

# Remo Rohs

## List of Publications by Year in descending order

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Version: 2024-02-01

72  
papers

8,231  
citations

61857

43  
h-index

71532

76  
g-index

83  
all docs

83  
docs citations

83  
times ranked

8471  
citing authors

#	ARTICLE	IF	CITATIONS
1	The role of DNA shape in protein-DNA recognition. <i>Nature</i> , 2009, 461, 1248-1253.	13.7	918
2	Origins of Specificity in Protein-DNA Recognition. <i>Annual Review of Biochemistry</i> , 2010, 79, 233-269.	5.0	791
3	Cofactor Binding Evokes Latent Differences in DNA Binding Specificity between Hox Proteins. <i>Cell</i> , 2011, 147, 1270-1282.	13.5	454
4	Absence of a simple code: how transcription factors read the genome. <i>Trends in Biochemical Sciences</i> , 2014, 39, 381-399.	3.7	447
5	Functional Specificity of a Hox Protein Mediated by the Recognition of Minor Groove Structure. <i>Cell</i> , 2007, 131, 530-543.	13.5	303
6	Genomic Regions Flanking E-Box Binding Sites Influence DNA Binding Specificity of bHLH Transcription Factors through DNA Shape. <i>Cell Reports</i> , 2013, 3, 1093-1104.	2.9	280
7	DNashape: a method for the high-throughput prediction of DNA structural features on a genomic scale. <i>Nucleic Acids Research</i> , 2013, 41, W56-W62.	6.5	265
8	Molecular flexibility in ab initio drug docking to DNA: binding-site and binding-mode transitions in all-atom Monte Carlo simulations. <i>Nucleic Acids Research</i> , 2005, 33, 7048-7057.	6.5	247
9	Quantitative modeling of transcription factor binding specificities using DNA shape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4654-4659.	3.3	218
10	Diversity in DNA recognition by p53 revealed by crystal structures with Hoogsteen base pairs. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 423-429.	3.6	214
11	Coregulation of Transcription Factor Binding and Nucleosome Occupancy through DNA Features of Mammalian Enhancers. <i>Molecular Cell</i> , 2014, 54, 844-857.	4.5	195
12	Deconvolving the Recognition of DNA Shape from Sequence. <i>Cell</i> , 2015, 161, 307-318.	13.5	174
13	Methylene Blue Binding to DNA with Alternating GC Base Sequence: A Modeling Study. <i>Journal of the American Chemical Society</i> , 2000, 122, 2860-2866.	6.6	163
14	ChEC-seq kinetics discriminates transcription factor binding sites by DNA sequence and shape in vivo. <i>Nature Communications</i> , 2015, 6, 8733.	5.8	153
15	Probing DNA shape and methylation state on a genomic scale with DNase I. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6376-6381.	3.3	151
16	Unraveling determinants of transcription factor binding outside the core binding site. <i>Genome Research</i> , 2015, 25, 1018-1029.	2.4	146
17	DNashapeR: an R/Bioconductor package for DNA shape prediction and feature encoding. <i>Bioinformatics</i> , 2016, 32, 1211-1213.	1.8	142
18	A widespread role of the motif environment in transcription factor binding across diverse protein families. <i>Genome Research</i> , 2015, 25, 1268-1280.	2.4	134

