

# 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	Structure-activity relationship for the folding intermediate-selective inhibition of DYRK1A. <i>European Journal of Medicinal Chemistry</i> , 2022, 227, 113948.	5.5	6
2	Characteristic H3 N-tail dynamics in the nucleosome core particle, nucleosome, and chromatosome. <i>IScience</i> , 2022, 25, 103937.	4.1	5
3	Design and Synthesis of Tranlylcyproamine-Derived LSD1 Inhibitors with Improved hERG and Microsomal Stability Profiles. <i>ACS Medicinal Chemistry Letters</i> , 2022, 13, 848-854.	2.8	9
4	Elucidation of binding preferences of YEATS domains to site-specific acetylated nucleosome core particles. <i>Journal of Biological Chemistry</i> , 2022, 298, 102164.	3.4	5
5	Visualization of the dynamic interaction between nucleosomal histone H3K9 tri-methylation and HP1± chromodomain in living cells. <i>Cell Chemical Biology</i> , 2022, 29, 1153-1161.e5.	5.2	5
6	Epidrugs: Toward Understanding and Treating Diverse Diseases. <i>Epigenomes</i> , 2022, 6, 18.	1.8	3
7	The methyltransferase METTL9 mediates pervasive 1-methylhistidine modification in mammalian proteomes. <i>Nature Communications</i> , 2021, 12, 891.	12.8	54
8	Structure-Based Identification of Potent Lysine-Specific Demethylase 1 Inhibitor Peptides and Temporary Cyclization to Enhance Proteolytic Stability and Cell Growth-Inhibitory Activity. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 3707-3719.	6.4	11
9	The N-terminal Tails of Histones H2A and H2B Adopt Two Distinct Conformations in the Nucleosome with Contact and Reduced Contact to DNA. <i>Journal of Molecular Biology</i> , 2021, 433, 167110.	4.2	16
10	Quantification of the effect of site-specific histone acetylation on chromatin transcription rate. <i>Nucleic Acids Research</i> , 2020, 48, 12648-12659.	14.5	6
11	Acetylated histone H4 tail enhances histone H3 tail acetylation by altering their mutual dynamics in the nucleosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19661-19663.	7.1	31
12	Rational design and implementation of a chemically inducible heterotrimerization system. <i>Nature Methods</i> , 2020, 17, 928-936.	19.0	30
13	Ultrasensitive Change in Nucleosome Binding by Multiple Phosphorylations to the Intrinsically Disordered Region of the Histone Chaperone FACT. <i>Journal of Molecular Biology</i> , 2020, 432, 4637-4657.	4.2	5
14	Design and Discovery of an Orally Efficacious Spiroindolinone-Based Tankyrase Inhibitor for the Treatment of Colon Cancer. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 4183-4204.	6.4	25
15	Development and Structural Evaluation of <i>N</i> -alkylated <i>trans</i> -phenylcyclopropylamine-Based LSD1 Inhibitors. <i>ChemMedChem</i> , 2020, 15, 787-793.	3.2	18
16	Chemoselective Arylation of Dialkyl Diselenides and Application to the Synthesis of a $\mu$ -N,N,N-trimethyllysine Derivative. <i>European Journal of Organic Chemistry</i> , 2020, 2020, 6649-6652.	2.4	2
17	Eradication of Central Nervous System Leukemia of T-Cell Origin with a Brain-Permeable LSD1 Inhibitor. <i>Clinical Cancer Research</i> , 2019, 25, 1601-1611.	7.0	17
18	Discovery of Novel Spiroindoline Derivatives as Selective Tankyrase Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 3407-3427.	6.4	43

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19	Inhibition of FAD-dependent lysine-specific demethylases by chiral polyamine analogues. RSC Advances, 2018, 8, 36895-36902.	3.6	2
20	Tri-methylation of ATF7IP by G9a/GLP recruits the chromodomain protein MPP8. Epigenetics and Chromatin, 2018, 11, 56.	3.9	43
21	JQ1 affects BRD2-dependent and independent transcription regulation without disrupting H4-hyperacetylated chromatin states. Epigenetics, 2018, 13, 410-431.	2.7	32
22	Crystal Structure of LSD1 in Complex with 4-[5-(Piperidin-4-ylmethoxy)-2-(p-tolyl)pyridin-3-yl]benzotrile. Molecules, 2018, 23, 1538.	3.8	20
23	Development of Novel Inhibitors for Histone Methyltransferase SET7/9 based on Cyproheptadine. ChemMedChem, 2018, 13, 1530-1540.	3.2	11
24	Lysine-specific demethylase 1 inhibitors prevent teratoma development from human induced pluripotent stem cells. Oncotarget, 2018, 9, 6450-6462.	1.8	14
25	IRS-1 acts as an endocytic regulator of IGF-I receptor to facilitate sustained IGF signaling. ELife, 2018, 7, .	6.0	43
26	Characterization of lysine acetylation of a phosphoenolpyruvate carboxylase involved in glutamate overproduction in <i>Corynebacterium glutamicum</i> . Molecular Microbiology, 2017, 104, 677-689.	2.5	12
27	Structural insight into inhibitors of flavin adenine dinucleotide-dependent lysine demethylases. Epigenetics, 2017, 12, 340-352.	2.7	45
28	Crystal structure of RNA polymerase II from <i>Komagataella pastoris</i> . Biochemical and Biophysical Research Communications, 2017, 487, 230-235.	2.1	15
29	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
30	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
31	Temperature-Sensitive Substrate and Product Binding Underlie Temperature-Compensated Phosphorylation in the Clock. Molecular Cell, 2017, 67, 783-798.e20.	9.7	79
32	Crystal structure of human nucleosome core particle containing enzymatically introduced CpG methylation. FEBS Open Bio, 2016, 6, 498-514.	2.3	11
33	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
34	Histone H4 lysine 20 acetylation is associated with gene repression in human cells. Scientific Reports, 2016, 6, 24318.	3.3	40
35	Single-Molecule Analysis of Colocalized Epigenetic Modifications. Biophysical Journal, 2016, 110, 66a.	0.5	0
36	Crystal structure of eukaryotic translation initiation factor 2B. Nature, 2016, 531, 122-125.	27.8	103

