Takashi Umehara

List of Publications by Year
in descending order

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84 papers	3,720 citations	109321 35 h-index	138484 58 g-index
91 all docs	91 docs citations	91 times ranked	5536 citing authors

#	Article	IF	Citations
1	Chromosomal gradient of histone acetylation established by Sas2p and Sir2p functions as a shield against gene silencing. Nature Genetics, 2002, 32, 370-377.	21.4	412
2	Genome-wide Expression Analysis of Mouse Liver Reveals CLOCK-regulated Circadian Output Genes. Journal of Biological Chemistry, 2003, 278, 41519-41527.	3.4	306
3	FAD-dependent lysine-specific demethylase-1 regulates cellular energy expenditure. Nature Communications, 2012, 3, 758.	12.8	181
4	Structurally Designed trans-2-Phenylcyclopropylamine Derivatives Potently Inhibit Histone Demethylase LSD1/KDM1,,. Biochemistry, 2010, 49, 6494-6503.	2.5	163
5	Crystal structure of histone demethylase LSD1 and tranylcypromine at 2.25 Ã.... Biochemical and Biophysical Research Communications, 2008, 366, 15-22.	2.1	120
6	Crystal Structure of the Human BRD2 Bromodomain. Journal of Biological Chemistry, 2007, 282, 4193-4201.	3.4	109
7	Structural Basis for Acetylated Histone H4 Recognition by the Human BRD2 Bromodomain. Journal of Biological Chemistry, 2010, 285, 7610-7618.	3.4	105
8	Structural Insight into the Zinc Finger CW Domain as a Histone Modification Reader. Structure, 2010, 18, 1127-1139.	3.3	103
9	Crystal structure of eukaryotic translation initiation factor 2B. Nature, 2016, 531, 122-125.	27.8	103
10	Real-Time Imaging of Histone H4K12â€“Specific Acetylation Determines the Modes of Action of Histone Deacetylase and Bromodomain Inhibitors. Chemistry and Biology, 2011, 18, 495-507.	6.0	99
11	Cell death with predominant apoptotic features in Saccharomyces cerevisiae mediated by deletion of the histone chaperone ASF1/CIA1. Genes To Cells, 2001, 6, 1043-1054.	1.2	86
12	Temperature-Sensitive Substrate and Product Binding Underlie Temperature-Compensated Phosphorylation in the Clock. Molecular Cell, 2017, 67, 783-798.e20.	9.7	79
13	Genetic-code evolution for protein synthesis with non-natural amino acids. Biochemical and Biophysical Research Communications, 2011, 411, 757-761.	2.1	72
14	Intra- and inter-nucleosomal interactions of the histone H4 tail revealed with a human nucleosome core particle with genetically-incorporated H4 tetra-acetylation. Scientific Reports, 2015, 5, 17204.	3.3	67
15	Mapping of the basic aminoâ€acid residues responsible for tubulation and cellular protrusion by the EFC/Fâ€BAR domain of pacsin2/Syndapin II. FEBS Letters, 2010, 584, 1111-1118.	2.8	66
16	Structure of the Oncoprotein Gankyrin in Complex with S6 ATPase of the 26S Proteasome. Structure, 2007, 15, 179-189.	3.3	64
17	Global analysis of functional surfaces of core histones with comprehensive point mutants. Genes To Cells, 2007, 12, 13-33.	1.2	63
18	Solution Structure of the SWIRM Domain of Human Histone Demethylase LSD1. Structure, 2006, 14, 457-468.	3.3	59

