Mehdi Mobli

List of Publications by Year
in descending order

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114	4,954	66343	110387
papers	citations	42 h-index	64 g-index

133	133	133	5936
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The transmembrane adapter SCIMP recruits tyrosine kinase Syk to phosphorylate Toll-like receptors to mediate selective inflammatory outputs. Journal of Biological Chemistry, 2022, 298, 101857.	3.4	5
2	Methyl probes in proteins for determining ligand binding mode in weak proteinâ€“ligand complexes. Scientific Reports, 2022, 12, .	3.3	3
3	Structural basis for the binding of the cancer targeting scorpion toxin, ClTx, to the vascular endothelia growth factor receptor neuropilin-1. Current Research in Structural Biology, 2021, 3, 179-186.	2.2	3
4	NUScon: a community-driven platform for quantitative evaluation of nonuniform sampling in NMR. Magnetic Resonance, 2021, 2, 843-861.	1.9	7
5	Recombinant production, bioconjugation and membrane binding studies of Pn3a, a selective NaV1.7 inhibitor. Biochemical Pharmacology, 2020, 181, 114148.	4.4	7
6	Structural venomics reveals evolution of a complex venom by duplication and diversification of an ancient peptide-encoding gene. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 11399-11408.	7.1	59
7	An amphipathic peptide with antibiotic activity against multidrug-resistant Gram-negative bacteria. Nature Communications, 2020, 11, 3184.	12.8	105
8	Mapping the Molecular Surface of the Analgesic NaV1.7-Selective Peptide Pn3a Reveals Residues Essential for Membrane and Channel Interactions. ACS Pharmacology and Translational Science, 2020, 3, 535-546.	4.9	16
9	Multi-species transcriptomics reveals evolutionary diversity in the mechanisms regulating shrimp tail muscle excitation-contraction coupling. Gene, 2020, 752, 144765.	2.2	4
10	Structural and functional characterisation of a novel peptide from the Australian sea anemone Actinia tenebrosa. Toxicon, 2019, 168, 104-112.	1.6	11
11	Framework for and evaluation of bursts in random sampling of multidimensional NMR experiments. Journal of Magnetic Resonance, 2019, 300, 103-113.	2.1	10
12	Elucidating the Lipid Binding Properties of Membrane-Active Peptides Using Cyclised Nanodiscs. Frontiers in Chemistry, 2019, 7, 238.	3.6	19
13	A new vector coupling ligation-independent cloning with sortase a fusion for efficient cloning and one-step purification of tag-free recombinant proteins. Protein Expression and Purification, 2019, 161, 1-7.	1.3	3
14	Bacillus anthracis Protective Antigen Shows High Specificity for a UV Induced Mouse Model of Cutaneous Squamous Cell Carcinoma. Frontiers in Medicine, 2019, 6, 22.	2.6	1
15	Optimizing the transformation of HYSCORE data using the maximum entropy algorithm. Journal of Magnetic Resonance, 2019, 301, 30-39.	2.1	2
16	Classification of the human phox homology (PX) domains based on their phosphoinositide binding specificities. Nature Communications, 2019, 10, 1528.	12.8	101
17	Enabling adoption of 2D-NMR for the higher order structure assessment of monoclonal antibody therapeutics. MAbs, 2019, 11, 94-105.	5.2	67
18	Video with Impact: Access to the Worldâ€™s Magnetic-Resonance Experts for the Scientific-Education Community. Journal of Chemical Education, 2019, 96, 159-164.	2.3	6

