

# Julie D Forman-Kay

## List of Publications by Citations

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|--------------------|--------------------------|---------------|-----------------|
| 171<br>papers      | 17,923<br>citations      | 73<br>h-index | 132<br>g-index  |
| 204<br>ext. papers | 20,551<br>ext. citations | 9<br>avg, IF  | 6.89<br>L-index |

| #   | Paper   | IF   | Citations |
|-----|---|------|-----------|
| 171 | Backbone dynamics of a free and phosphopeptide-complexed Src homology 2 domain studied by $^{15}\text{N}$ NMR relaxation. <i>Biochemistry</i> , <b>1994</b> , 33, 5984-6003   | 3.2  | 1979      |
| 170 | Phase transition of a disordered nuage protein generates environmentally responsive membraneless organelles. <i>Molecular Cell</i> , <b>2015</b> , 57, 936-947  | 17.6 | 952       |
| 169 | Backbone $^1\text{H}$ and $^{15}\text{N}$ resonance assignments of the N-terminal SH3 domain of drk in folded and unfolded states using enhanced-sensitivity pulsed field gradient NMR techniques. <i>Journal of Biomolecular NMR</i> , <b>1994</b> , 4, 845-58             | 3    | 617       |
| 168 | Sensitivity of secondary structure propensities to sequence differences between alpha- and gamma-synuclein: implications for fibrillation. <i>Protein Science</i> , <b>2006</b> , 15, 2795-804  | 6.3  | 547       |
| 167 | Slow dynamics in folded and unfolded states of an SH3 domain. <i>Journal of the American Chemical Society</i> , <b>2001</b> , 123, 11341-52   | 16.4 | 408       |
| 166 | Two-dimensional NMR experiments for correlating carbon-13.beta. and proton.delta./epsilon. chemical shifts of aromatic residues in $^{13}\text{C}$ -labeled proteins via scalar couplings. <i>Journal of the American Chemical Society</i> , <b>1993</b> , 115, 11054-11055 | 16.4 | 399       |
| 165 | A heteronuclear correlation experiment for simultaneous determination of $^{15}\text{N}$ longitudinal decay and chemical exchange rates of systems in slow equilibrium. <i>Journal of Biomolecular NMR</i> , <b>1994</b> , 4, 727-34  | 3.4  | 387       |
| 164 | Atomic-level characterization of disordered protein ensembles. <i>Current Opinion in Structural Biology</i> , <b>2007</b> , 17, 3-14  | 8.1  | 360       |
| 163 | Folding of an intrinsically disordered protein by phosphorylation as a regulatory switch. <i>Nature</i> , <b>2015</b> , 519, 106-9  | 50.4 | 344       |
| 162 | Pi-Pi contacts are an overlooked protein feature relevant to phase separation. <i>ELife</i> , <b>2018</b> , 7,  | 8.9  | 302       |
| 161 | Comparison of the backbone dynamics of a folded and an unfolded SH3 domain existing in equilibrium in aqueous buffer. <i>Biochemistry</i> , <b>1995</b> , 34, 868-78  | 3.2  | 289       |
| 160 | Solution structure and dynamics of the outer membrane enzyme PagP by NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 13560-5  | 11.5 | 282       |
| 159 | Protein dynamics and conformational disorder in molecular recognition. <i>Journal of Molecular Recognition</i> , <b>2010</b> , 23, 105-16   | 2.6  | 277       |
| 158 | Modulation of Intrinsically Disordered Protein Function by Post-translational Modifications. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 6696-705   | 5.4  | 262       |
| 157 | Dynamic equilibrium engagement of a polyvalent ligand with a single-site receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 17772-7  | 11.5 | 257       |
| 156 | Sequence determinants of compaction in intrinsically disordered proteins. <i>Biophysical Journal</i> , <b>2010</b> , 98, 2383-90  | 2.9  | 252       |
| 155 | CFTR regulatory region interacts with NBD1 predominantly via multiple transient helices. <i>Nature Structural and Molecular Biology</i> , <b>2007</b> , 14, 738-45  | 17.6 | 233       |

