Vladimir G Tumanyan

List of Publications by Year
in descending order

59 papers	847 citations	516710 16 h-index	526287 27 g-index
60 all docs	60 docs citations	60 times ranked	874 citing authors

#	Article	IF	Citations
1	Numeric analysis of reversibility of classic movement equations and constructive criteria of estimating quality of molecular dynamic simulations. Journal of Biomolecular Structure and Dynamics, 2021, 39, 4066-4076.	3.5	7
2	Structural coordinates: A novel approach to predict protein backbone conformation. PLoS ONE, 2021, 16, e0239793.	2.5	2
3	The ranging of amino acids substitution matrices of various types in accordance with the alignment accuracy criterion. BMC Bioinformatics, 2020, 21, 294.	2.6	5
4	Omnipresence of the polyproline II helix in fibrous and globular proteins. Current Opinion in Structural Biology, 2017, 42, 41-49.	5.7	13
5	The structural and physicochemical characteristics of conformationally stable Î±-helical oligopeptides. Biophysics (Russian Federation), 2015, 60, 348-360.	0.7	6
6	Disallowed conformations of a polypeptide chain as exemplified by the Î²-turn of the Î²-hairpin in the Î±-spectrin SH3 domain. Biophysics (Russian Federation), 2015, 60, 1-9.	0.7	7
7	On efficient in vitro purification of cell suspensions containing malignant cells. Biophysics (Russian) Tj ETQq1 1 0.784314 rgBT /Overlock	0.7	0
8	Alternatingly twisted Î²-hairpins and nonglycine residues in the disallowed IIâ€² region of the Ramachandran plot. Journal of Biomolecular Structure and Dynamics, 2014, 32, 198-208.	3.5	7
9	Estimation of the quality of global alignment of amino acid sequences based on evolution criterion. Biophysics (Russian Federation), 2013, 58, 137-141.	0.7	0
10	Classification of amino acids based on comparative analysis of contacts in DNA-protein complexes and specific DNA-protein interactions. Biophysics (Russian Federation), 2013, 58, 766-770.	0.7	1
11	Conformationally stable segments in helical structures of polypeptide chains of proteins and their role in high level structures formation. Biophysics (Russian Federation), 2013, 58, 841-844.	0.7	2
12	Long-range macromolecule interaction and â€œspeed readingâ€•long nucleotide sequences in DNA. Physics Letters, Section A: General, Atomic and Solid State Physics, 2013, 377, 323-328.	2.1	2
13	Structural attributes of nucleotide sequences in promoter regions of supercoiling-sensitive genes: How to relate microarray expression data with genomic sequences. Genomics, 2013, 101, 1-11.	2.9	10
14	DNA sequencing using specific long-range interaction between macromolecules. Biophysics (Russian) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.7	2
15	Coexistence of different base periodicities in prokaryotic genomes as related to DNA curvature, supercoiling, and transcription. Genomics, 2011, 98, 223-231.	2.9	17
16	On the optimal folding of protein molecules. Biophysics (Russian Federation), 2011, 56, 596-601.	0.7	8
17	Splice sites are overrepresented in Pasilla binding motif clusters in D. melanogaster genes. Biophysics (Russian Federation), 2011, 56, 1043-1046.	0.7	0
18	General theory of the long-range interactions in protein folding. Physics Letters, Section A: General, Atomic and Solid State Physics, 2011, 375, 2911-2915.	2.1	10

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19	Comparative analysis of the quality of a global algorithm and a local algorithm for alignment of two sequences. Algorithms for Molecular Biology, 2011, 6, 25.	1.2	44
20	A Novel Model System for Design of Biomaterials Based on Recombinant Analogs of Spider Silk Proteins. Journal of NeuroImmune Pharmacology, 2009, 4, 17-27.	4.1	77
21	Left helix of polyproline II type and genesis of Î²-structures in spidroins 1 and 2 and their recombinant analogs. Biophysics (Russian Federation), 2009, 54, 271-274.	0.7	3
22	Periodicities in nucleotide distribution in the immunoglobulin light chain locus of Gallus gallus. Biophysics (Russian Federation), 2009, 54, 415-418.	0.7	0
23	Relative occurrence of amino acid-nucleotide contacts assessed by Voronoi-Delaunay tessellation of protein-DNA interfaces. Biophysics (Russian Federation), 2008, 53, 199-201.	0.7	3
24	A new approach to assessing the validity of indels in algorithmic pair alignments. Biophysics (Russian) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.7	2
25	On the mechanisms of the effect of imino acids on the physical characteristics of collagens. Biophysics (Russian Federation), 2008, 53, 476-477.	0.7	2
26	Left-handed helix of polyproline ii type in linker regions of DNA-binding proteins. Biophysics (Russian) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.7	2
27	Reconstruction of Genuine Pair-Wise Sequence Alignment. Journal of Computational Biology, 2008, 15, 379-391.	1.6	7
28	Study and Prediction of Secondary Structure for Membrane Proteins. Journal of Biomolecular Structure and Dynamics, 2007, 24, 421-427.	3.5	2
29	Comprehensive statistical analysis of residues interaction specificity at protein-protein interfaces. Proteins: Structure, Function and Bioinformatics, 2007, 67, 1060-1077.	2.6	23
30	Computation of 3D structure and distribution of helical parameters for D-period segments of human fibrillar collagen III. Biophysics (Russian Federation), 2007, 52, 567-574.	0.7	3
31	Conformational properties of short oligopeptides: Prediction of the protein chain conformation. Biophysics (Russian Federation), 2006, 51, 54-55.	0.7	0
32	A tetrapeptide-based method for polyproline II-type secondary structure prediction. Proteins: Structure, Function and Bioinformatics, 2005, 61, 763-768.	2.6	13
33	Analysis of forces that determine helix formation in Â-proteins. Protein Science, 2004, 13, 351-357.	7.6	16
34	Use of molecular mechanics for secondary structure prediction. Is it possible to reveal Î±-helix?. FEBS Letters, 2002, 510, 13-16.	2.8	4
35	Molecular Modelling of Disease-Causing Single-Nucleotide Polymorphisms in Collagen. SAR and QSAR in Environmental Research, 2001, 12, 383-399.	2.2	3
36	Segmentation of long genomic sequences into domains with homogeneous composition with BASIO software. Bioinformatics, 2001, 17, 1065-1066.	4.1	7

