Yu-hang Chen

List of Publications by Year
in descending order

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69 papers	6,707 citations	136885 32 h-index	91828 69 g-index
73 all docs	73 docs citations	73 times ranked	11025 citing authors

#	Article	IF	Citations
1	Cryo-EM structure and electrophysiological characterization of ALMT from Glycine max reveal a previously uncharacterized class of anion channels. Science Advances, 2022, 8, eabm3238.	4.7	13
2	Global profiling of regulatory elements in the histone benzoylation pathway. Nature Communications, 2022, 13, 1369.	5.8	6
3	Distinct kinetic mechanisms of H3K4 methylation catalyzed by MLL3 and MLL4 core complexes. Journal of Biological Chemistry, 2021, 296, 100635.	1.6	6
4	Dri1 mediates heterochromatin assembly via RNAi and histone deacetylation. Genetics, 2021, 218, .	1.2	4
5	Structure and activity of SLAC1 channels for stomatal signaling in leaves. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	35
6	The ZAR1 resistosome is a calcium-permeable channel triggering plant immune signaling. Cell, 2021, 184, 3528-3541.e12.	13.5	308
7	Distinct functions of POT1 proteins contribute to the regulation of telomerase recruitment to telomeres. Nature Communications, 2021, 12, 5514.	5.8	20
8	Ccp1-Ndc80 switch at the N terminus of CENP-T regulates kinetochore assembly. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	3
9	The Structural Basis for Specific Recognition of H3K14 Acetylation by Sth1 in the RSC Chromatin Remodeling Complex. Structure, 2020, 28, 111-118.e3.	1.6	18
10	N-terminal modified cyclopeptidic mimetics of ApolloTBM as inhibitors of TRF2. Bioorganic and Medicinal Chemistry Letters, 2020, 30, 127401.	1.0	4
11	Rationally Designed APOBEC3B Cytosine Base Editors with Improved Specificity. Molecular Cell, 2020, 79, 728-740.e6.	4.5	104
12	Crystal Structure of MLL2 Complex Guides the Identification of a Methylation Site on P53 Catalyzed by KMT2 Family Methyltransferases. Structure, 2020, 28, 1141-1148.e4.	1.6	14
13	Molecular Architecture of the SARS-CoV-2 Virus. Cell, 2020, 183, 730-738.e13.	13.5	793
14	Taf14 recognizes a common motif in transcriptional machineries and facilitates their clustering by phase separation. Nature Communications, 2020, 11, 4206.	5.8	19
15	Microcephalin 1/BRIT1-TRF2 interaction promotes telomere replication and repair, linking telomere dysfunction to primary microcephaly. Nature Communications, 2020, 11, 5861.	5.8	13
16	The relationship between H19 and parameters of ovarian reserve. Reproductive Biology and Endocrinology, 2020, 18, 46.	1.4	12
17	Development and optimization of a cascade of screening assays for inhibitors of TRF2. Analytical Biochemistry, 2020, 602, 113796.	1.1	3
18	Targeted, random mutagenesis of plant genes with dual cytosine and adenine base editors. Nature Biotechnology, 2020, 38, 875-882.	9.4	259