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|-----|---|------|-----|
| 154 | Structural and hydrodynamic properties of an intrinsically disordered region of a germ cell-specific protein on phase separation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E8194-E8203 | 11.5 | 227 |
| 153 | Correlation between dynamics and high affinity binding in an SH2 domain interaction. <i>Biochemistry</i> , <b>1996</b> , 35, 361-8  | 3.2  | 225 |
| 152 | Structure/function implications in a dynamic complex of the intrinsically disordered Sic1 with the Cdc4 subunit of an SCF ubiquitin ligase. <i>Structure</i> , <b>2010</b> , 18, 494-506  | 5.2  | 208 |
| 151 | Autoinhibition of the HECT-type ubiquitin ligase Smurf2 through its C2 domain. <i>Cell</i> , <b>2007</b> , 130, 651-62  | 56.2 | 206 |
| 150 | Polyelectrostatic interactions of disordered ligands suggest a physical basis for ultrasensitivity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 9650-5                                    | 11.5 | 186 |
| 149 | Calculation of ensembles of structures representing the unfolded state of an SH3 domain. <i>Journal of Molecular Biology</i> , <b>2001</b> , 308, 1011-32   | 6.5  | 184 |
| 148 | Solution structure of a Nedd4 WW domain-ENaC peptide complex. <i>Nature Structural Biology</i> , <b>2001</b> , 8, 407-12  |      | 181 |
| 147 | What's in a name? Why these proteins are intrinsically disordered: Why these proteins are intrinsically disordered. <i>Intrinsically Disordered Proteins</i> , <b>2013</b> , 1, e24157  |      | 171 |
| 146 | Structural characterization of folded and unfolded states of an SH3 domain in equilibrium in aqueous buffer. <i>Biochemistry</i> , <b>1995</b> , 34, 6784-94  | 3.2  | 170 |
| 145 | RGG/RG Motif Regions in RNA Binding and Phase Separation. <i>Journal of Molecular Biology</i> , <b>2018</b> , 430, 4650-4665  | 6.5  | 166 |
| 144 | pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D326-35   | 20.1 | 159 |
| 143 | Distribution of molecular size within an unfolded state ensemble using small-angle X-ray scattering and pulse field gradient NMR techniques. <i>Journal of Molecular Biology</i> , <b>2002</b> , 316, 101-12  | 6.5  | 158 |
| 142 | Sequence-Specific Polyampholyte Phase Separation in Membraneless Organelles. <i>Physical Review Letters</i> , <b>2016</b> , 117, 178101   | 7.4  | 149 |
| 141 | NOE data demonstrating a compact unfolded state for an SH3 domain under non-denaturing conditions. <i>Journal of Molecular Biology</i> , <b>1999</b> , 289, 619-38  | 6.5  | 149 |
| 140 | Characterization of the backbone dynamics of folded and denatured states of an SH3 domain. <i>Biochemistry</i> , <b>1997</b> , 36, 2390-402   | 3.2  | 148 |
| 139 | Global folds of proteins with low densities of NOEs using residual dipolar couplings: application to the 370-residue maltodextrin-binding protein. <i>Journal of Molecular Biology</i> , <b>2000</b> , 300, 197-212                                       | 6.5  | 147 |
| 138 | Structural characterization of proteins with an attached ATCUN motif by paramagnetic relaxation enhancement NMR spectroscopy. <i>Journal of the American Chemical Society</i> , <b>2001</b> , 123, 9843-7   | 16.4 | 145 |
| 137 | From sequence and forces to structure, function, and evolution of intrinsically disordered proteins. <i>Structure</i> , <b>2013</b> , 21, 1492-9  | 5.2  | 144 |

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|-----|---|------|-----|
| 136 | A simple in vivo assay for increased protein solubility. <i>Protein Science</i> , <b>1999</b> , 8, 1908-11  | 6.3  | 140 |
