AndrÃ¡s Perczel

List of Publications by Year
in descending order

81 papers	2,244 citations	257450 24 h-index	243625 44 g-index
85 all docs	85 docs citations	85 times ranked	2363 citing authors

#	Article	IF	Citations
1	Directed Evolution-Driven Increase of Structural Plasticity Is a Prerequisite for Binding the Complement Lectin Pathway Blocking MASP-Inhibitor Peptides. ACS Chemical Biology, 2022, , .	3.4	1
2	Cryo-EM structure of acylpeptide hydrolase reveals substrate selection by multimerization and a multi-state serine-protease triad. Chemical Science, 2022, 13, 7132-7142.	7.4	5
3	Omicron Binding Mode: Contact Analysis and Dynamics of the Omicron Receptor-Binding Domain in Complex with ACE2. Journal of Chemical Information and Modeling, 2022, 62, 3844-3853.	5.4	11
4	Assessment of Tractable Cysteines for Covalent Targeting by Screening Covalent Fragments. ChemBioChem, 2021, 22, 743-753.	2.6	19
5	Cost-Effective Flow Peptide Synthesis: Metamorphosis of HPLC. Organic Process Research and Development, 2021, 25, 182-191.	2.7	14
6	Synthesis of chimera oligopeptide including furanoid Î²-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.	2.7	5
7	The Budapest Amyloid Predictor and Its Applications. Biomolecules, 2021, 11, 500.	4.0	11
8	Bacterial fermentation and isotope labelling optimized for amyloidogenic proteins. Microbial Biotechnology, 2021, 14, 1107-1119.	4.2	3
9	Solution Structure and Acidâ€Base Properties of Reduced Î±â€Conotoxin MI. Chemistry and Biodiversity, 2021, 18, e2100464.	2.1	1
10	Structural Water Stabilizes Protein Motifs in Liquid Protein Phase: The Folding Mechanism of Short Î²-Sheets Coupled to Phase Transition. International Journal of Molecular Sciences, 2021, 22, 8595.	4.1	3
11	Application of Sugar Amino Acids: Flow Chemistry Used for Î±/Î²â€Chimera Synthesis. European Journal of Organic Chemistry, 2021, 2021, 6071-6083.	2.4	3
12	The Route from the Folded to the Amyloid State: Exploring the Potential Energy Surface of a Drugâ€Like Miniprotein. Chemistry - A European Journal, 2020, 26, 1968-1978.	3.3	14
13	1H, 15N 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.	0.8	26
14	Compactness of Protein Folds Alters Disulfideâ€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.	2.6	5
15	Interplay of Structural Disorder and Short Binding Elements in the Cellular Chaperone Function of Plant Dehydrin ERD14. Cells, 2020, 9, 1856.	4.1	12
16	Dynamically encoded reactivity of Ras enzymes: opening new frontiers for drug discovery. Cancer and Metastasis Reviews, 2020, 39, 1075-1089.	5.9	16
17	Structural impact of GTP binding on downstream KRAS signaling. Chemical Science, 2020, 11, 9272-9289.	7.4	25
18	Off-pathway 3D-structure provides protection against spontaneous Asn/Asp isomerization: shielding proteins Achilles heel. Quarterly Reviews of Biophysics, 2020, 53, e2.	5.7	2

