Ptr S Tompa

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

| 187 | 19,582 | 58 | 139 |
|--------------------|-----------------------|-------------|-----------------|
| papers | citations | h-index | g-index |
| 194 ext. papers | 22,885 ext. citations | 8.6 avg, IF | 7.33 L-index |

| # | Paper | IF | Citations |
|-----|---|--------------|-----------|
| 187 | F/YGG-motif is an intrinsically disordered nucleic-acid binding motif RNA Biology, 2022 , 19, 622-635 | 4.8 | O |
| 186 | Degron masking outlines degronons, co-degrading functional modules in the proteome <i>Communications Biology</i> , 2022 , 5, 445 | 6.7 | O |
| 185 | DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2021 , | 20.1 | 13 |
| 184 | Integration of Data from Liquid-Liquid Phase Separation Databases Highlights Concentration and Dosage Sensitivity of LLPS Drivers. <i>International Journal of Molecular Sciences</i> , 2021 , 22, | 6.3 | 8 |
| 183 | Liquid-Liquid Phase Separation Enhances TDP-43 LCD Aggregation but Delays Seeded Aggregation. <i>Biomolecules</i> , 2021 , 11, | 5.9 | 9 |
| 182 | DNA-binding domain as the minimal region driving RNA-dependent liquid-liquid phase separation of androgen receptor. <i>Protein Science</i> , 2021 , 30, 1380-1392 | 6.3 | 4 |
| 181 | Cellular Chaperone Function of Intrinsically Disordered Dehydrin ERD14. <i>International Journal of Molecular Sciences</i> , 2021 , 22, | 6.3 | 3 |
| 180 | Exploring Curated Conformational Ensembles of Intrinsically Disordered Proteins in the Protein Ensemble Database. <i>Current Protocols</i> , 2021 , 1, e192 | | 1 |
| 179 | "Protein" no longer means what it used to. <i>Current Research in Structural Biology</i> , 2021 , 3, 146-152 | 2.8 | O |
| 178 | The role of ordered cooperative assembly in biomolecular condensates. <i>Nature Reviews Molecular Cell Biology</i> , 2021 , 22, 647-648 | 48.7 | 1 |
| 177 | PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. <i>Nucleic Acids Research</i> , 2021 , 49, D404-D411 | 20.1 | 31 |
| 176 | A generic approach to study the kinetics of liquid-liquid phase separation under near-native conditions. <i>Communications Biology</i> , 2021 , 4, 77 | 6.7 | 10 |
| 175 | Specific Conformational Dynamics and Expansion Underpin a Multi-Step Mechanism for Specific Binding of p27 with Cdk2/Cyclin A. <i>Journal of Molecular Biology</i> , 2020 , 432, 2998-3017 | 6.5 | 10 |
| 174 | WT and A53T Esynuclein Systems: Melting Diagram and Its New Interpretation. <i>International Journal of Molecular Sciences</i> , 2020 , 21, | 6.3 | 2 |
| 173 | A guide to regulation of the formation of biomolecular condensates. <i>FEBS Journal</i> , 2020 , 287, 1924-193 | 5 5.7 | 29 |
| 172 | Interaction between the scaffold proteins CBP by IQGAP1 provides an interface between gene expression and cytoskeletal activity. <i>Scientific Reports</i> , 2020 , 10, 5753 | 4.9 | 1 |
| 171 | PhaSePro: the database of proteins driving liquid-liquid phase separation. <i>Nucleic Acids Research</i> , 2020 , 48, D360-D367 | 20.1 | 43 |

