Akinori Sarai

List of Publications by Year
in descending order

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	Large-scale recognition of high-affinity proteaseâ€“inhibitor complexes using topological autocorrelation and support vector machines. Molecular Simulation, 2016, 42, 420-433.	2.0	2
2	Transcription Factors and DNA Elements in Eukaryote. , 2013, , 2224-2227.		0
3	A new method for evaluating the specificity of indirect readout in proteinâ€“DNA recognition. Nucleic Acids Research, 2012, 40, e129-e129.	14.5	19
4	Analysis of the relationships between evolvability, thermodynamics, and the functions of intrinsically disordered proteins/regions. Computational Biology and Chemistry, 2012, 41, 51-57.	2.3	18
5	Genetic algorithm optimization in drug design QSAR: Bayesian-regularized genetic neural networks (BRGNN) and genetic algorithm-optimized support vectors machines (GA-SVM). Molecular Diversity, 2011, 15, 269-289.	3.9	81
6	Analysis of electric moments of RNA-binding proteins: implications for mechanism and prediction. BMC Structural Biology, 2011, 11, 8.	2.3	24
7	CCRXP: exploring clusters of conserved residues in protein structures. Nucleic Acids Research, 2010, 38, W398-W401.	14.5	14
8	Proteochemometric Recognition of Stable Kinase Inhibition Complexes Using Topological Autocorrelation and Support Vector Machines. Journal of Chemical Information and Modeling, 2010, 50, 1179-1188.	5.4	30
9	Thermodynamic Database for Proteins: Features and Applications. Methods in Molecular Biology, 2010, 609, 97-112.	0.9	17
10	EVALUATION OF DNA INTRAMOLECULAR INTERACTIONS FOR NUCLEOSOME POSITIONING IN YEAST. , 2009, , .		0
11	A generalized conformational energy function of DNA derived from molecular dynamics simulations. Nucleic Acids Research, 2009, 37, e135-e135.	14.5	7
12	Prediction of mono- and di-nucleotide-specific DNA-binding sites in proteins using neural networks. BMC Structural Biology, 2009, 9, 30.	2.3	35
13	Î”Gâ€based prediction and experimental confirmation of SYCRP1â€binding sites on the Synechocystis genome. FEBS Journal, 2008, 275, 4786-4795.	4.7	11
14	uORFs, reinitiation and alternative translation start sites in human mRNAs. FEBS Letters, 2008, 582, 1293-1297.	2.8	57
15	Proteinâ€“DNA interactions: structural, thermodynamic and clustering patterns of conserved residues in DNA-binding proteins. Nucleic Acids Research, 2008, 36, 5922-5932.	14.5	79
16	Sequence-dependent DNA deformability studied using molecular dynamics simulations. Nucleic Acids Research, 2007, 35, 6063-6074.	14.5	111
17	Indirect readout in drug-DNA recognition: role of sequence-dependent DNA conformation. Nucleic Acids Research, 2007, 36, 376-386.	14.5	20
18	Dimensionality of amino acid space and solvent accessibility prediction with neural networks. Computational Biology and Chemistry, 2006, 30, 160-168.	2.3	7

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19	Atom-wise statistics and prediction of solvent accessibility in proteins. Biophysical Chemistry, 2006, 124, 145-154.	2.8	10
20	Classification of Protein-DNA Complexes Based on Structural Descriptors. Structure, 2006, 14, 1355-1367.	3.3	39
21	ProTherm and ProNIT: thermodynamic databases for proteins and protein-nucleic acid interactions. Nucleic Acids Research, 2006, 34, D204-D206.	14.5	361
22	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
23	PSSM-based prediction of DNA binding sites in proteins. BMC Bioinformatics, 2005, 6, 33.	2.6	224
24	The role of alternative translation start sites in the generation of human protein diversity. Molecular Genetics and Genomics, 2005, 273, 491-496.	2.1	61
25	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
26	Protein-DNA Recognition Patterns and Predictions. Annual Review of Biophysics and Biomolecular Structure, 2005, 34, 379-398.	18.3	164
27	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
28	Role of inter and intramolecular interactions in proteinâ€“DNA recognition. Gene, 2005, 364, 108-113.	2.2	28
29	Knowledge-based prediction of DNA atomic structure from nucleic sequence. Genome Informatics, 2005, 16, 12-21.	0.4	4
30	ProTherm, version 4.0: thermodynamic database for proteins and mutants. Nucleic Acids Research, 2004, 32, 120D-121.	14.5	307
31	Translational polymorphism as a potential source of plant proteins variety in Arabidopsis thaliana. Bioinformatics, 2004, 20, 445-447.	4.1	19
32	Analysis and prediction of DNA-binding proteins and their binding residues based on composition, sequence and structural information. Bioinformatics, 2004, 20, 477-486.	4.1	327
33	ASAView: Database and tool for solvent accessibility representation in proteins. BMC Bioinformatics, 2004, 5, 51.	2.6	248
34	Look-up tables for protein solvent accessibility prediction and nearest neighbor effect analysis. Biopolymers, 2004, 75, 209-216.	2.4	23
35	Intermolecular and Intramolecular Readout Mechanisms in Proteinâ€“DNA Recognition. Journal of Molecular Biology, 2004, 337, 285-294.	4.2	116
36	Moment-based Prediction of DNA-binding Proteins. Journal of Molecular Biology, 2004, 341, 65-71.	4.2	124

