## Mair E A Churchill

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Histone acetyltransferase activity of yeast Gcn5p is required for the activation of target genes inÂvivo. Genes and Development, 1998, 12, 627-639.	5.9	400
2	Structural Basis for the Histone Chaperone Activity of Asf1. Cell, 2006, 127, 495-508.	28.9	398
3	Nasal chemosensory cells use bitter taste signaling to detect irritants and bacterial signals. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 3210-3215.	7.1	349
4	[33] Hydroxyl radical footprinting: A high-resolution method for mapping protein-DNA contacts. Methods in Enzymology, 1987, 155, 537-558.	1.0	305
5	Structural Basis and Specificity of Acyl-Homoserine Lactone Signal Production in Bacterial Quorum Sensing. Molecular Cell, 2002, 9, 685-694.	9.7	230
6	A Holliday recombination intermediate is twofold symmetric Proceedings of the National Academy of Sciences of the United States of America, 1988, 85, 4653-4656.	7.1	221
7	Protein motifs that recognize structural features of DNA. Trends in Biochemical Sciences, 1991, 16, 92-97.	7.5	207
8	Structural Basis of Acyl-homoserine Lactone-Dependent Signaling. Chemical Reviews, 2011, 111, 68-85.	47.7	198
9	DNA chaperones: A solution to a persistence problem?. Cell, 1994, 77, 167-169.	28.9	176
10	The high mobility group box: the ultimate utility player of a cell. Trends in Biochemical Sciences, 2012, 37, 553-562.	7.5	173
11	The structure of a chromosomal high mobility group protein-DNA complex reveals sequence-neutral mechanisms important for non-sequence-specific DNA recognition. EMBO Journal, 1999, 18, 6610-6618.	7.8	169
12	The histone shuffle: histone chaperones in an energetic dance. Trends in Biochemical Sciences, 2010, 35, 476-489.	7.5	154
13	Structure of the Pseudomonas aeruginosa acyl-homoserinelactone synthase Lasl. Molecular Microbiology, 2004, 53, 1135-1146.	2.5	153
14	Specificity of Acyl-Homoserine Lactone Synthases Examined by Mass Spectrometry. Journal of Bacteriology, 2006, 188, 773-783.	2.2	131
15	Quorum-Sensing Control of Antibiotic Synthesis in <i>Burkholderia thailandensis</i> . Journal of Bacteriology, 2009, 191, 3909-3918.	2.2	129
16	Nonsequence-specific DNA recognition: a structural perspective. Structure, 2000, 8, R83-R89.	3.3	126
17	ASF1 Binds to a Heterodimer of Histones H3 and H4: A Two-Step Mechanism for the Assembly of the H3â^'H4 Heterotetramer on DNAâ€. Biochemistry, 2005, 44, 13673-13682.	2.5	121
18	The solution structure and dynamics of the DNA-binding domain of HMG-D from Drosophila melanogaster. Structure, 1994, 2, 609-627.	3.3	120

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19	DNA Binding and Bending by HMG Boxes: Energetic Determinants of Specificity. Journal of Molecular Biology, 2004, 343, 371-393.	4.2	114
20	Crystal structure of QscR, a <i>Pseudomonas aeruginosa</i> quorum sensing signal receptor. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 15763-15768.	7.1	108
21	Construction and analysis of monomobile DNA junctions. Biochemistry, 1988, 27, 6032-6038.	2.5	104
22	Mutational Analysis of <i>Burkholderia thailandensis</i> Quorum Sensing and Self-Aggregation. Journal of Bacteriology, 2009, 191, 5901-5909.	2.2	88
23	Structural analysis and DNA binding of the HMG domains of the human mitochondrial transcription factor A. Nucleic Acids Research, 2009, 37, 3153-3164.	14.5	83
24	DNA Binding of a Non-sequence-specific HMG-D Protein is Entropy Driven with a Substantial Non-electrostatic Contribution. Journal of Molecular Biology, 2003, 331, 795-813.	4.2	81
