

Hidetoshi Kono

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/349329/publications.pdf>

Version: 2024-02-01

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	Protein-DNA Recognition Patterns and Predictions. Annual Review of Biophysics and Biomolecular Structure, 2005, 34, 379-398.	18.3	164
2	Structure-based prediction of DNA target sites by regulatory proteins. Proteins: Structure, Function and Bioinformatics, 1999, 35, 114-131.	2.6	160
3	Computational Design and Characterization of a Monomeric Helical Dinuclear Metalloprotein. Journal of Molecular Biology, 2003, 334, 1101-1115.	4.2	138
4	ProTherm: Thermodynamic Database for Proteins and Mutants. Nucleic Acids Research, 1999, 27, 286-288.	14.5	137
5	Statistical theory for protein combinatorial libraries. packing interactions, backbone flexibility, and the sequence variability of a main-chain structure 11 Edited by J. Thornton. Journal of Molecular Biology, 2001, 306, 607-628.	4.2	130
6	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
7	De Novo Design of a Redox-Active Minimal Rubredoxin Mimic. Journal of the American Chemical Society, 2005, 127, 5804-5805.	13.7	126
8	Intermolecular and Intramolecular Readout Mechanisms in Protein-DNA Recognition. Journal of Molecular Biology, 2004, 337, 285-294.	4.2	116
9	Sequence-dependent DNA deformability studied using molecular dynamics simulations. Nucleic Acids Research, 2007, 35, 6063-6074.	14.5	111
10	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
11	Distinct Roles of Histone H3 and H2A Tails in Nucleosome Stability. Scientific Reports, 2016, 6, 31437.	3.3	79
12	Crystal structure of the overlapping dinucleosome composed of hexasome and octasome. Science, 2017, 356, 205-208.	12.6	77
13	Relationship between amino acid properties and protein stability: buried mutations. The Protein Journal, 1999, 18, 565-578.	1.1	72
14	Accessibility of the histone H3 tail in the nucleosome for binding of paired readers. Nature Communications, 2017, 8, 1489.	12.8	67
15	ProTherm, version 2.0: thermodynamic database for proteins and mutants. Nucleic Acids Research, 2000, 28, 283-285.	14.5	62
16	Specificity of Protein-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
17	Emerging BRAF Mutations in Cancer Progression and Their Possible Effects on Transcriptional Networks. Genes, 2020, 11, 1342.	2.4	58
18	Histone H3K23-specific acetylation by MORF is coupled to H3K14 acylation. Nature Communications, 2019, 10, 4724.	12.8	56

#	ARTICLE	IF	CITATIONS
19	H3 Histone Tail Conformation within the Nucleosome and the Impact of K14 Acetylation Studied Using Enhanced Sampling Simulation. <i>PLoS Computational Biology</i> , 2016, 12, e1004788.	3.2	52
20	Heterochromatin protein 1 (HP1): interactions with itself and chromatin components. <i>Biophysical Reviews</i> , 2020, 12, 387-400.	3.2	52
21	Sequence-Dependent Conformational Energy of DNA Derived from Molecular Dynamics Simulations: Toward Understanding the Indirect Readout Mechanism in Protein-DNA Recognition. <i>Journal of the American Chemical Society</i> , 2005, 127, 16074-16089.	13.7	50
22	Discovery of proteinaceous N-modification in lysine biosynthesis of <i>Thermus thermophilus</i> . <i>Nature Chemical Biology</i> , 2009, 5, 673-679.	8.0	49
23	Energy minimization method using automata network for sequence and side-chain conformation prediction from given backbone geometry. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 19, 244-255.	2.6	45
24	Importance of mutant position in Ramachandran plot for predicting protein stability of surface mutations. <i>Biopolymers</i> , 2002, 64, 210-220.	2.4	42
25	Importance of Surrounding Residues for Protein Stability of Partially Buried Mutations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2000, 18, 281-295.	3.5	41
26	Sequence analysis of the gliding protein Gli349 in <i>Mycoplasma mobile</i> . <i>Biophysics (Nagoya-shi, Japan)</i> , 2005, 1, 33-43.	0.4	39
27	A new method for side-chain conformation prediction using a Hopfield network and reproduced rotamers. <i>Journal of Computational Chemistry</i> , 1996, 17, 1667-1683.	3.3	38
28	Solvent density and long-range dipole field around a DNA-binding protein studied by molecular dynamics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 40, 193-206.	2.6	38
29	ReadOut: structure-based calculation of direct and indirect readout energies and specificities for protein-DNA recognition. <i>Nucleic Acids Research</i> , 2006, 34, W124-W127.	14.5	36
30	Covalent Modifications of Histone H3K9 Promote Binding of CHD3. <i>Cell Reports</i> , 2017, 21, 455-466.	6.4	36
31	Sequence Dependencies of DNA Deformability and Hydration in the Minor Groove. <i>Biophysical Journal</i> , 2009, 97, 1138-1147.	0.5	33
32	Two Arginine Residues Suppress the Flexibility of Nucleosomal DNA in the Canonical Nucleosome Core. <i>PLoS ONE</i> , 2015, 10, e0120635.	2.5	30
33	Role of inter and intramolecular interactions in protein-DNA recognition. <i>Gene</i> , 2005, 364, 108-113.	2.2	28
34	H4 Tails Potentially Produce the Diversity in the Orientation of Two Nucleosomes. <i>Biophysical Journal</i> , 2017, 113, 978-990.	0.5	25
35	Free energy profiles for unwrapping the outer superhelical turn of nucleosomal DNA. <i>PLoS Computational Biology</i> , 2018, 14, e1006024.	3.2	25
36	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. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2012, 68, 366-381.	0.3	24