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19	Characterization and Nonenzymatic Transformation of Three Types of Alkaloids from Streptomyces albogriseolus MGR072 and Discovery of Inhibitors of Indoleamine 2,3-Dioxygenase. Organic Letters, 2019, 21, 8577-8581.	2.4	10
20	Structural basis of nucleosome recognition and modification by MLL methyltransferases. Nature, 2019, 573, 445-449.	13.7	134
21	The internal interaction in RBBP5 regulates assembly and activity of MLL1 methyltransferase complex. Nucleic Acids Research, 2019, 47, 10426-10438.	6.5	16
22	Chromosome engineering of the TCA cycle in Halomonas bluephagenesis for production of copolymers of 3-hydroxybutyrate and 3-hydroxyvalerate (PHBV). Metabolic Engineering, 2019, 54, 69-82.	3.6	65
23	Microbial engineering for easy downstream processing. Biotechnology Advances, 2019, 37, 107365.	6.0	52
24	Absence of the long noncoding RNA H19 results in aberrant ovarian STAR and progesterone production. Molecular and Cellular Endocrinology, 2019, 490, 15-20.	1.6	22
25	Structural basis for activity of TRIC counter-ion channels in calcium release. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 4238-4243.	3.3	26
26	The Replisome Mediates A-NHEJ Repair of Telomeres Lacking POT1-TPP1 Independently of MRN Function. Cell Reports, 2019, 29, 3708-3725.e5.	2.9	10
27	Developmental ROS individualizes organismal stress resistance and lifespan. Nature, 2019, 576, 301-305.	13.7	151
28	Structural insights into chromosome attachment to the nuclear envelope by an inner nuclear membrane protein Bqt4 in fission yeast. Nucleic Acids Research, 2019, 47, 1573-1584.	6.5	16
29	The structural biology of the shelterin complex. Biological Chemistry, 2019, 400, 457-466.	1.2	19
30	The Inner Nuclear Membrane Protein Bqt4 in Fission Yeast Contains a DNA-Binding Domain Essential for Telomere Association with the Nuclear Envelope. Structure, 2019, 27, 335-343.e3.	1.6	8
31	Cyclic Peptidic Mimetics of Apollo Peptides Targeting Telomeric Repeat Binding Factor 2 (TRF2) and Apollo Interaction. ACS Medicinal Chemistry Letters, 2018, 9, 507-511.	1.3	10
32	CRISPRâ€“Cas9-mediated base-editing screening in mice identifies DND1 amino acids that are critical for primordial germ cell development. Nature Cell Biology, 2018, 20, 1315-1325.	4.6	54
33	Heterochromatin and RNAi regulate centromeres by protecting CENP-A from ubiquitin-mediated degradation. PLoS Genetics, 2018, 14, e1007572.	1.5	15
34	NBS1 Phosphorylation Status Dictates Repair Choice of Dysfunctional Telomeres. Molecular Cell, 2017, 65, 801-817.e4.	4.5	45
35	A sequential EMT-MET mechanism drives the differentiation of human embryonic stem cells towards hepatocytes. Nature Communications, 2017, 8, 15166.	5.8	106
36	Structural basis for conductance through TRIC cation channels. Nature Communications, 2017, 8, 15103.	5.8	12

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37	Discovery of a Highly Potent, Cell-Permeable Macrocyclic Peptidomimetic (MM-589) Targeting the WD Repeat Domain 5 Protein (WDR5)â€“Mixed Lineage Leukemia (MLL) Proteinâ€“Protein Interaction. Journal of Medicinal Chemistry, 2017, 60, 4818-4839.	2.9	72
38	Structural basis for DAXX interaction with ATRX. Protein and Cell, 2017, 8, 767-771.	4.8	10
39	Structural and functional analyses of the mammalian TIN2-TPP1-TRF2 telomeric complex. Cell Research, 2017, 27, 1485-1502.	5.7	76
40	Structure of the fission yeast S. pombe telomeric Tpz1-Poz1-Rap1 complex. Cell Research, 2017, 27, 1503-1520.	5.7	14
41	Coordinated regulation of heterochromatin inheritance by Dpb3â€“Dpb4 complex. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 12524-12529.	3.3	47
42	Dimerization of SLX4 contributes to functioning of the SLX4-nuclease complex. Nucleic Acids Research, 2016, 44, 4871-4880.	6.5	14
43	Ccp1 Homodimer Mediates Chromatin Integrity by Antagonizing CENP-A Loading. Molecular Cell, 2016, 64, 79-91.	4.5	20
44	TRF2-RAP1 is required to protect telomeres from engaging in homologous recombination-mediated deletions and fusions. Nature Communications, 2016, 7, 10881.	5.8	106
45	Design of High-Affinity Stapled Peptides To Target the Repressor Activator Protein 1 (RAP1)/Telomeric Repeat-Binding Factor 2 (TRF2) Proteinâ€“Protein Interaction in the Shelterin Complex. Journal of Medicinal Chemistry, 2016, 59, 328-334.	2.9	18
46	Structural basis for activity regulation of MLL family methyltransferases. Nature, 2016, 530, 447-452.	13.7	189
47	Targeting MLL1 H3K4 Methyltransferase Activity in Mixed-Lineage Leukemia. Molecular Cell, 2014, 53, 247-261.	4.5	252
48	Essential role of lncRNA binding for WDR5 maintenance of active chromatin and embryonic stem cell pluripotency. ELife, 2014, 3, e02046.	2.8	176
49	SLX4 Assembles a Telomere Maintenance Toolkit by Bridging Multiple Endonucleases with Telomeres. Cell Reports, 2013, 4, 861-869.	2.9	103
50	High-Affinity, Small-Molecule Peptidomimetic Inhibitors of MLL1/WDR5 Proteinâ€“Protein Interaction. Journal of the American Chemical Society, 2013, 135, 669-682.	6.6	157
51	Structure of the SPRY domain of human Ash2L and its interactions with RbBP5 and DPY30. Cell Research, 2012, 22, 598-602.	5.7	44
52	Dimeric SecA Couples the Preprotein Translocation in an Asymmetric Manner. PLoS ONE, 2011, 6, e16498.	1.1	8
53	A conserved motif within RAP1 has diversified roles in telomere protection and regulation in different organisms. Nature Structural and Molecular Biology, 2011, 18, 213-221.	3.6	100
54	A long noncoding RNA maintains active chromatin to coordinate homeotic gene expression. Nature, 2011, 472, 120-124.	13.7	1,760

