Hidetoshi Kono

List of Publications by Year
in descending order

118 papers	3,108 citations	159585 30 h-index	175258 52 g-index
124 all docs	124 docs citations	124 times ranked	2902 citing authors

#	Article	IF	Citations
1	Extended ensemble simulations of a SARS-CoV-2 nsp1â€“5â€™-UTR complex. PLoS Computational Biology, 2022, 18, e1009804.	3.2	5
2	HNF1A POU Domain Mutations Found in Japanese Liver Cancer Patients Cause Downregulation of HNF4A Promoter Activity with Possible Disruption in Transcription Networks. Genes, 2022, 13, 413.	2.4	3
3	Overall structure of fully assembled cyanobacterial KaiABC circadian clock complex by an integrated experimental-computational approach. Communications Biology, 2022, 5, 184.	4.4	5
4	RNAPII driven post-translational modifications of nucleosomal histones. Trends in Genetics, 2022, 38, 1076-1095.	6.7	9
5	Free Energy Landscape of H2A-H2B Displacement From Nucleosome. Journal of Molecular Biology, 2022, 434, 167707.	4.2	6
6	Torsional stress can regulate the unwrapping of two outer half superhelical turns of nucleosomal DNA. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	14
7	NRF2 DLG Domain Mutations Identified in Japanese Liver Cancer Patients Affect the Transcriptional Activity in HCC Cell Lines. International Journal of Molecular Sciences, 2021, 22, 5296.	4.1	1
8	The N-terminal Tails of Histones H2A and H2B Adopt Two Distinct Conformations in the Nucleosome with Contact and Reduced Contact to DNA. Journal of Molecular Biology, 2021, 433, 167110.	4.2	16
9	Interplay among transacting factors around promoter in the initial phases of transcription. Current Opinion in Structural Biology, 2021, 71, 7-15.	5.7	4
10	Structural basis of the regulation of the normal and oncogenic methylation of nucleosomal histone H3 Lys36 by NSD2. Nature Communications, 2021, 12, 6605.	12.8	23
11	Emerging BRAF Mutations in Cancer Progression and Their Possible Effects on Transcriptional Networks. Genes, 2020, 11, 1342.	2.4	58
12	Nucleosome unwrapping and unstacking. Current Opinion in Structural Biology, 2020, 64, 119-125.	5.7	16
13	Structural basis for designing an array of engrailed homeodomains. Acta Crystallographica Section D: Structural Biology, 2020, 76, 824-833.	2.3	0
14	Heterochromatin protein 1 (HP1): interactions with itself and chromatin components. Biophysical Reviews, 2020, 12, 387-400.	3.2	52
15	Structural Studies of Overlapping Dinucleosomes in Solution. Biophysical Journal, 2020, 118, 2209-2219.	0.5	15
16	Balance between DNAâ€binding affinity and specificity enables selective recognition of longer target sequences in vivo. Protein Science, 2019, 28, 1630-1639.	7.6	3
17	Histone H3K23-specific acetylation by MORF is coupled to H3K14 acylation. Nature Communications, 2019, 10, 4724.	12.8	56
18	Transcutaneous Codelivery of Tumor Antigen and Resiquimod in Solid-in-Oil Nanodispersions Promotes Antitumor Immunity. ACS Biomaterials Science and Engineering, 2019, 5, 2297-2306.	5.2	16