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37	Systematic single base-pair substitution analysis of DNA binding by the cAMP receptor protein in cyanobacteriumSynechocystissp. PCC 6803. FEBS Letters, 2004, 563, 55-58.	2.8	12
38	DNA-Protein Interactions. , 2004, , 241-278.		1
39	Real value prediction of solvent accessibility from amino acid sequence. Proteins: Structure, Function and Bioinformatics, 2003, 50, 629-635.	2.6	180
40	Free energy calculations for the relative binding affinity between DNA and ?-repressor. Proteins: Structure, Function and Bioinformatics, 2003, 52, 129-136.	2.6	12
41	Anatomy of specific interactions between ? repressor and operator DNA. Proteins: Structure, Function and Bioinformatics, 2003, 53, 33-43.	2.6	10
42	ProTherm, Thermodynamic Database for Proteins and Mutants: developments in version 3.0. Nucleic Acids Research, 2002, 30, 301-302.	14.5	59
43	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
44	Importance of mutant position in Ramachandran plot for predicting protein stability of surface mutations. Biopolymers, 2002, 64, 210-220.	2.4	42
45	Filling a cavity dramatically increases pressure stability of the c-Myb R2 subdomain. Proteins: Structure, Function and Bioinformatics, 2001, 45, 96-101.	2.6	39
46	Thermodynamic databases for proteins and protein-nucleic acid interactions. Biopolymers, 2001, 61, 121-126.	2.4	20
47	Stability analysis for the cavity-filling mutations of the Myb DNA-binding domain utilizing free-energy calculations. , 2000, 38, 197-209.		17
48	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
49	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
50	ProTherm, version 2.0: thermodynamic database for proteins and mutants. Nucleic Acids Research, 2000, 28, 283-285.	14.5	62
51	Importance of Surrounding Residues for Protein Stability of Partially Buried Mutations. Journal of Biomolecular Structure and Dynamics, 2000, 18, 281-295.	3.5	41
52	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
53	Prediction of DNA Target Sites by Regulatory Proteins.. Seibutsu Butsuri, 2000, 40, 162-166.	0.1	0
54	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

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55	Oligonucleotides Containing a 6-Substituted Pyrimidine Base: A Design for Myb Inhibitors. Nucleosides & Nucleotides, 1999, 18, 1501-1502.	0.5	1
56	Important amino acid properties for enhanced thermostability from mesophilic to thermophilic proteins. Biophysical Chemistry, 1999, 82, 51-67.	2.8	214
57	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
58	Relationship between amino acid properties and protein stability: buried mutations. The Protein Journal, 1999, 18, 565-578.	1.1	72
59	Properties of phosphorothioate DNA analogs. An ab initio study of prototype model linkages derived from dimethyl-phosphate anion. Computational and Theoretical Chemistry, 1999, 460, 103-116.	1.5	6
60	Structure-based prediction of DNA target sites by regulatory proteins. Proteins: Structure, Function and Bioinformatics, 1999, 35, 114-131.	2.6	160
61	Free-Energy Maps of Baseâ˜'Amino Acid Interactions for DNAâ˜'Protein Recognition. Journal of the American Chemical Society, 1999, 121, 6152-6157.	13.7	44
62	Shape and energetics of a cavity in c-Myb probed by natural and non-natural amino acid mutations. Journal of Molecular Biology, 1999, 292, 909-920.	4.2	33
63	The Mutant RecA Proteins, RecAR243Q and RecAK245N, Exhibit Defective DNA Binding in Homologous Pairing. Archives of Biochemistry and Biophysics, 1999, 365, 83-91.	3.0	29
64	Construction of an Artificial Tandem Protein of the c-Myb DNA-Binding Domain and Analysis of Its DNA Binding Specificity. Biochemical and Biophysical Research Communications, 1999, 262, 94-97.	2.1	12
65	Triplex Formation of Chemically Modified Homopyrimidine Oligonucleotides:â€‰ Thermodynamic and Kinetic Studies. Biochemistry, 1999, 38, 14653-14659.	2.5	30
66	Thermodynamics of specific and non-specific DNA binding by the c-myb DNA-binding domain. Journal of Molecular Biology, 1998, 276, 571-590.	4.2	100
67	Unique Mode of GCC Box Recognition by the DNA-binding Domain of Ethylene-responsive Element-binding Factor (ERF Domain) in Plant. Journal of Biological Chemistry, 1998, 273, 26857-26861.	3.4	355
68	Multi-state thermal transitions of proteins - DNA-binding domain of the c-Myb oncoprotein. Pure and Applied Chemistry, 1998, 70, 671-676.	1.9	3
69	Investigation of the Pyrimidine Preference by the c-Myb DNA-binding Domain at the Initial Base of the Consensus Sequence. Journal of Biological Chemistry, 1997, 272, 17966-17971.	3.4	20
70	Temperature Dependence and Sequence Specificity of DNA Triplex Formation:Â An Analysis Using Isothermal Titration Calorimetry. Journal of the American Chemical Society, 1996, 118, 4532-4538.	13.7	70
71	The cavity in the hydrophobic core of Myb DNA-binding domain is reserved for DNA recognition and trans-activation. Nature Structural Biology, 1996, 3, 178-187.	9.7	243
72	A Possible Role of the C-terminal Domain of the RecA Protein. Journal of Biological Chemistry, 1996, 271, 33515-33524.	3.4	72