25	Structure of RsrI methyltransferase, a member of the N6-adenine beta class of DNA methyltransferases. Nucleic Acids Research, 2000, 28, 3950-3961.	14.5	78
26	CAF-1-induced oligomerization of histones H3/H4 and mutually exclusive interactions with Asf1 guide H3/H4 transitions among histone chaperones and DNA. Nucleic Acids Research, 2012, 40, 11229-11239.	14.5	75
27	A complex LuxR–LuxI type quorum sensing network in a roseobacterial marine sponge symbiont activates flagellar motility and inhibits biofilm formation. Molecular Microbiology, 2012, 85, 916-933.	2.5	75
28	Structural and functional analysis of domains of the progesterone receptor. Molecular and Cellular Endocrinology, 2012, 348, 418-429.	3.2	74
29	Mode of interaction of the zinc finger protein TFIIIA with a 5S RNA gene of Xenopus Proceedings of the National Academy of Sciences of the United States of America, 1990, 87, 5528-5532.	7.1	67
30	Mechanistic insights into histone deposition and nucleosome assembly by the chromatin assembly factor-1. Nucleic Acids Research, 2018, 46, 9907-9917.	14.5	67
31	Crystal Structure of a Peptide Complex of Anti-influenza Peptide Antibody Fab 26/9. Journal of Molecular Biology, 1994, 241, 534-556.	4.2	65
32	Detection of drug binding to DNA by hydroxyl radical footprinting. Relationship of distamycin binding sites to DNA structure and positioned nucleosomes on 5S RNA genes of Xenopus. Biochemistry, 1990, 29, 6043-6050.	2.5	61
33	Structure of the Progesterone Receptor-Deoxyribonucleic Acid Complex: Novel Interactions Required for Binding to Half-Site Response Elements. Molecular Endocrinology, 2006, 20, 3042-3052.	3.7	60
34	Asymmetric structure of a three-arm DNA junction. Biochemistry, 1990, 29, 10927-10934.	2.5	59
35	Modifying the helical structure of DNA by design: recruitment of an architecture-specific protein to an enforced DNA bend. Chemistry and Biology, 1995, 2, 213-221.	6.0	58
36	Transcriptional activation by mitochondrial transcription factor A involves preferential distortion of promoter DNA. Nucleic Acids Research, 2012, 40, 614-624.	14.5	58

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37	The role of intercalating residues in chromosomal high-mobility-group protein DNA binding, bending and specificity. Nucleic Acids Research, 2003, 31, 2852-2864.	14.5	56
38	Harnessing the writhe: a role for DNA chaperonesin nucleoprotein- complex formation. Trends in Biochemical Sciences, 1994, 19, 185-187.	7.5	53
39	Nuclear PTEN functions as an essential regulator of SRF-dependent transcription to control smooth muscle differentiation. Nature Communications, 2016, 7, 10830.	12.8	53
40	The activity of the histone chaperone yeast Asf1 in the assembly and disassembly of histone H3/H4–DNA complexes. Nucleic Acids Research, 2011, 39, 5449-5458.	14.5	52
41	Binding of the histone chaperone ASF1 to the CBP bromodomain promotes histone acetylation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E1072-81.	7.1	52
42	De Novo Mutations in EBF3 Cause a Neurodevelopmental Syndrome. American Journal of Human Genetics, 2017, 100, 138-150.	6.2	52
43	N -(3-Hydroxyhexanoyl)- l -Homoserine Lactone Is the Biologically Relevant Quormone That Regulates the phz Operon of Pseudomonas chlororaphis Strain 30-84. Applied and Environmental Microbiology, 2007, 73, 7443-7455.	3.1	51
44	The Cac1 subunit of histone chaperone CAF-1 organizes CAF-1-H3/H4 architecture and tetramerizes histones. ELife, 2016, 5, .	6.0	51