#	Article	IF	Citations
19	Free energy profile for unwrapping outer superhelical turn of CENP-A nucleosome. Biophysics and Physicobiology, 2019, 16, 337-343.	1.0	8
20	Forewords to the special issue â€œProgress of theoretical and computational biophysicsâ€”in honor of Professor Nobuhiro Goâ€™s outstanding contribution on the occasion of his 80th birthdayâ€• Biophysics and Physicobiology, 2019, 16, 173-175.	1.0	0
21	Investigating the Influence of Arginine Dimethylation on Nucleosome Dynamics Using All-Atom Simulations and Kinetic Analysis. Journal of Physical Chemistry B, 2018, 122, 9625-9634.	2.6	11
22	MNase, as a probe to study the sequence-dependent site exposures in the +1 nucleosomes of yeast. Nucleic Acids Research, 2018, 46, 7124-7137.	14.5	12
23	Free energy profiles for unwrapping the outer superhelical turn of nucleosomal DNA. PLoS Computational Biology, 2018, 14, e1006024.	3.2	25
24	Loss-of-function mutations in Zn-finger DNA-binding domain of HNF4A cause aberrant transcriptional regulation in liver cancer. Oncotarget, 2018, 9, 26144-26156.	1.8	17
25	Crystal structure of the overlapping dinucleosome composed of hexasome and octasome. Science, 2017, 356, 205-208.	12.6	77
26	Covalent Modifications of Histone H3K9 Promote Binding of CHD3. Cell Reports, 2017, 21, 455-466.	6.4	36
27	H4 Tails Potentially Produce the Diversity in the Orientation of Two Nucleosomes. Biophysical Journal, 2017, 113, 978-990.	0.5	25
28	Accessibility of the histone H3 tail in the nucleosome for binding of paired readers. Nature Communications, 2017, 8, 1489.	12.8	67
29	Predicting conformational ensembles and genome-wide transcription factor binding sites from DNA sequences. Scientific Reports, 2017, 7, 4071.	3.3	11
30	DNA conformational transitions inferred from re-evaluation ofm|F_o| â^’D|F_c| electron-density maps. Acta Crystallographica Section D: Structural Biology, 2017, 73, 600-608.	2.3	3
31	H3 Histone Tail Conformation within the Nucleosome and the Impact of K14 Acetylation Studied Using Enhanced Sampling Simulation. PLoS Computational Biology, 2016, 12, e1004788.	3.2	52
32	Spotting the difference in molecular dynamics simulations of biomolecules. Journal of Chemical Physics, 2016, 145, 074116.	3.0	14
33	Distinct Roles of Histone H3 and H2A Tails in Nucleosome Stability. Scientific Reports, 2016, 6, 31437.	3.3	79
34	Two Arginine Residues Suppress the Flexibility of Nucleosomal DNA in the Canonical Nucleosome Core. PLoS ONE, 2015, 10, e0120635.	2.5	30
35	Adaptive lambda square dynamics simulation: An efficient conformational sampling method for biomolecules. Journal of Computational Chemistry, 2014, 35, 39-50.	3.3	16
36	Intensity of Diffracted X-rays from Biomolecules with Radiation Damage Caused by Strong X-ray Pulses. Journal of the Physical Society of Japan, 2014, 83, 094301.	1.6	1

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37	1P123 Free Energy Profile of Nucleosomal DNA Unwrapping(05B. Nucleic acid : Interaction &) Tj ETQq1 1 0.784314 rgBT /Overlock Seibutsu Butsuri, 2014, 54, S161.	0.1	0
38	3P088 Designing a new artificial transcription factor based on engrailed homeodomain(01F. Protein:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Butsuri, 2014, 54, S263.	0.1	0
39	Dissociation Free-Energy Profiles of Specific and Nonspecific DNAâ€“Protein Complexes. Journal of Physical Chemistry B, 2013, 117, 7535-7545.	2.6	16
40	2SCP-01 Free Energy Profile for Nucleosomal DNA unwrapping(2SCP Functional dynamics of) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 627	0.1	0
41	Calculation of Molecular-Structure-Based Damage Caused by Short-Pulse High-Intensity X-ray Lasers. Journal of the Physical Society of Japan, 2013, 82, 114301.	1.6	2
42	1P021 Adaptive lambda square dynamics simulation : an efficient conformational sampling method for biomolecules(01A. Protein:Structure,Poster). Seibutsu Butsuri, 2013, 53, S109.	0.1	0
43	Local Conformational Changes in the DNA Interfaces of Proteins. PLoS ONE, 2013, 8, e56080.	2.5	12
44	Molecular Structure of Isolated MvspI, a Variable Surface Protein of the Fish Pathogen Mycoplasma mobile. Journal of Bacteriology, 2012, 194, 3050-3057.	2.2	14
45	A new method for evaluating the specificity of indirect readout in proteinâ€“DNA recognition. Nucleic Acids Research, 2012, 40, e129-e129.	14.5	19
46	Phase retrieval from single biomolecule diffraction pattern. Optics Express, 2012, 20, 3375.	3.4	12
47	3PT108 The influence of solvent condition on DNA structures studied by molecular dynamics simulations(The 50th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2012, 52, S158-S159.	0.1	0
48	1B1522 Local conformational changes of proteins in DNA interfaces(Proteins: Structure &) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 30 Butsuri, 2012, 52, S22.	0.1	0
49	1SD-03 Differences in dissociation free-energy profiles between cognite and non-cognite protein-DNA complexes(1SD Molecular Dynamics in the Nucleus and Gene Regulation,Symposium,The 50th Annual) Tj ETQq1 1 0.784314 rgBT /Over	0.1	0
50	3PS026 Automatic similarity identification of 2D diffraction patterns with noisy background for 3D coherent x-ray diffractive imaging(The 50th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2012, 52, S150.	0.1	0
51	Rational design of DNA sequenceâ€specific zinc fingers. FEBS Letters, 2012, 586, 918-923.	2.8	5
52	What determines water-bridge lifetimes at the surface of DNA? Insight from systematic molecular dynamics analysis of water kinetics for various DNA sequences. Biophysical Chemistry, 2012, 160, 54-61.	2.8	21
53	Classifying and assembling two-dimensional X-ray laser diffraction patterns of a single particle to reconstruct the three-dimensional diffraction intensity function: resolution limit due to the quantum noise. Acta Crystallographica Section A: Foundations and Advances, 2012, 68, 366-381.	0.3	24
54	3B1434 Free energy profile of nucleosoma DNA sliding(3B Nucleic acid binding proteins,The 49th) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.1	0