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73	Determination of the NMR solution structure of a specific DNA complex of the Myb DNA-binding domain. Journal of Biomolecular NMR, 1995, 6, 294-305.	2.8	4
74	Comparison of the free and DNA-complexed forms of the DMA-binding domain from c-Myb. Nature Structural and Molecular Biology, 1995, 2, 309-320.	8.2	156
75	The Affinity Maturation of Anti-4-hydroxy-3-nitrophenylacetyl Mouse Monoclonal Antibody. Journal of Biological Chemistry, 1995, 270, 22218-22222.	3.4	41
76	Solution structure of a specific DNA complex of the Myb DNA-binding domain with cooperative recognition helices. Cell, 1994, 79, 639-648.	28.9	486
77	Thermodynamic and kinetic studies of DNA triplex formation of an oligohomopyrimidine and a matched duplex by filter binding assay. Biochemistry, 1993, 32, 8963-8969.	2.5	72
78	Thermodynamic and Kinetic Analyses of DNA Triplex Formation: Application of Filter-Binding Assay. Journal of Biomolecular Structure and Dynamics, 1993, 11, 245-252.	3.5	13
79	Sequence Context of Oligomer Tracts in Eukaryotic DNA: Biological and Conformational Implications. Journal of Biomolecular Structure and Dynamics, 1988, 6, 543-562.	3.5	9
80	Relationship Between Curved DNA Conformations and Slow Gel Migration. Journal of Biomolecular Structure and Dynamics, 1987, 4, 561-567.	3.5	18
81	Hydrophobic Interactions in the Major Groove Can Influence DNA Local Structure. Journal of Biomolecular Structure and Dynamics, 1986, 4, 41-48.	3.5	42
82	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. International Journal of Quantum Chemistry, 1985, 28, 399-409.	2.0	9
83	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. International Journal of Quantum Chemistry, 1984, 25, 527-533.	2.0	20
84	Comment on â€˜â€˜IRâ€spectroscopic study of isotope effects on the NH/ND stretching bands of mesoâ€tetraphenylporphine and vibrational hydrogen tunnelingâ€™â€™. Journal of Chemical Physics, 1984, 80, 5341-5343.	3.0	20
85	Dynamics of proton migration in free base porphines. Journal of Chemical Physics, 1982, 76, 5554-5563.	3.0	64
86	Theoretical Studies of Photoisomerization in Visual Pigments. II. Numerical Calculation. Journal of the Physical Society of Japan, 1982, 51, 3309-3317.	1.6	1
87	Theoretical Studies of Photoisomerization in Visual Pigments. I. Formulation. Journal of the Physical Society of Japan, 1982, 51, 3302-3308.	1.6	3
88	PROTON TRANSFER IN THE PRIMARY PROCESS OF VISION. Photochemistry and Photobiology, 1981, 33, 875-881.	2.5	8
89	TEMPERATURE DEPENDENCE OF PHOTOSYNTHETIC EXCITATION TRANSFERâ€”ACTIVATIONLESS TRANSFER. Photochemistry and Photobiology, 1980, 31, 579-583.	2.5	10
90	SIMULATION ANALYSIS OF THE PHOTOCONVERSION PROCESS OF SQUID RHODOPSIN AT LIQUID HELIUM TEMPERATURE. Photochemistry and Photobiology, 1980, 32, 199-206.	2.5	12

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