

# Mair E A Churchill

## List of Publications by Year in descending order

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89  
papers

6,520  
citations

61687

45  
h-index

73587

79  
g-index

93  
all docs

93  
docs citations

93  
times ranked

7402  
citing authors

#	ARTICLE	IF	CITATIONS
1	Histone acetyltransferase activity of yeast Gcn5p is required for the activation of target genes in vivo. <i>Genes and Development</i> , 1998, 12, 627-639.	2.7	400
2	Structural Basis for the Histone Chaperone Activity of Asf1. <i>Cell</i> , 2006, 127, 495-508.	13.5	398
3	Nasal chemosensory cells use bitter taste signaling to detect irritants and bacterial signals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3210-3215.	3.3	349
4	[33] Hydroxyl radical footprinting: A high-resolution method for mapping protein-DNA contacts. <i>Methods in Enzymology</i> , 1987, 155, 537-558.	0.4	305
5	Structural Basis and Specificity of Acyl-Homoserine Lactone Signal Production in Bacterial Quorum Sensing. <i>Molecular Cell</i> , 2002, 9, 685-694.	4.5	230
6	A Holliday recombination intermediate is twofold symmetric.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1988, 85, 4653-4656.	3.3	221
7	Protein motifs that recognize structural features of DNA. <i>Trends in Biochemical Sciences</i> , 1991, 16, 92-97.	3.7	207
8	Structural Basis of Acyl-homoserine Lactone-Dependent Signaling. <i>Chemical Reviews</i> , 2011, 111, 68-85.	23.0	198
9	DNA chaperones: A solution to a persistence problem?. <i>Cell</i> , 1994, 77, 167-169.	13.5	176
10	The high mobility group box: the ultimate utility player of a cell. <i>Trends in Biochemical Sciences</i> , 2012, 37, 553-562.	3.7	173
11	The structure of a chromosomal high mobility group protein-DNA complex reveals sequence-neutral mechanisms important for non-sequence-specific DNA recognition. <i>EMBO Journal</i> , 1999, 18, 6610-6618.	3.5	169
12	The histone shuffle: histone chaperones in an energetic dance. <i>Trends in Biochemical Sciences</i> , 2010, 35, 476-489.	3.7	154
13	Structure of the <i>Pseudomonas aeruginosa</i> acyl-homoserine lactone synthase LasI. <i>Molecular Microbiology</i> , 2004, 53, 1135-1146.	1.2	153
14	Specificity of Acyl-Homoserine Lactone Synthases Examined by Mass Spectrometry. <i>Journal of Bacteriology</i> , 2006, 188, 773-783.	1.0	131
15	Quorum-Sensing Control of Antibiotic Synthesis in <i>Burkholderia thailandensis</i> . <i>Journal of Bacteriology</i> , 2009, 191, 3909-3918.	1.0	129
16	Nonsequence-specific DNA recognition: a structural perspective. <i>Structure</i> , 2000, 8, R83-R89.	1.6	126
17	ASF1 Binds to a Heterodimer of Histones H3 and H4: A Two-Step Mechanism for the Assembly of the H3-H4 Heterotetramer on DNA. <i>Biochemistry</i> , 2005, 44, 13673-13682.	1.2	121
18	The solution structure and dynamics of the DNA-binding domain of HMG-D from <i>Drosophila melanogaster</i> . <i>Structure</i> , 1994, 2, 609-627.	1.6	120

