Andrs Perczel

List of Publications by Year in Descending Order

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	Application of Sugar Amino Acids: Flow Chemistry Used for β-Chimera Synthesis. *European Journal of Organic Chemistry*, **2021**, 2021, 6071	3.2	0
77	The Budapest Amyloid Predictor and Its Applications. *Biomolecules*, **2021**, 11,	5.9	3
76	Bacterial fermentation and isotope labelling optimized for amyloidogenic proteins. *Microbial Biotechnology*, **2021**, 14, 1107-1119	6.3	1
75	Assessment of Tractable Cysteines for Covalent Targeting by Screening Covalent Fragments. *ChemBioChem*, **2021**, 22, 743-753	3.8	10
74	Cost-Effective Flow Peptide Synthesis: Metamorphosis of HPLC. *Organic Process Research and Development*, **2021**, 25, 182-191	3.9	5
73	Synthesis of chimera oligopeptide including furanoid β-sugar amino acid derivatives with free OHs: mild but successful removal of the 1,2-O-isopropylidene from the building block. *Amino Acids*, **2021**, 53, 281-294	3.5	2
72	Solution Structure and Acid-Base Properties of Reduced β-Conotoxin MI. *Chemistry and Biodiversity*, **2021**, 18, e2100464	2.5	0
71	Structural Water Stabilizes Protein Motifs in Liquid Protein Phase: The Folding Mechanism of Short β-Sheets Coupled to Phase Transition. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	2
70	Off-pathway 3D-structure provides protection against spontaneous Asn/Asp isomerization: shielding proteins Achilles heel. *Quarterly Reviews of Biophysics*, **2020**, 53, e2	7	1
69	The Route from the Folded to the Amyloid State: Exploring the Potential Energy Surface of a Drug-Like Miniprotein. *Chemistry - A European Journal*, **2020**, 26, 1893	4.8	
68	Configuration-Controlled Crystal and/or Gel Formation of Protected d-Glucosamines Supported by Promiscuous Interaction Surfaces and a Conformationally Heterogeneous Solution State. *Chemistry - A European Journal*, **2020**, 26, 11643-11655	4.8	1
67	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. *ChemBioChem*, **2020**, 21, 681-695	3.8	3
66	Interplay of Structural Disorder and Short Binding Elements in the Cellular Chaperone Function of Plant Dehydrin ERD14. *Cells*, **2020**, 9,	7.9	6
65	Dynamically encoded reactivity of Ras enzymes: opening new frontiers for drug discovery. *Cancer and Metastasis Reviews*, **2020**, 39, 1075-1089	9.6	4
64	Structural impact of GTP binding on downstream KRAS signaling. *Chemical Science*, **2020**, 11, 9272-9289	9.4	9
63	The Route from the Folded to the Amyloid State: Exploring the Potential Energy Surface of a Drug-Like Miniprotein. *Chemistry - A European Journal*, **2020**, 26, 1968-1978	4.8	7
62	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. *Biomolecular NMR Assignments*, **2020**, 14, 1-7	0.7	11

