Guy Lippens

List of Publications by Year
in descending order

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86 papers	3,833 citations	109264 35 h-index	133188 59 g-index
88 all docs	88 docs citations	88 times ranked	4502 citing authors

#	Article	IF	Citations
1	Postâ€translational modification: nature's escape from genetic imprisonment and the basis for dynamic information encoding. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2012, 4, 565-583.	6.6	288
2	Identification of the Tau phosphorylation pattern that drives its aggregation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9080-9085.	3.3	168
3	Cell signaling, post-translational protein modifications and NMR spectroscopy. Journal of Biomolecular NMR, 2012, 54, 217-236.	1.6	153
4	DEB025 (Alisporivir) Inhibits Hepatitis C Virus Replication by Preventing a Cyclophilin A Induced Cis-Trans Isomerisation in Domain II of NS5A. PLoS ONE, 2010, 5, e13687.	1.1	151
5	Hepatitis C Virus NS5A Protein Is a Substrate for the Peptidyl-prolyl cis/trans Isomerase Activity of Cyclophilins A and B. Journal of Biological Chemistry, 2009, 284, 13589-13601.	1.6	149
6	Structural Impact of Heparin Binding to Full-Length Tau As Studied by NMR Spectroscopy. Biochemistry, 2006, 45, 12560-12572.	1.2	142
7	Identification of O-GlcNAc sites within peptides of the Tau protein and their impact on phosphorylation. Molecular BioSystems, 2011, 7, 1420.	2.9	108
8	NMR Analysis of a Tau Phosphorylation Pattern. Journal of the American Chemical Society, 2006, 128, 3575-3583.	6.6	107
9	NMR observation of Tau in Xenopus oocytes. Journal of Magnetic Resonance, 2008, 192, 252-257.	1.2	100
10	Domain 3 of NS5A Protein from the Hepatitis C Virus Has Intrinsic Î±-Helical Propensity and Is a Substrate of Cyclophilin A. Journal of Biological Chemistry, 2011, 286, 20441-20454.	1.6	98
11	NMR Investigation of the Interaction between the Neuronal Protein Tau and the Microtubulesâ€. Biochemistry, 2007, 46, 3055-3064.	1.2	86
12	Domain 3 of non-structural protein 5A from hepatitis C virus is natively unfolded. Biochemical and Biophysical Research Communications, 2009, 381, 634-638.	1.0	81
13	Alzheimer disease specific phosphoepitopes of Tau interfere with assembly of tubulin but not binding to microtubules. FASEB Journal, 2009, 23, 1146-1152.	0.2	80
14	Structural characterization by nuclear magnetic resonance of the impact of phosphorylation in the prolineâ€rich region of the disordered Tau protein. Proteins: Structure, Function and Bioinformatics, 2012, 80, 454-462.	1.5	79
15	The Peptidyl Prolyl cis/trans-Isomerase Pin1 Recognizes the Phospho-Thr212-Pro213 Site on Tau. Biochemistry, 2004, 43, 2032-2040.	1.2	77
16	Accepting its Random Coil Nature Allows a Partial NMR Assignment of the Neuronal Tau Protein. ChemBioChem, 2004, 5, 1639-1646.	1.3	74
17	Spectroscopic Studies of GSK3Î² Phosphorylation of the Neuronal Tau Protein and Its Interaction with the N-terminal Domain of Apolipoprotein E. Journal of Biological Chemistry, 2010, 285, 33435-33444.	1.6	71
18	3â€Oâ€Sulfation of Heparan Sulfate Enhances Tau Interaction and Cellular Uptake. Angewandte Chemie - International Edition, 2020, 59, 1818-1827.	7.2	71