(2018-2020)

| 170 | DisProt: intrinsic protein disorder annotation in 2020. Nucleic Acids Research, 2020, 48, D269-D276 | 20.1 | 91 |
|-----|---|---------------|-----|
| 169 | Targeting an Intrinsically Disordered Protein by Covalent Modification. <i>Methods in Molecular Biology</i> , 2020 , 2141, 835-854 | 1.4 | 1 |
| 168 | Distance-Based Metrics for Comparing Conformational Ensembles of Intrinsically Disordered Proteins. <i>Biophysical Journal</i> , 2020 , 118, 2952-2965 | 2.9 | 6 |
| 167 | Learning of Signaling Networks: Molecular Mechanisms. <i>Trends in Biochemical Sciences</i> , 2020 , 45, 284-29 | 94 0.3 | 11 |
| 166 | Dehydrin ERD14 activates glutathione transferase Phi9 in Arabidopsis thaliana under osmotic stress. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020 , 1864, 129506 | 4 | 13 |
| 165 | Interplay of Structural Disorder and Short Binding Elements in the Cellular Chaperone Function of Plant Dehydrin ERD14. <i>Cells</i> , 2020 , 9, | 7.9 | 6 |
| 164 | Chasing coevolutionary signals in intrinsically disordered proteins complexes. <i>Scientific Reports</i> , 2020 , 10, 17962 | 4.9 | 2 |
| 163 | Focusing of Microcrystals and Liquid Condensates in Acoustofluidics. <i>Crystals</i> , 2019 , 9, 120 | 2.3 | 5 |
| 162 | The Balancing Act of Intrinsically Disordered Proteins: Enabling Functional Diversity while Minimizing Promiscuity. <i>Journal of Molecular Biology</i> , 2019 , 431, 1650-1670 | 6.5 | 24 |
| 161 | Emergent functions of proteins in non-stoichiometric supramolecular assemblies. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019 , 1867, 970-979 | 4 | 27 |
| 160 | Dynamic anticipation by Cdk2/Cyclin A-bound p27 mediates signal integration in cell cycle regulation. <i>Nature Communications</i> , 2019 , 10, 1676 | 17.4 | 43 |
| 159 | Spontaneous driving forces give rise to protein-RNA condensates with coexisting phases and complex material properties. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 7889-7898 | 11.5 | 186 |
| 158 | Misprediction of Structural Disorder in Halophiles. <i>Molecules</i> , 2019 , 24, | 4.8 | 4 |
| 157 | An intrinsically disordered proteins community for ELIXIR. F1000Research, 2019, 8, | 3.6 | 7 |
| 156 | Calpain Purification Through Calpastatin and Calcium: Strategy and Procedures. <i>Methods in Molecular Biology</i> , 2019 , 1929, 233-244 | 1.4 | 1 |
| 155 | Does Intrinsic Disorder in Proteins Favor Their Interaction with Lipids?. <i>Proteomics</i> , 2019 , 19, e1800098 | 4.8 | 11 |
| 154 | Chemical shift assignments of the partially deuterated Fyn SH2-SH3 domain. <i>Biomolecular NMR Assignments</i> , 2018 , 12, 117-122 | 0.7 | |
| 153 | Molecular Motions and Interactions in Aqueous Solutions of Thymosin-D Stabilin C-Terminal Domain (CTD) and Their 1:1 Complex Studied by H NMR Spectroscopy. <i>ChemPhysChem</i> , 2018 , 19, 848-85 | 5ĝ.2 | 2 |

