

Akinori Sarai

List of Publications by Year in descending order

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91
papers

5,906
citations

87888

38
h-index

74163

75
g-index

92
all docs

92
docs citations

92
times ranked

5625
citing authors

#	ARTICLE	IF	CITATIONS
1	Solution structure of a specific DNA complex of the Myb DNA-binding domain with cooperative recognition helices. <i>Cell</i> , 1994, 79, 639-648.	28.9	486
2	ProTherm and ProNIT: thermodynamic databases for proteins and protein-nucleic acid interactions. <i>Nucleic Acids Research</i> , 2006, 34, D204-D206.	14.5	361
3	Unique Mode of GCC Box Recognition by the DNA-binding Domain of Ethylene-responsive Element-binding Factor (ERF Domain) in Plant. <i>Journal of Biological Chemistry</i> , 1998, 273, 26857-26861.	3.4	355
4	Analysis and prediction of DNA-binding proteins and their binding residues based on composition, sequence and structural information. <i>Bioinformatics</i> , 2004, 20, 477-486.	4.1	327
5	ProTherm, version 4.0: thermodynamic database for proteins and mutants. <i>Nucleic Acids Research</i> , 2004, 32, 120D-121.	14.5	307
6	ASAView: Database and tool for solvent accessibility representation in proteins. <i>BMC Bioinformatics</i> , 2004, 5, 51.	2.6	248
7	The cavity in the hydrophobic core of Myb DNA-binding domain is reserved for DNA recognition and trans-activation. <i>Nature Structural Biology</i> , 1996, 3, 178-187.	9.7	243
8	PSSM-based prediction of DNA binding sites in proteins. <i>BMC Bioinformatics</i> , 2005, 6, 33.	2.6	224
9	Important amino acid properties for enhanced thermostability from mesophilic to thermophilic proteins. <i>Biophysical Chemistry</i> , 1999, 82, 51-67.	2.8	214
10	Real value prediction of solvent accessibility from amino acid sequence. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 50, 629-635.	2.6	180
11	Protein-DNA Recognition Patterns and Predictions. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2005, 34, 379-398.	18.3	164
12	Structure-based prediction of DNA target sites by regulatory proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 35, 114-131.	2.6	160
13	Comparison of the free and DNA-complexed forms of the DNA-binding domain from c-Myb. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 309-320.	8.2	156
14	Role of structural and sequence information in the prediction of protein stability changes: comparison between buried and partially buried mutations. <i>Protein Engineering, Design and Selection</i> , 1999, 12, 549-555.	2.1	128
15	Moment-based Prediction of DNA-binding Proteins. <i>Journal of Molecular Biology</i> , 2004, 341, 65-71.	4.2	124
16	Intermolecular and Intramolecular Readout Mechanisms in Protein-DNA Recognition. <i>Journal of Molecular Biology</i> , 2004, 337, 285-294.	4.2	116
17	Sequence-dependent DNA deformability studied using molecular dynamics simulations. <i>Nucleic Acids Research</i> , 2007, 35, 6063-6074.	14.5	111
18	Thermodynamics of specific and non-specific DNA binding by the c-myb DNA-binding domain. <i>Journal of Molecular Biology</i> , 1998, 276, 571-590.	4.2	100

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19	Genetic algorithm optimization in drug design QSAR: Bayesian-regularized genetic neural networks (BRGNN) and genetic algorithm-optimized support vectors machines (GA-SVM). <i>Molecular Diversity</i> , 2011, 15, 269-289.	3.9	81
20	Protein-DNA interactions: structural, thermodynamic and clustering patterns of conserved residues in DNA-binding proteins. <i>Nucleic Acids Research</i> , 2008, 36, 5922-5932.	14.5	79
21	Thermodynamic and kinetic studies of DNA triplex formation of an oligohomopyrimidine and a matched duplex by filter binding assay. <i>Biochemistry</i> , 1993, 32, 8963-8969.	2.5	72
22	A Possible Role of the C-terminal Domain of the RecA Protein. <i>Journal of Biological Chemistry</i> , 1996, 271, 33515-33524.	3.4	72
23	Relationship between amino acid properties and protein stability: buried mutations. <i>The Protein Journal</i> , 1999, 18, 565-578.	1.1	72
24	Temperature Dependence and Sequence Specificity of DNA Triplex Formation: An Analysis Using Isothermal Titration Calorimetry. <i>Journal of the American Chemical Society</i> , 1996, 118, 4532-4538.	13.7	70
25	Dynamics of proton migration in free base porphines. <i>Journal of Chemical Physics</i> , 1982, 76, 5554-5563.	3.0	64
26	ProTherm, version 2.0: thermodynamic database for proteins and mutants. <i>Nucleic Acids Research</i> , 2000, 28, 283-285.	14.5	62
27	The role of alternative translation start sites in the generation of human protein diversity. <i>Molecular Genetics and Genomics</i> , 2005, 273, 491-496.	2.1	61
28	Specificity of Protein-DNA Recognition Revealed by Structure-based Potentials: Symmetric/Asymmetric and Cognate/Non-cognate Binding. <i>Journal of Molecular Biology</i> , 2002, 322, 907-915.	4.2	60
29	ProTherm, Thermodynamic Database for Proteins and Mutants: developments in version 3.0. <i>Nucleic Acids Research</i> , 2002, 30, 301-302.	14.5	59
30	uORFs, reinitiation and alternative translation start sites in human mRNAs. <i>FEBS Letters</i> , 2008, 582, 1293-1297.	2.8	57
31	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
32	Free-Energy Maps of Base-Amino Acid Interactions for DNA-Protein Recognition. <i>Journal of the American Chemical Society</i> , 1999, 121, 6152-6157.	13.7	44
33	Hydrophobic Interactions in the Major Groove Can Influence DNA Local Structure. <i>Journal of Biomolecular Structure and Dynamics</i> , 1986, 4, 41-48.	3.5	42
34	Importance of mutant position in Ramachandran plot for predicting protein stability of surface mutations. <i>Biopolymers</i> , 2002, 64, 210-220.	2.4	42
35	The Affinity Maturation of Anti-4-hydroxy-3-nitrophenylacetyl Mouse Monoclonal Antibody. <i>Journal of Biological Chemistry</i> , 1995, 270, 22218-22222.	3.4	41
36	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