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19	The Route from the Folded to the Amyloid State: Exploring the Potential Energy Surface of a Drugâ€Like Miniprotein. Chemistry - A European Journal, 2020, 26, 1893-1893.	3.3	0
20	Configurationâ€Controlled Crystal and/or Gel Formation of Protected d â€Glucosamines Supported by Promiscuous Interaction Surfaces and a Conformationally Heterogeneous Solution State. Chemistry - A European Journal, 2020, 26, 11643-11655.	3.3	3
21	Assignment of Vibrational Circular Dichroism Crossâ€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.	3.3	2
22	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.	3.3	7
23	DUckCov: a Dynamic Undockingâ€Based Virtual Screening Protocol for Covalent Binders. ChemMedChem, 2019, 14, 1011-1021.	3.2	18
24	Î±/Î²-Chimera peptide synthesis with cyclic Î²-sugar amino acids: the efficient coupling protocol. Amino Acids, 2019, 51, 669-678.	2.7	16
25	Unwanted hydrolysis or Î±/Î²-peptide bond formation: how long should the rate-limiting coupling step take?. RSC Advances, 2019, 9, 30720-30728.	3.6	11
26	Protein Aggregation in a Nutshell: The Splendid Molecular Architecture of the Dreaded Amyloid Fibrils. Current Protein and Peptide Science, 2019, 20, 1077-1088.	1.4	7
27	C-terminal oligomerization of podocin mediates interallelic interactions. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 2448-2457.	3.8	15
28	Approaches to Pyranuronic Î²â€Sugar Amino Acid Building Blocks of Peptidosaccharide Foldamers. European Journal of Organic Chemistry, 2018, 2018, 355-361.	2.4	6
29	Biochemical and pharmacological characterization of three opioid-nociceptin hybrid peptide ligands reveals substantially differing modes of their actions. Peptides, 2018, 99, 205-216.	2.4	6
30	Four faces of the interaction between ions and aromatic rings. Journal of Computational Chemistry, 2017, 38, 1762-1773.	3.3	9
31	Predictable Conformational Diversity in Foldamers of Sugar Amino Acids. Journal of Chemical Information and Modeling, 2017, 57, 757-768.	5.4	4
32	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.	2.0	1
33	The Piwiâ€pi<scp>RNA</scp> pathway: road to immortality. Aging Cell, 2017, 16, 906-911.	6.7	39
34	C-3 epimers of sugar amino acids as foldameric building blocks: improved synthesis, useful derivatives, coupling strategies. Amino Acids, 2017, 49, 223-240.	2.7	17
35	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.	3.8	23
36	Hydrogenâ€Bonding Network Anchors the Cyclic Form of Sugar Arylhydrazones. European Journal of Organic Chemistry, 2016, 2016, 3419-3426.	2.4	1

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37	Small Peptides Derived from Penetratin as Antibacterial Agents. Archiv Der Pharmazie, 2016, 349, 242-251.	4.1	8
38	Aromatic Cluster Sensor of Protein Folding: Nearâ€UV Electronic Circular Dichroism Bands Assigned to Fold Compactness. Chemistry - A European Journal, 2016, 22, 13871-13883.	3.3	6
39	Origin of problems related to Staudinger reduction in carbopeptoid syntheses. Amino Acids, 2016, 48, 2619-2633.	2.7	7
40	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, 147-155.	1.4	17
41	Mutation-dependent recessive inheritance of NPHS2-associated steroid-resistant nephrotic syndrome. Nature Genetics, 2014, 46, 299-304.	21.4	134
42	Rational Design of Î±-Helix-Stabilized Exendin-4 Analogues. Biochemistry, 2014, 53, 3540-3552.	2.5	21
43	Structural Insights into the Trpâ€Cage Folding Intermediate Formation. Chemistry - A European Journal, 2013, 19, 2628-2640.	3.3	49
44	Penetratin and Derivatives Acting as Antibacterial Agents. Chemical Biology and Drug Design, 2013, 82, 167-177.	3.2	13
45	Foldamer Stability Coupled to Aggregation Propensity of Elongated Trpâ€Cage Miniproteins. European Journal of Organic Chemistry, 2013, 2013, 3513-3522.	2.4	10
46	Multiple fuzzy interactions in the moonlighting function of thymosin-Î²4. Intrinsically Disordered Proteins, 2013, 1, e26204.	1.9	12
47	Cooperativity network of Trpâ€cage miniproteins: probing saltâ€bridges. Journal of Peptide Science, 2011, 17, 610-619.	1.4	34
48	Penetratin analogues acting as antifungal agents. European Journal of Medicinal Chemistry, 2011, 46, 370-377.	5.5	17
49	Reconciling the lockâ€andâ€key and dynamic views of canonical serine protease inhibitor action. FEBS Letters, 2010, 584, 203-206.	2.8	20
50	Protein Dynamics as Reported by NMR. Annual Reports on NMR Spectroscopy, 2010, , 35-75.	1.5	17
51	The inherent flexibility of peptides and protein fragments quantitized by CD in conjunction with CCA+. Journal of Peptide Science, 2009, 15, 738-752.	1.4	10
52	Corrigendum to â€œCalcium-induced tripartite binding of intrinsically disordered calpastatin to its cognate enzyme, calpainâ€•[FEBS Lett. 582 (2008) 2149-2154]. FEBS Letters, 2008, 582, 2816-2816.	2.8	0
53	Cooperation between a Salt Bridge and the Hydrophobic Core Triggers Fold Stabilization in a Trp-Cage Miniprotein. Biochemistry, 2008, 47, 1007-1016.	2.5	53
54	Dead-End Street of Protein Folding: Thermodynamic Rationale of Amyloid Fibril Formation. Journal of the American Chemical Society, 2007, 129, 14959-14965.	13.7	53