| 152 | In vivo biotinylated calpastatin improves the affinity purification of human m-calpain. <i>Protein Expression and Purification</i> , 2018 , 145, 77-84 | 2 | 5 |
|-----|---|------|-----|
| 151 | A comprehensive assessment of long intrinsic protein disorder from the DisProt database. <i>Bioinformatics</i> , 2018 , 34, 445-452 | 7.2 | 42 |
| 150 | Protein Phase Separation: A New Phase in Cell Biology. <i>Trends in Cell Biology</i> , 2018 , 28, 420-435 | 18.3 | 869 |
| 149 | AmyPro: a database of proteins with validated amyloidogenic regions. <i>Nucleic Acids Research</i> , 2018 , 46, D387-D392 | 20.1 | 30 |
| 148 | Disordered Substrates of the 20S Proteasome Link Degradation with Phase Separation. <i>Proteomics</i> , 2018 , 18, e1800276 | 4.8 | 1 |
| 147 | Phasing in on the cell cycle. <i>Cell Division</i> , 2018 , 13, 1 | 2.8 | 21 |
| 146 | Quantification of Intrinsically Disordered Proteins: A Problem Not Fully Appreciated. <i>Frontiers in Molecular Biosciences</i> , 2018 , 5, 83 | 5.6 | 14 |
| 145 | MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. <i>Nucleic Acids Research</i> , 2018 , 46, D471-D476 | 20.1 | 143 |
| 144 | Yeast and Cancer: Common Mechanism Underlying Activation of Ras by Glycolytic Flux. <i>FASEB Journal</i> , 2018 , 32, lb143 | 0.9 | |
| 143 | The Melting Diagram of Protein Solutions and Its Thermodynamic Interpretation. <i>International Journal of Molecular Sciences</i> , 2018 , 19, | 6.3 | 2 |
| 142 | Co-Evolution of Intrinsically Disordered Proteins with Folded Partners Witnessed by Evolutionary Couplings. <i>International Journal of Molecular Sciences</i> , 2018 , 19, | 6.3 | 12 |
| 141 | Challenges in the Structural-Functional Characterization of Multidomain, Partially Disordered Proteins CBP and p300: Preparing Native Proteins and Developing Nanobody Tools. <i>Methods in Enzymology</i> , 2018 , 611, 607-675 | 1.7 | 4 |
| 140 | Unique Physicochemical Patterns of Residues in Protein-Protein Interfaces. <i>Journal of Chemical Information and Modeling</i> , 2018 , 58, 2164-2173 | 6.1 | 5 |
| 139 | Hydrogen Mobility and Protein-Water Interactions in Proteins in the Solid State. <i>ChemPhysChem</i> , 2017 , 18, 677-682 | 3.2 | 8 |
| 138 | H, N, C resonance assignment of plant dehydrin early response to dehydration 10 (ERD10). <i>Biomolecular NMR Assignments</i> , 2017 , 11, 127-131 | 0.7 | 3 |
| 137 | Bioinformatics Approaches to the Structure and Function of Intrinsically Disordered Proteins 2017 , 167- | -203 | 2 |
| 136 | DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , 2017 , 45, D219-D227 | 20.1 | 182 |
| 135 | To be disordered or not to be disordered: is that still a question for proteins in the cell?. <i>Cellular and Molecular Life Sciences</i> , 2017 , 74, 3185-3204 | 10.3 | 23 |

(2016-2017)

