Lin Chen

List of Publications by Year
in descending order

86	9,037	76326	53230
papers	citations	40 h-index	85 g-index

124	124	124	11986
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Mechanism of forkhead transcription factors binding to a novel palindromic DNA site. Nucleic Acids Research, 2021, 49, 3573-3583.	14.5	28
2	Structural insight into the molecular mechanism of p53-mediated mitochondrial apoptosis. Nature Communications, 2021, 12, 2280.	12.8	33
3	Hypertonic Dextrose Stimulates Chondrogenic Cells to Deposit Collagen and Proliferate. Cartilage, 2021, , 194760352110145.	2.7	5
4	Novel Few-Shot Learning Neural Network for Predicting Carbohydrate-Active Enzyme Affinity Toward Fructo-Oligosaccharides. Journal of Computational Biology, 2021, 28, 1208-1218.	1.6	1
5	Landscape of DNA binding signatures of myocyte enhancer factor-2B reveals a unique interplay of base and shape readout. Nucleic Acids Research, 2020, 48, 8529-8544.	14.5	17
6	Crystal Structures of Ternary Complexes of MEF2 and NKX2â€“5 Bound to DNA Reveal a Disease Related Proteinâ€“Protein Interaction Interface. Journal of Molecular Biology, 2020, 432, 5499-5508.	4.2	3
7	Dissection of Anti-tumor Activity of Histone Deacetylase Inhibitor SAHA in Nasopharyngeal Carcinoma Cells via Quantitative Phosphoproteomics. Frontiers in Cell and Developmental Biology, 2020, 8, 577784.	3.7	7
8	A small molecular compound CC1007 induces cross-lineage differentiation by inhibiting HDAC7 expression and HDAC7/MEF2C interaction in BCR-ABL1â^' pre-B-ALL. Cell Death and Disease, 2020, 11, 738.	6.3	6
9	p53 destabilizing protein skews asymmetric division and enhances NOTCH activation to direct self-renewal of TICs. Nature Communications, 2020, 11, 3084.	12.8	26
10	Acetylation-mediated degradation of HSD17B4 regulates the progression of prostate cancer. Aging, 2020, 12, 14699-14717.	3.1	16
11	Structure-Based Approaches to Antigen-Specific Therapy of Myasthenia Gravis. , 2019, , .		0
12	Structural basis for DNA recognition by FOXC2. Nucleic Acids Research, 2019, 47, 3752-3764.	14.5	36
13	Structural basis of binding of homodimers of the nuclear receptor NR4A2 to selective Nur-responsive DNA elements. Journal of Biological Chemistry, 2019, 294, 19795-19803.	3.4	23
14	Overexpression of MEF2D contributes to oncogenic malignancy and chemotherapeutic resistance in ovarian carcinoma. American Journal of Cancer Research, 2019, 9, 887-905.	1.4	5
15	Molecular Characterization, Spatialâ€“Temporal Expression Profiles, and Injuryâ€responsive Regulation of Myocyteâ€specific Enhancer Factor 2 Gene Family in the Ricefield Eel, Monopterus albus. Journal of the World Aquaculture Society, 2018, 49, 396-411.	2.4	1
16	The Cancer Mutation D83V Induces an Î±-Helix to Î²-Strand Conformation Switch in MEF2B. Journal of Molecular Biology, 2018, 430, 1157-1172.	4.2	31
17	Crystal Structure of Apo MEF2B Reveals New Insights in DNA Binding and Cofactor Interaction. Biochemistry, 2018, 57, 4047-4051.	2.5	11
18	Î±1-FANGs: Protein Ligands Selective for the Î±-Bungarotoxin Site of the Î±1-Nicotinic Acetylcholine Receptor. ACS Chemical Biology, 2018, 13, 2568-2576.	3.4	8