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19	Residual Dipolar Couplings for Resolving Cysteine Bridges in Disulfide-Rich Peptides. Frontiers in Chemistry, 2019, 7, 889.	3.6	9
20	A complicated complex: Ion channels, voltage sensing, cell membranes and peptide inhibitors. Neuroscience Letters, 2018, 679, 35-47.	2.1	27
21	Structural insights into the mechanism of inhibition of AHAS by herbicides. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1945-E1954.	7.1	44
22	Secreted Cysteine-Rich Repeat Proteins â€œSCREPsâ€• A Novel Multi-Domain Architecture. Frontiers in Pharmacology, 2018, 9, 1333.	3.5	15
23	Efficient biosynthesis of heterodimeric C3-aryl pyrroloindoline alkaloids. Nature Communications, 2018, 9, 4428.	12.8	53
24	Evaluation of Chemical Strategies for Improving the Stability and Oral Toxicity of Insecticidal Peptides. Biomedicines, 2018, 6, 90.	3.2	7
25	Selective Na ‹sub›V‹/sub› 1.1 activation rescues Dravet syndrome mice from seizures and premature death. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8077-E8085.	7.1	105
26	Nonuniform Sampling in Biomolecular NMR. , 2018, , 2035-2054.		3
27	A non-uniform sampling approach enables studies of dilute and unstable proteins. Journal of Biomolecular NMR, 2017, 68, 119-127.	2.8	11
28	Synthesis of Multivalent [Lys8]-Oxytocin Dendrimers that Inhibit Visceral Nociceptive Responses. Australian Journal of Chemistry, 2017, 70, 162.	0.9	9
29	The tarantula toxin Î²/Î´-TRTX-Pre1a highlights the importance of the S1-S2 voltage-sensor region for sodium channel subtype selectivity. Scientific Reports, 2017, 7, 974.	3.3	16
30	Two proteins for the price of one: Structural studies of the dual-destiny protein preproalbumin with sunflower trypsin inhibitor-1. Journal of Biological Chemistry, 2017, 292, 12398-12411.	3.4	12
31	Potent neuroprotection after stroke afforded by a double-knot spider-venom peptide that inhibits acid-sensing ion channel 1a. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3750-3755.	7.1	180
32	NaV1.7 as a pain target â€“ From gene to pharmacology. , 2017, 172, 73-100.		104
33	Modulation of Ion Channels by Cysteine-Rich Peptides. Advances in Pharmacology, 2017, 79, 199-223.	2.0	22
34	Solution structure of the TLR adaptor MAL/TIRAP reveals an intact BB loop and supports MAL Cys91 glutathionylation for signaling. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6480-E6489.	7.1	33
35	Structural basis of TIR-domain-assembly formation in MAL- and MyD88-dependent TLR4 signaling. Nature Structural and Molecular Biology, 2017, 24, 743-751.	8.2	140
36	The structure, dynamics and selectivity profile of a NaV1.7 potency-optimised huwentoxin-IV variant. PLoS ONE, 2017, 12, e0173551.	2.5	33

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37	Nonuniform Sampling in Biomolecular NMR. , 2017, , 1-21.		2
38	Inhibition of the norepinephrine transporter by Ï‡â€conotoxin dendrimers. Journal of Peptide Science, 2016, 22, 280-289.	1.4	8
39	Correction: Sparse sampling methods in multidimensional NMR. Physical Chemistry Chemical Physics, 2016, 18, 19482-19482.	2.8	0
40	Toxin structures as evolutionary tools: Using conserved 3D folds to study the evolution of rapidly evolving peptides. BioEssays, 2016, 38, 539-548.	2.5	76
41	Rational Design and Synthesis of a Novel Membrane Binding NaV1.8 Selective Inhibitor with in vivo Activity in Pain Models. Biophysical Journal, 2016, 110, 33a.	0.5	0
42	Determination of ligand binding modes in weak proteinâ€“ligand complexes using sparse NMR data. Journal of Biomolecular NMR, 2016, 66, 195-208.	2.8	19
43	Molecular basis of the interaction between gating modifier spider toxins and the voltage sensor of voltage-gated ion channels. Scientific Reports, 2016, 6, 34333.	3.3	44
44	The CC domain structure from the wheat stem rust resistance protein Sr33 challenges paradigms for dimerization in plant NLR proteins. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12856-12861.	7.1	105
45	Development of a Î¼O-Conotoxin Analogue with Improved Lipid Membrane Interactions and Potency for the Analgesic Sodium Channel NaV1.8. Journal of Biological Chemistry, 2016, 291, 11829-11842.	3.4	37
46	Molecular dynamics and functional studies define a hot spot of crystal contacts essential for PcTx1 inhibition of acidâ€sensing ion channel 1a. British Journal of Pharmacology, 2015, 172, 4985-4995.	5.4	35
47	Intradomain Confinement of Disulfides in the Folding of Two Consecutive Modules of the LDL Receptor. PLoS ONE, 2015, 10, e0132141.	2.5	3
48	Reducing seed dependent variability of non-uniformly sampled multidimensional NMR data. Journal of Magnetic Resonance, 2015, 256, 60-69.	2.1	26
49	Backbone and side chain NMR assignments of Geobacillus stearothermophilus ZapA allow identification of residues that mediate the interaction of ZapA with FtsZ. Biomolecular NMR Assignments, 2015, 9, 387-391.	0.8	1
50	Weaponization of a Hormone: Convergent Recruitment of Hyperglycemic Hormone into the Venom of Arthropod Predators. Structure, 2015, 23, 1283-1292.	3.3	66
51	RNA polymerase-induced remodelling of NusA produces a pause enhancement complex. Nucleic Acids Research, 2015, 43, 2829-2840.	14.5	31
52	Rational Engineering Defines a Molecular Switch That Is Essential for Activity of Spider-Venom Peptides against the Analgesics Target Na_V1.7. Molecular Pharmacology, 2015, 88, 1002-1010.	2.3	32
53	CHAPTER 2. The Structural Universe of Disulfide-Rich Venom Peptides. RSC Drug Discovery Series, 2015, , 37-79.	0.3	13
54	The insecticidal spider toxin <scp>SFI</scp>1 is a knottin peptide that blocks the pore of insect voltageâ€gated sodium channels via a large Î²â€hairpin loop. FEBS Journal, 2015, 282, 904-920.	4.7	34