| 134 | Phase Separation of C9orf72 Dipeptide Repeats Perturbs Stress Granule Dynamics. <i>Molecular Cell</i> , 2017 , 65, 1044-1055.e5 | 17.6 | 307 |
|-----|---|------|-----|
| 133 | Simultaneous quantification of protein order and disorder. <i>Nature Chemical Biology</i> , 2017 , 13, 339-342 | 11.7 | 83 |
| 132 | Affinity purification of human m-calpain through an intrinsically disordered inhibitor, calpastatin. <i>PLoS ONE</i> , 2017 , 12, e0174125 | 3.7 | 2 |
| 131 | Linking functions: an additional role for an intrinsically disordered linker domain in the transcriptional coactivator CBP. <i>Scientific Reports</i> , 2017 , 7, 4676 | 4.9 | 28 |
| 130 | Phosphorylation of MAP65-1 by Arabidopsis Aurora Kinases Is Required for Efficient Cell Cycle Progression. <i>Plant Physiology</i> , 2017 , 173, 582-599 | 6.6 | 27 |
| 129 | Protein Delivery into Plant Cells: Toward Structural Biology. Frontiers in Plant Science, 2017, 8, 519 | 6.2 | 8 |
| 128 | Arginine-rich Peptides Can Actively Mediate Liquid-liquid Phase Separation. <i>Bio-protocol</i> , 2017 , 7, e2525 | 0.9 | 14 |
| 127 | Coding Regions of Intrinsic Disorder Accommodate Parallel Functions. <i>Trends in Biochemical Sciences</i> , 2016 , 41, 898-906 | 10.3 | 16 |
| 126 | Computational analysis of translational readthrough proteins in Drosophila and yeast reveals parallels to alternative splicing. <i>Scientific Reports</i> , 2016 , 6, 32142 | 4.9 | 4 |
| 125 | Three reasons protein disorder analysis makes more sense in the light of collagen. <i>Protein Science</i> , 2016 , 25, 1030-6 | 6.3 | 6 |
| 124 | The principle of conformational signaling. <i>Chemical Society Reviews</i> , 2016 , 45, 4252-84 | 58.5 | 29 |
| 123 | Just a Flexible Linker? The Structural and Dynamic Properties of CBP-ID4 Revealed by NMR Spectroscopy. <i>Biophysical Journal</i> , 2016 , 110, 372-381 | 2.9 | 18 |
| 122 | Design Principles Involving Protein Disorder Facilitate Specific Substrate Selection and Degradation by the Ubiquitin-Proteasome System. <i>Journal of Biological Chemistry</i> , 2016 , 291, 6723-31 | 5.4 | 29 |
| 121 | Tripartite degrons confer diversity and specificity on regulated protein degradation in the ubiquitin-proteasome system. <i>Nature Communications</i> , 2016 , 7, 10239 | 17.4 | 71 |
| 120 | A Novel Method for Assessing the Chaperone Activity of Proteins. <i>PLoS ONE</i> , 2016 , 11, e0161970 | 3.7 | 9 |
| 119 | Wide-line NMR and DSC studies on intrinsically disordered p53 transactivation domain and its helically pre-structured segment. <i>BMB Reports</i> , 2016 , 49, 497-501 | 5.5 | 4 |
| 118 | Numerous proteins with unique characteristics are degraded by the 26S proteasome following monoubiquitination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E4639-47 | 11.5 | 91 |
| 117 | Essential functions linked with structural disorder in organisms of minimal genome. <i>Biology Direct</i> , 2016 , 11, 45 | 7.2 | 4 |
| , | 2016 , 11, 45 | / | |

| 116 | Start2Fold: a database of hydrogen/deuterium exchange data on protein folding and stability. <i>Nucleic Acids Research</i> , 2016 , 44, D429-34 | 20.1 | 17 |
|-----|--|------|-----|
| 115 | The role of structural disorder in cell cycle regulation, related clinical proteomics, disease development and drug targeting. <i>Expert Review of Proteomics</i> , 2015 , 12, 221-33 | 4.2 | 12 |
| 114 | Intrinsically disordered proteins: emerging interaction specialists. <i>Current Opinion in Structural Biology</i> , 2015 , 35, 49-59 | 8.1 | 136 |
| 113 | Polymer physics of intracellular phase transitions. <i>Nature Physics</i> , 2015 , 11, 899-904 | 16.2 | 705 |
| 112 | The Protein Ensemble Database. Advances in Experimental Medicine and Biology, 2015, 870, 335-49 | 3.6 | 19 |
| 111 | Ensemble Methods Enable a New Definition for the Solution to Gas-Phase Transfer of Intrinsically Disordered Proteins. <i>Journal of the American Chemical Society</i> , 2015 , 137, 13807-17 | 16.4 | 37 |
| 110 | Disordered regions in transmembrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015 , 1848, 2839-48 | 3.8 | 18 |
| 109 | Towards Understanding Protein Disorder In-Cell. <i>Advances in Experimental Medicine and Biology</i> , 2015 , 870, 319-34 | 3.6 | 2 |
| 108 | Bioinformatics Approaches for Predicting Disordered Protein Motifs. <i>Advances in Experimental Medicine and Biology</i> , 2015 , 870, 291-318 | 3.6 | 15 |
| 107 | Redefining the BH3 Death Domain as a Q hort Linear MotifQ <i>Trends in Biochemical Sciences</i> , 2015 , 40, 736-748 | 10.3 | 40 |
| 106 | Computational approaches for inferring the functions of intrinsically disordered proteins. <i>Frontiers in Molecular Biosciences</i> , 2015 , 2, 45 | 5.6 | 32 |
| 105 | Functional Advantages of Conserved Intrinsic Disorder in RNA-Binding Proteins. <i>PLoS ONE</i> , 2015 , 10, e0139731 | 3.7 | 71 |
| 104 | SnapShot: Intrinsic Structural Disorder. <i>Cell</i> , 2015 , 161, 1230-1230.e1 | 56.2 | 12 |
| 103 | DisCons: a novel tool to quantify and classify evolutionary conservation of intrinsic protein disorder. <i>BMC Bioinformatics</i> , 2015 , 16, 153 | 3.6 | 21 |
| 102 | Predicting the predictive power of IDP ensembles. Structure, 2014, 22, 177-8 | 5.2 | 19 |
| 101 | Introducing protein intrinsic disorder. <i>Chemical Reviews</i> , 2014 , 114, 6561-88 | 68.1 | 487 |
| 100 | Multisteric regulation by structural disorder in modular signaling proteins: an extension of the concept of allostery. <i>Chemical Reviews</i> , 2014 , 114, 6715-32 | 68.1 | 72 |
| 99 | Contribution of proline to the pre-structuring tendency of transient helical secondary structure elements in intrinsically disordered proteins. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014 , 1840, 993-1003 | 4 | 26 |