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19	Glycan Determinants of Heparin-Tau Interaction. Biophysical Journal, 2017, 112, 921-932.	0.2	68
20	Tau phosphorylation regulates the interaction between BIN1â€™s SH3 domain and Tauâ€™s proline-rich domain. Acta Neuropathologica Communications, 2015, 3, 58.	2.4	66
21	Molecular Implication of PP2A and Pin1 in the Alzheimer's Disease Specific Hyperphosphorylation of Tau. PLoS ONE, 2011, 6, e21521.	1.1	61
22	Nuclear Magnetic Resonance Analysis of the Acetylation Pattern of the Neuronal Tau Protein. Biochemistry, 2014, 53, 3020-3032.	1.2	60
23	Systematic Identification of Tubulin-interacting Fragments of the Microtubule-associated Protein Tau Leads to a Highly Efficient Promoter of Microtubule Assembly. Journal of Biological Chemistry, 2011, 286, 33358-33368.	1.6	56
24	Molecular mechanisms of the phosphoâ€dependent prolyl cis/trans isomerase Pin1. FEBS Journal, 2007, 274, 5211-5222.	2.2	55
25	Immunophilin FKBP52 induces Tau-P301L filamentous assembly in vitro and modulates its activity in a model of tauopathy. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4584-4589.	3.3	55
26	Characterization of Neuronal Tau Protein as a Target of Extracellular Signal-regulated Kinase. Journal of Biological Chemistry, 2016, 291, 7742-7753.	1.6	54
27	Proline-Directed Random-Coil Chemical Shift Values as a Tool for the NMR Assignment of the Tau Phosphorylation Sites. ChemBioChem, 2004, 5, 73-78.	1.3	53
28	The Neuronal Tau Protein Blocks in Vitro Fibrillation of the Amyloid-Î² (AÎ²) Peptide at the Oligomeric Stage. Journal of the American Chemical Society, 2018, 140, 8138-8146.	6.6	49
29	Selective intracellular accumulation of the major metabolite issued from the activation of the prodrug ethionamide in mycobacteria. Journal of Antimicrobial Chemotherapy, 2006, 58, 768-772.	1.3	47
30	In Vivo Detection of the Cyclic Osmoregulated Periplasmic Glucan of Ralstonia solanacearum by High-Resolution Magic Angle Spinning NMR. Journal of Magnetic Resonance, 2001, 151, 118-123.	1.2	45
31	The Domain 2 of the HCV NS5A Protein Is Intrinsically Unstructured. Protein and Peptide Letters, 2010, 17, 1012-1018.	0.4	42
32	A Phosphorylationâ€Induced Turn Defines the Alzheimerâ€™s Disease AT8 Antibody Epitope on the Tau Protein. Angewandte Chemie - International Edition, 2015, 54, 6819-6823.	7.2	41
33	Characterization of the AT180 epitope of phosphorylated Tau protein by a combined nuclear magnetic resonance and fluorescence spectroscopy approach. Biochemical and Biophysical Research Communications, 2011, 412, 743-746.	1.0	40
34	Mechanism of Tau-Promoted Microtubule Assembly As Probed by NMR Spectroscopy. Journal of the American Chemical Society, 2014, 136, 12615-12623.	6.6	40
35	Monitoring of the ethionamide pro-drug activation in mycobacteria by 1H high resolution magic angle spinning NMR. Biochemical and Biophysical Research Communications, 2005, 331, 452-458.	1.0	38
36	Comparative analysis of Erk phosphorylation suggests a mixed strategy for measuring phosphoâ€form distributions. Molecular Systems Biology, 2011, 7, 482.	3.2	38