45	Two high-mobility group box domains act together to underwind and kink DNA. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1423-1432.	2.5	50
46	The C-terminal Extension (CTE) of the Nuclear Hormone Receptor DNA Binding Domain Determines Interactions and Functional Response to the HMGB-1/-2 Co-regulatory Proteins. Journal of Biological Chemistry, 2002, 277, 25115-25124.	3.4	49
47	The Role of the C-terminal Extension (CTE) of the Estrogen Receptor α and β DNA Binding Domain in DNA Binding and Interaction with HMGB. Journal of Biological Chemistry, 2004, 279, 14763-14771.	3.4	49
48	Quorum-Sensing Signal Synthesis by the Yersinia pestis Acyl-Homoserine Lactone Synthase Yspl. Journal of Bacteriology, 2006, 188, 784-788.	2.2	47
49	dHMG-Z, a second HMG-1-related protein in Drosophila melanogaster. Nucleic Acids Research, 1993, 21, 4369-4371.	14.5	45
50	Interactions of high mobility group box proteins with DNA and chromatin. Methods in Enzymology, 1999, 304, 99-133.	1.0	42
51	Pseudomonas aeruginosa AlgR Phosphorylation Modulates Rhamnolipid Production and Motility. Journal of Bacteriology, 2013, 195, 5499-5515.	2.2	40
52	The Aurora A and Aurora B Protein Kinases: A Single Amino Acid Difference Controls Intrinsic Activity and Activation by TPX2. Cell Cycle, 2005, 4, 784-789.	2.6	39
53	Mechanism of high-mobility group protein B enhancement of progesterone receptor sequence-specific DNA binding. Nucleic Acids Research, 2008, 36, 3655-3666.	14.5	38
54	The <i>Burkholderia mallei</i> BmaR3-BmaI3 Quorum-Sensing System Produces and Responds to <i>N</i> -3-Hydroxy-Octanoyl Homoserine Lactone. Journal of Bacteriology, 2008, 190, 5137-5141.	2.2	38

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55	Mechanism of agonism and antagonism of the <i>Pseudomonas aeruginosa</i> quorum sensing regulator QscR with nonâ€native ligands. Molecular Microbiology, 2018, 108, 240-257.	2.5	33
56	Functional Impact of Chromatin Remodeling Gene Mutations and Predictive Signature for Therapeutic Response in Bladder Cancer. Molecular Cancer Research, 2018, 16, 69-77.	3.4	33
57	Animal Protection and Structural Studies of a Consensus Sequence Vaccine Targeting the Receptor Binding Domain of the Type IV Pilus of Pseudomonas aeruginosa. Journal of Molecular Biology, 2007, 374, 426-442.	4.2	31
58	A Progesterone Receptor Co-activator (JDP2) Mediates Activity through Interaction with Residues in the Carboxyl-terminal Extension of the DNA Binding Domain. Journal of Biological Chemistry, 2009, 284, 24415-24424.	3.4	31
59	Structure prediction of a complex between the chromosomal protein HMG-D and DNA. , 1998, 30, 113-135.		30
60	Discovery of a distinct domain in cyclin A sufficient for centrosomal localization independently of Cdk binding. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2932-2937.	7.1	27
61	Cytosine methylation of mitochondrial DNA at CpG sequences impacts transcription factor A DNA binding and transcription. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2019, 1862, 598-607.	1.9	26
62	Oxidation of a critical methionine modulates DNA binding of theDrosophila melanogasterhigh mobility group protein, HMG-D. FEBS Letters, 1997, 414, 514-520.	2.8	24
63	Structural Studies of the High Mobility Group Globular Domain and Basic Tail of HMG-D Bound to Disulfide Cross-Linked DNA. Biochemistry, 2000, 39, 9725-9736.	2.5	24
64	Structures of Liganded and Unliganded RsrI N6-Adenine DNA Methyltransferase. Journal of Biological Chemistry, 2003, 278, 26094-26101.	3.4	21
65	Histone transfer among chaperones. Biochemical Society Transactions, 2012, 40, 357-363.	3.4	21