| 98 | A million peptide motifs for the molecular biologist. <i>Molecular Cell</i> , 2014 , 55, 161-9 | 17.6 | 310 |
|----|--|--------|------|
| 97 | Classification of intrinsically disordered regions and proteins. <i>Chemical Reviews</i> , 2014 , 114, 6589-631 | 68.1 | 1141 |
| 96 | pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. <i>Nucleic Acids Research</i> , 2014 , 42, D326-35 | 20.1 | 159 |
| 95 | Synonymous constraint elements show a tendency to encode intrinsically disordered protein segments. <i>PLoS Computational Biology</i> , 2014 , 10, e1003607 | 5 | 18 |
| 94 | The DynaMine webserver: predicting protein dynamics from sequence. <i>Nucleic Acids Research</i> , 2014 , 42, W264-70 | 20.1 | 89 |
| 93 | Discrete molecular dynamics can predict helical prestructured motifs in disordered proteins. <i>PLoS ONE</i> , 2014 , 9, e95795 | 3.7 | 17 |
| 92 | From protein sequence to dynamics and disorder with DynaMine. <i>Nature Communications</i> , 2013 , 4, 274 | 1 17.4 | 103 |
| 91 | Molecular mechanism of SSR128129E, an extracellularly acting, small-molecule, allosteric inhibitor of FGF receptor signaling. <i>Cancer Cell</i> , 2013 , 23, 489-501 | 24.3 | 99 |
| 90 | New m-calpain substrate-based azapeptide inhibitors. <i>Journal of Peptide Science</i> , 2013 , 19, 370-6 | 2.1 | 4 |
| 89 | Intrinsic structural disorder in cytoskeletal proteins. <i>Cytoskeleton</i> , 2013 , 70, 550-71 | 2.4 | 43 |
| 88 | Multiple fuzzy interactions in the moonlighting function of thymosin-图. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e26204 | | 8 |
| 87 | Hydrogel formation by multivalent IDPs: A reincarnation of the microtrabecular lattice?. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e24068 | | 8 |
| 86 | Polycation-Interactions are a driving force for molecular recognition by an intrinsically disordered oncoprotein family. <i>PLoS Computational Biology</i> , 2013 , 9, e1003239 | 5 | 50 |
| 85 | What@in a name? Why these proteins are intrinsically disordered: Why these proteins are intrinsically disordered. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e24157 | | 171 |
| 84 | Structural disorder provides increased adaptability for vesicle trafficking pathways. <i>PLoS Computational Biology</i> , 2013 , 9, e1003144 | 5 | 29 |
| 83 | Hydrogen skeleton, mobility and protein architecture. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e25767 | | 2 |
| 82 | The alphabet of intrinsic disorder: I. Act like a Pro: On the abundance and roles of proline residues in intrinsically disordered proteins. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e24360 | | 143 |
| 81 | Exon-phase symmetry and intrinsic structural disorder promote modular evolution in the human genome. <i>Nucleic Acids Research</i> , 2013 , 41, 4409-22 | 20.1 | 11 |