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55	3I1048 Phase retrieval from noisy x-ray diffraction patterns of single molecules(3I Protein:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 Butsuri, 2011, 51, S137.	0.1	0
56	1C1412 Local conformational changes of proteins in DNA interfaces(Nucleic acid,The 49th Annual) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.1	0
57	2B1624 What determines water lifetimes at the surface of biomolecules?(Water & Hydration &) Tj ETQq1 1 0.784314 rgBT /O	0.1	0
58	2P131 Sequence dependencies of DNA deformability and hydration(The 48th Annual Meeting of the) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.1	0
59	1P129 Sequence and environmental effects on the B-A transition of DNA studied by molecular dynamics simulations(Nucleic acid:Structure & Property,The 48th Annual Meeting of the Biophysical Society of) Tj ETQq1 1 0.784314 rgBT /Ove	0.1	0
60	2P011 Estimation of attainable structural resolution by computer simulation for single biomolecule imaging with X-ray Free Electron Laser(The 48th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2010, 50, S83-S84.	0.1	0
61	1SC1005 Dynamics of water molecules and proteins interacting with DNA(1SC Fluctuation and) Tj ETQq1 1 0.784314 rgBT /Overlock 1 Butsuri, 2010, 50, S2.	0.1	0
62	EVALUATION OF DNA INTRAMOLECULAR INTERACTIONS FOR NUCLEOSOME POSITIONING IN YEAST. , 2009, , .		0
63	A generalized conformational energy function of DNA derived from molecular dynamics simulations. Nucleic Acids Research, 2009, 37, e135-e135.	14.5	7
64	Discovery of proteinaceous N-modification in lysine biosynthesis of Thermus thermophilus. Nature Chemical Biology, 2009, 5, 673-679.	8.0	49
65	Crystal structures of the regulatory subunit of Thrâ€sensitive aspartate kinase from Thermus thermophilus. FEBS Journal, 2009, 276, 3124-3136.	4.7	15
66	Sequence Dependencies of DNA Deformability and Hydration in the Minor Groove. Biophysical Journal, 2009, 97, 1138-1147.	0.5	33
67	Rotamer Libraries For Molecular Modeling And Design Of Proteins. , 2009, , .		2
68	3P-097 Structure-based Analysis of Cooperativity in Protein-DNA Recognition(Nucleic acid:Interaction) Tj ETQq0 0 0 rgBT /Overlock 10 T 2009, 49, S167.	0.1	0
69	2P-088 Role of indirect readout in protein-DNA recognition assessed by a Bayesian approach(Nucleic) Tj ETQq1 1 0.784314 rgBT /Ove	0.1	0
70	3P-069 Theory of single molecule imaging by X-ray free-electron laser(Protein:Measurement &) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.1	0
71	1TP5-08 The free energy profile of a nucleosome core particle through the molecular dynamics simulation(The 47th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2009, 49, S38.	0.1	0
72	3P-104 Comparison of DNA hydration patterns obtained from MD simulation and 3D-RISM theory(Water,) Tj ETQq0 0 0 rgBT /Overlock 1 Butsuri, 2009, 49, S168-S169.	0.1	0