| 135 | High-resolution three-dimensional structure of reduced recombinant human thioredoxin in solution. <i>Biochemistry</i> , <b>1991</b> , 30, 2685-98   | 3.2  | 137 |
| 134 | Contributions to protein entropy and heat capacity from bond vector motions measured by NMR spin relaxation. <i>Journal of Molecular Biology</i> , <b>1997</b> , 272, 790-804   | 6.5  | 134 |
| 133 | Phospho-dependent phase separation of FMRP and CAPRIN1 recapitulates regulation of translation and deadenylation. <i>Science</i> , <b>2019</b> , 365, 825-829   | 33.3 | 128 |
| 132 | NMR studies of unfolded states of an SH3 domain in aqueous solution and denaturing conditions. <i>Biochemistry</i> , <b>1997</b> , 36, 3959-70  | 3.2  | 128 |
| 131 | Structure and disorder in an unfolded state under nondenaturing conditions from ensemble models consistent with a large number of experimental restraints. <i>Journal of Molecular Biology</i> , <b>2009</b> , 391, 359-74                                  | 6.5  | 126 |
| 130 | Phosphoregulated FMRP phase separation models activity-dependent translation through bidirectional control of mRNA granule formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 4218-4227 | 11.5 | 125 |
| 129 | Dynamic Protein Interaction Networks and New Structural Paradigms in Signaling. <i>Chemical Reviews</i> , <b>2016</b> , 116, 6424-62  | 68.1 | 118 |
| 128 | Liquid-liquid phase separation in cellular signaling systems. <i>Current Opinion in Structural Biology</i> , <b>2016</b> , 41, 180-186  | 8.1  | 116 |
| 127 | Relationship between electrostatics and redox function in human thioredoxin: characterization of pH titration shifts using two-dimensional homo- and heteronuclear NMR. <i>Biochemistry</i> , <b>1992</b> , 31, 3442-52                                     | 3.2  | 116 |
| 126 | Theories for Sequence-Dependent Phase Behaviors of Biomolecular Condensates. <i>Biochemistry</i> , <b>2018</b> , 57, 2499-2508  | 3.2  | 115 |
| 125 | Characterization of disordered proteins with ENSEMBLE. <i>Bioinformatics</i> , <b>2013</b> , 29, 398-9  | 7.2  | 115 |
| 124 | Regulatory R region of the CFTR chloride channel is a dynamic integrator of phospho-dependent intra- and intermolecular interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, E4427-36  | 11.5 | 110 |
| 123 | Properties of Stress Granule and P-Body Proteomes. <i>Molecular Cell</i> , <b>2019</b> , 76, 286-294  | 17.6 | 105 |
| 122 | Diversity in protein recognition by PTB domains. <i>Current Opinion in Structural Biology</i> , <b>1999</b> , 9, 690-5  | 8.1  | 103 |
| 121 | Improved structural characterizations of the drkN SH3 domain unfolded state suggest a compact ensemble with native-like and non-native structure. <i>Journal of Molecular Biology</i> , <b>2007</b> , 367, 1494-510   | 6.5  | 99  |
| 120 | Structure of a Numb PTB domain-peptide complex suggests a basis for diverse binding specificity. <i>Nature Structural Biology</i> , <b>1998</b> , 5, 1075-83  |      | 98  |
| 119 | Correlation between binding and dynamics at SH2 domain interfaces. <i>Nature Structural Biology</i> , <b>1998</b> , 5, 156-63   |      | 97  |

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|-----|---|------|----|
| 118 | Novel mode of ligand binding by the SH2 domain of the human XLP disease gene product SAP/SH2D1A. <i>Current Biology</i> , <b>1999</b> , 9, 1355-62  | 6.3  | 97 |
| 117 | Ensemble modeling of protein disordered states: experimental restraint contributions and validation. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2012</b> , 80, 556-72                                 | 4.2  | 95 |
| 116 | Multidimensional NMR methods for protein structure determination. <i>IUBMB Life</i> , <b>2001</b> , 52, 291-302   | 4.7  | 95 |
