

# Swapna Gurla

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2080026/publications.pdf>

Version: 2024-02-01

16  
papers

249  
citations

1040056

9  
h-index

996975

15  
g-index

19  
all docs

19  
docs citations

19  
times ranked

387  
citing authors

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | Structural evolution of the ancient enzyme, dissimilatory sulfite reductase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1331-1345.   | 2.6 | 5         |
| 2  | Assessment of prediction methods for protein structures determined by <i>NMR</i> in <i>CASP14</i> : Impact of <i>AlphaFold2</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1959-1976.  | 2.6 | 30        |
| 3  | Protein structure prediction assisted with sparse NMR data in <i>CASP13</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1315-1332.  | 2.6 | 21        |
| 4  | Combining Evolutionary Covariance and NMR Data for Protein Structure Determination. <i>Methods in Enzymology</i> , 2019, 614, 363-392.  | 1.0 | 8         |
| 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  | 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         |
| 7  | Cover Image, Volume 85, Issue 4. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, C1.  | 2.6 | 0         |
| 8  | <sup>13</sup> C metabolic flux profiling of <i>Pichia pastoris</i> grown in aerobic batch cultures on glucose revealed high relative anabolic use of <i>TCA</i> cycle and limited incorporation of provided precursors of branched-chain amino acids. <i>FEBS Journal</i> , 2017, 284, 3100-3113. | 4.7 | 10        |
| 9  | <sup>19</sup> F 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        |
| 10 | 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         |
| 11 | Letter to the Editor: Backbone <sup>1</sup> H, <sup>15</sup> N and <sup>13</sup> 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         |
| 12 | Automated protein fold determination using a minimal NMR constraint strategy. <i>Protein Science</i> , 2003, 12, 1232-1246.   | 7.6 | 53        |
| 13 | 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        |
| 14 | 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         |
| 15 | Solution NMR evidence for a cis Tyr-Ala peptide group in the structure of [Pro <sup>93</sup> Ala] bovine pancreatic ribonuclease A. <i>Protein Science</i> , 2000, 9, 421-426.  | 7.6 | 10        |
| 16 | Application of multiple-quantum line narrowing with simultaneous <sup>1</sup> H and <sup>13</sup> 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        |