Sanzo Miyazawa

List of Publications by Year
in descending order

38 papers	4,194 citations	623734 14 h-index	414414 32 g-index
38 all docs	38 docs citations	38 times ranked	2847 citing authors

#	Article	IF	Citations
1	Boltzmann Machine Learning and Regularization Methods for Inferring Evolutionary Fields and Couplings From a Multiple Sequence Alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 328-342.	3.0	0
2	Prediction of Structures and Interactions from Genome Information. Advances in Experimental Medicine and Biology, 2018, 1105, 123-152.	1.6	2
3	Selection originating from protein stability/foldability: Relationships between protein folding free energy, sequence ensemble, and fitness. Journal of Theoretical Biology, 2017, 433, 21-38.	1.7	10
4	Selection maintaining protein stability at equilibrium. Journal of Theoretical Biology, 2016, 391, 21-34.	1.7	3
5	Prediction of Residue-Contacts Based on Coevolution between Amino Acid Sites: Toward the Prediction of Protein Structure. Seibutsu Butsuri, 2014, 54, 091-095.	0.1	0
6	Superiority of a mechanistic codon substitution model even for protein sequences in Phylogenetic analysis. BMC Evolutionary Biology, 2013, 13, 257.	3.2	8
7	Prediction of Contact Residue Pairs Based on Co-Substitution between Sites in Protein Structures. PLoS ONE, 2013, 8, e54252.	2.5	14
8	Selective Constraints on Amino Acids Estimated by a Mechanistic Codon Substitution Model with Multiple Nucleotide Changes. PLoS ONE, 2011, 6, e17244.	2.5	11
9	Advantages of a Mechanistic Codon Substitution Model for Evolutionary Analysis of Protein-Coding Sequences. PLoS ONE, 2011, 6, e28892.	2.5	13
10	On the optimal contact potential of proteins. Chemical Physics Letters, 2008, 451, 132-135.	2.6	7
11	Properties of contact matrices induced by pairwise interactions in proteins. Physical Review E, 2008, 77, 051910.	2.1	1
12	3P-301 A Codon-based Model for Evolution of Protein-coding DNA Sequences(The 46th Annual Meeting) Tj ETQq0 0 0 rgBT /Overlock 10	0.1	0
13	Numerical Evaluation of Biocide Treatment against Sulfate Reducing Bacteria in Oilfield Water Pipelines. Journal of the Japan Petroleum Institute, 2007, 50, 208-217.	0.6	2
14	How effective for fold recognition is a potential of mean force that includes relative orientations between contacting residues in proteins?. Journal of Chemical Physics, 2005, 122, 024901.	3.0	57
15	Long- and short-range interactions in native protein structures are consistent/minimally frustrated in sequence space. Proteins: Structure, Function and Bioinformatics, 2002, 50, 35-43.	2.6	20
16	Identifying sequenceâ€“structure pairs undetected by sequence alignments. Protein Engineering, Design and Selection, 2000, 13, 459-475.	2.1	25
17	Self-consistent estimation of inter-residue protein contact energies based on an equilibrium mixture approximation of residues. , 1999, 34, 49-68.		159
18	Evaluation of short-range interactions as secondary structure energies for protein fold and sequence recognition. Proteins: Structure, Function and Bioinformatics, 1999, 36, 347-356.	2.6	35

#	Article	IF	Citations
19	An empirical energy potential with a reference state for protein fold and sequence recognition. , 1999, 36, 357-369.		93
20	Selfâ€consistent estimation of interâ€residue protein contact energies based on an equilibrium mixture approximation of residues. Proteins: Structure, Function and Bioinformatics, 1999, 34, 49-68.	2.6	2
21	Evaluation of shortâ€range interactions as secondary structure energies for protein fold and sequence recognition. Proteins: Structure, Function and Bioinformatics, 1999, 36, 347-356.	2.6	2
22	Residue â€“ Residue Potentials with a Favorable Contact Pair Term and an Unfavorable High Packing Density Term, for Simulation and Threading. Journal of Molecular Biology, 1996, 256, 623-644.	4.2	1,140
23	A reliable sequence alignment method based on probabilities of residue correspondences. Protein Engineering, Design and Selection, 1995, 8, 999-1009.	2.1	80
24	Protein stability for single substitution mutants and the extent of local compactness in the denatured state. Protein Engineering, Design and Selection, 1994, 7, 1209-1220.	2.1	60
25	Monte Carlo calculation of the quantum J1â^'J2 model on the square lattice. Physics Letters, Section A: General, Atomic and Solid State Physics, 1994, 193, 370-374.	2.1	5
26	A new substitution matrix for protein sequence searches based on contact frequencies in protein structures. Protein Engineering, Design and Selection, 1993, 6, 267-278.	2.1	70
27	Basigin, a New, Broadly Distributed Member of the Immunoglobulin Superfamily, Has Strong Homology with Both the Immunoglobulin V Domain and the Î²-Chain of Major Histocompatibility Complex Class II Antigen. Journal of Biochemistry, 1990, 107, 316-323.	1.7	183
28	Only d_{fl16}, d_{sp2}, and d_{q52} gene families exist in mouse immunoglobulin heavy chain diversity gene loci, of which d_{fl16} and d_{sp2} originate from the same primordial d_h gene. European Journal of Immunology, 1989, 19, 1849-1854.	2.9	141
29	Statistical mechanics of supercoilingâ€induced Bâ€toâ€Z transitions in a closed circular DNA: Oneâ€dimensional model system with a double quadratic displacement potential and long range interactions. Journal of Chemical Physics, 1985, 83, 859-883.	3.0	4
30	Estimation of effective interresidue contact energies from protein crystal structures: quasi-chemical approximation. Macromolecules, 1985, 18, 534-552.	4.8	1,489
31	Equilibrium folding pathways for model proteins. Journal of Statistical Physics, 1983, 30, 549-559.	1.2	2
32	Equilibrium folding-unfolding pathways of model proteins: Effect of myoglobin-heme contacts. Biopolymers, 1983, 22, 79-85.	2.4	6
33	Cooperative ligand binding on multidimensional lattices: Bethe approximation. Biopolymers, 1983, 22, 2253-2271.	2.4	8
34	Most probable intermediates in protein folding-unfolding with a noninteracting globule-coil model. Biochemistry, 1982, 21, 5203-5213.	2.5	15
35	Kerr Effects of Flexible Macromolecules. , 1981, , 163-179.		3
36	RELATIONSHIP BETWEEN MUTABILITY, POLARITY AND EXTERIORITY OF AMINO ACID RESIDUES IN PROTEIN EVOLUTION. International Journal of Peptide and Protein Research, 1980, 15, 211-224.	0.1	72

#	Article	IF	Citations
37	Two types of amino acid substitutions in protein evolution. Journal of Molecular Evolution, 1979, 12, 219-236.	1.8	442
38	VOLUME AND POLARITY CHANGES ACCOMPANIED BY AMINO ACID SUBSTITUTIONS IN PROTEIN EVOLUTION. International Journal of Peptide and Protein Research, 1978, 12, 237-241.	0.1	10