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19	DNA Binding and Bending by HMG Boxes: Energetic Determinants of Specificity. <i>Journal of Molecular Biology</i> , 2004, 343, 371-393.	2.0	114
20	Crystal structure of QscR, a <i>Pseudomonas aeruginosa</i> quorum sensing signal receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15763-15768.	3.3	108
21	Construction and analysis of monomobile DNA junctions. <i>Biochemistry</i> , 1988, 27, 6032-6038.	1.2	104
22	Mutational Analysis of <i>Burkholderia thailandensis</i> Quorum Sensing and Self-Aggregation. <i>Journal of Bacteriology</i> , 2009, 191, 5901-5909.	1.0	88
23	Structural analysis and DNA binding of the HMG domains of the human mitochondrial transcription factor A. <i>Nucleic Acids Research</i> , 2009, 37, 3153-3164.	6.5	83
24	DNA Binding of a Non-sequence-specific HMG-D Protein is Entropy Driven with a Substantial Non-electrostatic Contribution. <i>Journal of Molecular Biology</i> , 2003, 331, 795-813.	2.0	81
25	Structure of RsrI methyltransferase, a member of the N6-adenine beta class of DNA methyltransferases. <i>Nucleic Acids Research</i> , 2000, 28, 3950-3961.	6.5	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. <i>Nucleic Acids Research</i> , 2012, 40, 11229-11239.	6.5	75
27	A complex LuxR-LuxI type quorum sensing network in a roseobacterial marine sponge symbiont activates flagellar motility and inhibits biofilm formation. <i>Molecular Microbiology</i> , 2012, 85, 916-933.	1.2	75
28	Structural and functional analysis of domains of the progesterone receptor. <i>Molecular and Cellular Endocrinology</i> , 2012, 348, 418-429.	1.6	74
29	Mode of interaction of the zinc finger protein TFIIIA with a 5S RNA gene of <i>Xenopus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1990, 87, 5528-5532.	3.3	67
30	Mechanistic insights into histone deposition and nucleosome assembly by the chromatin assembly factor-1. <i>Nucleic Acids Research</i> , 2018, 46, 9907-9917.	6.5	67
31	Crystal Structure of a Peptide Complex of Anti-influenza Peptide Antibody Fab 26/9. <i>Journal of Molecular Biology</i> , 1994, 241, 534-556.	2.0	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 <i>Xenopus</i> . <i>Biochemistry</i> , 1990, 29, 6043-6050.	1.2	61
33	Structure of the Progesterone Receptor-Deoxyribonucleic Acid Complex: Novel Interactions Required for Binding to Half-Site Response Elements. <i>Molecular Endocrinology</i> , 2006, 20, 3042-3052.	3.7	60
34	Asymmetric structure of a three-arm DNA junction. <i>Biochemistry</i> , 1990, 29, 10927-10934.	1.2	59
35	Modifying the helical structure of DNA by design: recruitment of an architecture-specific protein to an enforced DNA bend. <i>Chemistry and Biology</i> , 1995, 2, 213-221.	6.2	58
36	Transcriptional activation by mitochondrial transcription factor A involves preferential distortion of promoter DNA. <i>Nucleic Acids Research</i> , 2012, 40, 614-624.	6.5	58