| 80 | Structural characterization of intrinsically disordered proteins by NMR spectroscopy. <i>Molecules</i> , 2013 , 18, 10802-28 | 4.8 | 118 |
|----|--|----------------|-----|
| 79 | Functional diversity and structural disorder in the human ubiquitination pathway. <i>PLoS ONE</i> , 2013 , 8, e65443 | 3.7 | 22 |
| 78 | Intrinsic disorder in cell signaling and gene transcription. <i>Molecular and Cellular Endocrinology</i> , 2012 , 348, 457-65 | 4.4 | 87 |
| 77 | Intrinsically disordered proteins: a 10-year recap. <i>Trends in Biochemical Sciences</i> , 2012 , 37, 509-16 | 10.3 | 451 |
| 76 | Intrinsically Disordered Proteins 2012 , 136-152 | | 5 |
| 75 | Structural disorder in proteins brings order to crystal growth in biomineralization. <i>Bone</i> , 2012 , 51, 528-3 | 3 4 1.7 | 91 |
| 74 | On the supertertiary structure of proteins. <i>Nature Chemical Biology</i> , 2012 , 8, 597-600 | 11.7 | 53 |
| 73 | Fuzzy complexes: a more stochastic view of protein function. <i>Advances in Experimental Medicine and Biology</i> , 2012 , 725, 1-14 | 3.6 | 162 |
| 72 | Long-range interactions in nonsense-mediated mRNA decay are mediated by intrinsically disordered protein regions. <i>Journal of Molecular Biology</i> , 2012 , 424, 125-31 | 6.5 | 7 |
| 71 | Increased structural disorder of proteins encoded on human sex chromosomes. <i>Molecular BioSystems</i> , 2012 , 8, 229-36 | | 22 |
| 70 | Diverse functional manifestations of intrinsic structural disorder in molecular chaperones. <i>Biochemical Society Transactions</i> , 2012 , 40, 963-8 | 5.1 | 25 |
| 69 | Structural disorder in eukaryotes. <i>PLoS ONE</i> , 2012 , 7, e34687 | 3.7 | 141 |
| 68 | Unstructural biology coming of age. Current Opinion in Structural Biology, 2011, 21, 419-25 | 8.1 | 251 |
| 67 | Full backbone assignment and dynamics of the intrinsically disordered dehydrin ERD14. <i>Biomolecular NMR Assignments</i> , 2011 , 5, 189-93 | 0.7 | 33 |
| 66 | The Levinthal paradox of the interactome. <i>Protein Science</i> , 2011 , 20, 2074-9 | 6.3 | 21 |
| 65 | Structural flexibility allows the functional diversity of potyvirus genome-linked protein VPg. <i>Journal of Virology</i> , 2011 , 85, 2449-57 | 6.6 | 38 |
| 64 | Verification of alternative splicing variants based on domain integrity, truncation length and intrinsic protein disorder. <i>Nucleic Acids Research</i> , 2011 , 39, 1208-19 | 20.1 | 41 |
| 63 | Accessory proteins in signal transduction: scaffold proteins and beyond. FEBS Journal, 2010, 277, 4347 | 5.7 | 6 |