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73	Comparison of DNA hydration patterns obtained using two distinct computational methods, molecular dynamics simulation and three-dimensional reference interaction site model theory. Journal of Chemical Physics, 2008, 128, 185102.	3.0	16
74	3P-065 Theoretical approach for solving 3D structures of biomolecules with single-molecule X-ray diffraction patterns(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S137.	0.1	0
75	2P-114 Sequence-dependent DNA deformability and hydration studied by molecular dynamics simulations(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S92-S93.	0.1	0
76	Combinatorial Protein Design Strategies Using Computational Methods. , 2007, 352, 3-22.		3
77	DNA deformability and hydration studied by molecular dynamics simulation. Molecular Simulation, 2007, 33, 103-107.	2.0	7
78	coliSNP database server mapping nsSNPs on protein structures. Nucleic Acids Research, 2007, 36, D409-D413.	14.5	16
79	Sequence-dependent DNA deformability studied using molecular dynamics simulations. Nucleic Acids Research, 2007, 35, 6063-6074.	14.5	111
80	1P138 Analysis of Transcriptonal Regulation Network in Saccharomyces cerevisiae(Nucleic acid,Poster) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.1	0
81	1P136 Interaction Free Energy Landscapes between DMA Bases and Protein Side Chains(Nucleic) Tj ETQq1 1 0.784314 rgBT /Overloc	0.1	0
82	Protein-DNA Recognition Mechanism and Prediction. Seibutsu Butsuri, 2007, 47, 160-166.	0.1	1
83	ReadOut: structure-based calculation of direct and indirect readout energies and specificities for protein-DNA recognition. Nucleic Acids Research, 2006, 34, W124-W127.	14.5	36
84	Progress in the development and application of computational methods for probabilistic protein design. Computers and Chemical Engineering, 2005, 29, 407-421.	3.8	22
85	INTEGRATION OF BIOINFORMATICS AND COMPUTATIONAL BIOLOGY TO UNDERSTAND PROTEIN-DNA RECOGNITION MECHANISM. Journal of Bioinformatics and Computational Biology, 2005, 03, 169-183.	0.8	9
86	Protein-DNA Recognition Patterns and Predictions. Annual Review of Biophysics and Biomolecular Structure, 2005, 34, 379-398.	18.3	164
87	Sequence-Dependent Conformational Energy of DNA Derived from Molecular Dynamics Simulations:Â Toward Understanding the Indirect Readout Mechanism in Proteinâ˜'DNA Recognition. Journal of the American Chemical Society, 2005, 127, 16074-16089.	13.7	50
88	De Novo Design of a Redox-Active Minimal Rubredoxin Mimic. Journal of the American Chemical Society, 2005, 127, 5804-5805.	13.7	126
89	Role of inter and intramolecular interactions in proteinâ€“DNA recognition. Gene, 2005, 364, 108-113.	2.2	28
90	Sequence analysis of the gliding protein Gli349 in Mycoplasma mobile. Biophysics (Nagoya-shi, Japan), 2005, 1, 33-43.	0.4	39