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19	Quantum annealing versus classical machine learning applied to a simplified computational biology problem. <i>Npj Quantum Information</i> , 2018, 4, .	2.8	126
20	Evolving insights on how cytosine methylation affects protein-DNA binding. <i>Briefings in Functional Genomics</i> , 2015, 14, 61-73.	1.3	122
21	DNA Shape Features Improve Transcription Factor Binding Site Predictions In Vivo. <i>Cell Systems</i> , 2016, 3, 278-286.e4.	2.9	119
22	TFBSshape: a motif database for DNA shape features of transcription factor binding sites. <i>Nucleic Acids Research</i> , 2014, 42, D148-D155.	6.5	111
23	Epigenetic stress responses induce muscle stem-cell ageing by Hoxa9 developmental signals. <i>Nature</i> , 2016, 540, 428-432.	13.7	108
24	Mechanistic insights into metal ion activation and operator recognition by the ferric uptake regulator. <i>Nature Communications</i> , 2015, 6, 7642.	5.8	107
25	Transcription factor family-specific <scp>DNA</scp> shape readout revealed by quantitative specificity models. <i>Molecular Systems Biology</i> , 2017, 13, 910.	3.2	105
26	Unraveling Proteins: A Molecular Mechanics Study. <i>Biophysical Journal</i> , 1999, 76, 2760-2768.	0.2	103
27	Nuance in the double-helix and its role in protein-DNA recognition. <i>Current Opinion in Structural Biology</i> , 2009, 19, 171-177.	2.6	99
28	DNA Binding by GATA Transcription Factor Suggests Mechanisms of DNA Looping and Long-Range Gene Regulation. <i>Cell Reports</i> , 2012, 2, 1197-1206.	2.9	94
29	Expanding the repertoire of DNA shape features for genome-scale studies of transcription factor binding. <i>Nucleic Acids Research</i> , 2017, 45, 12877-12887.	6.5	81
30	A Map of Minor Groove Shape and Electrostatic Potential from Hydroxyl Radical Cleavage Patterns of DNA. <i>ACS Chemical Biology</i> , 2011, 6, 1314-1320.	1.6	78
31	Structural and Energetic Origins of Sequence-Specific DNA Bending: Monte Carlo Simulations of Papillomavirus E2-DNA Binding Sites. <i>Structure</i> , 2005, 13, 1499-1509.	1.6	76
32	Methylene Blue Binding to DNA with Alternating AT Base Sequence: Minor Groove Binding is Favored over Intercalation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2004, 21, 699-711.	2.0	75
33	Electrostatic Interactions between Arginines and the Minor Groove in the Nucleosome. <i>Journal of Biomolecular Structure and Dynamics</i> , 2010, 27, 861-866.	2.0	75
34	Control of DNA minor groove width and Fis protein binding by the purine 2-amino group. <i>Nucleic Acids Research</i> , 2013, 41, 6750-6760.	6.5	74
35	High-Resolution Profiling of Drosophila Replication Start Sites Reveals a DNA Shape and Chromatin Signature of Metazoan Origins. <i>Cell Reports</i> , 2015, 11, 821-834.	2.9	72
36	Systematic prediction of DNA shape changes due to CpG methylation explains epigenetic effects on protein-DNA binding. <i>Epigenetics and Chromatin</i> , 2018, 11, 6.	1.8	65

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37	Structure of p53 binding to the BAX response element reveals DNA unwinding and compression to accommodate base-pair insertion. <i>Nucleic Acids Research</i> , 2013, 41, 8368-8376.	6.5	64
38	Genome-wide prediction of minor-groove electrostatic potential enables biophysical modeling of protein-DNA binding. <i>Nucleic Acids Research</i> , 2017, 45, 12565-12576.	6.5	63
39	Structural studies of p53 inactivation by DNA-contact mutations and its rescue by suppressor mutations via alternative protein-DNA interactions. <i>Nucleic Acids Research</i> , 2013, 41, 8748-8759.	6.5	60
40	DNAproDB: an interactive tool for structural analysis of DNA-protein complexes. <i>Nucleic Acids Research</i> , 2017, 45, W89-W97.	6.5	59
41	GBshape: a genome browser database for DNA shape annotations. <i>Nucleic Acids Research</i> , 2015, 43, D103-D109.	6.5	58
42	Covariation between homeodomain transcription factors and the shape of their DNA binding sites. <i>Nucleic Acids Research</i> , 2014, 42, 430-441.	6.5	54
43	Toward a Mechanistic Understanding of DNA Methylation Readout by Transcription Factors. <i>Journal of Molecular Biology</i> , 2020, 432, 1801-1815.	2.0	54
44	Relationship between histone modifications and transcription factor binding is protein family specific. <i>Genome Research</i> , 2018, 28, 321-333.	2.4	51
45	Mechanism of Origin DNA Recognition and Assembly of an Initiator-Helicase Complex by SV40 Large Tumor Antigen. <i>Cell Reports</i> , 2013, 3, 1117-1127.	2.9	48
46	How motif environment influences transcription factor search dynamics: Finding a needle in a haystack. <i>BioEssays</i> , 2016, 38, 605-612.	1.2	48
47	Sequences flanking the core-binding site modulate glucocorticoid receptor structure and activity. <i>Nature Communications</i> , 2016, 7, 12621.	5.8	48
48	Expansion of GA Dinucleotide Repeats Increases the Density of CLAMP Binding Sites on the X-Chromosome to Promote <i>Drosophila</i> Dosage Compensation. <i>PLoS Genetics</i> , 2016, 12, e1006120.	1.5	48
49	DNAproDB: an expanded database and web-based tool for structural analysis of DNA-protein complexes. <i>Nucleic Acids Research</i> , 2019, 48, D277-D287.	6.5	41
50	Structure of the Forkhead Domain of FOXA2 Bound to a Complete DNA Consensus Site. <i>Biochemistry</i> , 2017, 56, 3745-3753.	1.2	39
51	Using internal and collective variables in Monte Carlo simulations of nucleic acid structures: Chain breakage/closure algorithm and associated Jacobians. <i>Journal of Computational Chemistry</i> , 2006, 27, 309-315.	1.5	27
52	TFBSshape: an expanded motif database for DNA shape features of transcription factor binding sites. <i>Nucleic Acids Research</i> , 2020, 48, D246-D255.	6.5	27
53	Genome information processing by the INO80 chromatin remodeler positions nucleosomes. <i>Nature Communications</i> , 2021, 12, 3231.	5.8	27
54	DNA sequence+shape kernel enables alignment-free modeling of transcription factor binding. <i>Bioinformatics</i> , 2017, 33, 3003-3010.	1.8	25