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55	Seven novel modulators of the analgesic target <scp>Na_V</scp>1.7 uncovered using a highâ€throughput venomâ€based discovery approach. British Journal of Pharmacology, 2015, 172, 2445-2458.	5.4	74
56	Î±-Conotoxin Dendrimers Have Enhanced Potency and Selectivity for Homomeric Nicotinic Acetylcholine Receptors. Journal of the American Chemical Society, 2015, 137, 3209-3212.	13.7	32
57	Solution structure of the RNA-binding cold-shock domain of the Chlamydomonas reinhardtii NAB1 protein and insights into RNA recognition. Biochemical Journal, 2015, 469, 97-106.	3.7	4
58	Solution Structure, Membrane Interactions, and Protein Binding Partners of the Tetraspanin Sm-TSP-2, a Vaccine Antigen from the Human Blood Fluke Schistosoma mansoni. Journal of Biological Chemistry, 2014, 289, 7151-7163.	3.4	33
59	Measuring Interactions of FERM Domain-Containing Sorting Nexin Proteins with Endosomal Lipids and Cargo Molecules. Methods in Enzymology, 2014, 534, 331-349.	1.0	12
60	Selenoether oxytocin analogues have analgesic properties in a mouse model of chronic abdominal pain. Nature Communications, 2014, 5, 3165.	12.8	122
61	Total Synthesis of Human Hepcidin through Regioselective Disulfideâ€Bond Formation by using the Safetyâ€Catch Cysteine Protecting Group 4,4â€²â€Dimethylsulfinylbenzhydryl. Angewandte Chemie - International Edition, 2014, 53, 2931-2934.	13.8	46
62	Chemical Synthesis, 3D Structure, and ASIC Binding Site of the Toxin Mambalginâ€2. Angewandte Chemie - International Edition, 2014, 53, 1017-1020.	13.8	66
63	Functional implications of large backbone amplitude motions of the glycoprotein 130â€binding epitope of interleukinâ€6. FEBS Journal, 2014, 281, 2471-2483.	4.7	7
64	Understanding the Molecular Basis of Toxin Promiscuity: The Analgesic Sea Anemone Peptide APETx2 Interacts with Acid-Sensing Ion Channel 3 and hERG Channels via Overlapping Pharmacophores. Journal of Medicinal Chemistry, 2014, 57, 9195-9203.	6.4	40
65	Nonuniform sampling and non-Fourier signal processing methods in multidimensional NMR. Progress in Nuclear Magnetic Resonance Spectroscopy, 2014, 83, 21-41.	7.5	197
66	Non-uniform sampling in EPR â€“ optimizing data acquisition for HYSCORE spectroscopy. Physical Chemistry Chemical Physics, 2014, 16, 16378-16382.	2.8	8
67	A Tarantula-Venom Peptide Antagonizes the TRPA1 Nociceptor Ion Channel by Binding to the S1â€“S4 Gating Domain. Current Biology, 2014, 24, 473-483.	3.9	56
68	A distinct sodium channel voltage-sensor locus determines insect selectivity of the spider toxin Dc1a. Nature Communications, 2014, 5, 4350.	12.8	63
69	Isolation, synthesis and characterization of Ï‰-TRTX-Cc1a, a novel tarantula venom peptide that selectively targets L-type CaV channels. Biochemical Pharmacology, 2014, 89, 276-286.	4.4	19
70	Nonuniform Sampling and Maximum Entropy Reconstruction in Multidimensional NMR. Accounts of Chemical Research, 2014, 47, 708-717.	15.6	115
71	Molecular Insights into the Interaction between Plasmodium falciparum Apical Membrane Antigen 1 and an Invasion-Inhibitory Peptide. PLoS ONE, 2014, 9, e109674.	2.5	10
72	Vicinal Disulfide Constrained Cyclic Peptidomimetics: a Turn Mimetic Scaffold Targeting the Norepinephrine Transporter. Angewandte Chemie - International Edition, 2013, 52, 12020-12023.	13.8	32