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19	Species-Specific Deamidation of cGAS by Herpes Simplex Virus UL37 Protein Facilitates Viral Replication. Cell Host and Microbe, 2018, 24, 234-248.e5.	11.0	140
20	Conserved forkhead dimerization motif controls DNA replication timing and spatial organization of chromosomes in S. cerevisiae. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2411-E2419.	7.1	40
21	Remarkably Stereospecific Utilization of ATP Î±,Î²-Halomethylene Analogues by Protein Kinases. Journal of the American Chemical Society, 2017, 139, 7701-7704.	13.7	13
22	DNA-binding properties of FOXP3 transcription factor. Acta Biochimica Et Biophysica Sinica, 2017, 49, 792-799.	2.0	12
23	Structure of the Forkhead Domain of FOXA2 Bound to a Complete DNA Consensus Site. Biochemistry, 2017, 56, 3745-3753.	2.5	39
24	Reversal of pathological cardiac hypertrophy via the MEF2-coregulator interface. JCI Insight, 2017, 2, .	5.0	33
25	Structural insights into the molecular mechanisms of myasthenia gravis and their therapeutic implications. ELife, 2017, 6, .	6.0	22
26	Mining 3D genome structure populations identifies major factors governing the stability of regulatory communities. Nature Communications, 2016, 7, 11549.	12.8	36
27	Expression and purification of the kinase domain of PINK1 in Pichia pastoris. Protein Expression and Purification, 2016, 128, 67-72.	1.3	5
28	Nicotinic acetylcholine receptor agonist attenuates ILC2-dependent airway hyperreactivity. Nature Communications, 2016, 7, 13202.	12.8	108
29	Population-based 3D genome structure analysis reveals driving forces in spatial genome organization. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1663-72.	7.1	182
30	DNA binding by FOXP3 domain-swapped dimer suggests mechanisms of long-range chromosomal interactions. Nucleic Acids Research, 2015, 43, 1268-1282.	14.5	49
31	Conformations of p53 response elements in solution deduced using site-directed spin labeling and Monte Carlo sampling. Nucleic Acids Research, 2014, 42, 2789-2797.	14.5	23
32	Inter-residue coupling contributes to high-affinity subtype-selective binding of Î±-bungarotoxin to nicotinic receptors. Biochemical Journal, 2013, 454, 311-321.	3.7	16
33	Complex between Î±-bungarotoxin and an Î±7 nicotinic receptor ligand-binding domain chimaera. Biochemical Journal, 2013, 454, 303-310.	3.7	73
34	Structure of p53 binding to the BAX response element reveals DNA unwinding and compression to accommodate base-pair insertion. Nucleic Acids Research, 2013, 41, 8368-8376.	14.5	64
35	Inhibition of the function of class IIa HDACs by blocking their interaction with MEF2. Nucleic Acids Research, 2012, 40, 5378-5388.	14.5	44
36	DNA Binding by GATA Transcription Factor Suggests Mechanisms of DNA Looping and Long-Range Gene Regulation. Cell Reports, 2012, 2, 1197-1206.	6.4	94

