

Swapna Gurla

List of Publications by Year in descending order

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16
papers

249
citations

1040056

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15
g-index

19
all docs

19
docs citations

19
times ranked

387
citing authors

#	ARTICLE	IF	CITATIONS
1	Automated protein fold determination using a minimal NMR constraint strategy. <i>Protein Science</i> , 2003, 12, 1232-1246.	7.6	53
2	19F NMR Reveals Multiple Conformations at the Dimer Interface of the Nonstructural Protein 1 Effector Domain from Influenza A Virus. <i>Structure</i> , 2014, 22, 515-525.	3.3	41
3	Assessment of prediction methods for protein structures determined by ¹ H NMR in CASP14: Impact of AlphaFold2. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1959-1976.	2.6	30
4	Protein structure prediction assisted with sparse NMR data in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1315-1332.	2.6	21
5	Antiparallel Coiled-Coil Interactions Mediate the Homodimerization of the DNA Damage-Repair Protein PALB2. <i>Biochemistry</i> , 2018, 57, 6581-6591.	2.5	17
6	Application of multiple-quantum line narrowing with simultaneous ¹ H and ¹³ C constant-time scalar-coupling evolution in PFG-HACANH and PFG-HACA(CO)NH triple-resonance experiments. <i>Journal of Biomolecular NMR</i> , 1997, 9, 105-111.	2.8	16
7	Semi-automated backbone resonance assignments of the extracellular ligand-binding domain of an ionotropic glutamate receptor. <i>Journal of Biomolecular NMR</i> , 2002, 22, 297-298.	2.8	13
8	Solution NMR evidence for a cis Tyr-Ala peptide group in the structure of [Pro93Ala] bovine pancreatic ribonuclease A. <i>Protein Science</i> , 2000, 9, 421-426.	7.6	10
9	¹³ C metabolic flux profiling of <i>Pichia pastoris</i> grown in aerobic batch cultures on glucose revealed high relative anabolic use of TCA cycle and limited incorporation of provided precursors of branched-chain amino acids. <i>FEBS Journal</i> , 2017, 284, 3100-3113.	4.7	10
10	Combining Evolutionary Covariance and NMR Data for Protein Structure Determination. <i>Methods in Enzymology</i> , 2019, 614, 363-392.	1.0	8
11	Resonance assignments for cold-shock protein ribosome-binding factor A (RbfA) from <i>Escherichia coli</i> . <i>Journal of Biomolecular NMR</i> , 2001, 21, 389-390.	2.8	7
12	Letter to the Editor: Backbone ¹ H, ¹⁵ N and ¹³ C assignments for the 21 kDa <i>Caenorhabditis elegans</i> homologue of 'brain-specific' protein. <i>Journal of Biomolecular NMR</i> , 2004, 28, 91-92.	2.8	7
13	Multiple helical conformations of the helix-turn-helix region revealed by NOE-restrained MD simulations of tryptophan aporepressor, TrpR. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 731-740.	2.6	6
14	Structural evolution of the ancient enzyme, dissimilatory sulfite reductase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1331-1345.	2.6	5
15	Solution NMR structure of <i>Escherichia coli</i> ytfP expands the structural coverage of the UPF0131 protein domain family. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 789-795.	2.6	4
16	Cover Image, Volume 85, Issue 4. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, C1.	2.6	0