| 62 | Functional classification of scaffold proteins and related molecules. FEBS Journal, 2010, 277, 4348-55 | 5.7 | 59 |
|----|---|------|-----|
| 61 | Reduction in structural disorder and functional complexity in the thermal adaptation of prokaryotes. <i>PLoS ONE</i> , 2010 , 5, e12069 | 3.7 | 56 |
| 60 | Dual coding in alternative reading frames correlates with intrinsic protein disorder. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 5429-34 | 11.5 | 60 |
| 59 | Power law distribution defines structural disorder as a structural element directly linked with function. <i>Journal of Molecular Biology</i> , 2010 , 403, 346-50 | 6.5 | 27 |
| 58 | Intrinsically disordered chaperones in plants and animals. <i>Biochemistry and Cell Biology</i> , 2010 , 88, 167-7 | 43.6 | 112 |
| 57 | Intrinsic structural disorder confers cellular viability on oncogenic fusion proteins. <i>PLoS Computational Biology</i> , 2009 , 5, e1000552 | 5 | 63 |
| 56 | The androgen receptor gene polyglycine repeat polymorphism is associated with memory performance in healthy Chinese individuals. <i>Psychoneuroendocrinology</i> , 2009 , 34, 947-52 | 5 | 9 |
| 55 | Fuzzy interactome: the limitations of models in molecular biology. <i>Trends in Biochemical Sciences</i> , 2009 , 34, 3 | 10.3 | 10 |
| 54 | Janus chaperones: assistance of both RNA- and protein-folding by ribosomal proteins. <i>FEBS Letters</i> , 2009 , 583, 88-92 | 3.8 | 36 |
| 53 | Cold stability of intrinsically disordered proteins. <i>FEBS Letters</i> , 2009 , 583, 465-9 | 3.8 | 37 |
| 52 | Close encounters of the third kind: disordered domains and the interactions of proteins. <i>BioEssays</i> , 2009 , 31, 328-35 | 4.1 | 197 |
| 51 | High levels of structural disorder in scaffold proteins as exemplified by a novel neuronal protein, CASK-interactive protein1. <i>FEBS Journal</i> , 2009 , 276, 3744-56 | 5.7 | 61 |
| 50 | Interfacial water at protein surfaces: wide-line NMR and DSC characterization of hydration in ubiquitin solutions. <i>Biophysical Journal</i> , 2009 , 96, 2789-98 | 2.9 | 36 |
| 49 | Malleable machines take shape in eukaryotic transcriptional regulation. <i>Nature Chemical Biology</i> , 2008 , 4, 728-37 | 11.7 | 161 |
| 48 | Calcium-induced tripartite binding of intrinsically disordered calpastatin to its cognate enzyme, calpain. <i>FEBS Letters</i> , 2008 , 582, 2149-54 | 3.8 | 25 |
| 47 | Fuzzy complexes: polymorphism and structural disorder in protein-protein interactions. <i>Trends in Biochemical Sciences</i> , 2008 , 33, 2-8 | 10.3 | 788 |
| 46 | Structural and dynamic characterization of intrinsically disordered human securin by NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 2008 , 130, 16873-9 | 16.4 | 63 |
| 45 | Intrinsic structural disorder of DF31, a Drosophila protein of chromatin decondensation and remodeling activities. <i>Journal of Proteome Research</i> , 2008 , 7, 2291-9 | 5.6 | 16 |