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37	Filling a cavity dramatically increases pressure stability of the c-Myb R2 subdomain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 96-101.	2.6	39
38	Classification of Protein-DNA Complexes Based on Structural Descriptors. <i>Structure</i> , 2006, 14, 1355-1367.	3.3	39
39	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
40	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
41	Prediction of mono- and di-nucleotide-specific DNA-binding sites in proteins using neural networks. <i>BMC Structural Biology</i> , 2009, 9, 30.	2.3	35
42	Shape and energetics of a cavity in c-Myb probed by natural and non-natural amino acid mutations. <i>Journal of Molecular Biology</i> , 1999, 292, 909-920.	4.2	33
43	Triplex Formation of Chemically Modified Homopyrimidine Oligonucleotides: Thermodynamic and Kinetic Studies. <i>Biochemistry</i> , 1999, 38, 14653-14659.	2.5	30
44	Proteochemometric Recognition of Stable Kinase Inhibition Complexes Using Topological Autocorrelation and Support Vector Machines. <i>Journal of Chemical Information and Modeling</i> , 2010, 50, 1179-1188.	5.4	30
45	The Mutant RecA Proteins, RecAR243Q and RecAK245N, Exhibit Defective DNA Binding in Homologous Pairing. <i>Archives of Biochemistry and Biophysics</i> , 1999, 365, 83-91.	3.0	29
46	Role of inter and intramolecular interactions in protein-DNA recognition. <i>Gene</i> , 2005, 364, 108-113.	2.2	28
47	Analysis of electric moments of RNA-binding proteins: implications for mechanism and prediction. <i>BMC Structural Biology</i> , 2011, 11, 8.	2.3	24
48	Look-up tables for protein solvent accessibility prediction and nearest neighbor effect analysis. <i>Biopolymers</i> , 2004, 75, 209-216.	2.4	23
49	Theoretical studies on the interaction of proteins with base pairs. I. Ab initio calculation for the effect of H-bonding interaction of proteins on the stability of adenine-uracil pair. <i>International Journal of Quantum Chemistry</i> , 1984, 25, 527-533.	2.0	20
50	Comment on "Raman spectroscopic study of isotope effects on the NH/ND stretching bands of meso-tetraphenylporphine and vibrational hydrogen tunneling". <i>Journal of Chemical Physics</i> , 1984, 80, 5341-5343.	3.0	20
51	Investigation of the Pyrimidine Preference by the c-Myb DNA-binding Domain at the Initial Base of the Consensus Sequence. <i>Journal of Biological Chemistry</i> , 1997, 272, 17966-17971.	3.4	20
52	Thermodynamic databases for proteins and protein-nucleic acid interactions. <i>Biopolymers</i> , 2001, 61, 121-126.	2.4	20
53	Indirect readout in drug-DNA recognition: role of sequence-dependent DNA conformation. <i>Nucleic Acids Research</i> , 2007, 36, 376-386.	14.5	20
54	Translational polymorphism as a potential source of plant proteins variety in <i>Arabidopsis thaliana</i> . <i>Bioinformatics</i> , 2004, 20, 445-447.	4.1	19

