Benjamin Bardiaux

List of Publications by Year
in descending order

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59

papers

3,331

citations

230014

27

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53

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68

all docs

68

docs citations

68

times ranked

4431

citing authors

#	Article	IF	Citations
1	Characterization of the Interaction Domains between the Phosphoprotein and the Nucleoprotein of Human Metapneumovirus. Journal of Virology, 2022, 96, JVI0090921.	1.5	4
2	Structural and molecular basis of cross-seeding barriers in amyloids. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	34
3	Exploring Exhaustively the Conformations of a Tandem Domains Protein using a Discrete Distance Geometry Approach. Biophysical Journal, 2021, 120, 277a.	0.2	0
4	Host-Pathogen Adhesion as the Basis of Innovative Diagnostics for Emerging Pathogens. Diagnostics, 2021, 11, 1259.	1.3	5
5	Structures of Pathological and Functional Amyloids and Prions, a Solid-State NMR Perspective. Frontiers in Molecular Neuroscience, 2021, 14, 670513.	1.4	18
6	A Structural and Dynamic Analysis of the Partially Disordered Polymerase-Binding Domain in RSV Phosphoprotein. Biomolecules, 2021, 11, 1225.	1.8	6
7	1H, 15ÂN and 13C resonance assignments of the C-terminal domain of PulL, a component of the Klebsiella oxytoca type II secretion system. Biomolecular NMR Assignments, 2021, 15, 455-459.	0.4	2
8	Computational and biochemical analysis of type IV pilus dynamics and stability. Structure, 2021, 29, 1397-1409.e6.	1.6	5
9	Quantitative Structural Interpretation of Protein Crosslinks. Structure, 2020, 28, 75-82.e4.	1.6	5
10	Structure and function of minor pilins of type IV pili. Medical Microbiology and Immunology, 2020, 209, 301-308.	2.6	40
11	ARIAweb: a server for automated NMR structure calculation. Nucleic Acids Research, 2020, 48, W41-W47.	6.5	14
12	AÎ²(1-42) tetramer and octamer structures reveal edge conductivity pores as a mechanism for membrane damage. Nature Communications, 2020, 11, 3014.	5.8	162
13	Dynamics of a type 2 secretion system pseudopilus unraveled by complementary approaches. Journal of Biomolecular NMR, 2019, 73, 293-303.	1.6	9
14	Structure and Assembly of the Enterohemorrhagic Escherichia coli Type 4 Pilus. Structure, 2019, 27, 1082-1093.e5.	1.6	33
15	Single-site phosphorylation within the His-tag sequence attached to a recombinant protein. Analytical Biochemistry, 2019, 570, 62-64.	1.1	0
16	Minimal NMR distance information for rigidity of protein graphs. Discrete Applied Mathematics, 2019, 256, 91-104.	0.5	26
17	3D structure determination of amyloid fibrils using solid-state NMR spectroscopy. Methods, 2018, 138-139, 26-38.	1.9	60
18	Sequence-specific DNA binding activity of the cross-brace zinc finger motif of the piggyBac transposase. Nucleic Acids Research, 2018, 46, 2660-2677.	6.5	22

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19	Ordering Protein Contact Matrices. Computational and Structural Biotechnology Journal, 2018, 16, 140-156.	1.9	0
20	Tuning interval Branch-and-Prune for protein structure determination. Journal of Global Optimization, 2018, 72, 109-127.	1.1	19
21	Integrative Structural Biology of the Calcium Dependent Type 2 Secretion Pseudopilus. Biophysical Journal, 2018, 114, 229a.	0.2	0
22	Automatic Building of Protein Atomic Models from Cryo-EM Maps. Biophysical Journal, 2018, 114, 190a-191a.	0.2	2
23	Structure and dynamics of Helicobacter pylori nickel-chaperone HypA: an integrated approach using NMR spectroscopy, functional assays and computational tools. Journal of Biological Inorganic Chemistry, 2018, 23, 1309-1330.	1.1	20
24	Biogenesis and structure of a type VI secretion baseplate. Nature Microbiology, 2018, 3, 1404-1416.	5.9	76
25	The protofilament architecture of a de novo designed coiled coil-based amyloidogenic peptide. Journal of Structural Biology, 2018, 203, 263-272.	1.3	6
26	Integrative Structural Biology of a Type II Secretion Pseudopilus. Biophysical Journal, 2017, 112, 486a.	0.2	0
27	The Interval Branch-And-Prune Algorithm for the Protein Structure Determination. Biophysical Journal, 2017, 112, 56a.	0.2	0
28	Structural Characterization of Whirlin Reveals an Unexpected and Dynamic Supramodule Conformation of Its PDZ Tandem. Structure, 2017, 25, 1645-1656.e5.	1.6	22
29	Structure of the calcium-dependent type 2 secretion pseudopilus. Nature Microbiology, 2017, 2, 1686-1695.	5.9	68
30	Structure of outer membrane protein G in lipid bilayers. Nature Communications, 2017, 8, 2073.	5.8	91
31	Structure determination of helical filaments by solid-state NMR spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E272-81.	3.3	25
32	Solidâ€state NMR Study of the YadA Membraneâ€Anchor Domain in the Bacterial Outer Membrane. Angewandte Chemie - International Edition, 2015, 54, 12602-12606.	7.2	22
33	NMR Exchange Format: a unified and open standard for representation of NMR restraint data. Nature Structural and Molecular Biology, 2015, 22, 433-434.	3.6	40
34	Biogenesis and structure of a type VI secretion membrane core complex. Nature, 2015, 523, 555-560.	13.7	241
35	Improved reliability, accuracy and quality in automated NMR structure calculation with ARIA. Journal of Biomolecular NMR, 2015, 62, 425-438.	1.6	34
36	An algorithm to enumerate all possible protein conformations verifying a set of distance constraints. BMC Bioinformatics, 2015, 16, 23.	1.2	42

