal, 2016, 02, .	0.3	1
9	Integrated molecular mechanism directing nucleosome reorganization by human FACT. Genes and Development, 2016, 30, 673-686.	2.7	132
10	Construction and characterization of Cy3- or Cy5-conjugated hairpin pyrroleâ€“imidazole polyamides binding to DNA in the nucleosome. Biomaterials Science, 2014, 2, 297-307.	2.6	19
11	Phosphorylation-Coupled Intramolecular Dynamics of Unstructured Regions in Chromatin Remodeler FACT. Biophysical Journal, 2013, 104, 2222-2234.	0.2	26
12	Phosphorylated Intrinsically Disordered Region of FACT Masks Its Nucleosomal DNA Binding Elements. Journal of Biological Chemistry, 2009, 284, 24610-24621.	1.6	50
13	Visualization of Intrinsically Disordered Regions of Proteins by Highâ€Speed Atomic Force Microscopy. ChemPhysChem, 2008, 9, 1859-1866.	1.0	95
14	Solution structure of the HMG-box domain in the SSRP1 subunit of FACT. Journal of Biomolecular NMR, 2005, 32, 83-88.	1.6	19
15	Alteration of the nucleosomal DNA path in the crystal structure of a human nucleosome core particle. Nucleic Acids Research, 2005, 33, 3424-3434.	6.5	127
16	Identification of Single Mn2+ Binding Sites Required for Activation of the Mutant Proteins of E.coli RNase HI at Glu48 and/or Asp134 by X-ray Crystallography. Journal of Molecular Biology, 2005, 345, 1171-1183.	2.0	34
17	Structural basis for channelling mechanism of a fatty acid Î²-oxidation multienzyme complex. EMBO Journal, 2004, 23, 2745-2754.	3.5	101
18	Dispensability of Glutamic Acid 48 and Aspartic Acid 134 for Mn2+-Dependent Activity ofEscherichia coliRibonuclease HIâ€. Biochemistry, 2003, 42, 3366-3374.	1.2	21

#	Article	IF	Citations
19	Laser Irradiated Growth of Protein Crystal. Japanese Journal of Applied Physics, 2003, 42, L798-L800.	0.8	124
20	Site-specific cleavage of MS2 RNA by a thermostable DNA-linked RNase H. Protein Engineering, Design and Selection, 2002, 15, 683-688.	1.0	3
21	Cleavage of a DNA-RNA-DNA/DNA chimeric substrate containing a single ribonucleotide at the DNA-RNA junction with prokaryotic RNases HII. FEBS Letters, 2002, 531, 204-208.	1.3	60
22	Strong nucleic acid binding to the Escherichia coli RNase HI mutant with two arginine residues at the active site. BBA - Proteins and Proteomics, 2001, 1547, 135-142.	2.1	4
23	Efficient cleavage of RNA at high temperatures by a thermostable DNA-linked ribonuclease H. Protein Engineering, Design and Selection, 2000, 13, 881-886.	1.0	3
24	Catalysis byEscherichia coliRibonuclease HI Is Facilitated by a Phosphate Group of the Substrate. Biochemistry, 2000, 39, 13939-13944.	1.2	34