Jurgen F Doreleijers

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/12143712/publications.pdf

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21 papers 2,941 citations

16 h-index 752698 20 g-index

21 all docs

21 docs citations

times ranked

21

4858 citing authors

#	Article	IF	Citations
1	An overview of tools for the validation of protein NMR structures. Journal of Biomolecular NMR, 2014, 58, 259-285.	2.8	34
2	NRG-CING: integrated validation reports of remediated experimental biomolecular NMR data and coordinates in wwPDB. Nucleic Acids Research, 2012, 40, D519-D524.	14.5	34
3	WeNMR: Structural Biology on the Grid. Journal of Grid Computing, 2012, 10, 743-767.	3.9	170
4	CING: an integrated residue-based structure validation program suite. Journal of Biomolecular NMR, 2012, 54, 267-283.	2.8	106
5	Blind Testing of Routine, Fully Automated Determination of Protein Structures from NMR Data. Structure, 2012, 20, 227-236.	3.3	75
6	Overview on the Use of NMR to Examine Protein Structure. Current Protocols in Protein Science, 2011, 64, Unit17.5.	2.8	9
7	The NMR restraints grid at BMRB for 5,266 protein and nucleic acid PDB entries. Journal of Biomolecular NMR, 2009, 45, 389-396.	2.8	26
8	CASD-NMR: critical assessment of automated structure determination by NMR. Nature Methods, 2009, 6, 625-626.	19.0	80
9	Remediation of the protein data bank archive. Nucleic Acids Research, 2007, 36, D426-D433.	14.5	136
10	BioMagResBank. Nucleic Acids Research, 2007, 36, D402-D408.	14.5	1,450
11	BioMagResBank databases DOCR and FRED containing converted and filtered sets of experimental NMR restraints and coordinates from over 500 protein PDB structures. Journal of Biomolecular NMR, 2005, 32, 1-12.	2.8	50
12	RECOORD: A recalculated coordinate database of 500+ proteins from the PDB using restraints from the BioMagResBank. Proteins: Structure, Function and Bioinformatics, 2005, 59, 662-672.	2.6	323
13	Solution structure of T4moC, the Rieske ferredoxin component of the toluene 4-monooxygenase complex. Journal of Biological Inorganic Chemistry, 2004, 9, 945-953.	2.6	11
14	DRESS: a database of REfined solution NMR structures. Proteins: Structure, Function and Bioinformatics, 2004, 55, 483-486.	2.6	91
15	BioMagResBank database with sets of experimental NMR constraints corresponding to the structures of over 1400 biomolecules deposited in the Protein Data Bank. Journal of Biomolecular NMR, 2003, 26, 139-146.	2.8	84
16	Joint refinement as a tool for thorough comparison between NMR and X-ray data and structures of HU protein. Journal of Biomolecular NMR, 2001, 21, 235-248.	2.8	16
17	Structure and mechanism of formation of the H-y5 isomer of an intramolecular DNA triple helix. Nature Structural Biology, 1999, 6, 854-859.	9.7	15
18	Completeness of NOEs in protein structure: a statistical analysis of NMR. Journal of Biomolecular NMR, 1999, 14, 123-132.	2.8	66

#	Article	IF	CITATIONS
19	Validation of nuclear magnetic resonance structures of proteins and nucleic acids: Hydrogen geometry and nomenclature., 1999, 37, 404-416.		21
20	Quality assessment of NMR structures: a statistical survey. Journal of Molecular Biology, 1998, 281, 149-164.	4.2	106
21	Solution Structure of the Immunodominant Region of Protein G of Bovine Respiratory Syncytial Virusâ€,‡. Biochemistry, 1996, 35, 14684-14688.	2.5	38