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37	Investigations on the Determinants Responsible for Low Molar Mass Dextran Formation by DSR-M Dextransucrase. ACS Catalysis, 2017, 7, 7106-7119.	5.5	37
38	Elucidating Tau function and dysfunction in the era of cryo-EM. Journal of Biological Chemistry, 2019, 294, 9316-9325.	1.6	36
39	Hepatitis C Virus NS5B and Host Cyclophilin A Share a Common Binding Site on NS5A. Journal of Biological Chemistry, 2012, 287, 44249-44260.	1.6	35
40	Major Differences between the Self-Assembly and Seeding Behavior of Heparin-Induced and in Vitro Phosphorylated Tau and Their Modulation by Potential Inhibitors. ACS Chemical Biology, 2019, 14, 1363-1379.	1.6	34
41	An Improved Homonuclear TOCSY Experiment with Minimal Water Saturation. Journal of Magnetic Resonance Series B, 1996, 111, 168-170.	1.6	33
42	The FK506-binding protein FKBP52in vitroinduces aggregation of truncated Tau forms with prion-like behavior. FASEB Journal, 2015, 29, 3171-3181.	0.2	33
43	Regions of Tau Implicated in the Paired Helical Fragment Core as Defined by NMR. ChemBioChem, 2005, 6, 1849-1856.	1.3	32
44	Proline Conformation in a Functional Tau Fragment. Journal of Molecular Biology, 2016, 428, 79-91.	2.0	31
45	Overall Structural Model of NS5A Protein from Hepatitis C Virus and Modulation by Mutations Confering Resistance of Virus Replication to Cyclosporin A. Biochemistry, 2017, 56, 3029-3048.	1.2	29
46	Studying the Natively Unfolded Neuronal Tau Protein by Solution NMR Spectroscopy. Protein and Peptide Letters, 2006, 13, 235-246.	0.4	28
47	Unraveling a phosphorylation event in a folded protein by NMR spectroscopy: phosphorylation of the Pin1 WW domain by PKA. Journal of Biomolecular NMR, 2013, 55, 323-337.	1.6	26
48	Isomerization and Oligomerization of Truncated and Mutated Tau Forms by FKBP52 are Independent Processes. Journal of Molecular Biology, 2016, 428, 1080-1090.	2.0	26
49	NMR Meets Tau: Insights into Its Function and Pathology. Biomolecules, 2016, 6, 28.	1.8	25
50	Efficient in vivo synthesis of lasso peptide pseudomycoidin proceeds in the absence of both the leader and the leader peptidase. Chemical Science, 2019, 10, 9699-9707.	3.7	25
51	High-Resolution Magic Angle Spinning NMR of the Neuronal Tau Protein Integrated in Alzheimer's-Like Paired Helical Fragments. Journal of the American Chemical Society, 2005, 127, 10138-10139.	6.6	23
52	A functional fragment of Tau forms fibers without the need for an intermolecular cysteine bridge. Biochemical and Biophysical Research Communications, 2014, 445, 299-303.	1.0	23
53	¹⁵N-NMR-Based Approach for Amino Acids-Based ¹³C-Metabolic Flux Analysis of Metabolism. Analytical Chemistry, 2017, 89, 2101-2106.	3.2	23
54	Graphical interpretation of Boolean operators for protein NMR assignments. Journal of Biomolecular NMR, 2008, 42, 11-21.	1.6	22

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55	A Proline-Tryptophan Turn in the Intrinsically Disordered Domain 2 of NS5A Protein Is Essential for Hepatitis C Virus RNA Replication. Journal of Biological Chemistry, 2015, 290, 19104-19120.	1.6	22
56	Tau Monoclonal Antibody Generation Based on Humanized Yeast Models. Journal of Biological Chemistry, 2015, 290, 4059-4074.	1.6	21
57	Towards understanding the phosphorylation code of tau. Biochemical Society Transactions, 2012, 40, 698-703.	1.6	20
58	In-cell NMR: from metabolites to macromolecules. Analyst, The, 2018, 143, 620-629.	1.7	20
59	The Zebra Mussel (Dreissena polymorpha) as a Model Organism for Ecotoxicological Studies: A Prior 1H NMR Spectrum Interpretation of a Whole Body Extract for Metabolism Monitoring. Metabolites, 2020, 10, 256.	1.3	19
60	Identification and characterization of andalusicin: N-terminally dimethylated class III lantibiotic from Bacillus thuringiensis sv. andalousiensis. IScience, 2021, 24, 102480.	1.9	18
61	Studying Posttranslational Modifications by In-Cell NMR. Chemistry and Biology, 2008, 15, 311-312.	6.2	17
62	Nuclear Magnetic Resonance Spectroscopy for the Identification of Multiple Phosphorylations of Intrinsically Disordered Proteins. Journal of Visualized Experiments, 2016, , .	0.2	17
63	Studying Intrinsically Disordered Proteins under True Inâ€…Vivo Conditions by Combined Crossâ€Polarization and Carbonylâ€Detection NMR Spectroscopy. Angewandte Chemie - International Edition, 2016, 55, 7418-7422.	7.2	17
64	Tuning the catalytic activity and selectivity of water-soluble bimetallic RuPt nanoparticles by modifying their surface metal distribution. Nanoscale, 2019, 11, 16544-16552.	2.8	16
65	Futile Encounter Engineering of the DSR-M Dextransucrase Modifies the Resulting Polymer Length. Biochemistry, 2019, 58, 2853-2859.	1.2	15
66	Integrated pH Measurement during Reaction Monitoring with Dual-Reception ‹sup›1‹/sup›Hâ€“‹sup›31‹/sup›P NMR Spectroscopy. Analytical Chemistry, 2019, 91, 3959-3963.	3.2	13
67	A Î²-Turn Motif in the Steroid Hormone Receptorâ€™s Ligand-Binding Domains Interacts with the Peptidyl-prolyl Isomerase (PPIase) Catalytic Site of the Immunophilin FKBP52. Biochemistry, 2016, 55, 5366-5376.	1.2	10
68	Improved Isotopic Profiling by Pure Shift Heteronuclear 2D J-Resolved NMR Spectroscopy. Analytical Chemistry, 2018, 90, 4025-4031.	3.2	10
69	Cyclophilin A allows the allosteric regulation of a structural motif in the disordered domain 2 of NS5A and thereby fine-tunes HCV RNA replication. Journal of Biological Chemistry, 2019, 294, 13171-13185.	1.6	10
70	A new strategy for sequential assignment of intrinsically unstructured proteins based on 15N single isotope labelling. Journal of Magnetic Resonance, 2013, 236, 1-6.	1.2	9
71	An NMR look at an engineered PET depolymerase. Biophysical Journal, 2022, 121, 2882-2894.	0.2	9
72	Selective backbone labelling of ILV methyl labelled proteins. Journal of Biomolecular NMR, 2009, 43, 219-227.	1.6	8

