

Andrs Perczel

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78
papers

1,909
citations

25
h-index

41
g-index

85
ext. papers

2,072
ext. citations

5.4
avg. IF

4.45
L-index

#	Paper	IF	Citations
78	Peptide models. 1. Topology of selected peptide conformational potential energy surfaces (glycine and alanine derivatives). <i>Journal of the American Chemical Society</i> , 1991 , 113, 6256-6265	16.4	233
77	Conformational analysis of pseudocyclic hexapeptides based on quantitative circular dichroism (CD), NOE, and x-ray data. The pure CD spectra of type I and type II .beta.-turns. <i>Journal of the American Chemical Society</i> , 1991 , 113, 9772-9784	16.4	109
76	Mutation-dependent recessive inheritance of NPHS2-associated steroid-resistant nephrotic syndrome. <i>Nature Genetics</i> , 2014 , 46, 299-304	36.3	108
75	Vicinal disulfide turns. <i>Protein Engineering, Design and Selection</i> , 2003 , 16, 637-9	1.9	96
74	Peptide models 6. New .beta.-turn conformations from ab initio calculations confirmed by x-ray data of proteins. <i>Journal of the American Chemical Society</i> , 1993 , 115, 4849-4858	16.4	94
73	alpha- and 3(10)-helix interconversion: a quantum-chemical study on polyalanine systems in the gas phase and in aqueous solvent. <i>Journal of the American Chemical Society</i> , 2001 , 123, 6054-60	16.4	88
72	Turns 1996 , 285-380		78
71	Structure and stability of beta-pleated sheets. <i>Journal of Computational Chemistry</i> , 2005 , 26, 1155-68	3.5	56
70	Peptide models. XXXIII. Extrapolation of low-level Hartree-Fock data of peptide conformation to large basis set SCF, MP2, DFT, and CCSD(T) results. The Ramachandran surface of alanine dipeptide computed at various levels of theory. <i>Journal of Computational Chemistry</i> , 2003 , 24, 1026-42	3.5	54
69	Cooperation between a salt bridge and the hydrophobic core triggers fold stabilization in a Trp-cage miniprotein. <i>Biochemistry</i> , 2008 , 47, 1007-16	3.2	51
68	Dead-end street of protein folding: thermodynamic rationale of amyloid fibril formation. <i>Journal of the American Chemical Society</i> , 2007 , 129, 14959-65	16.4	50
67	Toward a computed peptide structure database: The role of a universal atomic numbering system of amino acids in peptides and internal hierarchy of database. <i>International Journal of Quantum Chemistry</i> , 2002 , 90, 933-968	2.1	50
66	Peptide Models. 18. Hydroxymethyl Side-Chain Induced Backbone Conformational Shifts of L-Serine Amide. All ab Initio Conformers of For-L-Ser-NH ₂ . <i>Journal of the American Chemical Society</i> , 1996 , 118, 7809-7817	16.4	48
65	On the flexibility of beta-peptides. <i>Journal of Computational Chemistry</i> , 2004 , 25, 285-307	3.5	47
64	Structural insights into the Trp-cage folding intermediate formation. <i>Chemistry - A European Journal</i> , 2013 , 19, 2628-40	4.8	45
63	Investigation of penetratin peptides. Part 1. The environment dependent conformational properties of penetratin and two of its derivatives. <i>Journal of Peptide Science</i> , 2002 , 8, 151-71	2.1	42
62	Toward a rational design of beta-peptide structures. <i>Journal of Computational Chemistry</i> , 2006 , 27, 20-38	3.5	39