#	ARTICLE	IF	CITATIONS
37	Structural basis of the regulation of the normal and oncogenic methylation of nucleosomal histone H3 Lys36 by NSD2. <i>Nature Communications</i> , 2021, 12, 6605.	12.8	23
38	Progress in the development and application of computational methods for probabilistic protein design. <i>Computers and Chemical Engineering</i> , 2005, 29, 407-421.	3.8	22
39	What determines water-bridge lifetimes at the surface of DNA? Insight from systematic molecular dynamics analysis of water kinetics for various DNA sequences. <i>Biophysical Chemistry</i> , 2012, 160, 54-61.	2.8	21
40	Thermodynamic databases for proteins and protein-nucleic acid interactions. <i>Biopolymers</i> , 2001, 61, 121-126.	2.4	20
41	A new method for evaluating the specificity of indirect readout in protein-DNA recognition. <i>Nucleic Acids Research</i> , 2012, 40, e129-e129.	14.5	19
42	Molecular dynamics study on mobility and dipole ordering of solvent around proteins: effects of periodic-box size and protein charge. <i>Chemical Physics Letters</i> , 1999, 306, 395-401.	2.6	18
43	Multicanonical Monte Carlo calculation of the free-energy map of the base-amino acid interaction. <i>Journal of Computational Chemistry</i> , 2000, 21, 954-962.	3.3	18
44	Probabilistic approach to the design of symmetric protein quaternary structures. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 971-977.	2.1	18
45	Stability analysis for the cavity-filling mutations of the Myb DNA-binding domain utilizing free-energy calculations. <i>Journal of Molecular Biology</i> , 2000, 38, 197-209.		17
46	Loss-of-function mutations in Zn-finger DNA-binding domain of <i>HNF4A</i> cause aberrant transcriptional regulation in liver cancer. <i>Oncotarget</i> , 2018, 9, 26144-26156.	1.8	17
47	coliSNP database server mapping nsSNPs on protein structures. <i>Nucleic Acids Research</i> , 2007, 36, D409-D413.	14.5	16
48	Comparison of DNA hydration patterns obtained using two distinct computational methods, molecular dynamics simulation and three-dimensional reference interaction site model theory. <i>Journal of Chemical Physics</i> , 2008, 128, 185102.	3.0	16
49	Dissociation Free-Energy Profiles of Specific and Nonspecific DNA-Protein Complexes. <i>Journal of Physical Chemistry B</i> , 2013, 117, 7535-7545.	2.6	16
50	Adaptive lambda square dynamics simulation: An efficient conformational sampling method for biomolecules. <i>Journal of Computational Chemistry</i> , 2014, 35, 39-50.	3.3	16
51	Transcutaneous Codelivery of Tumor Antigen and Resiquimod in Solid-in-Oil Nanodispersions Promotes Antitumor Immunity. <i>ACS Biomaterials Science and Engineering</i> , 2019, 5, 2297-2306.	5.2	16
52	Nucleosome unwrapping and unstacking. <i>Current Opinion in Structural Biology</i> , 2020, 64, 119-125.	5.7	16
53	The N-terminal Tails of Histones H2A and H2B Adopt Two Distinct Conformations in the Nucleosome with Contact and Reduced Contact to DNA. <i>Journal of Molecular Biology</i> , 2021, 433, 167110.	4.2	16
54	Crystal structures of the regulatory subunit of Thr-sensitive aspartate kinase from <i>Thermus thermophilus</i> . <i>FEBS Journal</i> , 2009, 276, 3124-3136.	4.7	15