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73	The insecticidal neurotoxin Aps III is an atypical knottin peptide that potently blocks insect voltage-gated sodium channels. Biochemical Pharmacology, 2013, 85, 1542-1554.	4.4	33
74	Do Vicinal Disulfide Bridges Mediate Functionally Important Redox Transformations in Proteins?. Antioxidants and Redox Signaling, 2013, 19, 1976-1980.	5.4	16
75	Vicinal Disulfide Constrained Cyclic Peptidomimetics: a Turn Mimetic Scaffold Targeting the Norepinephrine Transporter. Angewandte Chemie, 2013, 125, 12242-12245.	2.0	9
76	Production of Recombinant Disulfide-Rich Venom Peptides for Structural and Functional Analysis via Expression in the Periplasm of E. coli. PLoS ONE, 2013, 8, e63865.	2.5	140
77	Solution Structure and Peptide Binding of the PTB Domain from the AIDA1 Postsynaptic Signaling Scaffolding Protein. PLoS ONE, 2013, 8, e65605.	2.5	8
78	Isolation of an Orally Active Insecticidal Toxin from the Venom of an Australian Tarantula. PLoS ONE, 2013, 8, e73136.	2.5	55
79	Insulin-like growth factor binding protein-2: NMR analysis and structural characterization of the N-terminal domain. Biochimie, 2012, 94, 608-616.	2.6	15
80	Cyclization of Peptides by using Selenolanthionine Bridges. Angewandte Chemie - International Edition, 2012, 51, 10298-10302.	13.8	51
81	Cyclisation Increases the Stability of the Sea Anemone Peptide APETx2 but Decreases Its Activity at Acid-Sensing Ion Channel 3. Marine Drugs, 2012, 10, 1511-1527.	4.6	19
82	Functional Expression in Escherichia coli of the Disulfide-Rich Sea Anemone Peptide APETx2, a Potent Blocker of Acid-Sensing Ion Channel 3. Marine Drugs, 2012, 10, 1605-1618.	4.6	41
83	Sparse sampling methods in multidimensional NMR. Physical Chemistry Chemical Physics, 2012, 14, 10835-10843.	2.8	77
84	Data Sampling in Multidimensional NMR: Fundamentals and Strategies. Topics in Current Chemistry, 2011, 316, 49-77.	4.0	41
85	A Dynamic Pharmacophore Drives the Interaction between Psalmotoxin-1 and the Putative Drug Target Acid-Sensing Ion Channel 1a. Molecular Pharmacology, 2011, 80, 796-808.	2.3	85
86	The Nâ€“Terminal Tail of hERG Contains an Amphipathic Î±â€“Helix That Regulates Channel Deactivation. PLoS ONE, 2011, 6, e16191.	2.5	79
87	Macromolecular NMR spectroscopy for the nonâ€spectroscopist. FEBS Journal, 2011, 278, 687-703.	4.7	140
88	Macromolecular NMR spectroscopy for the nonâ€spectroscopist: beyond macromolecular solution structure determination. FEBS Journal, 2011, 278, 704-715.	4.7	53
89	Venomics: a new paradigm for natural products-based drug discovery. Amino Acids, 2011, 40, 15-28.	2.7	172
90	Siteâ€Specific pK_a Determination of Selenocysteine Residues in Selenovasopressin by Using ⁷⁷Se NMR Spectroscopy. Angewandte Chemie - International Edition, 2011, 50, 11952-11955.	13.8	44