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37	The role of intercalating residues in chromosomal high-mobility-group protein DNA binding, bending and specificity. <i>Nucleic Acids Research</i> , 2003, 31, 2852-2864.	6.5	56
38	Harnessing the writhe: a role for DNA chaperones in nucleoprotein- complex formation. <i>Trends in Biochemical Sciences</i> , 1994, 19, 185-187.	3.7	53
39	Nuclear PTEN functions as an essential regulator of SRF-dependent transcription to control smooth muscle differentiation. <i>Nature Communications</i> , 2016, 7, 10830.	5.8	53
40	The activity of the histone chaperone yeast Asf1 in the assembly and disassembly of histone H3/H4-DNA complexes. <i>Nucleic Acids Research</i> , 2011, 39, 5449-5458.	6.5	52
41	Binding of the histone chaperone ASF1 to the CBP bromodomain promotes histone acetylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1072-81.	3.3	52
42	De Novo Mutations in EBF3 Cause a Neurodevelopmental Syndrome. <i>American Journal of Human Genetics</i> , 2017, 100, 138-150.	2.6	52
43	N-(3-Hydroxyhexanoyl)-L-Homoserine Lactone Is the Biologically Relevant Quorumone That Regulates the phz Operon of <i>Pseudomonas chlororaphis</i> Strain 30-84. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7443-7455.	1.4	51
44	The Cac1 subunit of histone chaperone CAF-1 organizes CAF-1-H3/H4 architecture and tetramerizes histones. <i>ELife</i> , 2016, 5, .	2.8	51
45	Two high-mobility group box domains act together to underwind and kink DNA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 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. <i>Journal of Biological Chemistry</i> , 2002, 277, 25115-25124.	1.6	49
47	The Role of the C-terminal Extension (CTE) of the Estrogen Receptor $\beta$ and $\beta$ DNA Binding Domain in DNA Binding and Interaction with HMGB. <i>Journal of Biological Chemistry</i> , 2004, 279, 14763-14771.	1.6	49
48	Quorum-Sensing Signal Synthesis by the <i>Yersinia pestis</i> Acyl-Homoserine Lactone Synthase Yspl. <i>Journal of Bacteriology</i> , 2006, 188, 784-788.	1.0	47
49	dHMG-Z, a second HMG-1-related protein in <i>Drosophila melanogaster</i> . <i>Nucleic Acids Research</i> , 1993, 21, 4369-4371.	6.5	45
50	Interactions of high mobility group box proteins with DNA and chromatin. <i>Methods in Enzymology</i> , 1999, 304, 99-133.	0.4	42
51	<i>Pseudomonas aeruginosa</i> AlgR Phosphorylation Modulates Rhamnolipid Production and Motility. <i>Journal of Bacteriology</i> , 2013, 195, 5499-5515.	1.0	40
52	The Aurora A and Aurora B Protein Kinases: A Single Amino Acid Difference Controls Intrinsic Activity and Activation by TPX2. <i>Cell Cycle</i> , 2005, 4, 784-789.	1.3	39
53	Mechanism of high-mobility group protein B enhancement of progesterone receptor sequence-specific DNA binding. <i>Nucleic Acids Research</i> , 2008, 36, 3655-3666.	6.5	38
54	The <i>Burkholderia mallei</i> BmaR3-BmaI3 Quorum-Sensing System Produces and Responds to N-3-Hydroxy-Octanoyl Homoserine Lactone. <i>Journal of Bacteriology</i> , 2008, 190, 5137-5141.	1.0	38