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55	pKaoptimized catalysis in serine proteinases, an ab initio study on the catalaytic His. International Journal of Quantum Chemistry, 2007, 107, 2178-2183.	2.0	3
56	Toward a rational design of Î²-peptide structures. Journal of Computational Chemistry, 2006, 27, 20-38.	3.3	43
57	Structure and stability of Î²-pleated sheets. Journal of Computational Chemistry, 2005, 26, 1155-1168.	3.3	68
58	Vicinal disulfide bridge conformers by experimental methods and by ab initio and DFT molecular computations. Proteins: Structure, Function and Bioinformatics, 2004, 55, 152-168.	2.6	28
59	On the flexibility of ?-peptides. Journal of Computational Chemistry, 2004, 25, 285-307.	3.3	47
60	Stability issues of covalently and noncovalently bonded peptide subunits. Journal of Computational Chemistry, 2004, 25, 1084-1100.	3.3	15
61	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, 1026-1042.	3.3	54
62	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, 1157-1171.	3.3	6
63	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, 5332-5342.	3.3	26
64	Vicinal disulfide turns. Protein Engineering, Design and Selection, 2003, 16, 637-639.	2.1	107
65	Investigation of penetratin peptides Part 1. The environment dependent conformational properties of penetratin and two of its derivatives. Journal of Peptide Science, 2002, 8, 151-171.	1.4	45
66	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.	2.0	54
67	Î±- and 310-Helix Interconversion:Â A Quantum-Chemical Study on Polyalanine Systems in the Gas Phase and in Aqueous Solvent. Journal of the American Chemical Society, 2001, 123, 6054-6060.	13.7	96
68	Peptide models XXXI. Conformational properties of hydrophobic residues shaping the core of proteins. Anab initiostudy of N-formyl-L-valinamide and N-formyl-L-phenylalaninamide. Journal of Computational Chemistry, 2001, 22, 732-751.	3.3	17
69	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.	3.3	28
70	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.	3.3	37
71	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.	2.0	20
72	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

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73	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.	13.7	49
74	Peptide models XVI. The identification of selected HCO?L?SER?NH2 conformers via a systematic grid search usingab initio potential energy surfaces. Journal of Computational Chemistry, 1996, 17, 821-834.	3.3	37
75	A search for the ideal type I Î²-turn. , 1996, 38, 723-732.		13
76	Turns. , 1996, , 285-380.		83
77	Searching for the simplest structural units to describe the three-dimensional structure of proteins. International Reviews in Physical Chemistry, 1995, 14, 127-168.	2.3	31
78	Synthesis and conformational analysis of N-glycopeptides. II. CD, molecular dynamics, and nmr spectroscopic studies on linear N-glycopeptides. Biopolymers, 1993, 33, 665-685.	2.4	31
79	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.	13.7	99
80	Peptide models. 1. Topology of selected peptide conformational potential energy surfaces (glycine and) Tj ETQq0 0 0 rgBT /Overlock 10	13.7	244
81	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.	13.7	115