Martin Tollinger

List of Publications by Year
in descending order

73 papers	2,592 citations	218592 26 h-index	206029 48 g-index
79 all docs	79 docs citations	79 times ranked	3047 citing authors

#	Article	IF	Citations
1	Formic acid reduction and CO₂ activation at Mo₂C: The important role of surface oxide. Electrochemical Science Advances, 2022, 2, e2100130.	1.2	7
2	3D-Printed High-Pressure-Resistant Immobilized Enzyme Microreactor (Î¼IMER) for Protein Analysis. Analytical Chemistry, 2022, 94, 8580-8587.	3.2	6
3	NMR resonance assignments of the FinO-domain of the RNA chaperone RocC. Biomolecular NMR Assignments, 2021, 15, 61-64.	0.4	3
4	Inverse relation between structural flexibility and IgE reactivity of Cor a 1 hazelnut allergens. Scientific Reports, 2021, 11, 4173.	1.6	14
5	Oral birch pollen immunotherapy with apples: Results of a phase II clinical pilot study. Immunity, Inflammation and Disease, 2021, 9, 503-511.	1.3	10
6	Cosolute modulation of protein oligomerization reactions in the homeostatic timescale. Biophysical Journal, 2021, 120, 2067-2077.	0.2	2
7	Microdroplet Mass Spectrometry Enables Extremely Accelerated Pepsin Digestion of Proteins. Journal of the American Society for Mass Spectrometry, 2021, 32, 1841-1845.	1.2	9
8	NMR resonance assignments of the PR-10 allergens Act c 8 and Act d 8 from golden and green kiwifruit. Biomolecular NMR Assignments, 2021, 15, 367-371.	0.4	4
9	Structure and Zeatin Binding of the Peach Allergen Pru p 1. Journal of Agricultural and Food Chemistry, 2021, 69, 8120-8129.	2.4	10
10	(3Î¾,4Î¾,5Î¾,6Î¾,7Î¾,11Î¾)-3,6-Dihydroxy-8-oxo-9-eremophilene-12-oic Acid, a New Phytotoxin of Alternaria alternata ssp. tenuissima Isolates Associated with Fruit Spots on Apple (Malus Ã—) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.8	6
11	A drug library screen identifies Carbenoxolone as novel FOXO inhibitor that overcomes FOXO3-mediated chemoprotection in high-stage neuroblastoma. Oncogene, 2020, 39, 1080-1097.	2.6	31
12	NMR resonance assignments of the four isoforms of the hazelnut allergen Cor a 1.04. Biomolecular NMR Assignments, 2020, 14, 45-49.	0.4	5
13	In silico Design of Phl p 6 Variants With Altered Fold-Stability Significantly Impacts Antigen Processing, Immunogenicity and Immune Polarization. Frontiers in Immunology, 2020, 11, 1824.	2.2	8
14	Allergenâ€specific immunotherapy with apples: selected cultivars could be a promising tool for birch pollen allergy. Journal of the European Academy of Dermatology and Venereology, 2020, 34, 1286-1292.	1.3	16
15	Branch site bulge conformations in domain 6 determine functional sugar puckers in group II intron splicing. Nucleic Acids Research, 2019, 47, 11430-11440.	6.5	10
16	pH-Dependent Protonation of the Phl p 6 Pollen Allergen Studied by NMR and cpH-aMD. Journal of Chemical Theory and Computation, 2019, 15, 5716-5726.	2.3	10
17	Pathogenic Mutations Associated with Legius Syndrome Modify the Spred1 Surface and Are Involved in Direct Binding to the Ras Inactivator Neurofibromin. Journal of Molecular Biology, 2019, 431, 3889-3899.	2.0	4
18	NMR resonance assignments of the pathogenesis-related peach allergen Pru p 1.0101. Biomolecular NMR Assignments, 2019, 13, 127-130.	0.4	5