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55	Mechanism of agonism and antagonism of the <i>Pseudomonas aeruginosa</i> quorum sensing regulator QscR with non-native ligands. <i>Molecular Microbiology</i> , 2018, 108, 240-257.	1.2	33
56	Functional Impact of Chromatin Remodeling Gene Mutations and Predictive Signature for Therapeutic Response in Bladder Cancer. <i>Molecular Cancer Research</i> , 2018, 16, 69-77.	1.5	33
57	Animal Protection and Structural Studies of a Consensus Sequence Vaccine Targeting the Receptor Binding Domain of the Type IV Pilus of <i>Pseudomonas aeruginosa</i> . <i>Journal of Molecular Biology</i> , 2007, 374, 426-442.	2.0	31
58	A Progesterone Receptor Co-activator (JDP2) Mediates Activity through Interaction with Residues in the Carboxyl-terminal Extension of the DNA Binding Domain. <i>Journal of Biological Chemistry</i> , 2009, 284, 24415-24424.	1.6	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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2932-2937.	3.3	27
61	Cytosine methylation of mitochondrial DNA at CpG sequences impacts transcription factor A DNA binding and transcription. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2019, 1862, 598-607.	0.9	26
62	Oxidation of a critical methionine modulates DNA binding of the <i>Drosophila melanogaster</i> high mobility group protein, HMG-D. <i>FEBS Letters</i> , 1997, 414, 514-520.	1.3	24
63	Structural Studies of the High Mobility Group Globular Domain and Basic Tail of HMG-D Bound to Disulfide Cross-Linked DNA. <i>Biochemistry</i> , 2000, 39, 9725-9736.	1.2	24
64	Structures of Liganded and Unliganded RsrI N6-Adenine DNA Methyltransferase. <i>Journal of Biological Chemistry</i> , 2003, 278, 26094-26101.	1.6	21
65	Histone transfer among chaperones. <i>Biochemical Society Transactions</i> , 2012, 40, 357-363.	1.6	21
66	PKC $\delta$ phosphorylation of RhoGDI2 at Ser31 disrupts interactions with Rac1 and decreases GDI activity. <i>Oncogene</i> , 2013, 32, 1010-1017.	2.6	21
67	Class I HDAC inhibition stimulates cardiac protein SUMOylation through a post-translational mechanism. <i>Cellular Signalling</i> , 2014, 26, 2912-2920.	1.7	21
68	A solo luxI-type gene directs acylhomoserine lactone synthesis and contributes to motility control in the marine sponge symbiont <i>Ruegeria</i> sp. KLH11. <i>Microbiology (United Kingdom)</i> , 2015, 161, 50-56.	0.7	21
69	The conformational flexibility of the C-terminus of histone H4 promotes histone octamer and nucleosome stability and yeast viability. <i>Epigenetics and Chromatin</i> , 2012, 5, 5.	1.8	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. <i>Molecular and Cellular Biology</i> , 2013, 33, 605-621.	1.1	20
71	Defining the Structure and Function of Acyl-Homoserine Lactone Autoinducers. <i>Methods in Molecular Biology</i> , 2011, 692, 159-171.	0.4	20
72	Genetic and Structure-Function Studies of Missense Mutations in Human Endothelial Lipase. <i>PLoS ONE</i> , 2013, 8, e55716.	1.1	13

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73	Structural Analysis of HMG-DNA Complexes Reveals Influence of Intercalation on Sequence Selectivity and DNA Bending. <i>Journal of Molecular Biology</i> , 2010, 403, 88-102.	2.0	12
74	Development of novel Asf1-H3/H4 inhibitors. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2015, 25, 963-968.	1.0	10
75	Crystallization and rhenium MAD phasing of the acyl-homoserine lactone synthase Esal. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1945-1949.	2.5	9
76	Centrosomal localization of cyclins E and A. <i>Cell Cycle</i> , 2011, 10, 199-205.	1.3	9
77	Reversed-phase ion-pair liquid chromatography method for purification of duplex DNA with single base pair resolution. <i>Nucleic Acids Research</i> , 2013, 41, e194-e194.	6.5	9
78	Analysis of Histone Chaperone Antisilencing Function 1 Interactions. <i>Methods in Enzymology</i> , 2012, 512, 223-241.	0.4	8
79	Co-crystallization and preliminary crystallographic analysis of the high mobility group domain of HMG-D bound to DNA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1594-1597.	2.5	6
80	A New GNAT in Bacterial Signaling?. <i>Structure</i> , 2006, 14, 1342-1344.	1.6	6
81	Crystallization of <i>Pseudomonas aeruginosa</i> AHL synthase LasI using $\hat{\nu}^2$ -turn crystal engineering. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 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. <i>Mitochondrion</i> , 2016, 29, 1-6.	1.6	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. <i>PLoS ONE</i> , 2011, 6, e26105.	1.1	2
86	Mechanism of Mitochondrial Transcription Factor A Attenuation of CpG-Induced Antibody Production. <i>PLoS ONE</i> , 2016, 11, e0157157.	1.1	1
87	Structure of barium guanosine 5'-monophosphate. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 1992, 48, 1223-1227.	0.4	0
88	A complex $\langle \text{LuxR} \rangle \langle \text{LuxI} \rangle$ type quorum sensing network in a roseobacterial marine sponge symbiont activates flagellar motility and inhibits biofilm formation. <i>Molecular Microbiology</i> , 2012, 86, 500-500.	1.2	0
89	Lessons from the QSCR Structure for Quorum Sensing. , 2015, , 189-214.		0