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19	Polyanionic stretch-deleted histone chaperone cia1/Asf1p is functional bothin vivoandin vitro. Genes To Cells, 2002, 7, 59-73.	1.2	55
20	The methyltransferase METTL9 mediates pervasive 1-methylhistidine modification in mammalian proteomes. Nature Communications, 2021, 12, 891.	12.8	54
21	Crystal Structures of Fission Yeast Histone Chaperone Asf1 Complexed with the Hip1 B-domain or the Cac2 C Terminus. Journal of Biological Chemistry, 2008, 283, 14022-14031.	3.4	53
22	ST1710â€“DNA complex crystal structure reveals the DNA binding mechanism of the MarR family of regulators. Nucleic Acids Research, 2009, 37, 4723-4735.	14.5	50
23	Structural basis for the recognition between the regulatory particles Nas6 and Rpt3 of the yeast 26S proteasome. Biochemical and Biophysical Research Communications, 2007, 359, 503-509.	2.1	49
24	Distribution of histone H4 modifications as revealed by a panel of specific monoclonal antibodies. Chromosome Research, 2015, 23, 753-766.	2.2	49
25	Crystallographic Study of a Site-Specifically Cross-Linked Protein Complex with a Genetically Incorporated Photoreactive Amino Acid,. Biochemistry, 2011, 50, 250-257.	2.5	48
26	Identification of Cyproheptadine as an Inhibitor of SET Domain Containing Lysine Methyltransferase 7/9 (Set7/9) That Regulates Estrogen-Dependent Transcription. Journal of Medicinal Chemistry, 2016, 59, 3650-3660.	6.4	47
27	Structural implications for K5/K12â€diâ€acetylated histone H4 recognition by the second bromodomain of BRD2. FEBS Letters, 2010, 584, 3901-3908.	2.8	46
28	Structural insight into inhibitors of flavin adenine dinucleotide-dependent lysine demethylases. Epigenetics, 2017, 12, 340-352.	2.7	45
29	Solution structure of the extraterminal domain of the bromodomainâ€containing protein BRD4. Protein Science, 2008, 17, 2174-2179.	7.6	43
30	Tri-methylation of ATF7IP by G9a/GLP recruits the chromodomain protein MPP8. Epigenetics and Chromatin, 2018, 11, 56.	3.9	43
31	Discovery of Novel Spiroindoline Derivatives as Selective Tankyrase Inhibitors. Journal of Medicinal Chemistry, 2019, 62, 3407-3427.	6.4	43
32	IRS-1 acts as an endocytic regulator of IGF-I receptor to facilitate sustained IGF signaling. ELife, 2018, 7, .	6.0	43
33	Structural and Functional Differences of SWIRM Domain Subtypes. Journal of Molecular Biology, 2007, 369, 222-238.	4.2	41
34	Histone H4 lysine 20 acetylation is associated with gene repression in human cells. Scientific Reports, 2016, 6, 24318.	3.3	40
35	Multiple Siteâ€Specific Installations of N^{Îµ}â€Monomethylâ€<scp>L</scp>â€Lysine into Histone Proteins by Cellâ€Based and Cellâ€Free Protein Synthesis. ChemBioChem, 2014, 15, 1830-1838.	2.6	36
36	Solution Structure of Histone Chaperone ANP32B: Interaction with Core Histones H3â€“H4 through Its Acidic Concave Domain. Journal of Molecular Biology, 2010, 401, 97-114.	4.2	35