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91	Phox homology band 4.1/ezrin/radixin/moesin-like proteins function as molecular scaffolds that interact with cargo receptors and Ras GTPases. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7763-7768.	7.1	99
92	Chemical Synthesis and Structure of the Prokineticin Bv8. ChemBioChem, 2010, 11, 1882-1888.	2.6	22
93	A non-uniformly sampled 4D HCC(CO)NH-TOCSY experiment processed using maximum entropy for rapid protein sidechain assignment. Journal of Magnetic Resonance, 2010, 204, 160-164.	2.1	57
94	NMR methods for determining disulfide-bond connectivities. Toxicon, 2010, 56, 849-854.	1.6	56
95	Derivation of Peptide and Protein Structure using NMR Spectroscopy. , 2010, , 279-325.		6
96	Derivation of Peptide and Protein Structure using NMR Spectroscopy. , 2010, , 14-49.		0
97	Direct Visualization of Disulfide Bonds through Diselenide Proxies Using ⁷⁷Se NMR Spectroscopy. Angewandte Chemie - International Edition, 2009, 48, 9312-9314.	13.8	63
98	Nonuniform sampling and spectral aliasing. Journal of Magnetic Resonance, 2009, 199, 88-93.	2.1	76
99	Effective Protocol for Database Similarity Searching of Heteronuclear Single Quantum Coherence Spectra. Analytical Chemistry, 2009, 81, 9329-9335.	6.5	8
100	A Nuclear Localization Signal at the SAMâ€“SAM Domain Interface of AIDA-1 Suggests a Requirement for Domain Uncoupling Prior to Nuclear Import. Journal of Molecular Biology, 2009, 392, 1168-1177.	4.2	26
101	The structural plasticity of heparan sulfate NA-domains and hence their role in mediating multivalent interactions is confirmed by high-accuracy 15N-NMR relaxation studies. Glycoconjugate Journal, 2008, 25, 401-414.	2.7	40
102	Maximum entropy spectral reconstruction of nonuniformly sampled data. Concepts in Magnetic Resonance Part A: Bridging Education and Research, 2008, 32A, 436-448.	0.5	65
103	N-Acetylated amino sugars: the dependence of NMR 3J(HNH2)-couplings on conformation, dynamics and solvent. Organic and Biomolecular Chemistry, 2007, 5, 2243.	2.8	49
104	An NMR, IR and theoretical investigation of ¹H Chemical Shifts and hydrogen bonding in phenols. Magnetic Resonance in Chemistry, 2007, 45, 865-877.	1.9	78
105	An automated tool for maximum entropy reconstruction of biomolecular NMR spectra. Nature Methods, 2007, 4, 467-468.	19.0	64
106	Automatic maximum entropy spectral reconstruction in NMR. Journal of Biomolecular NMR, 2007, 39, 133-139.	2.8	59
107	Three-Dimensional13C-Detected CH3-TOCSY Using Selectively Protonated Proteins:Â Facile Methyl Resonance Assignment and Protein Structure Determination. Journal of the American Chemical Society, 2006, 128, 9119-9128.	13.7	23
108	Conformational analysis, Part 41. A modelling and LIS/NMR investigation of the conformations ofÎ±,Î²-unsaturated carbonyl compounds. Journal of Physical Organic Chemistry, 2006, 19, 384-392.	1.9	16

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109	Spectral reconstruction methods in fast NMR: Reduced dimensionality, random sampling and maximum entropy. Journal of Magnetic Resonance, 2006, 182, 96-105.	2.1	92
110	Quantum vs. classical models of the nitro group for proton chemical shift calculations and conformational analysis. Journal of Computational Chemistry, 2005, 26, 389-398.	3.3	2
111	1H chemical shifts in NMR. Part 21?Prediction of the1H chemical shifts of molecules containing the ester group: a modelling andab initio investigation. Magnetic Resonance in Chemistry, 2005, 43, 3-15.	1.9	19
112	1H chemical shifts in NMR. Part 20â€" Anisotropic and steric effects in halogen substituent chemical shifts(SCS), a modelling andab initio investigation. Magnetic Resonance in Chemistry, 2004, 42, 436-444.	1.9	14
113	1H chemical shifts in NMR: Part 19. Carbonyl anisotropies and steric effects in aromatic aldehydes and ketones. Magnetic Resonance in Chemistry, 2003, 41, 26-36.	1.9	81
114	Chapter 9. Maximum Entropy Reconstruction. New Developments in NMR, 0, , 252-266.	0.1	2