61	Peptide models XXIII. Conformational model for polar side-chain containing amino acid residues: A comprehensive analysis of RHF, DFT, and MP2 properties of HCO-L-SER-NH ₂ . <i>Journal of Computational Chemistry</i> , 2000 , 21, 626-655	3.5	36
60	Peptide models XVI. The identification of selected HCO-L-SER-NH ₂ conformers via a systematic grid search using ab initio potential energy surfaces. <i>Journal of Computational Chemistry</i> , 1996 , 17, 821-834	3.5	36
59	Cooperativity network of Trp-cage miniproteins: probing salt-bridges. <i>Journal of Peptide Science</i> , 2011 , 17, 610-9	2.1	30
58	Searching for the simplest structural units to describe the three-dimensional structure of proteins. <i>International Reviews in Physical Chemistry</i> , 1995 , 14, 127-168	7	29
57	Synthesis and conformational analysis of N-glycopeptides. II. CD, molecular dynamics, and NMR spectroscopic studies on linear N-glycopeptides. <i>Biopolymers</i> , 1993 , 33, 665-85	2.2	28
56	Vicinal disulfide bridge conformers by experimental methods and by ab initio and DFT molecular computations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 55, 152-68	4.2	27
55	The Piwi-piRNA pathway: road to immortality. <i>Aging Cell</i> , 2017 , 16, 906-911	9.9	26
54	Toward direct determination of conformations of protein building units from multidimensional NMR experiments I. A theoretical case study of For-Gly-NH ₂ and For-L-Ala-NH ₂ . <i>Journal of Computational Chemistry</i> , 2000 , 21, 882-900	3.5	26
53	Intrinsically stable secondary structure elements of proteins: a comprehensive study of folding units of proteins by computation and by analysis of data determined by X-ray crystallography. <i>Chemistry - A European Journal</i> , 2003 , 9, 5332-42	4.8	21
52	Peptide models. XIV. Ab initio study on the role of side-chain backbone interaction stabilizing the building unit of right- and left-handed helices in peptides and proteins. <i>International Journal of Quantum Chemistry</i> , 1997 , 61, 797-814	2.1	20
51	Rational design of Helix-stabilized exendin-4 analogues. <i>Biochemistry</i> , 2014 , 53, 3540-52	3.2	18
50	Reconciling the lock-and-key and dynamic views of canonical serine protease inhibitor action. <i>FEBS Letters</i> , 2010 , 584, 203-6	3.8	18
49	DUckCov: a Dynamic Undocking-Based Virtual Screening Protocol for Covalent Binders. <i>ChemMedChem</i> , 2019 , 14, 1011-1021	3.7	17
48	Stability issues of covalently and noncovalently bonded peptide subunits. <i>Journal of Computational Chemistry</i> , 2004 , 25, 1084-100	3.5	15
47	Challenging drug target for Parkinson's disease: Pathological complex of the chameleon TPPP/p25 and alpha-synuclein proteins. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2017 , 1863, 310-323	6.9	14
46	Penetratin analogues acting as antifungal agents. <i>European Journal of Medicinal Chemistry</i> , 2011 , 46, 370-7	6.8	14
45	Peptide models XXXI. Conformational properties of hydrophobic residues shaping the core of proteins. An ab initio study of N-formyl-L-valinamide and N-formyl-L-phenylalaninamide. <i>Journal of Computational Chemistry</i> , 2001 , 22, 732-751	3.5	14
44	Protein Dynamics as Reported by NMR. <i>Annual Reports on NMR Spectroscopy</i> , 2010 , 35-75	1.7	13