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37	Transcription Initiation Factor IID-interactive Histone Chaperone CIA-II Implicated in Mammalian Spermatogenesis. Journal of Biological Chemistry, 2003, 278, 35660-35667.	3.4	33
38	JQ1 affects BRD2-dependent and independent transcription regulation without disrupting H4-hyperacetylated chromatin states. Epigenetics, 2018, 13, 410-431.	2.7	32
39	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.	7.1	31
40	Rational design and implementation of a chemically inducible heterotrimerization system. Nature Methods, 2020, 17, 928-936.	19.0	30
41	Cell-permeable Carboxyl-terminal p27Kip1 Peptide Exhibits Anti-tumor Activity by Inhibiting Pim-1 Kinase. Journal of Biological Chemistry, 2011, 286, 2681-2688.	3.4	29
42	Expanded Genetic Code Technologies for Incorporating Modified Lysine at Multiple Sites. ChemBioChem, 2014, 15, 2181-2187.	2.6	29
43	Lysine-Specific Demethylase 2 Suppresses Lipid Influx and Metabolism in Hepatic Cells. Molecular and Cellular Biology, 2015, 35, 1068-1080.	2.3	28
44	Design and Discovery of an Orally Efficacious Spiroindolinone-Based Tankyrase Inhibitor for the Treatment of Colon Cancer. Journal of Medicinal Chemistry, 2020, 63, 4183-4204.	6.4	25
45	Crystal Structure Analysis of the PHD Domain of the Transcription Co-activator Pygopus. Journal of Molecular Biology, 2007, 370, 80-92.	4.2	23
46	Solution structure of the zinc finger HIT domain in protein FON. Protein Science, 2007, 16, 1577-1587.	7.6	23
47	Development and crystallographic evaluation of histone H3 peptide with N-terminal serine substitution as a potent inhibitor of lysine-specific demethylase 1. Bioorganic and Medicinal Chemistry, 2017, 25, 2617-2624.	3.0	22
48	Isolation and characterization of a cDNA encoding a new type of human transcription elongation factor S-II. Gene, 1995, 167, 297-302.	2.2	21
49	Crystal Structure of LSD1 in Complex with 4-[5-(Piperidin-4-ylmethoxy)-2-(p-tolyl)pyridin-3-yl]benzonitrile. Molecules, 2018, 23, 1538.	3.8	20
50	Structures of histone methyltransferase SET7/9 in complexes with adenosylmethionine derivatives. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 595-602.	2.5	19
51	Development and Structural Evaluation of Nâ€Alkylated transâ€2â€Phenylcyclopropylamineâ€Based LSD1 Inhibitors. ChemMedChem, 2020, 15, 787-793.	3.2	18
52	Solution structures of the DNA-binding domains of immune-related zinc-finger protein ZFAT. Journal of Structural and Functional Genomics, 2015, 16, 55-65.	1.2	17
53	Activation of lysine-specific demethylase 1 inhibitor peptide by redox-controlled cleavage of a traceless linker. Bioorganic and Medicinal Chemistry, 2017, 25, 1227-1234.	3.0	17
54	Eradication of Central Nervous System Leukemia of T-Cell Origin with a Brain-Permeable LSD1 Inhibitor. Clinical Cancer Research, 2019, 25, 1601-1611.	7.0	17