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19	5â€Oxyacetic Acid Modification Destabilizes Double Helical Stem Structures and Favors Anionic Watsonâ€“Crick like cmo⁵Uâ€C Base Pairs. Chemistry - A European Journal, 2018, 24, 18903-18906.	1.7	18
20	Studying sparsely populated conformational states in RNA combining chemical synthesis and solution NMR spectroscopy. Methods, 2018, 148, 39-47.	1.9	23
21	Structure of the Major Apple Allergen MalÂdÂ1. Journal of Agricultural and Food Chemistry, 2017, 65, 1606-1612.	2.4	50
22	NMR resonance assignments of the EVH1 domain of neurofibrominâ€™s recruitment factor Spred1. Biomolecular NMR Assignments, 2017, 11, 305-308.	0.4	4
23	Synthesis and incorporation of 13C-labeled DNA building blocks to probe structural dynamics of DNA by NMR. Nucleic Acids Research, 2017, 45, 9178-9192.	6.5	14
24	NMR resonance assignments of a hypoallergenic isoform of the major birch pollen allergen Bet v 1. Biomolecular NMR Assignments, 2017, 11, 231-234.	0.4	4
25	Conformational Flexibility Differentiates Naturally Occurring Bet v 1 Isoforms. International Journal of Molecular Sciences, 2017, 18, 1192.	1.8	18
26	Excited States of Nucleic Acids Probed by Proton Relaxation Dispersion NMR Spectroscopy. Angewandte Chemie, 2016, 128, 12187-12191.	1.6	8
27	Excited States of Nucleic Acids Probed by Proton Relaxation Dispersion NMR Spectroscopy. Angewandte Chemie - International Edition, 2016, 55, 12008-12012.	7.2	48
28	Measurement of Ligandâ€“Target Residence Times by ¹H Relaxation Dispersion NMR Spectroscopy. Journal of Medicinal Chemistry, 2016, 59, 10788-10793.	2.9	24
29	NMR resonance assignments of the major apple allergen Mal d 1. Biomolecular NMR Assignments, 2016, 10, 287-290.	0.4	10
30	Fold stability during endolysosomal acidification is a key factor for allergenicity and immunogenicity of the major birch pollen allergen. Journal of Allergy and Clinical Immunology, 2016, 137, 1525-1534.	1.5	69
31	NMR Methods to Study Dynamic Allostery. PLoS Computational Biology, 2016, 12, e1004620.	1.5	61
32	Ligandâ€Detected Relaxation Dispersion NMR Spectroscopy: Dynamics of preQ₁â€“RNA Binding. Angewandte Chemie - International Edition, 2015, 54, 560-563.	7.2	28
33	Cross-correlated relaxation measurements under adiabatic sweeps: determination of local order in proteins. Journal of Biomolecular NMR, 2015, 63, 353-365.	1.6	6
34	Ice nucleation by water-soluble macromolecules. Atmospheric Chemistry and Physics, 2015, 15, 4077-4091.	1.9	198
35	NMR resonance assignments of the archaeal ribosomal protein L7Ae in the apo form and bound to a 25 nt RNA. Biomolecular NMR Assignments, 2015, 9, 177-180.	0.4	2
36	relax: the analysis of biomolecular kinetics and thermodynamics using NMR relaxation dispersion data. Bioinformatics, 2014, 30, 2219-2220.	1.8	45

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37	Ligand Binding Modulates the Structural Dynamics and Compactness of the Major Birch Pollen Allergen. Biophysical Journal, 2014, 107, 2972-2981.	0.2	35
38	A kinetic study of domain swapping of Protein L. Physical Chemistry Chemical Physics, 2014, 16, 6383.	1.3	15
39	Allosteric Communication in the KIX Domain Proceeds through Dynamic Repacking of the Hydrophobic Core. ACS Chemical Biology, 2013, 8, 1600-1610.	1.6	62
40	The allosteric communication pathways in KIX domain of CBP. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14237-14242.	3.3	57
41	Synthesis of (6-¹³C)Pyrimidine Nucleotides as Spin-Labels for RNA Dynamics. Journal of the American Chemical Society, 2012, 134, 7558-7569.	6.6	73
42	Site-Resolved Measurement of Microsecond-to-Millisecond Conformational-Exchange Processes in Proteins by Solid-State NMR Spectroscopy. Journal of the American Chemical Society, 2012, 134, 14800-14807.	6.6	61
43	Mathematical treatment of adiabatic fast passage pulses for the computation of nuclear spin relaxation rates in proteins with conformational exchange. Journal of Biomolecular NMR, 2011, 51, 35-47.	1.6	7
44	Siderocalin Q83 exhibits differential slow dynamics upon ligand binding. Journal of Biomolecular NMR, 2011, 51, 83-88.	1.6	5
45	Longitudinal exchange: an alternative strategy towards quantification of dynamics parameters in ZZ exchange spectroscopy. Journal of Biomolecular NMR, 2011, 51, 123-129.	1.6	16
46	Electrostatic Stabilization of a Native Protein Structure in the Gas Phase. Angewandte Chemie - International Edition, 2011, 50, 873-877.	7.2	111
47	Kinetics of DNA Refolding from Longitudinal Exchange NMR Spectroscopy. ChemBioChem, 2011, 12, 2007-2010.	1.3	6
48	Probing RNA dynamics via longitudinal exchange and CPMG relaxation dispersion NMR spectroscopy using a sensitive 13C-methyl label. Nucleic Acids Research, 2011, 39, 4340-4351.	6.5	49
49	Autocorrelation Analysis of NOESY Data Provides Residue Compactness for Folded and Unfolded Proteins. Journal of the American Chemical Society, 2009, 131, 6038-6039.	6.6	13
50	Direct Observation of the Dynamic Process Underlying Allosteric Signal Transmission. Journal of the American Chemical Society, 2009, 131, 3063-3068.	6.6	111
51	Direct methods and residue type specific isotope labeling in NMR structure determination and model-driven sequential assignment. Journal of Biomolecular NMR, 2008, 42, 111-127.	1.6	4
52	Folding of the KIX Domain: Characterization of the Equilibrium Analog of a Folding Intermediate using 15N/13C Relaxation Dispersion and Fast 1H/2H Amide Exchange NMR Spectroscopy. Journal of Molecular Biology, 2008, 380, 726-741.	2.0	34
53	Calculation of Residual Dipolar Couplings from Disordered State Ensembles Using Local Alignment. Journal of the American Chemical Society, 2008, 130, 7804-7805.	6.6	67
54	Characterization of the Hydrodynamic Properties of the Folding Transition State of an SH3 Domain by Magnetization Transfer NMR Spectroscopy. Biochemistry, 2006, 45, 6434-6445.	1.2	8