#	ARTICLE	IF	CITATIONS
55	Structural Studies of Overlapping Dinucleosomes in Solution. <i>Biophysical Journal</i> , 2020, 118, 2209-2219.	0.5	15
56	Effect of recombinant human erythropoietin administration on peripheral blood neutrophil counts of premature infants. <i>Journal of Pediatrics</i> , 1994, 124, 467-470.	1.8	14
57	Molecular Structure of Isolated Mvspl, a Variable Surface Protein of the Fish Pathogen <i>Mycoplasma mobile</i> . <i>Journal of Bacteriology</i> , 2012, 194, 3050-3057.	2.2	14
58	Spotting the difference in molecular dynamics simulations of biomolecules. <i>Journal of Chemical Physics</i> , 2016, 145, 074116.	3.0	14
59	Torsional stress can regulate the unwrapping of two outer half superhelical turns of nucleosomal DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	14
60	Cavity-Filling Mutations Enhance Protein Stability by Lowering the Free Energy of Native State. <i>Journal of Physical Chemistry B</i> , 2000, 104, 3705-3711.	2.6	13
61	Phase retrieval from single biomolecule diffraction pattern. <i>Optics Express</i> , 2012, 20, 3375.	3.4	12
62	MNase, as a probe to study the sequence-dependent site exposures in the +1 nucleosomes of yeast. <i>Nucleic Acids Research</i> , 2018, 46, 7124-7137.	14.5	12
63	Local Conformational Changes in the DNA Interfaces of Proteins. <i>PLoS ONE</i> , 2013, 8, e56080.	2.5	12
64	Predicting conformational ensembles and genome-wide transcription factor binding sites from DNA sequences. <i>Scientific Reports</i> , 2017, 7, 4071.	3.3	11
65	Investigating the Influence of Arginine Dimethylation on Nucleosome Dynamics Using All-Atom Simulations and Kinetic Analysis. <i>Journal of Physical Chemistry B</i> , 2018, 122, 9625-9634.	2.6	11
66	Anatomy of specific interactions between λ repressor and operator DNA. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 33-43.	2.6	10
67	INTEGRATION OF BIOINFORMATICS AND COMPUTATIONAL BIOLOGY TO UNDERSTAND PROTEIN-DNA RECOGNITION MECHANISM. <i>Journal of Bioinformatics and Computational Biology</i> , 2005, 03, 169-183.	0.8	9
68	RNAPII driven post-translational modifications of nucleosomal histones. <i>Trends in Genetics</i> , 2022, 38, 1076-1095.	6.7	9
69	Free energy profile for unwrapping outer superhelical turn of CENP-A nucleosome. <i>Biophysics and Physicobiology</i> , 2019, 16, 337-343.	1.0	8
70	A new method for side-chain conformation prediction using a Hopfield network and reproduced rotamers. <i>Journal of Computational Chemistry</i> , 1996, 17, 1667-1683.	3.3	8
71	DNA deformability and hydration studied by molecular dynamics simulation. <i>Molecular Simulation</i> , 2007, 33, 103-107.	2.0	7
72	A generalized conformational energy function of DNA derived from molecular dynamics simulations. <i>Nucleic Acids Research</i> , 2009, 37, e135-e135.	14.5	7

#	ARTICLE	IF	CITATIONS
73	Free Energy Landscape of H2A-H2B Displacement From Nucleosome. <i>Journal of Molecular Biology</i> , 2022, 434, 167707.	4.2	6
74	Rational design of DNA sequence-specific zinc fingers. <i>FEBS Letters</i> , 2012, 586, 918-923.	2.8	5
75	Extended ensemble simulations of a SARS-CoV-2 nsp1-5'-UTR complex. <i>PLoS Computational Biology</i> , 2022, 18, e1009804.	3.2	5
76	Overall structure of fully assembled cyanobacterial KaiABC circadian clock complex by an integrated experimental-computational approach. <i>Communications Biology</i> , 2022, 5, 184.	4.4	5
77	Interplay among transacting factors around promoter in the initial phases of transcription. <i>Current Opinion in Structural Biology</i> , 2021, 71, 7-15.	5.7	4
78	Solvent density and long-range dipole field around a DNA-binding protein studied by molecular dynamics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 40, 193-206.	2.6	4
79	Combinatorial Protein Design Strategies Using Computational Methods. , 2007, 352, 3-22.		3
80	Balance between DNA-binding affinity and specificity enables selective recognition of longer target sequences in vivo. <i>Protein Science</i> , 2019, 28, 1630-1639.	7.6	3
81	DNA conformational transitions inferred from re-evaluation of cryo-EM cryo-EM electron-density maps. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 600-608.	2.3	3
82	HNF1A POU Domain Mutations Found in Japanese Liver Cancer Patients Cause Downregulation of HNF4A Promoter Activity with Possible Disruption in Transcription Networks. <i>Genes</i> , 2022, 13, 413.	2.4	3
83	Rotamer Libraries For Molecular Modeling And Design Of Proteins. , 2009, , .		2
84	Calculation of Molecular-Structure-Based Damage Caused by Short-Pulse High-Intensity X-ray Lasers. <i>Journal of the Physical Society of Japan</i> , 2013, 82, 114301.	1.6	2
85	Intensity of Diffracted X-rays from Biomolecules with Radiation Damage Caused by Strong X-ray Pulses. <i>Journal of the Physical Society of Japan</i> , 2014, 83, 094301.	1.6	1
86	NRF2 DLG Domain Mutations Identified in Japanese Liver Cancer Patients Affect the Transcriptional Activity in HCC Cell Lines. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5296.	4.1	1
87	DNA-Protein Interactions. , 2004, , 241-278.		1
88	Protein-DNA Recognition Mechanism and Prediction. <i>Seibutsu Butsuri</i> , 2007, 47, 160-166.	0.1	1
89	1P138 Analysis of Transcriptional Regulation Network in <i>Saccharomyces cerevisiae</i> (Nucleic acid,Poster) Tj ETQq1 1 0,784314 rgBT /Over	0.1	0
90	1P136 Interaction Free Energy Landscapes between DMA Bases and Protein Side Chains(Nucleic) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6	0.1	0