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55	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.	4.2	16
56	Crystal structure of RNA polymerase II from Komagataella pastoris. Biochemical and Biophysical Research Communications, 2017, 487, 230-235.	2.1	15
57	Restricted Expression of a Member of the Transcription Elongation Factor S-II Family in Testicular Germ Cells during and after Meiosis. Journal of Biochemistry, 1997, 121, 598-603.	1.7	14
58	Lysine-specific demethylase 1 inhibitors prevent teratoma development from human induced pluripotent stem cells. Oncotarget, 2018, 9, 6450-6462.	1.8	14
59	Development of a hexahistidine-3Ã— FLAG-tandem affinity purification method for endogenous protein complexes in Pichia pastoris. Journal of Structural and Functional Genomics, 2014, 15, 191-199.	1.2	12
60	Characterization of lysine acetylation of a phosphoenolpyruvate carboxylase involved in glutamate overproduction in <scp>C</scp>orynebacterium glutamicum. Molecular Microbiology, 2017, 104, 677-689.	2.5	12
61	Crystal structure of human nucleosome core particle containing enzymatically introduced CpG methylation. FEBS Open Bio, 2016, 6, 498-514.	2.3	11
62	Development of Novel Inhibitors for Histone Methyltransferase SET7/9 based on Cyproheptadine. ChemMedChem, 2018, 13, 1530-1540.	3.2	11
63	Structure-Based Identification of Potent Lysine-Specific Demethylase 1 Inhibitor Peptides and Temporary Cyclization to Enhance Proteolytic Stability and Cell Growth-Inhibitory Activity. Journal of Medicinal Chemistry, 2021, 64, 3707-3719.	6.4	11
64	Structural Similarity between Histone Chaperone Cia1p/Asf1p and DNA-Binding Protein NF-Î°B. Journal of Biochemistry, 2005, 138, 821-829.	1.7	10
65	Design and Synthesis of Tranylcypromine-Derived LSD1 Inhibitors with Improved hERG and Microsomal Stability Profiles. ACS Medicinal Chemistry Letters, 2022, 13, 848-854.	2.8	9
66	A tandem insertion vector for large-scale preparation of nucleosomal DNA. Analytical Biochemistry, 2012, 423, 184-186.	2.4	8
67	Crystallization of the archaeal transcription termination factor NusA: a significant decrease in twinning under microgravity conditions. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 69-73.	0.7	6
68	A series of bacterial co-expression vectors with rare-cutter recognition sequences. Protein Expression and Purification, 2010, 74, 88-98.	1.3	6
69	Quantification of the effect of site-specific histone acetylation on chromatin transcription rate. Nucleic Acids Research, 2020, 48, 12648-12659.	14.5	6
70	Structure-activity relationship for the folding intermediate-selective inhibition of DYRK1A. European Journal of Medicinal Chemistry, 2022, 227, 113948.	5.5	6
71	Ultrasensitive Change in Nucleosome Binding by Multiple Phosphorylations to the Intrinsically Disordered Region of the Histone Chaperone FACT. Journal of Molecular Biology, 2020, 432, 4637-4657.	4.2	5
72	Characteristic H3 N-tail dynamics in the nucleosome core particle, nucleosome, and chromatosome. IScience, 2022, 25, 103937.	4.1	5

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73	Elucidation of binding preferences of YEATS domains to site-specific acetylated nucleosome core particles. Journal of Biological Chemistry, 2022, 298, 102164.	3.4	5
74	Visualization of the dynamic interaction between nucleosomal histone H3K9 tri-methylation and HP1Î± chromodomain in living cells. Cell Chemical Biology, 2022, 29, 1153-1161.e5.	5.2	5
75	Isolation of a cDNA encoding a mouse TFIID subunit containing histone H4 homology. Gene, 1995, 161, 301-302.	2.2	4
76	Three distinct regions in a rat TFIID subunit containing histone H4 homology. Gene, 1995, 161, 303-304.	2.2	4
77	Purification, crystallization and preliminary X-ray diffraction of the C-terminal bromodomain from human BRD2. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 613-615.	0.7	3
78	Epidrugs: Toward Understanding and Treating Diverse Diseases. Epigenomes, 2022, 6, 18.	1.8	3
79	Purification, crystallization and preliminary X-ray diffraction analysis of the non-ATPase subunit Nas6 in complex with the ATPase subunit Rpt3 of the 26S proteasome fromSaccharomyces cerevisiae. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 190-192.	0.7	2
80	Inhibition of FAD-dependent lysine-specific demethylases by chiral polyamine analogues. RSC Advances, 2018, 8, 36895-36902.	3.6	2
81	Chemoselective Arylation of Dialkyl Diselenides and Application to the Synthesis of a Îµâ€•N,N,N â€Trimethyllysine Derivative. European Journal of Organic Chemistry, 2020, 2020, 6649-6652.	2.4	2
82	Purification, crystallization and preliminary X-ray diffraction analysis of the histone chaperone cia1 from fission yeast. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 971-973.	0.7	1
83	Structural Biology Toward Rational Drug Development in Collaboration with Molecular Imaging. Current Medical Imaging, 2012, 8, 308-313.	0.8	0
84	Single-Molecule Analysis of Colocalized Epigenetic Modifications. Biophysical Journal, 2016, 110, 66a.	0.5	0