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55	An Isolated Helix Persists in a Sparsely Populated Form of KIX under Native Conditions. Biochemistry, 2006, 45, 8885-8893.	1.2	32
56	Measuring pKaValues in Protein Folding Transition State Ensembles by NMR Spectroscopy. Journal of the American Chemical Society, 2005, 127, 8904-8905.	6.6	16
57	Structural Comparison of the Unstable drkN SH3 Domain and a Stable Mutantâ€,â€¡. Biochemistry, 2005, 44, 15550-15560.	1.2	39
58	Site-specific contributions to the pH dependence of protein stability. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 4545-4550.	3.3	86
59	Measurement of Side-Chain Carboxyl pKaValues of Glutamate and Aspartate Residues in an Unfolded Protein by Multinuclear NMR Spectroscopy. Journal of the American Chemical Society, 2002, 124, 5714-5717.	6.6	68
60	Cooperative Interactions and a Non-native Buried Trp in the Unfolded State of an SH3 Domain. Journal of Molecular Biology, 2002, 322, 163-178.	2.0	64
61	The B12-Binding Subunit of Glutamate Mutase from Clostridium tetanomorphum Traps the Nucleotide Moiety of Coenzyme B12. Journal of Molecular Biology, 2001, 309, 777-791.	2.0	33
62	A Protein Pre-Organized to Trap the Nucleotide Moiety of Coenzyme B12: Refined Solution Structure of the B12-Binding Subunit of Glutamate Mutase from Clostridium tetanomorphum. ChemBioChem, 2001, 2, 643-655.	1.3	9
63	Mapping the ligand binding site at protein side-chains in protein-ligand complexes through NOE difference spectroscopy. Journal of Biomolecular NMR, 2001, 20, 195-202.	1.6	15
64	Direct structure refinement of high molecular weight proteins against residual dipolar couplings and carbonyl chemical shift changes upon alignment: an application to maltose binding protein. Journal of Biomolecular NMR, 2001, 21, 31-40.	1.6	50
65	Slow Dynamics in Folded and Unfolded States of an SH3 Domain. Journal of the American Chemical Society, 2001, 123, 11341-11352.	6.6	454
66	NMR Techniques to Study Hydrogen Bondingin Aqueous Solution. Monatshefte FÃ¼r Chemie, 1999, 130, 961-982.	0.9	15
67	Heteronuclear relaxation in time-dependent spin systems: (15)N-T1 (rho) dispersion during adiabatic fast passage. Journal of Biomolecular NMR, 1999, 13, 213-221.	1.6	11
68	Electrochemical Synthesis and Structure Analysis of Neocoenzyme B12 - An Epimer of Coenzyme B12 with a Remarkably Flexible Organometallic Group. Helvetica Chimica Acta, 1999, 82, 848-869.	1.0	16
69	The Structure of Methylcob(III)alamin in Aqueous Solution - A Water Molecule as Structuring Element of the Nucleotide Loop. Helvetica Chimica Acta, 1999, 82, 1596-1609.	1.0	21
70	Relaxation-Induced Polarization Transfer and the Determination of Methyl Group 13C Chemical Shielding Anisotropy. Journal of Physical Chemistry A, 1999, 103, 5253-5258.	1.1	0
71	NMR Techniques to Study Hydrogen Bonding in Aqueous Solution. , 1999, , 17-38.		1
72	How a protein prepares for B12 binding: structure and dynamics of the B12-binding subunit of glutamate mutase from Clostridium tetanomorphum. Structure, 1998, 6, 1021-1033.	1.6	72

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73	An efficient method for the preparation of methylcobalamin, nature's organometallic methyl transfer catalyst. Journal of Molecular Catalysis A, 1997, 116, 147-155.	4.8	27