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55	Crystal structure of the Nâ€terminal region of human Ash2L shows a wingedâ€helix motif involved in DNA binding. EMBO Reports, 2011, 12, 797-803.	2.0	49
56	An Ash2L/RbBP5 Heterodimer Stimulates the MLL1 Methyltransferase Activity through Coordinated Substrate Interactions with the MLL1 SET Domain. PLoS ONE, 2010, 5, e14102.	1.1	98
57	Structural Basis of Selective Ubiquitination of TRF1 by SCFFbx4. Developmental Cell, 2010, 18, 214-225.	3.1	55
58	Activation of DegP chaperone-protease via formation of large cage-like oligomers upon binding to substrate proteins. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 11939-11944.	3.3	151
59	Full-length Escherichia coli SecA Dimerizes in a Closed Conformation in Solution as Determined by Cryo-electron Microscopy. Journal of Biological Chemistry, 2008, 283, 28783-28787.	1.6	19
60	A Shared Docking Motif in TRF1 and TRF2 Used for Differential Recruitment of Telomeric Proteins. Science, 2008, 319, 1092-1096.	6.0	227
61	The active ring-like structure of SecA revealed by electron crystallography: Conformational change upon interaction with SecB. Journal of Structural Biology, 2007, 159, 149-153.	1.3	16
62	The identification of a new actin-binding region in p57. Cell Research, 2006, 16, 106-112.	5.7	20
63	Crystal structure of human histone lysine-specific demethylase 1 (LSD1). Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13956-13961.	3.3	248
64	Escherichia coli CorA Periplasmic Domain Functions as a Homotetramer to Bind Substrate. Journal of Biological Chemistry, 2006, 281, 26813-26820.	1.6	13
65	Two-dimensional crystallization of a small heat shock protein HSP16.3 on lipid layer. Biochemical and Biophysical Research Communications, 2003, 310, 360-366.	1.0	8
66	Practical aspects of overexpressing bacterial secondary membrane transporters for structural studies. Biochimica Et Biophysica Acta - Biomembranes, 2003, 1610, 23-36.	1.4	71
67	DnaK and DnaJ facilitated the folding process and reduced inclusion body formation of magnesium transporter CorA overexpressed in Escherichia coli. Protein Expression and Purification, 2003, 32, 221-231.	0.6	80
68	Ring-like pore structures of SecA: Implication for bacterial protein-conducting channels. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 4221-4226.	3.3	69
69	Polymorphism of structural forms of C-reactive protein. International Journal of Molecular Medicine, 2002, 9, 665.	1.8	10