66	PKCα phosphorylation of RhoGDI2 at Ser31 disrupts interactions with Rac1 and decreases GDI activity. Oncogene, 2013, 32, 1010-1017.	5.9	21
67	Class I HDAC inhibition stimulates cardiac protein SUMOylation through a post-translational mechanism. Cellular Signalling, 2014, 26, 2912-2920.	3.6	21
68	A solo luxI-type gene directs acylhomoserine lactone synthesis and contributes to motility control in the marine sponge symbiont Ruegeria sp. KLH11. Microbiology (United Kingdom), 2015, 161, 50-56.	1.8	21
69	The conformational flexibility of the C-terminus of histone H4 promotes histone octamer and nucleosome stability and yeast viability. Epigenetics and Chromatin, 2012, 5, 5.	3.9	20
70	The C Terminus of the Histone Chaperone Asf1 Cross-Links to Histone H3 in Yeast and Promotes Interaction with Histones H3 and H4. Molecular and Cellular Biology, 2013, 33, 605-621.	2.3	20
71	Defining the Structure and Function of Acyl-Homoserine Lactone Autoinducers. Methods in Molecular Biology, 2011, 692, 159-171.	0.9	20
72	Genetic and Structure-Function Studies of Missense Mutations in Human Endothelial Lipase. PLoS ONE, 2013, 8, e55716.	2.5	13

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73	Structural Analysis of HMGD–DNA Complexes Reveals Influence of Intercalation on Sequence Selectivity and DNA Bending. Journal of Molecular Biology, 2010, 403, 88-102.	4.2	12
74	Development of novel Asf1–H3/H4 inhibitors. Bioorganic and Medicinal Chemistry Letters, 2015, 25, 963-968.	2.2	10
75	Crystallization and rhenium MAD phasing of the acyl-homoserinelactone synthase Esal. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1945-1949.	2.5	9
76	Centrosomal localization of cyclins E and A. Cell Cycle, 2011, 10, 199-205.	2.6	9
77	Reversed-phase ion-pair liquid chromatography method for purification of duplex DNA with single base pair resolution. Nucleic Acids Research, 2013, 41, e194-e194.	14.5	9
78	Analysis of Histone Chaperone Antisilencing Function 1 Interactions. Methods in Enzymology, 2012, 512, 223-241.	1.0	8
79	Co-crystallization and preliminary crystallographic analysis of the high mobility group domain of HMG-D bound to DNA. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1594-1597.	2.5	6
80	A New GNAT in Bacterial Signaling?. Structure, 2006, 14, 1342-1344.	3.3	6
81	Crystallization ofPseudomonas aeruginosaAHL synthase Lasl using β-turn crystal engineering. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 518-520.	2.5	5
82	The sea urchin mitochondrial transcription factor A binds and bends DNA efficiently despite its unusually short C-terminal tail. Mitochondrion, 2016, 29, 1-6.	3.4	3
83	Acyl-Homoserine Lactone Biosynthesis: Structure and Mechanism. , 0, , 273-289.		3
84	Watching flipping junctions. , 2003, 10, 73-75.		2
85	Bayesian Analysis of High-Throughput Quantitative Measurement of Protein-DNA Interactions. PLoS ONE, 2011, 6, e26105.	2.5	2
86	Mechanism of Mitochondrial Transcription Factor A Attenuation of CpG-Induced Antibody Production. PLoS ONE, 2016, 11, e0157157.	2.5	1
87	Structure of barium guanosine 5'-monophosphate. Acta Crystallographica Section C: Crystal Structure Communications, 1992, 48, 1223-1227.	0.4	0
88	A complex <scp>LuxR–LuxI</scp> type quorum sensing network in a roseobacterial marine sponge symbiont activates flagellar motility and inhibits biofilm formation. Molecular Microbiology, 2012, 86, 500-500.	2.5	0
89	Lessons from the QSCR Structure for Quorum Sensing. , 2015, , 189-214.		0