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List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/12079533/publications.pdf

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17 papers	1,572 citations	686830 13 h-index	839053 18 g-index
19 all docs	19 docs citations	19 times ranked	2565 citing authors

#	ARTICLE	IF	CITATIONS
1	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.	6.5	17
2	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.	2.0	3
3	The RNA Polymerase Î± Subunit Recognizes the DNA Shape of the Upstream Promoter Element. Biochemistry, 2020, 59, 4523-4532.	1.2	12
4	Structure of the Forkhead Domain of FOXA2 Bound to a Complete DNA Consensus Site. Biochemistry, 2017, 56, 3745-3753.	1.2	39
5	Exposing the secrets of sex determination. Nature Structural and Molecular Biology, 2015, 22, 437-438.	3.6	2
6	Mechanistic insights into metal ion activation and operator recognition by the ferric uptake regulator. Nature Communications, 2015, 6, 7642.	5.8	107
7	Unraveling determinants of transcription factor binding outside the core binding site. Genome Research, 2015, 25, 1018-1029.	2.4	146
8	Evolving insights on how cytosine methylation affects protein-DNA binding. Briefings in Functional Genomics, 2015, 14, 61-73.	1.3	122
9	Conformations of p53 response elements in solution deduced using site-directed spin labeling and Monte Carlo sampling. Nucleic Acids Research, 2014, 42, 2789-2797.	6.5	23
10	Absence of a simple code: how transcription factors read the genome. Trends in Biochemical Sciences, 2014, 39, 381-399.	3.7	447
11	Mechanism of Origin DNA Recognition and Assembly of an Initiator-Helicase Complex by SV40 Large Tumor Antigen. Cell Reports, 2013, 3, 1117-1127.	2.9	48
12	DNAshape: a method for the high-throughput prediction of DNA structural features on a genomic scale. Nucleic Acids Research, 2013, 41, W56-W62.	6.5	265
13	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.	6.5	64
14	Probing DNA shape and methylation state on a genomic scale with DNase I. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6376-6381.	3.3	151
15	Proteopedia: 3D visualization and annotation of transcription factorâ€“DNA readout modes. Biochemistry and Molecular Biology Education, 2012, 40, 400-401.	0.5	8
16	DNA Binding by GATA Transcription Factor Suggests Mechanisms of DNA Looping and Long-Range Gene Regulation. Cell Reports, 2012, 2, 1197-1206.	2.9	94
17	Opposites Attract: Shape and Electrostatic Complementarity in Protein-DNA Complexes. RSC Biomolecular Sciences, 2012, , 53-80.	0.4	17