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91	DISENTANGLING THE ROLE OF TETRANUCLEOTIDES IN THE SEQUENCE-DEPENDENCE OF DNA CONFORMATION: A MOLECULAR DYNAMICS APPROACH. , 2005, , .		0
92	Computational design of water-soluble analogues of the potassium channel KcsA. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1828-1833.	7.1	106
93	Intermolecular and Intramolecular Readout Mechanisms in Proteinâ€“DNA Recognition. Journal of Molecular Biology, 2004, 337, 285-294.	4.2	116
94	DNA-Protein Interactions. , 2004, , 241-278.		1
95	Anatomy of specific interactions between ? repressor and operator DNA. Proteins: Structure, Function and Bioinformatics, 2003, 53, 33-43.	2.6	10
96	Computational Design and Characterization of a Monomeric Helical Dinuclear Metalloprotein. Journal of Molecular Biology, 2003, 334, 1101-1115.	4.2	138
97	Probabilistic approach to the design of symmetric protein quaternary structures. Protein Engineering, Design and Selection, 2003, 16, 971-977.	2.1	18
98	Specificity of Proteinâ€“DNA Recognition Revealed by Structure-based Potentials: Symmetric/Asymmetric and Cognate/Non-cognate Binding. Journal of Molecular Biology, 2002, 322, 907-915.	4.2	60
99	Importance of mutant position in Ramachandran plot for predicting protein stability of surface mutations. Biopolymers, 2002, 64, 210-220.	2.4	42
100	Statistical theory for protein combinatorial libraries. packing interactions, backbone flexibility, and the sequence variability of a main-chain structure11Edited by J. Thornton. Journal of Molecular Biology, 2001, 306, 607-628.	4.2	130
101	Thermodynamic databases for proteins and protein-nucleic acid interactions. Biopolymers, 2001, 61, 121-126.	2.4	20
102	Stability analysis for the cavity-filling mutations of the Myb DNA-binding domain utilizing free-energy calculations. , 2000, 38, 197-209.		17
103	Solvent density and long-range dipole field around a DNA-binding protein studied by molecular dynamics. Proteins: Structure, Function and Bioinformatics, 2000, 40, 193-206.	2.6	38
104	Multicanonical Monte Carlo calculation of the free-energy map of the base-amino acid interaction. Journal of Computational Chemistry, 2000, 21, 954-962.	3.3	18
105	ProTherm, version 2.0: thermodynamic database for proteins and mutants. Nucleic Acids Research, 2000, 28, 283-285.	14.5	62
106	Importance of Surrounding Residues for Protein Stability of Partially Buried Mutations. Journal of Biomolecular Structure and Dynamics, 2000, 18, 281-295.	3.5	41
107	Cavity-Filling Mutations Enhance Protein Stability by Lowering the Free Energy of Native State. Journal of Physical Chemistry B, 2000, 104, 3705-3711.	2.6	13
108	Solvent density and longâ€range dipole field around a DNAâ€binding protein studied by molecular dynamics. Proteins: Structure, Function and Bioinformatics, 2000, 40, 193-206.	2.6	4

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109	Prediction of DNA Target Sites by Regulatory Proteins.. Seibutsu Butsuri, 2000, 40, 162-166.	0.1	0
110	ProTherm: Thermodynamic Database for Proteins and Mutants. Nucleic Acids Research, 1999, 27, 286-288.	14.5	137
111	Role of structural and sequence information in the prediction of protein stability changes: comparison between buried and partially buried mutations. Protein Engineering, Design and Selection, 1999, 12, 549-555.	2.1	128
112	Molecular dynamics study on mobility and dipole ordering of solvent around proteins: effects of periodic-box size and protein charge. Chemical Physics Letters, 1999, 306, 395-401.	2.6	18
113	Relationship between amino acid properties and protein stability: buried mutations. The Protein Journal, 1999, 18, 565-578.	1.1	72
114	Structure-based prediction of DNA target sites by regulatory proteins. Proteins: Structure, Function and Bioinformatics, 1999, 35, 114-131.	2.6	160
115	A new method for side-chain conformation prediction using a Hopfield network and reproduced rotamers. Journal of Computational Chemistry, 1996, 17, 1667-1683.	3.3	38
116	A new method for side-chain conformation prediction using a Hopfield network and reproduced rotamers. Journal of Computational Chemistry, 1996, 17, 1667-1683.	3.3	8
117	Energy minimization method using automata network for sequence and side-chain conformation prediction from given backbone geometry. Proteins: Structure, Function and Bioinformatics, 1994, 19, 244-255.	2.6	45
118	Effect of recombinant human erythropoietin administration on peripheral blood neutrophil counts of premature infants. Journal of Pediatrics, 1994, 124, 467-470.	1.8	14