Sanzo Miyazawa

List of Publications by Year
in descending order

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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	Estimation of effective interresidue contact energies from protein crystal structures: quasi-chemical approximation. Macromolecules, 1985, 18, 534-552.	4.8	1,489
2	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
3	Two types of amino acid substitutions in protein evolution. Journal of Molecular Evolution, 1979, 12, 219-236.	1.8	442
4	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
5	Self-consistent estimation of inter-residue protein contact energies based on an equilibrium mixture approximation of residues. , 1999, 34, 49-68.		159
6	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
7	An empirical energy potential with a reference state for protein fold and sequence recognition. , 1999, 36, 357-369.		93
8	A reliable sequence alignment method based on probabilities of residue correspondences. Protein Engineering, Design and Selection, 1995, 8, 999-1009.	2.1	80
9	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
10	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
11	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
12	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
13	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
14	Identifying sequenceâ€“structure pairs undetected by sequence alignments. Protein Engineering, Design and Selection, 2000, 13, 459-475.	2.1	25
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	Most probable intermediates in protein folding-unfolding with a noninteracting globule-coil model. Biochemistry, 1982, 21, 5203-5213.	2.5	15
17	Prediction of Contact Residue Pairs Based on Co-Substitution between Sites in Protein Structures. PLoS ONE, 2013, 8, e54252.	2.5	14
18	Advantages of a Mechanistic Codon Substitution Model for Evolutionary Analysis of Protein-Coding Sequences. PLoS ONE, 2011, 6, e28892.	2.5	13

#	Article	IF	Citations
19	Selective Constraints on Amino Acids Estimated by a Mechanistic Codon Substitution Model with Multiple Nucleotide Changes. PLoS ONE, 2011, 6, e17244.	2.5	11
20	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
21	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
22	Cooperative ligand binding on multidimensional lattices: Bethe approximation. Biopolymers, 1983, 22, 2253-2271.	2.4	8
23	Superiority of a mechanistic codon substitution model even for protein sequences in Phylogenetic analysis. BMC Evolutionary Biology, 2013, 13, 257.	3.2	8
24	On the optimal contact potential of proteins. Chemical Physics Letters, 2008, 451, 132-135.	2.6	7
25	Equilibrium folding-unfolding pathways of model proteins: Effect of myoglobin-heme contacts. Biopolymers, 1983, 22, 79-85.	2.4	6
26	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
27	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
28	Selection maintaining protein stability at equilibrium. Journal of Theoretical Biology, 2016, 391, 21-34.	1.7	3
29	Kerr Effects of Flexible Macromolecules. , 1981, , 163-179.		3
30	Equilibrium folding pathways for model proteins. Journal of Statistical Physics, 1983, 30, 549-559.	1.2	2
31	Prediction of Structures and Interactions from Genome Information. Advances in Experimental Medicine and Biology, 2018, 1105, 123-152.	1.6	2
32	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
33	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
34	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
35	Properties of contact matrices induced by pairwise interactions in proteins. Physical Review E, 2008, 77, 051910.	2.1	1
36	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

#	Article	IF	Citations
37	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
38	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