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37	The chaperone Î±B-crystallin uses different interfaces to capture an amorphous and an amyloid client. Nature Structural and Molecular Biology, 2015, 22, 898-905.	3.6	130
38	Neisseria meningitidis Type IV Pili Composed of Sequence Invariable Pilins Are Masked by Multisite Glycosylation. PLoS Pathogens, 2015, 11, e1005162.	2.1	55
39	Solid-State NMR Structure Determination from Diagonal-Compensated, Sparsely Nonuniform-Sampled 4D Protonâ€"Proton Restraints. Journal of the American Chemical Society, 2014, 136, 11002-11010.	6.6	61
40	The Mechanism of Denaturation and the Unfolded State of the Î±-Helical Membrane-Associated Protein Mistic. Journal of the American Chemical Society, 2013, 135, 18884-18891.	6.6	16
41	Structural and Mechanistic Implications of Metal Binding in the Small Heat-shock Protein Î±B-crystallin. Journal of Biological Chemistry, 2012, 287, 1128-1138.	1.6	67
42	Membrane-protein structure determination by solid-state NMR spectroscopy of microcrystals. Nature Methods, 2012, 9, 1212-1217.	9.0	140
43	Efficient Modeling of Symmetric Protein Aggregates from NMR Data. Angewandte Chemie - International Edition, 2012, 51, 6916-6919.	7.2	7
44	ARIA for Solution and Solid-State NMR. Methods in Molecular Biology, 2012, 831, 453-483.	0.4	54
45	Structure Calculation from Unambiguous Long-Range Amide and Methyl ¹Hâ^'¹H Distance Restraints for a Microcrystalline Protein with MAS Solid-State NMR Spectroscopy. Journal of the American Chemical Society, 2011, 133, 5905-5912.	6.6	152
46	A software framework for analysing solid-state MAS NMR data. Journal of Biomolecular NMR, 2011, 51, 437-447.	1.6	138
47	Bayesian estimation of NMR restraint potential and weight: A validation on a representative set of protein structures. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1525-1537.	1.5	23
48	N-terminal domain of Î±B-crystallin provides a conformational switch for multimerization and structural heterogeneity. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6409-6414.	3.3	185
49	Solid-state NMR and SAXS studies provide a structural basis for the activation of Î±B-crystallin oligomers. Nature Structural and Molecular Biology, 2010, 17, 1037-1042.	3.6	263
50	Simultaneous use of solution, solid-state NMR and X-ray crystallography to study the conformational landscape of the Crh protein during oligomerization and crystallization. Advances and Applications in Bioinformatics and Chemistry, 2010, 3, 25.	1.6	0
51	Structural Insights into Serine-rich Fimbriae from Gram-positive Bacteria. Journal of Biological Chemistry, 2010, 285, 32446-32457.	1.6	48
52	Influence of different assignment conditions on the determination of symmetric homodimeric structures with ARIA. Proteins: Structure, Function and Bioinformatics, 2009, 75, 569-585.	1.5	33
53	CASD-NMR: critical assessment of automated structure determination by NMR. Nature Methods, 2009, 6, 625-626.	9.0	80
54	Graphical analysis of NMR structural quality and interactive contact map of NOE assignments in ARIA. BMC Structural Biology, 2008, 8, 30.	2.3	5

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55	Accurate NMR Structures Through Minimization of an Extended Hybrid Energy. Structure, 2008, 16, 1305-1312.	1.6	58
56	3D Structure Determination of the Crh Protein from Highly Ambiguous Solid-State NMR Restraints. Journal of the American Chemical Society, 2008, 130, 3579-3589.	6.6	135
57	ARIA2: Automated NOE assignment and data integration in NMR structure calculation. Bioinformatics, 2007, 23, 381-382.	1.8	506
58	Comparison of Different Torsion Angle Approaches for NMR Structure Determination. Journal of Biomolecular NMR, 2006, 34, 153-166.	1.6	7
59	Data mining techniques to study the disulfide-bonding state in proteins: signal peptide is a strong descriptor. Bioinformatics, 2004, 20, 2509-2512.	1.8	7