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37	Intra- and inter-nucleosomal interactions of the histone H4 tail revealed with a human nucleosome core particle with genetically-incorporated H4 tetra-acetylation. <i>Scientific Reports</i> , 2015, 5, 17204.	3.3	67
38	Lysine-Specific Demethylase 2 Suppresses Lipid Influx and Metabolism in Hepatic Cells. <i>Molecular and Cellular Biology</i> , 2015, 35, 1068-1080.	2.3	28
39	Solution structures of the DNA-binding domains of immune-related zinc-finger protein ZFAT. <i>Journal of Structural and Functional Genomics</i> , 2015, 16, 55-65.	1.2	17
40	Distribution of histone H4 modifications as revealed by a panel of specific monoclonal antibodies. <i>Chromosome Research</i> , 2015, 23, 753-766.	2.2	49
41	Multiple Site-Specific Installations of $\mu$ -Monomethyl-Lysine into Histone Proteins by Cell-Based and Cell-Free Protein Synthesis. <i>ChemBioChem</i> , 2014, 15, 1830-1838.	2.6	36
42	Development of a hexahistidine-3 $\times$ FLAG-tandem affinity purification method for endogenous protein complexes in <i>Pichia pastoris</i> . <i>Journal of Structural and Functional Genomics</i> , 2014, 15, 191-199.	1.2	12
43	Expanded Genetic Code Technologies for Incorporating Modified Lysine at Multiple Sites. <i>ChemBioChem</i> , 2014, 15, 2181-2187.	2.6	29
44	Structures of histone methyltransferase SET7/9 in complexes with adenosylmethionine derivatives. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 595-602.	2.5	19
45	FAD-dependent lysine-specific demethylase-1 regulates cellular energy expenditure. <i>Nature Communications</i> , 2012, 3, 758.	12.8	181
46	Structural Biology Toward Rational Drug Development in Collaboration with Molecular Imaging. <i>Current Medical Imaging</i> , 2012, 8, 308-313.	0.8	0
47	A tandem insertion vector for large-scale preparation of nucleosomal DNA. <i>Analytical Biochemistry</i> , 2012, 423, 184-186.	2.4	8
48	Crystallographic Study of a Site-Specifically Cross-Linked Protein Complex with a Genetically Incorporated Photoreactive Amino Acid. <i>Biochemistry</i> , 2011, 50, 250-257.	2.5	48
49	Genetic-code evolution for protein synthesis with non-natural amino acids. <i>Biochemical and Biophysical Research Communications</i> , 2011, 411, 757-761.	2.1	72
50	Real-Time Imaging of Histone H4K12-Specific Acetylation Determines the Modes of Action of Histone Deacetylase and Bromodomain Inhibitors. <i>Chemistry and Biology</i> , 2011, 18, 495-507.	6.0	99
51	Cell-permeable Carboxyl-terminal p27Kip1 Peptide Exhibits Anti-tumor Activity by Inhibiting Pim-1 Kinase. <i>Journal of Biological Chemistry</i> , 2011, 286, 2681-2688.	3.4	29
52	Structural Insight into the Zinc Finger CW Domain as a Histone Modification Reader. <i>Structure</i> , 2010, 18, 1127-1139.	3.3	103
53	Mapping of the basic amino acid residues responsible for tubulation and cellular protrusion by the EFC/F $\bar{A}$ BAR domain of pacsin2/Syndapin II. <i>FEBS Letters</i> , 2010, 584, 1111-1118.	2.8	66
54	Structural implications for K5/K12-acetylated histone H4 recognition by the second bromodomain of BRD2. <i>FEBS Letters</i> , 2010, 584, 3901-3908.	2.8	46