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73	Improved NMR Detection of Phospho-Metabolites in a Complex Mixture. Analytical Chemistry, 2021, 93, 4818-4824.	3.2	8
74	Ranking High Affinity Ligands of Low Solubility by NMR Spectroscopy. ACS Medicinal Chemistry Letters, 2011, 2, 485-487.	1.3	7
75	NMR reveals the intrinsically disordered domain 2 of NS5A protein as an allosteric regulator of the hepatitis C virus RNA polymerase NS5B. Journal of Biological Chemistry, 2017, 292, 18024-18043.	1.6	7
76	Studying Intrinsically Disordered Proteins under True Inâ€…Vivo Conditions by Combined Crossâ€Polarization and Carbonylâ€Detection NMR Spectroscopy. Angewandte Chemie, 2016, 128, 7544-7548.	1.6	6
77	IsoSolve: An Integrative Framework to Improve Isotopic Coverage and Consolidate Isotopic Measurements by Mass Spectrometry and/or Nuclear Magnetic Resonance. Analytical Chemistry, 2021, 93, 9428-9436.	3.2	5
78	The Jo-In protein welding system is a relevant tool to create CBM-containing plant cell wall degrading enzymes. New Biotechnology, 2021, 65, 31-41.	2.4	5
79	Dissociation Kinetics of a Binary Complex in Solution by Protein Displacement. Angewandte Chemie - International Edition, 2013, 52, 12587-12591.	7.2	4
80	Interaction study between HCV NS5A-D2 and NS5B using 19F NMR. Journal of Biomolecular NMR, 2018, 70, 67-76.	1.6	4
81	3â€•O â€Sulfation of Heparan Sulfate Enhances Tau Interaction and Cellular Uptake. Angewandte Chemie, 2020, 132, 1834-1843.	1.6	2
82	Increasing field strength versus advanced isotope labeling for NMRâ€based fluxomics. Magnetic Resonance in Chemistry, 2020, 58, 305-311.	1.1	1
83	Virtual decoupling to break the simplification versus resolution trade-off in nuclear magnetic resonance of complex metabolic mixtures. Magnetic Resonance, 2021, 2, 619-627.	0.8	1
84	Frontispiz: 3â€Oâ€Sulfation of Heparan Sulfate Enhances Tau Interaction and Cellular Uptake. Angewandte Chemie, 2020, 132, .	1.6	0
85	Frontispiece: 3â€Oâ€Sulfation of Heparan Sulfate Enhances Tau Interaction and Cellular Uptake. Angewandte Chemie - International Edition, 2020, 59, .	7.2	0
86	The covalent complex of Jo-In results from a long-lived, non-covalent intermediate state with near-native structure. Biochemical and Biophysical Research Communications, 2022, 589, 223-228.	1.0	0