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37	In Search of Allosteric Modulators of Î±7-nAChR by Solvent Density Guided Virtual Screening. Journal of Biomolecular Structure and Dynamics, 2011, 28, 695-715.	3.5	22
38	Ligand-binding domain of an Î±7-nicotinic receptor chimera and its complex with agonist. Nature Neuroscience, 2011, 14, 1253-1259.	14.8	183
39	Structure of a Domain-Swapped FOXP3 Dimer on DNA and Its Function in Regulatory T Cells. Immunity, 2011, 34, 479-491.	14.3	140
40	Structure of p300 bound to MEF2 on DNA reveals a mechanism of enhanceosome assembly. Nucleic Acids Research, 2011, 39, 4464-4474.	14.5	53
41	Packing of the Extracellular Domain Hydrophobic Core Has Evolved to Facilitate Pentameric Ligand-gated Ion Channel Function. Journal of Biological Chemistry, 2011, 286, 3658-3670.	3.4	18
42	Crystal Structure of the p53 Core Domain Bound to a Full Consensus Site as a Self-Assembled Tetramer. Structure, 2010, 18, 246-256.	3.3	129
43	In pursuit of the high-resolution structure of nicotinic acetylcholine receptors. Journal of Physiology, 2010, 588, 557-564.	2.9	20
44	Structure of the MADS-box/MEF2 Domain of MEF2A Bound to DNA and Its Implication for Myocardin Recruitment. Journal of Molecular Biology, 2010, 397, 520-533.	4.2	42
45	Structural Basis of HIV-1 Activation by NF-ÎºBâ€"A Higher-Order Complex of p50:RelA Bound to the HIV-1 LTR. Journal of Molecular Biology, 2009, 393, 98-112.	4.2	69
46	DNA Binding Site Sequence Directs Glucocorticoid Receptor Structure and Activity. Science, 2009, 324, 407-410.	12.6	618
47	A Cytokineâ€"Cytokine Interaction in the Assembly of Higher-Order Structure and Activation of the Interleukine-3:Receptor Complex. PLoS ONE, 2009, 4, e5188.	2.5	36
48	Crystal Structure of NFAT Bound to the HIV-1 LTR Tandem ÎºB Enhancer Element. Structure, 2008, 16, 684-694.	3.3	29
49	Crystal Structures of Multiple GATA Zinc Fingers Bound to DNA Reveal New Insights into DNA Recognition and Self-Association by GATA. Journal of Molecular Biology, 2008, 381, 1292-1306.	4.2	88
50	Crystal structure of a conserved N-terminal domain of histone deacetylase 4 reveals functional insights into glutamine-rich domains. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 4297-4302.	7.1	70
51	Structural Determinants for Î±-Neurotoxin Sensitivity in Muscle nAChR and Their Implications for the Gating Mechanism. Channels, 2007, 1, 234-237.	2.8	19
52	Crystal structure of the extracellular domain of nAChR Î±1 bound to Î±-bungarotoxin at 1.94 Ã... resolution. Nature Neuroscience, 2007, 10, 953-962.	14.8	398
53	FOXP3 Controls Regulatory T Cell Function through Cooperation with NFAT. Cell, 2006, 126, 375-387.	28.9	1,019
54	Structure of the Forkhead Domain of FOXP2 Bound to DNA. Structure, 2006, 14, 159-166.	3.3	176

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55	NFAT and MEF2, Two Families of Calcium-dependent Transcription Regulators. , 2006, , 293-307.		0
56	Solution Structure of Prosurvival Mcl-1 and Characterization of Its Binding by Proapoptotic BH3-only Ligands. Journal of Biological Chemistry, 2005, 280, 4738-4744.	3.4	187
57	Mechanism of Recruitment of Class II Histone Deacetylases by Myocyte Enhancer Factor-2. Journal of Molecular Biology, 2005, 345, 91-102.	4.2	100
58	Molecular and Biochemical Characterization of the Skp2-Cks1 Binding Interface. Journal of Biological Chemistry, 2004, 279, 51362-51369.	3.4	13
59	A Distal Enhancer in the Interferon-Î³ (IFN-Î³) Locus Revealed by Genome Sequence Comparison. Journal of Biological Chemistry, 2004, 279, 4802-4810.	3.4	123
60	Structural, Biochemical, and Functional Analyses of CED-9 Recognition by the Proapoptotic Proteins EGL-1 and CED-4. Molecular Cell, 2004, 15, 999-1006.	9.7	92
61	Docking Motif Interactions in MAP Kinases Revealed by Hydrogen Exchange Mass Spectrometry. Molecular Cell, 2004, 14, 43-55.	9.7	278
62	An asymmetric NFAT1 dimer on a pseudo-palindromic ÎºB-like DNA site. Nature Structural and Molecular Biology, 2003, 10, 807-811.	8.2	56
63	Structure of NFAT1 bound as a dimer to the HIV-1 LTR ÎºB element. Nature Structural and Molecular Biology, 2003, 10, 800-806.	8.2	92
64	Sequence-specific recruitment of transcriptional co-repressor Cabin1 by myocyte enhancer factor-2. Nature, 2003, 422, 730-734.	27.8	99
65	Structure of NFAT Bound to DNA as a Monomer. Journal of Molecular Biology, 2003, 334, 1009-1022.	4.2	32
66	The Sir4 C-terminal Coiled Coil is Required for Telomeric and Mating Type Silencing in Saccharomyces cerevisiae. Journal of Molecular Biology, 2003, 334, 769-780.	4.2	29
67	Transcriptional regulation by calcium, calcineurin, and NFAT. Genes and Development, 2003, 17, 2205-2232.	5.9	1,675
68	A Negatively Charged Amino Acid in Skp2 Is Required for Skp2-Cks1 Interaction and Ubiquitination of p27Kip1. Journal of Biological Chemistry, 2003, 278, 32390-32396.	3.4	24
69	Structure of a TonEBPâ€“DNA complex reveals DNA encircled by a transcription factor. Nature Structural Biology, 2002, 9, 90-94.	9.7	106
70	Demonstration of the in vivo interaction of key cell death regulators by structure-based design of second-site suppressors. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 11916-11921.	7.1	46
71	Combinatorial gene regulation by eukaryotic transcription factors. Current Opinion in Structural Biology, 1999, 9, 48-55.	5.7	66
72	Signal Integration by Transcription-factor Assemblies: Interactions of NF-AT1 and AP-1 on the IL-2 Promoter. Cold Spring Harbor Symposia on Quantitative Biology, 1999, 64, 527-532.	1.1	22