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37	Towards hierarchy of protein domain structure. Biochemical Society Transactions, 2000, 28, A457-A457.	3.4	0
38	A New Approach for the Calculation of the Energy of van der Waals Interactions in Macromolecules of Globular Proteins. Journal of Biomolecular Structure and Dynamics, 2000, 17, 799-809.	3.5	8
39	Hierarchy of Regions of Amino Acid Sequence with Respect to Their Role in the Protein Spatial Structure. Journal of Computational Biology, 2000, 7, 183-192.	1.6	5
40	DNA Segmentation Through the Bayesian Approach. Journal of Computational Biology, 2000, 7, 215-231.	1.6	36
41	PSIC: profile extraction from sequence alignments with position-specific counts of independent observations. Protein Engineering, Design and Selection, 1999, 12, 387-394.	2.1	184
42	Amino acid composition of protein termini are biased in different manners. Protein Engineering, Design and Selection, 1999, 12, 23-30.	2.1	46
43	Hierarchy of the Interaction Energy Distribution in the Spatial Structure of Globular Proteins and the Problem of Domain Definition. Journal of Biomolecular Structure and Dynamics, 1999, 17, 133-155.	3.5	24
44	Are knowledge-based potentials derived from protein structure sets discriminative with respect to amino acid types?. , 1998, 31, 225-246.		15
45	Protein sequence-structure compatibility criteria in terms of statistical hypothesis testing. Protein Engineering, Design and Selection, 1997, 10, 635-646.	2.1	6
46	COOH-terminal decamers in proteins are non-random. FEBS Letters, 1997, 404, 140-142.	2.8	16
47	Representation of amino acid sequences in terms of interaction energy in protein globules. FEBS Letters, 1997, 418, 43-46.	2.8	27
48	The third nucleotide of the Gly coding triplet remembers the periodicity of the collagen chain. FEBS Letters, 1995, 366, 33-36.	2.8	1
49	Structural principles of B-DNA grooves hydration in fibers as revealed by Monte Carlo simulations and x-ray diffraction. Biopolymers, 1990, 29, 1453-1464.	2.4	16
50	Structure of the hydration shells of oligo(dA-dT)Â·oligo(dA-dT) and oligo(dA)Â·oligo(dT) tracts in B-type conformation on the basis of Monte Carlo calculations. Biopolymers, 1990, 30, 563-581.	2.4	11
51	Hydration of B-DNA: Comparison between the water network around poly(dG) Â· poly(dC) and poly(dG-dC) Â· poly(dG-dC) on the basis of Monte Carlo computations. Biopolymers, 1989, 28, 741-761.	2.4	13
52	Third type of secondary structure: Noncooperative mobile conformation. Protein Data Bank analysis. Biochemical and Biophysical Research Communications, 1987, 146, 934-938.	2.1	36
53	Rigorous conformational analysis of right and left DNA helices and junction between them. Journal of Biosciences, 1985, 8, 593-602.	1.1	0
54	Conformational analysis of polytripeptides (Gly-Pro-Ala)n, (Gly-Ala-Hyp)n, and (Gly-Ala-Ala)n in connection with the problem of collagen structure. Biopolymers, 1984, 23, 1499-1512.	2.4	12

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55	Comprehensive conformational analysis of (Gly-Pro-Pro)n and (Gly-Pro-Hyp)n related to collagen. Biopolymers, 1982, 21, 475-497.	2.4	16
56	Conformational studies of double-helical polynucleotides by the method of pair-wise potential functions. International Journal of Quantum Chemistry, 1980, 17, 321-326.	2.0	5
57	A code controlling specific binding of regulatory proteins to DNA. Molecular Biology Reports, 1976, 2, 413-425.	2.3	24
58	A model for the binding of lac repressor to the lac operator. Molecular Biology Reports, 1976, 2, 427-434.	2.3	16
59	On the Conformation of Pyridoxal Phosphate Imine in Solution and in Aspartate-Aminotransferase Active Site. FEBS Journal, 1974, 50, 119-127.	0.2	19