43	Bacterial expression and/or solid phase peptide synthesis of 20-40 amino acid long polypeptides and miniproteins, the case study of Class B GPCR ligands. <i>Current Protein and Peptide Science</i> , 2016 , 17, 147-55	2.8	12
42	H, N backbone assignment and comparative analysis of the wild type and G12C, G12D, G12V mutants of K-Ras bound to GDP at physiological pH. <i>Biomolecular NMR Assignments</i> , 2020 , 14, 1-7	0.7	11
41	C-terminal oligomerization of podocin mediates interallelic interactions. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018 , 1864, 2448-2457	6.9	10
40	C-3 epimers of sugar amino acids as foldameric building blocks: improved synthesis, useful derivatives, coupling strategies. <i>Amino Acids</i> , 2017 , 49, 223-240	3.5	10
39	Penetratin and derivatives acting as antibacterial agents. <i>Chemical Biology and Drug Design</i> , 2013 , 82, 167-77	2.9	10
38	Chimera peptide synthesis with cyclic sugar amino acids: the efficient coupling protocol. <i>Amino Acids</i> , 2019 , 51, 669-678	3.5	10
37	Assessment of Tractable Cysteines for Covalent Targeting by Screening Covalent Fragments. <i>ChemBioChem</i> , 2021 , 22, 743-753	3.8	10
36	Foldamer Stability Coupled to Aggregation Propensity of Elongated Trp-Cage Miniproteins. <i>European Journal of Organic Chemistry</i> , 2013 , 2013, 3513-3522	3.2	9
35	The inherent flexibility of peptides and protein fragments quantitized by CD in conjunction with CCA+. <i>Journal of Peptide Science</i> , 2009 , 15, 738-52	2.1	9
34	A search for the ideal type I turn 1996 , 38, 723-732		9
33	Structural impact of GTP binding on downstream KRAS signaling. <i>Chemical Science</i> , 2020 , 11, 9272-9289	9.4	9
32	Multiple fuzzy interactions in the moonlighting function of thymosin- β . <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e26204		8
31	Origin of problems related to Staudinger reduction in carbopeptoid syntheses. <i>Amino Acids</i> , 2016 , 48, 2619-2633	3.5	7
30	Unwanted hydrolysis or peptide bond formation: how long should the rate-limiting coupling step take?. <i>RSC Advances</i> , 2019 , 9, 30720-30728	3.7	7
29	The Route from the Folded to the Amyloid State: Exploring the Potential Energy Surface of a Drug-Like Miniprotein. <i>Chemistry - A European Journal</i> , 2020 , 26, 1968-1978	4.8	7
28	Four faces of the interaction between ions and aromatic rings. <i>Journal of Computational Chemistry</i> , 2017 , 38, 1762-1773	3.5	6
27	Hydration shell differentiates folded and disordered states of a Trp-cage miniprotein, allowing characterization of structural heterogeneity by wide-line NMR measurements. <i>Scientific Reports</i> , 2019 , 9, 2947	4.9	6
26	Toward direct determination of conformations of protein building units from multidimensional NMR experiments. V. NMR chemical shielding analysis of N-formyl-serinamide, a model for polar side-chain containing peptides. <i>Journal of Computational Chemistry</i> , 2003 , 24, 1157-71	3.5	6