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55	Experimental maps of DNA structure at nucleotide resolution distinguish intrinsic from protein-induced DNA deformations. <i>Nucleic Acids Research</i> , 2018, 46, 2636-2647.	6.5	25
56	Epigenetic competition reveals density-dependent regulation and target site plasticity of phosphorothioate epigenetics in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 14322-14330.	3.3	25
57	CRISPR-Cas9 Mediated DNA Unwinding Detected Using Site-Directed Spin Labeling. <i>ACS Chemical Biology</i> , 2017, 12, 1489-1493.	1.6	24
58	Humanizing the yeast origin recognition complex. <i>Nature Communications</i> , 2021, 12, 33.	5.8	24
59	Conformations of p53 response elements in solution deduced using site-directed spin labeling and Monte Carlo sampling. <i>Nucleic Acids Research</i> , 2014, 42, 2789-2797.	6.5	23
60	Genome-wide features of neuroendocrine regulation in <i>Drosophila</i> by the basic helix-loop-helix transcription factor DIMMED. <i>Nucleic Acids Research</i> , 2015, 43, 2199-2215.	6.5	23
61	Flipping Watson and Crick. <i>Nature</i> , 2011, 470, 472-473.	13.7	22
62	An Integrated Spin-Labeling/Computational-Modeling Approach for Mapping Global Structures of Nucleic Acids. <i>Methods in Enzymology</i> , 2015, 564, 427-453.	0.4	18
63	Regulatory encoding of quantitative variation in spatial activity of a <i>Drosophila</i> enhancer. <i>Science Advances</i> , 2020, 6, .	4.7	18
64	Opposites Attract: Shape and Electrostatic Complementarity in Protein-DNA Complexes. <i>RSC Biomolecular Sciences</i> , 2012, , 53-80.	0.4	17
65	Landscape of DNA binding signatures of myocyte enhancer factor-2B reveals a unique interplay of base and shape readout. <i>Nucleic Acids Research</i> , 2020, 48, 8529-8544.	6.5	17
66	Analysis of Genetic Variation Indicates DNA Shape Involvement in Purifying Selection. <i>Molecular Biology and Evolution</i> , 2018, 35, 1958-1967.	3.5	14
67	The RNA Polymerase $\hat{\pm}$ Subunit Recognizes the DNA Shape of the Upstream Promoter Element. <i>Biochemistry</i> , 2020, 59, 4523-4532.	1.2	12
68	Proteopedia: 3D visualization and annotation of transcription factor-DNA readout modes. <i>Biochemistry and Molecular Biology Education</i> , 2012, 40, 400-401.	0.5	8
69	Deep Graph Embedding for Ranking Optimization in E-commerce. , 2018, 2018, 2007-2015.		6
70	Crystal Structures of Ternary Complexes of MEF2 and NKX2-5 Bound to DNA Reveal a Disease Related Protein-Protein Interaction Interface. <i>Journal of Molecular Biology</i> , 2020, 432, 5499-5508.	2.0	3
71	Exposing the secrets of sex determination. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 437-438.	3.6	2
72	Correspondence: Reply to "DNA shape is insufficient to explain binding". <i>Nature Communications</i> , 2017, 8, 15644.	5.8	1