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55	Structural Basis for Acetylated Histone H4 Recognition by the Human BRD2 Bromodomain. <i>Journal of Biological Chemistry</i> , 2010, 285, 7610-7618.	3.4	105
56	Solution Structure of Histone Chaperone ANP32B: Interaction with Core Histones H3&H4 through Its Acidic Concave Domain. <i>Journal of Molecular Biology</i> , 2010, 401, 97-114.	4.2	35
57	A series of bacterial co-expression vectors with rare-cutter recognition sequences. <i>Protein Expression and Purification</i> , 2010, 74, 88-98.	1.3	6
58	Structurally Designed <i>trans</i> -2-Phenylcyclopropylamine Derivatives Potently Inhibit Histone Demethylase LSD1/KDM1,, <i>Biochemistry</i> , 2010, 49, 6494-6503.	2.5	163
59	ST1710&DNA complex crystal structure reveals the DNA binding mechanism of the MarR family of regulators. <i>Nucleic Acids Research</i> , 2009, 37, 4723-4735.	14.5	50
60	Solution structure of the extraterminal domain of the bromodomain&containing protein BRD4. <i>Protein Science</i> , 2008, 17, 2174-2179.	7.6	43
61	Crystal structure of histone demethylase LSD1 and tranlycypromine at 2.25 Å... <i>Biochemical and Biophysical Research Communications</i> , 2008, 366, 15-22.	2.1	120
62	Crystal Structures of Fission Yeast Histone Chaperone Asf1 Complexed with the Hip1 B-domain or the Cac2 C Terminus. <i>Journal of Biological Chemistry</i> , 2008, 283, 14022-14031.	3.4	53
63	Crystal Structure of the Human BRD2 Bromodomain. <i>Journal of Biological Chemistry</i> , 2007, 282, 4193-4201.	3.4	109
64	Structural basis for the recognition between the regulatory particles Nas6 and Rpt3 of the yeast 26S proteasome. <i>Biochemical and Biophysical Research Communications</i> , 2007, 359, 503-509.	2.1	49
65	Structural and Functional Differences of SWIRM Domain Subtypes. <i>Journal of Molecular Biology</i> , 2007, 369, 222-238.	4.2	41
66	Crystal Structure Analysis of the PHD Domain of the Transcription Co-activator Pygopus. <i>Journal of Molecular Biology</i> , 2007, 370, 80-92.	4.2	23
67	Crystallization of the archaeal transcription termination factor NusA: a significant decrease in twinning under microgravity conditions. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 69-73.	0.7	6
68	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 from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 190-192.	0.7	2
69	Purification, crystallization and preliminary X-ray diffraction of the C-terminal bromodomain from human BRD2. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 613-615.	0.7	3
70	Global analysis of functional surfaces of core histones with comprehensive point mutants. <i>Genes To Cells</i> , 2007, 12, 13-33.	1.2	63
71	Structure of the Oncoprotein Gankyrin in Complex with S6 ATPase of the 26S Proteasome. <i>Structure</i> , 2007, 15, 179-189.	3.3	64
72	Solution structure of the zinc finger HIT domain in protein FON. <i>Protein Science</i> , 2007, 16, 1577-1587.	7.6	23

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73	Solution Structure of the SWIRM Domain of Human Histone Demethylase LSD1. <i>Structure</i> , 2006, 14, 457-468.	3.3	59
74	Purification, crystallization and preliminary X-ray diffraction analysis of the histone chaperone cia1 from fission yeast. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 971-973.	0.7	1
75	Structural Similarity between Histone Chaperone Cia1p/Asf1p and DNA-Binding Protein NF- $\kappa$ B. <i>Journal of Biochemistry</i> , 2005, 138, 821-829.	1.7	10
76	Genome-wide Expression Analysis of Mouse Liver Reveals CLOCK-regulated Circadian Output Genes. <i>Journal of Biological Chemistry</i> , 2003, 278, 41519-41527.	3.4	306
77	Transcription Initiation Factor IID-interactive Histone Chaperone CIA-II Implicated in Mammalian Spermatogenesis. <i>Journal of Biological Chemistry</i> , 2003, 278, 35660-35667.	3.4	33
78	Polyanionic stretch-deleted histone chaperone cia1/Asf1p is functional both in vivo and in vitro. <i>Genes To Cells</i> , 2002, 7, 59-73.	1.2	55
79	Chromosomal gradient of histone acetylation established by Sas2p and Sir2p functions as a shield against gene silencing. <i>Nature Genetics</i> , 2002, 32, 370-377.	21.4	412
80	Cell death with predominant apoptotic features in <i>Saccharomyces cerevisiae</i> mediated by deletion of the histone chaperone ASF1/CIA1. <i>Genes To Cells</i> , 2001, 6, 1043-1054.	1.2	86
81	Restricted Expression of a Member of the Transcription Elongation Factor S-II Family in Testicular Germ Cells during and after Meiosis. <i>Journal of Biochemistry</i> , 1997, 121, 598-603.	1.7	14
82	Isolation of a cDNA encoding a mouse TFIID subunit containing histone H4 homology. <i>Gene</i> , 1995, 161, 301-302.	2.2	4
83	Three distinct regions in a rat TFIID subunit containing histone H4 homology. <i>Gene</i> , 1995, 161, 303-304.	2.2	4
84	Isolation and characterization of a cDNA encoding a new type of human transcription elongation factor S-II. <i>Gene</i> , 1995, 167, 297-302.	2.2	21