25	Interplay of Structural Disorder and Short Binding Elements in the Cellular Chaperone Function of Plant Dehydrin ERD14. <i>Cells</i> , 2020 , 9,	7.9	6
24	Biochemical and pharmacological characterization of three opioid-nociceptin hybrid peptide ligands reveals substantially differing modes of their actions. <i>Peptides</i> , 2018 , 99, 205-216	3.8	5
23	Cost-Effective Flow Peptide Synthesis: Metamorphosis of HPLC. <i>Organic Process Research and Development</i> , 2021 , 25, 182-191	3.9	5
22	Approaches to Pyranuronic Sugar Amino Acid Building Blocks of Peptidosaccharide Foldamers. <i>European Journal of Organic Chemistry</i> , 2018 , 2018, 355-361	3.2	4
21	Aromatic Cluster Sensor of Protein Folding: Near-UV Electronic Circular Dichroism Bands Assigned to Fold Compactness. <i>Chemistry - A European Journal</i> , 2016 , 22, 13871-13883	4.8	4
20	Protein Aggregation in a Nutshell: The Splendid Molecular Architecture of the Dreaded Amyloid Fibrils. <i>Current Protein and Peptide Science</i> , 2019 , 20, 1077-1088	2.8	4
19	Dynamically encoded reactivity of Ras enzymes: opening new frontiers for drug discovery. <i>Cancer and Metastasis Reviews</i> , 2020 , 39, 1075-1089	9.6	4
18	Small Peptides Derived from Penetratin as Antibacterial Agents. <i>Archiv Der Pharmazie</i> , 2016 , 349, 242-514.3	4.3	4
17	pKa optimized catalysis in serine proteinases, an ab initio study on the catalytic His. <i>International Journal of Quantum Chemistry</i> , 2007 , 107, 2178-2183	2.1	3
16	Compactness of Protein Folds Alters Disulfide-Bond Reducibility by Three Orders of Magnitude: A Comprehensive Kinetic Case Study on the Reduction of Differently Sized Tryptophan Cage Model Proteins. <i>ChemBioChem</i> , 2020 , 21, 681-695	3.8	3
15	The Budapest Amyloid Predictor and Its Applications. <i>Biomolecules</i> , 2021 , 11,	5.9	3
14	Predictable Conformational Diversity in Foldamers of Sugar Amino Acids. <i>Journal of Chemical Information and Modeling</i> , 2017 , 57, 757-768	6.1	2
13	Synthesis of chimera oligopeptide including furanoid Sugar amino acid derivatives with free OHs: mild but successful removal of the 1,2-O-isopropylidene from the building block. <i>Amino Acids</i> , 2021 , 53, 281-294	3.5	2
12	Structural Water Stabilizes Protein Motifs in Liquid Protein Phase: The Folding Mechanism of Short Sheets Coupled to Phase Transition. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	2
11	How weak an acid can be? Variations of H-bond and/or van der Waals Interaction of Weak Acids. <i>Structural Chemistry</i> , 2017 , 28, 371-378	1.8	1
10	Off-pathway 3D-structure provides protection against spontaneous Asn/Asp isomerization: shielding proteins Achilles heel. <i>Quarterly Reviews of Biophysics</i> , 2020 , 53, e2	7	1
9	Configuration-Controlled Crystal and/or Gel Formation of Protected d-Glucosamines Supported by Promiscuous Interaction Surfaces and a Conformationally Heterogeneous Solution State. <i>Chemistry - A European Journal</i> , 2020 , 26, 11643-11655	4.8	1
8	Assignment of Vibrational Circular Dichroism Cross-Referenced Electronic Circular Dichroism Spectra of Flexible Foldamer Building Blocks: Towards Assigning Pure Chiroptical Properties of Foldamers. <i>Chemistry - A European Journal</i> , 2019 , 25, 14890-14900	4.8	1

7	Bacterial fermentation and isotope labelling optimized for amyloidogenic proteins. <i>Microbial Biotechnology</i> , 2021 , 14, 1107-1119	6.3	1
6	Peptide models. XIV. Ab initio study on the role of side-chain backbone interaction stabilizing the building unit of right- and left-handed helices in peptides and proteins 1997 , 61, 797		1
5	Application of Sugar Amino Acids: Flow Chemistry Used for β -Chimera Synthesis. <i>European Journal of Organic Chemistry</i> , 2021 , 2021, 6071	3.2	0
4	Hydrogen-Bonding Network Anchors the Cyclic Form of Sugar Arylhydrazones. <i>European Journal of Organic Chemistry</i> , 2016 , 2016, 3419-3426	3.2	0
3	Solution Structure and Acid-Base Properties of Reduced β -Conotoxin M1. <i>Chemistry and Biodiversity</i> , 2021 , 18, e2100464	2.5	0
2	The Route from the Folded to the Amyloid State: Exploring the Potential Energy Surface of a Drug-Like Mini-protein. <i>Chemistry - A European Journal</i> , 2020 , 26, 1893	4.8	
1	Corrigendum to Calcium-induced tripartite binding of intrinsically disordered calpastatin to its cognate enzyme, calpain [FEBS Lett. 582 (2008) 2149-2154]. <i>FEBS Letters</i> , 2008 , 582, 2816-2816	3.8	