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73	Structure of the DNA-binding domains from NFAT, Fos and Jun bound specifically to DNA. Nature, 1998, 392, 42-48.	27.8	498
74	Unusual Rel-like architecture in the DNA-binding domain of the transcription factor NFATc. Nature, 1997, 385, 172-176.	27.8	103
75	Selective base-pair destabilization enhances binding of a DNA methyltransferase. Tetrahedron, 1997, 53, 12041-12056.	1.9	9
76	Only one of the two DNA-bound orientations of AP-1 found in solution cooperates with NFATp. Current Biology, 1995, 5, 882-889.	3.9	63
77	The crystal structure of HaeIII methyltransferase covalently complexed to DNA: An extrahelical cytosine and rearranged base pairing. Cell, 1995, 82, 143-153.	28.9	399
78	Crystallization and Preliminary Crystallographic Analysis of a DNA (Cytosine-5)-Methyltransferase from Haemophilus aegyptius Bound Covalently to DNA. Journal of Molecular Biology, 1994, 238, 626-629.	4.2	12
79	A multifunctional plasmid for protein expression by ECPCR: overproduction of the p50 subunit of NF-ÎºB. Bioorganic and Medicinal Chemistry Letters, 1993, 3, 1089-1094.	2.2	44
80	Limited proteolysis and site-directed mutagenesis of the NF-ÎºB p50 DNA-binding subunit. Bioorganic and Medicinal Chemistry Letters, 1993, 3, 1095-1100.	2.2	42
81	Mutational separation of DNA binding from catalysis in a DNA cytosine methyltransferase. Journal of the American Chemical Society, 1993, 115, 5318-5319.	13.7	64
82	DNA methylation through a locally unpaired intermediate. Journal of the American Chemical Society, 1993, 115, 12583-12584.	13.7	85
83	[7] Overproduction of proteins using expression-cassette polymerase chain reaction. Methods in Enzymology, 1993, 217, 79-102.	1.0	26
84	Synthesis of an oligonucleotide suicide substrate for DNA methyltransferases. Journal of Organic Chemistry, 1992, 57, 2989-2991.	3.2	25
85	Direct identification of the active-site nucleophile in a DNA (cytosine-5)-methyltransferase. Biochemistry, 1991, 30, 11018-11025.	2.5	245
86	Phenomena of weak electroluminescence of iron and other metal electrodes and their application potentiality in electrochemistry research. Electrochimica Acta, 1991, 36, 1591-1593.	5.2	2