| 115 | Structural diversity in free and bound states of intrinsically disordered protein phosphatase 1 regulators. <i>Structure</i> , <b>2010</b> , 18, 1094-103   | 5.2  | 94 |
| 114 | Finding Our Way in the Dark Proteome. <i>Journal of the American Chemical Society</i> , <b>2016</b> , 138, 9730-42  | 16.4 | 93 |
| 113 | Similarities between the spectrin SH3 domain denatured state and its folding transition state. <i>Journal of Molecular Biology</i> , <b>2000</b> , 297, 1217-29   | 6.5  | 90 |
| 112 | Probing the diverse landscape of protein flexibility and binding. <i>Current Opinion in Structural Biology</i> , <b>2012</b> , 22, 643-50   | 8.1  | 87 |
| 111 | NMR evidence for differential phosphorylation-dependent interactions in WT and DeltaF508 CFTR. <i>EMBO Journal</i> , <b>2010</b> , 29, 263-77   | 13   | 87 |
| 110 | Studies on the solution conformation of human thioredoxin using heteronuclear 15N-1H nuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , <b>1990</b> , 29, 1566-72   | 3.2  | 86 |
| 109 | A change in conformational dynamics underlies the activation of Eph receptor tyrosine kinases. <i>EMBO Journal</i> , <b>2006</b> , 25, 4686-96  | 13   | 82 |
| 108 | Site-specific contributions to the pH dependence of protein stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 4545-50                              | 11.5 | 79 |
| 107 | Aromatic and methyl NOEs highlight hydrophobic clustering in the unfolded state of an SH3 domain. <i>Biochemistry</i> , <b>2003</b> , 42, 8687-95   | 3.2  | 77 |
| 106 | Transient structure and dynamics in the disordered c-Myc transactivation domain affect Bin1 binding. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, 6353-66  | 20.1 | 75 |
| 105 | Affinity and specificity of interactions between Nedd4 isoforms and the epithelial Na <sup>+</sup> channel. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 20019-28  | 5.4  | 74 |
| 104 | Analysis of deuterium relaxation-derived methyl axis order parameters and correlation with local structure. <i>Journal of Biomolecular NMR</i> , <b>1999</b> , 13, 181-5  | 3    | 74 |
| 103 | Random-phase-approximation theory for sequence-dependent, biologically functional liquid-liquid phase separation of intrinsically disordered proteins. <i>Journal of Molecular Liquids</i> , <b>2017</b> , 228, 176-193 | 6    | 73 |
| 102 | A "three-pronged" binding mechanism for the SAP/SH2D1A SH2 domain: structural basis and relevance to the XLP syndrome. <i>EMBO Journal</i> , <b>2002</b> , 21, 314-23   | 13   | 73 |
| 101 | Dramatic stabilization of an SH3 domain by a single substitution: roles of the folded and unfolded states. <i>Journal of Molecular Biology</i> , <b>2001</b> , 307, 913-28  | 6.5  | 73 |

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| 100 | NMR Pulse Schemes for the Sequence-Specific Assignment of Arginine Guanidino 15N and 1H Chemical Shifts in Proteins. <i>Journal of the American Chemical Society</i> , <b>1995</b> , 117, 3556-3564  | 16.4 | 73 |
| 99  | Triple-resonance NOESY-based experiments with improved spectral resolution: applications to structural characterization of unfolded, partially folded and folded proteins. <i>Journal of Biomolecular NMR</i> , <b>1997</b> , 9, 181-200                         | 3    | 69 |
| 98  | Complex regulatory mechanisms mediated by the interplay of multiple post-translational modifications. <i>Current Opinion in Structural Biology</i> , <b>2018</b> , 48, 58-67   | 8.1  | 68 |
| 97  | Structural determinants for high-affinity binding in a Nedd4 WW3* domain-Comm PY motif complex. <i>Structure</i> , <b>2006</b> , 14, 543-53  | 5.2  | 67 |