| 44 | Chaperone activity of ERD10 and ERD14, two disordered stress-related plant proteins. <i>Plant Physiology</i> , 2008 , 147, 381-90 | 6.6 | 308 |
|----|---|------|-----|
| 43 | Disordered plant LEA proteins as molecular chaperones. <i>Plant Signaling and Behavior</i> , 2008 , 3, 710-3 | 2.5 | 52 |
| 42 | Intrinsically disordered proteins display no preference for chaperone binding in vivo. <i>PLoS Computational Biology</i> , 2008 , 4, e1000017 | 5 | 43 |
| 41 | DisProt: the Database of Disordered Proteins. <i>Nucleic Acids Research</i> , 2007 , 35, D786-93 | 20.1 | 631 |
| 40 | Synthesis of cell-penetrating conjugates of calpain activator peptides. <i>Bioconjugate Chemistry</i> , 2007 , 18, 130-7 | 6.3 | 13 |
| 39 | Structural disorder promotes assembly of protein complexes. <i>BMC Structural Biology</i> , 2007 , 7, 65 | 2.7 | 78 |
| 38 | Prediction of protein disorder at the domain level. Current Protein and Peptide Science, 2007, 8, 161-71 | 2.8 | 65 |
| 37 | Towards proteomic approaches for the identification of structural disorder. <i>Current Protein and Peptide Science</i> , 2007 , 8, 173-9 | 2.8 | 16 |
| 36 | Local structural disorder imparts plasticity on linear motifs. <i>Bioinformatics</i> , 2007 , 23, 950-6 | 7.2 | 335 |
| 35 | Molecular principles of the interactions of disordered proteins. <i>Journal of Molecular Biology</i> , 2007 , 372, 549-61 | 6.5 | 220 |
| 34 | A novel two-dimensional electrophoresis technique for the identification of intrinsically unstructured proteins. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 265-73 | 7.6 | 56 |
| 33 | Disorder and sequence repeats in hub proteins and their implications for network evolution. <i>Journal of Proteome Research</i> , 2006 , 5, 2985-95 | 5.6 | 273 |
| 32 | Prevalent structural disorder in E. coli and S. cerevisiae proteomes. <i>Journal of Proteome Research</i> , 2006 , 5, 1996-2000 | 5.6 | 102 |
| 31 | CG15031/PPYR1 is an intrinsically unstructured protein that interacts with protein phosphatase Y. <i>Archives of Biochemistry and Biophysics</i> , 2006 , 451, 59-67 | 4.1 | 10 |
| 30 | Phosphorylation-induced transient intrinsic structure in the kinase-inducible domain of CREB facilitates its recognition by the KIX domain of CBP. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 64, 749-57 | 4.2 | 27 |
| 29 | Primary contact sites in intrinsically unstructured proteins: the case of calpastatin and microtubule-associated protein 2. <i>Biochemistry</i> , 2005 , 44, 3955-64 | 3.2 | 88 |
| 28 | The pairwise energy content estimated from amino acid composition discriminates between folded and intrinsically unstructured proteins. <i>Journal of Molecular Biology</i> , 2005 , 347, 827-39 | 6.5 | 767 |
| 27 | The interplay between structure and function in intrinsically unstructured proteins. <i>FEBS Letters</i> , 2005 , 579, 3346-54 | 3.8 | 563 |

(1998-2005)

| 26 | NMR relaxation studies on the hydrate layer of intrinsically unstructured proteins. <i>Biophysical Journal</i> , 2005 , 88, 2030-7 | 2.9 | 72 |
|----|---|-----------------|------|
| 25 | Structural disorder throws new light on moonlighting. <i>Trends in Biochemical Sciences</i> , 2005 , 30, 484-9 | 10.3 | 381 |
| 24 | IUPred: web server for the prediction of intrinsically unstructured regions of proteins based on estimated energy content. <i>Bioinformatics</i> , 2005 , 21, 3433-4 | 7.2 | 1571 |
| 23 | The role of structural disorder in the function of RNA and protein chaperones. <i>FASEB Journal</i> , 2004 , 18, 1169-75 | 0.9 | 456 |
| 22 | On the sequential determinants of calpain cleavage. Journal of Biological Chemistry, 2004, 279, 20775- | 855.4 | 245 |
| 21 | Contribution of distinct structural elements to activation of calpain by Ca2+ ions. <i>Journal of Biological Chemistry</i> , 2004 , 279, 20118-26 | 5.4 | 22 |
| 20 | Differential distribution of calpain small subunit 1 and 2 in rat brain. <i>European Journal of Neuroscience</i> , 2004 , 19, 1819-25 | 3.5 | 10 |
| 19 | Calpain as a multi-site regulator of cell cycle. <i>Biochemical Pharmacology</i> , 2004 , 67, 1513-21 | 6 | 44 |
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