#	ARTICLE	IF	CITATIONS
91	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
92	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
93	EVALUATION OF DNA INTRAMOLECULAR INTERACTIONS FOR NUCLEOSOME POSITIONING IN YEAST. , 2009, , .		0
94	3P-097 Structure-based Analysis of Cooperativity in Protein-DNA Recognition(Nucleic acid:Interaction) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 Td 2009, 49, S167.	0.1	0
95	2P-088 Role of indirect readout in protein-DNA recognition assessed by a Bayesian approach(Nucleic Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 227 Td	0.1	0
96	3P-069 Theory of single molecule imaging by X-ray free-electron laser(Protein:Measurement & Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 Td	0.1	0
97	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
98	3P-104 Comparison of DNA hydration patterns obtained from MD simulation and 3D-RISM theory(Water,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 Td Butsuri, 2009, 49, S168-S169.	0.1	0
99	2P131 Sequence dependencies of DNA deformability and hydration(The 48th Annual Meeting of the Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 227 Td	0.1	0
100	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 ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 Td	0.1	0
101	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
102	1SC1005 Dynamics of water molecules and proteins interacting with DNA(1SC Fluctuation and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 Td Butsuri, 2010, 50, S2.	0.1	0
103	3B1434 Free energy profile of nucleosoma DNA sliding(3B Nucleic acid binding proteins,The 49th) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 227 Td	0.1	0
104	3I1048 Phase retrieval from noisy x-ray diffraction patterns of single molecules(3I Protein:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 Td Butsuri, 2011, 51, S137.	0.1	0
105	1C1412 Local conformational changes of proteins in DNA interfaces(Nucleic acid,The 49th Annual) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 227 Td	0.1	0
106	2B1624 What determines water lifetimes at the surface of biomolecules?(Water & Hydration &) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 Td	0.1	0
107	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
108	1B1522 Local conformational changes of proteins in DNA interfaces(Proteins: Structure &) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 Td Butsuri, 2012, 52, S22.	0.1	0

#	ARTICLE	IF	CITATIONS
109	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 0.784314rgBT /Overlock 10	0.1	0
110	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
111	2SCP-01 Free Energy Profile for Nucleosomal DNA unwrapping(2SCP Functional dynamics of) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.1	0
112	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
113	1P123 Free Energy Profile of Nucleosomal DNA Unwrapping(05B. Nucleic acid : Interaction &) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Seibutsu Butsuri, 2014, 54, S161.	0.1	0
114	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
115	Structural basis for designing an array of engrailed homeodomains. Acta Crystallographica Section D: Structural Biology, 2020, 76, 824-833.	2.3	0
116	Prediction of DNA Target Sites by Regulatory Proteins.. Seibutsu Butsuri, 2000, 40, 162-166.	0.1	0
117	DISENTANGLING THE ROLE OF TETRANUCLEOTIDES IN THE SEQUENCE-DEPENDENCE OF DNA CONFORMATION: A MOLECULAR DYNAMICS APPROACH. , 2005, , .		0
118	Forewords to the special issue “Progress of theoretical and computational biophysics” in honor of Professor Nobuhiro Go’s outstanding contribution on the occasion of his 80th birthday” Biophysics and Physicobiology, 2019, 16, 173-175.	1.0	0