| 96  | Interaction of the eukaryotic initiation factor 4E with 4E-BP2 at a dynamic bipartite interface. <i>Structure</i> , <b>2013</b> , 21, 2186-96  | 5.2  | 64 |
| 95  | Sequential assignment of proline-rich regions in proteins: application to modular binding domain complexes. <i>Journal of Biomolecular NMR</i> , <b>2000</b> , 16, 253-9   | 3    | 64 |
| 94  | Structure of a regulatory complex involving the Abl SH3 domain, the Crk SH2 domain, and a Crk-derived phosphopeptide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 14053-8                         | 11.5 | 63 |
| 93  | Cooperative interactions and a non-native buried Trp in the unfolded state of an SH3 domain. <i>Journal of Molecular Biology</i> , <b>2002</b> , 322, 163-78   | 6.5  | 63 |
| 92  | First-generation predictors of biological protein phase separation. <i>Current Opinion in Structural Biology</i> , <b>2019</b> , 58, 88-96   | 8.1  | 62 |
| 91  | Measurement of side-chain carboxyl pK(a) values of glutamate and aspartate residues in an unfolded protein by multinuclear NMR spectroscopy. <i>Journal of the American Chemical Society</i> , <b>2002</b> , 124, 5714-7   | 16.4 | 62 |
| 90  | Charge pattern matching as a fuzzy mode of molecular recognition for the functional phase separations of intrinsically disordered proteins. <i>New Journal of Physics</i> , <b>2017</b> , 19, 115003   | 2.9  | 61 |
| 89  | Calculation of residual dipolar couplings from disordered state ensembles using local alignment. <i>Journal of the American Chemical Society</i> , <b>2008</b> , 130, 7804-5   | 16.4 | 61 |
| 88  | Structural and dynamic characterization of the phosphotyrosine binding region of a Src homology 2 domain--phosphopeptide complex by NMR relaxation, proton exchange, and chemical shift approaches. <i>Biochemistry</i> , <b>1995</b> , 34, 11353-62             | 3.2  | 60 |
| 87  | Coupling of tandem Smad ubiquitination regulatory factor (Smurf) WW domains modulates target specificity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 18404-9                                    | 11.5 | 57 |
| 86  | Comparative roles of charge, , and hydrophobic interactions in sequence-dependent phase separation of intrinsically disordered proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 28795-28805 | 11.5 | 56 |
| 85  | Comprehensive NOE characterization of a partially folded large fragment of staphylococcal nuclease Delta131Delta, using NMR methods with improved resolution. <i>Journal of Molecular Biology</i> , <b>1997</b> , 272, 9-20                                      | 6.5  | 56 |
| 84  | The ubiquitin binding region of the Smurf HECT domain facilitates polyubiquitylation and binding of ubiquitylated substrates. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 6308-15  | 5.4  | 55 |
| 83  | Congenital chloride-losing diarrhea causing mutations in the STAS domain result in misfolding and mistrafficking of SLC26A3. <i>Journal of Biological Chemistry</i> , <b>2008</b> , 283, 8711-22   | 5.4  | 54 |



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|----|--|------|----|
| 82 | Proteome-wide signatures of function in highly diverged intrinsically disordered regions. <i>ELife</i> , <b>2019</b> , 8,  | 8.9  | 53 |
| 81 | Direct Binding of the Corrector VX-809 to Human CFTR NBD1: Evidence of an Allosteric Coupling between the Binding Site and the NBD1:CL4 Interface. <i>Molecular Pharmacology</i> , <b>2017</b> , 92, 124-135   | 4.3  | 51 |
| 80 | Composite low affinity interactions dictate recognition of the cyclin-dependent kinase inhibitor Sic1 by the SCFCdc4 ubiquitin ligase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 3287-92 | 11.5 | 51 |