61	Hydration shell differentiates folded and disordered states of a Trp-cage miniprotein, allowing characterization of structural heterogeneity by wide-line NMR measurements. *Scientific Reports*, **2019**, 9, 2947	4.9	6
60	DUckCov: a Dynamic Undocking-Based Virtual Screening Protocol for Covalent Binders. *ChemMedChem*, **2019**, 14, 1011-1021	3.7	17
59	Assignment of Vibrational Circular Dichroism Cross-Referenced Electronic Circular Dichroism Spectra of Flexible Foldamer Building Blocks: Towards Assigning Pure Chiroptical Properties of Foldamers. *Chemistry - A European Journal*, **2019**, 25, 14890-14900	4.8	1
58	Protein Aggregation in a Nutshell: The Splendid Molecular Architecture of the Dreaded Amyloid Fibrils. *Current Protein and Peptide Science*, **2019**, 20, 1077-1088	2.8	4
57	Chimera peptide synthesis with cyclic sugar amino acids: the efficient coupling protocol. *Amino Acids*, **2019**, 51, 669-678	3.5	10
56	Unwanted hydrolysis or peptide bond formation: how long should the rate-limiting coupling step take?. *RSC Advances*, **2019**, 9, 30720-30728	3.7	7
55	C-terminal oligomerization of podocin mediates interallelic interactions. *Biochimica Et Biophysica Acta - Molecular Basis of Disease*, **2018**, 1864, 2448-2457	6.9	10
54	Approaches to Pyranuronic Sugar Amino Acid Building Blocks of Peptidosaccharide Foldamers. *European Journal of Organic Chemistry*, **2018**, 2018, 355-361	3.2	4
53	Biochemical and pharmacological characterization of three opioid-nociceptin hybrid peptide ligands reveals substantially differing modes of their actions. *Peptides*, **2018**, 99, 205-216	3.8	5
52	Four faces of the interaction between ions and aromatic rings. *Journal of Computational Chemistry*, **2017**, 38, 1762-1773	3.5	6
51	Predictable Conformational Diversity in Foldamers of Sugar Amino Acids. *Journal of Chemical Information and Modeling*, **2017**, 57, 757-768	6.1	2
50	How weak an acid can be? Variations of H-bond and/or van der Waals Interaction of Weak Acids. *Structural Chemistry*, **2017**, 28, 371-378	1.8	1
49	The Piwi-piRNA pathway: road to immortality. *Aging Cell*, **2017**, 16, 906-911	9.9	26
48	C-3 epimers of sugar amino acids as foldameric building blocks: improved synthesis, useful derivatives, coupling strategies. *Amino Acids*, **2017**, 49, 223-240	3.5	10
47	Challenging drug target for Parkinson's disease: Pathological complex of the chameleon TPPP/p25 and alpha-synuclein proteins. *Biochimica Et Biophysica Acta - Molecular Basis of Disease*, **2017**, 1863, 310-323	6.9	14
46	Aromatic Cluster Sensor of Protein Folding: Near-UV Electronic Circular Dichroism Bands Assigned to Fold Compactness. *Chemistry - A European Journal*, **2016**, 22, 13871-13883	4.8	4
45	Origin of problems related to Staudinger reduction in carbopeptoid syntheses. *Amino Acids*, **2016**, 48, 2619-2633	3.5	7
44	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. *Current Protein and Peptide Science*, **2016**, 17, 147-55	2.8	12

43	Hydrogen-Bonding Network Anchors the Cyclic Form of Sugar Arylhydrazones. *European Journal of Organic Chemistry*, **2016**, 2016, 3419-3426	3.2	0
42	Small Peptides Derived from Penetratin as Antibacterial Agents. *Archiv Der Pharmazie*, **2016**, 349, 242-51	4.3	4
41	Mutation-dependent recessive inheritance of NPHS2-associated steroid-resistant nephrotic syndrome. *Nature Genetics*, **2014**, 46, 299-304	36.3	108
40	Rational design of α-helix-stabilized exendin-4 analogues. *Biochemistry*, **2014**, 53, 3540-52	3.2	18
39	Structural insights into the Trp-cage folding intermediate formation. *Chemistry - A European Journal* , **2013**, 19, 2628-40	4.8	45
38	Penetratin and derivatives acting as antibacterial agents. *Chemical Biology and Drug Design*, **2013**, 82, 167-77	2.9	10
37	Foldamer Stability Coupled to Aggregation Propensity of Elongated Trp-Cage Miniproteins. *European Journal of Organic Chemistry*, **2013**, 2013, 3513-3522	3.2	9
36	Multiple fuzzy interactions in the moonlighting function of thymosin-β4. *Intrinsically Disordered Proteins*, **2013**, 1, e26204		8
35	Cooperativity network of Trp-cage miniproteins: probing salt-bridges. *Journal of Peptide Science*, **2011**, 17, 610-9	2.1	30
34	Penetratin analogues acting as antifungal agents. *European Journal of Medicinal Chemistry*, **2011**, 46, 370-7	6.8	14
33	Protein Dynamics as Reported by NMR. *Annual Reports on NMR Spectroscopy*, **2010**, 35-75	1.7	13
32	Reconciling the lock-and-key and dynamic views of canonical serine protease inhibitor action. *FEBS Letters*, **2010**, 584, 203-6	3.8	18
31	The inherent flexibility of peptides and protein fragments quantitized by CD in conjunction with CCA+. *Journal of Peptide Science*, **2009**, 15, 738-52	2.1	9
30	Corrigendum to "Calcium-induced tripartite binding of intrinsically disordered calpastatin to its cognate enzyme, calpain" [FEBS Lett. 582 (2008) 2149–2154]. *FEBS Letters*, **2008**, 582, 2816-2816	3.8	
29	Cooperation between a salt bridge and the hydrophobic core triggers fold stabilization in a Trp-cage miniprotein. *Biochemistry*, **2008**, 47, 1007-16	3.2	51
28	pKa optimized catalysis in serine proteinases, an ab initio study on the catalaytic His. *International Journal of Quantum Chemistry*, **2007**, 107, 2178-2183	2.1	3
27	Dead-end street of protein folding: thermodynamic rationale of amyloid fibril formation. *Journal of the American Chemical Society*, **2007**, 129, 14959-65	16.4	50
26	Toward a rational design of beta-peptide structures. *Journal of Computational Chemistry*, **2006**, 27, 20-38	3.5	39