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55	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
56	Relationship Between Curved DNA Conformations and Slow Gel Migration. <i>Journal of Biomolecular Structure and Dynamics</i> , 1987, 4, 561-567.	3.5	18
57	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
58	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
59	Analysis of the relationships between evolvability, thermodynamics, and the functions of intrinsically disordered proteins/regions. <i>Computational Biology and Chemistry</i> , 2012, 41, 51-57.	2.3	18
60	Stability analysis for the cavity-filling mutations of the Myb DNA-binding domain utilizing free-energy calculations. , 2000, 38, 197-209.		17
61	Thermodynamic Database for Proteins: Features and Applications. <i>Methods in Molecular Biology</i> , 2010, 609, 97-112.	0.9	17
62	CCRXP: exploring clusters of conserved residues in protein structures. <i>Nucleic Acids Research</i> , 2010, 38, W398-W401.	14.5	14
63	Thermodynamic and Kinetic Analyses of DNA Triplex Formation: Application of Filter-Binding Assay. <i>Journal of Biomolecular Structure and Dynamics</i> , 1993, 11, 245-252.	3.5	13
64	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
65	SIMULATION ANALYSIS OF THE PHOTOCONVERSION PROCESS OF SQUID RHODOPSIN AT LIQUID HELIUM TEMPERATURE. <i>Photochemistry and Photobiology</i> , 1980, 32, 199-206.	2.5	12
66	Construction of an Artificial Tandem Protein of the c-Myb DNA-Binding Domain and Analysis of Its DNA Binding Specificity. <i>Biochemical and Biophysical Research Communications</i> , 1999, 262, 94-97.	2.1	12
67	Free energy calculations for the relative binding affinity between DNA and λ -repressor. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 129-136.	2.6	12
68	Systematic single base-pair substitution analysis of DNA binding by the cAMP receptor protein in cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>FEBS Letters</i> , 2004, 563, 55-58.	2.8	12
69	λ -based prediction and experimental confirmation of SYCRP1-binding sites on the <i>Synechocystis</i> genome. <i>FEBS Journal</i> , 2008, 275, 4786-4795.	4.7	11
70	TEMPERATURE DEPENDENCE OF PHOTOSYNTHETIC EXCITATION TRANSFER-ASSISTED TRANSFER. <i>Photochemistry and Photobiology</i> , 1980, 31, 579-583.	2.5	10
71	Anatomy of specific interactions between λ repressor and operator DNA. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 33-43.	2.6	10
72	Atom-wise statistics and prediction of solvent accessibility in proteins. <i>Biophysical Chemistry</i> , 2006, 124, 145-154.	2.8	10

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73	Theoretical studies on the interaction of proteins with base pairs. II. Effect of external H-bond interactions on the stability of guanine-cytosine and non-Watson-Crick pairs. <i>International Journal of Quantum Chemistry</i> , 1985, 28, 399-409.	2.0	9
74	Sequence Context of Oligomer Tracts in Eukaryotic DNA: Biological and Conformational Implications. <i>Journal of Biomolecular Structure and Dynamics</i> , 1988, 6, 543-562.	3.5	9
75	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
76	PROTON TRANSFER IN THE PRIMARY PROCESS OF VISION. <i>Photochemistry and Photobiology</i> , 1981, 33, 875-881.	2.5	8
77	Dimensionality of amino acid space and solvent accessibility prediction with neural networks. <i>Computational Biology and Chemistry</i> , 2006, 30, 160-168.	2.3	7
78	A generalized conformational energy function of DNA derived from molecular dynamics simulations. <i>Nucleic Acids Research</i> , 2009, 37, e135-e135.	14.5	7
79	Properties of phosphorothioate DNA analogs. An ab initio study of prototype model linkages derived from dimethyl-phosphate anion. <i>Computational and Theoretical Chemistry</i> , 1999, 460, 103-116.	1.5	6
80	Determination of the NMR solution structure of a specific DNA complex of the Myb DNA-binding domain. <i>Journal of Biomolecular NMR</i> , 1995, 6, 294-305.	2.8	4
81	Knowledge-based prediction of DNA atomic structure from nucleic sequence. <i>Genome Informatics</i> , 2005, 16, 12-21.	0.4	4
82	Theoretical Studies of Photoisomerization in Visual Pigments. I. Formulation. <i>Journal of the Physical Society of Japan</i> , 1982, 51, 3302-3308.	1.6	3
83	Multi-state thermal transitions of proteins - DNA-binding domain of the c-Myb oncoprotein. <i>Pure and Applied Chemistry</i> , 1998, 70, 671-676.	1.9	3
84	Large-scale recognition of high-affinity protease-inhibitor complexes using topological autocorrelation and support vector machines. <i>Molecular Simulation</i> , 2016, 42, 420-433.	2.0	2
85	Theoretical Studies of Photoisomerization in Visual Pigments. II. Numerical Calculation. <i>Journal of the Physical Society of Japan</i> , 1982, 51, 3309-3317.	1.6	1
86	Oligonucleotides Containing a 6-Substituted Pyrimidine Base: A Design for Myb Inhibitors. <i>Nucleosides & Nucleotides</i> , 1999, 18, 1501-1502.	0.5	1
87	DNA-Protein Interactions. , 2004, , 241-278.		1
88	EVALUATION OF DNA INTRAMOLECULAR INTERACTIONS FOR NUCLEOSOME POSITIONING IN YEAST. , 2009, , .		0
89	Prediction of DNA Target Sites by Regulatory Proteins.. <i>Seibutsu Butsuri</i> , 2000, 40, 162-166.	0.1	0
90	Transcription Factors and DNA Elements in Eukaryote. , 2013, , 2224-2227.		0

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91	Excitation and Electron Transfer in Photosynthesis. Seibutsu Butsuri, 1980, 20, 75-83.	0.1	0