| 79 | High populations of non-native structures in the denatured state are compatible with the formation of the native folded state. <i>Journal of Molecular Biology</i> , <b>1998</b> , 284, 1153-64  | 6.5  | 49 |
| 78 | 15N H/D-SOLEXSY experiment for accurate measurement of amide solvent exchange rates: application to denatured drkN SH3. <i>Journal of Biomolecular NMR</i> , <b>2010</b> , 46, 227-44  | 3    | 48 |
| 77 | Synuclein-gamma targeting peptide inhibitor that enhances sensitivity of breast cancer cells to antimicrotubule drugs. <i>Cancer Research</i> , <b>2007</b> , 67, 626-33   | 10.1 | 48 |
| 76 | Phenotypic profiling of CFTR modulators in patient-derived respiratory epithelia. <i>Npj Genomic Medicine</i> , <b>2017</b> , 2, 12  | 6.2  | 46 |
| 75 | Side-chain dynamics of the SAP SH2 domain correlate with a binding hot spot and a region with conformational plasticity. <i>Journal of Molecular Biology</i> , <b>2002</b> , 322, 605-20   | 6.5  | 46 |
| 74 | Phosphorylation-dependent 14-3-3 protein interactions regulate CFTR biogenesis. <i>Molecular Biology of the Cell</i> , <b>2012</b> , 23, 996-1009  | 3.5  | 45 |
| 73 | An expanded WW domain recognition motif revealed by the interaction between Smad7 and the E3 ubiquitin ligase Smurf2. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 17069-17075  | 5.4  | 45 |
| 72 | Structural changes of CFTR R region upon phosphorylation: a plastic platform for intramolecular and intermolecular interactions. <i>FEBS Journal</i> , <b>2013</b> , 280, 4407-16  | 5.7  | 44 |
| 71 | The effect of intrachain electrostatic repulsion on conformational disorder and dynamics of the Sic1 protein. <i>Journal of Physical Chemistry B</i> , <b>2014</b> , 118, 4088-97  | 3.4  | 43 |
| 70 | Determination of the positions of bound water molecules in the solution structure of reduced human thioredoxin by heteronuclear three-dimensional nuclear magnetic resonance spectroscopy. <i>Journal of Molecular Biology</i> , <b>1991</b> , 220, 209-16 | 6.5  | 43 |
| 69 | Conformational changes relevant to channel activity and folding within the first nucleotide binding domain of the cystic fibrosis transmembrane conductance regulator. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 28480-94                | 5.4  | 42 |
| 68 | Conformational Ensembles of an Intrinsically Disordered Protein Consistent with NMR, SAXS, and Single-Molecule FRET. <i>Journal of the American Chemical Society</i> , <b>2020</b> , 142, 15697-15710  | 16.4 | 41 |
| 67 | <sup>1</sup> H- <sup>13</sup> C Dipole-Dipole Cross-Correlated Spin Relaxation As a Probe of Dynamics in Unfolded Proteins: Application to the DrkN SH3 Domain. <i>Journal of the American Chemical Society</i> , <b>1999</b> , 121, 3555-3556             | 16.4 | 40 |
| 66 | Structural signature of the MYPT1-PP1 interaction. <i>Journal of the American Chemical Society</i> , <b>2011</b> , 133, 73-80  | 16.4 | 37 |
| 65 | pH titration studies of an SH2 domain-phosphopeptide complex: unusual histidine and phosphate pKa values. <i>Protein Science</i> , <b>1997</b> , 6, 1910-9   | 6.3  | 37 |

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| 64 | Identification of a molecular locus for normalizing dysregulated GABA release from interneurons in the Fragile X brain. <i>Molecular Psychiatry</i> , <b>2020</b> , 25, 2017-2035  | 15.1  | 35 |
| 63 | Phase Separation as a Missing Mechanism for Interpretation of Disease Mutations. <i>Cell</i> , <b>2020</b> , 183, 1742-1756  | 36.56 | 34 |
| 62 | NMR studies of tandem WW domains of Nedd4 in complex with a PY motif-containing region of the epithelial sodium channel. <i>Biochemistry and Cell Biology</i> , <b>1998</b> , 76, 341-350                                  | 3.6   | 34 |