25	Structure and stability of beta-pleated sheets. *Journal of Computational Chemistry*, **2005**, 26, 1155-68	3.5	56
24	Vicinal disulfide bridge conformers by experimental methods and by ab initio and DFT molecular computations. *Proteins: Structure, Function and Bioinformatics*, **2004**, 55, 152-68	4.2	27
23	On the flexibility of beta-peptides. *Journal of Computational Chemistry*, **2004**, 25, 285-307	3.5	47
22	Stability issues of covalently and noncovalently bonded peptide subunits. *Journal of Computational Chemistry*, **2004**, 25, 1084-100	3.5	15
21	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. *Journal of Computational Chemistry*, **2003**, 24, 1026-42	3.5	54
20	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. *Journal of Computational Chemistry*, **2003**, 24, 1157-71	3.5	6
19	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. *Chemistry - A European Journal*, **2003**, 9, 5332-42	4.8	21
18	Vicinal disulfide turns. *Protein Engineering, Design and Selection*, **2003**, 16, 637-9	1.9	96
17	Investigation of penetratin peptides. Part 1. The environment dependent conformational properties of penetratin and two of its derivatives. *Journal of Peptide Science*, **2002**, 8, 151-71	2.1	42
16	Toward a computed peptide structure database: The role of a universal atomic numbering system of amino acids in peptides and internal hierarchy of database. *International Journal of Quantum Chemistry*, **2002**, 90, 933-968	2.1	50
15	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. *Journal of Computational Chemistry*, **2001**, 22, 732-751	3.5	14
14	alpha- and 3(10)-helix interconversion: a quantum-chemical study on polyalanine systems in the gas phase and in aqueous solvent. *Journal of the American Chemical Society*, **2001**, 123, 6054-60	16.4	88
13	Toward direct determination of conformations of protein building units from multidimensional NMR experiments I. A theoretical case study of For-Gly-NH2 and For-L-Ala-NH2. *Journal of Computational Chemistry*, **2000**, 21, 882-900	3.5	26
12	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-NH2. *Journal of Computational Chemistry*, **2000**, 21, 626-655	3.5	36
11	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. *International Journal of Quantum Chemistry*, **1997**, 61, 797-814	2.1	20
10	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
9	Peptide Models. 18. Hydroxymethyl Side-Chain Induced Backbone Conformational Shifts of l-Serine Amide. All ab Initio Conformers of For-l-Ser-NH2. *Journal of the American Chemical Society*, **1996**, 118, 7809-7817	16.4	48
8	Peptide models XVI. The identification of selected HCOL-SER-NH2 conformers via a systematic grid search using ab initio potential energy surfaces. *Journal of Computational Chemistry* , **1996**, 17, 821-834	3.5	36

7	A search for the ideal type I Eturn **1996**, 38, 723-732		9
6	Turns **1996**, 285-380		78
5	Searching for the simplest structural units to describe the three-dimensional structure of proteins. *International Reviews in Physical Chemistry*, **1995**, 14, 127-168	7	29
4	Peptide models 6. New .beta.-turn conformations from ab initio calculations confirmed by x-ray data of proteins. *Journal of the American Chemical Society*, **1993**, 115, 4849-4858	16.4	94
3	Synthesis and conformational analysis of N-glycopeptides. II. CD, molecular dynamics, and NMR spectroscopic studies on linear N-glycopeptides. *Biopolymers*, **1993**, 33, 665-85	2.2	28
2	Peptide models. 1. Topology of selected peptide conformational potential energy surfaces (glycine and alanine derivatives). *Journal of the American Chemical Society*, **1991**, 113, 6256-6265	16.4	233
1	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. *Journal of the American Chemical Society*, **1991**, 113, 9772-9784	16.4	109