| 61 | NMR characterization of copper-binding domains 4-6 of ATP7B. <i>Biochemistry</i> , <b>2010</b> , 49, 8468-77   | 3.2   | 33 |
| 60 | Autism-Misregulated eIF4G Microexons Control Synaptic Translation and Higher Order Cognitive Functions. <i>Molecular Cell</i> , <b>2020</b> , 77, 1176-1192.e16  | 17.6  | 32 |
| 59 | Synergy of cAMP and calcium signaling pathways in CFTR regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E2086-E2095                                 | 11.5  | 31 |
| 58 | Structural comparison of the unstable drkN SH3 domain and a stable mutant. <i>Biochemistry</i> , <b>2005</b> , 44, 15550-60  | 3.2   | 31 |
| 57 | PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D404-D411  | 20.1  | 31 |
| 56 | Tryptophan solvent exposure in folded and unfolded states of an SH3 domain by 19F and 1H NMR. <i>Biochemistry</i> , <b>2006</b> , 45, 14120-8  | 3.2   | 30 |
| 55 | An allosteric conduit facilitates dynamic multisite substrate recognition by the SCF ubiquitin ligase. <i>Nature Communications</i> , <b>2017</b> , 8, 13943   | 17.4  | 28 |
| 54 | Oxygen as a paramagnetic probe of clustering and solvent exposure in folded and unfolded states of an SH3 domain. <i>Journal of the American Chemical Society</i> , <b>2007</b> , 129, 1826-35                             | 16.4  | 27 |
| 53 | NMR dynamics-derived insights into the binding properties of a peptide interacting with an SH2 domain. <i>Biochemistry</i> , <b>2005</b> , 44, 694-703   | 3.2   | 27 |
| 52 | Hydration and packing along the folding pathway of SH3 domains by pressure-dependent NMR. <i>Biochemistry</i> , <b>2006</b> , 45, 4711-9   | 3.2   | 27 |
| 51 | Differential dynamic engagement within 24 SH3 domain: peptide complexes revealed by co-linear chemical shift perturbation analysis. <i>PLoS ONE</i> , <b>2012</b> , 7, e51282  | 3.7   | 27 |
| 50 | NMR structure of neuromedin C, a neurotransmitter with an amino terminal Cull-, Nill-binding (ATCUN) motif. <i>Chemical Biology and Drug Design</i> , <b>1997</b> , 49, 500-9  |       | 26 |
| 49 | A proton nuclear magnetic resonance assignment and secondary structure determination of recombinant human thioredoxin. <i>Biochemistry</i> , <b>1989</b> , 28, 7088-97   | 3.2   | 26 |
| 48 | Structural, functional, and bioinformatic studies demonstrate the crucial role of an extended peptide binding site for the SH3 domain of yeast Abp1p. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 26918-27 | 5.4   | 25 |
| 47 | Dynamics intrinsic to cystic fibrosis transmembrane conductance regulator function and stability. <i>Cold Spring Harbor Perspectives in Medicine</i> , <b>2013</b> , 3, a009522  | 5.4   | 24 |



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|----|---|------|----|
| 46 | Allosteric coupling between the intracellular coupling helix 4 and regulatory sites of the first nucleotide-binding domain of CFTR. <i>PLoS ONE</i> , <b>2013</b> , 8, e74347   | 3.7  | 24 |
| 45 | NMR Experiments for Studies of Dilute and Condensed Protein Phases: Application to the Phase-Separating Protein CAPRIN1. <i>Journal of the American Chemical Society</i> , <b>2020</b> , 142, 2471-2489   | 16.4 | 23 |
| 44 | Entropy and Information within Intrinsically Disordered Protein Regions. <i>Entropy</i> , <b>2019</b> , 21,   | 2.8  | 22 |
| 43 | Extended Experimental Inferential Structure Determination Method in Determining the Structural Ensembles of Disordered Protein States. <i>Communications Chemistry</i> , <b>2020</b> , 3,   | 6.3  | 21 |
| 42 | Translating Material Science into Biological Function. <i>Molecular Cell</i> , <b>2019</b> , 75, 1-2  | 17.6 | 21 |
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