

Vladimir N Uversky

List of Publications by Year in Descending Order

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Version: 2024-04-10

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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.

996 papers	65,541 citations	125 h-index	235 g-index
1,452 ext. papers	74,278 ext. citations	5.6 avg, IF	8.58 L-index

#	Paper	IF	Citations
996	New Evidence of the Importance of Weak Interactions in the Formation of PML-Bodies.. <i>International Journal of Molecular Sciences</i> , 2022 , 23,	6.3	2
995	Age-dependent aggregation of β -synuclein in the nervous system of gut-brain axis is associated with caspase-1 activation.. <i>Metabolic Brain Disease</i> , 2022 , 1	3.9	0
994	Latent potentials of camel's milk.. <i>European Food Research and Technology</i> , 2022 , 248, 1-2	3.4	
993	Experimental methods to study intrinsically disordered proteins 2022 , 505-533		2
992	Bioactive Peptides: Synthesis, Sources, Applications, and Proposed Mechanisms of Action.. <i>International Journal of Molecular Sciences</i> , 2022 , 23,	6.3	14
991	Methods to study the effect of solution variables on the conformational dynamics of intrinsically disordered proteins 2022 , 551-563		
990	Computational methods to study intrinsically disordered proteins 2022 , 489-504		1
989	Identification of the SARS-CoV-2 surface therapeutic targets and drugs using molecular modeling methods for inhibition the virus entry.. <i>Journal of Molecular Structure</i> , 2022 , 132488	3.4	1
988	The importance of accessory protein variants in the pathogenicity of SARS-CoV-2.. <i>Archives of Biochemistry and Biophysics</i> , 2022 , 717, 109124	4.1	2
987	The aqueous humor proteome is intrinsically disordered.. <i>Biochemistry and Biophysics Reports</i> , 2022 , 29, 101202	2.2	
986	The amyloid state of proteins: A boon or bane?. <i>International Journal of Biological Macromolecules</i> , 2022 , 200, 593-617	7.9	0
985	Computational, Experimental, and Clinical Evidence of a Specific but Peculiar Evolutionary Nature of (COVID-19) SARS-CoV-2.. <i>Journal of Proteome Research</i> , 2022 ,	5.6	3
984	Co-opting disorder into order: Intrinsically disordered proteins and the early evolution of complex multicellularity.. <i>International Journal of Biological Macromolecules</i> , 2022 , 201, 29-36	7.9	1
983	Phase separation of FG-nucleoporins in nuclear pore complexes.. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2022 , 1869, 119205	4.9	4
982	From Quantum Mechanics, Classical Mechanics, and Bioinformatics to Artificial Intelligence Studies in Neurodegenerative Diseases.. <i>Methods in Molecular Biology</i> , 2022 , 2340, 139-173	1.4	
981	Intrinsically Disordered Proteins: Critical Components of the Wetware.. <i>Chemical Reviews</i> , 2022 ,	68.1	4
980	Ferritinophagy and β -synuclein: Pharmacological Targeting of Autophagy to Restore Iron Regulation in Parkinson's Disease.. <i>International Journal of Molecular Sciences</i> , 2022 , 23,	6.3	1

979	Identification of intrinsically disorder regions in non-structural proteins of SARS-CoV-2: New insights into drug and vaccine resistance.. <i>Molecular and Cellular Biochemistry</i> , 2022 , 477, 1607	4.2	0
978	Intrinsically disordered proteins play diverse roles in cell signaling.. <i>Cell Communication and Signaling</i> , 2022 , 20, 20	7.5	8
977	Intrinsic disorder in proteins associated with oxidative stress-induced JNK signaling.. <i>Cellular and Molecular Life Sciences</i> , 2022 , 79, 202	10.3	2
976	ATP synthase FF structure, function, and structure-based drug design.. <i>Cellular and Molecular Life Sciences</i> , 2022 , 79, 179	10.3	0
975	BMI1 Silencing Induces Mitochondrial Dysfunction in Lung Epithelial Cells Exposed to Hyperoxia.. <i>Frontiers in Physiology</i> , 2022 , 13, 814510	4.6	
974	Intrinsically disordered proteins: Ensembles at the limits of Anfinsen's dogma. <i>Biophysics Reviews</i> , 2022 , 3, 011306	2.6	1
973	An issue of concern: unique truncated ORF8 protein variants of SARS-CoV-2.. <i>PeerJ</i> , 2022 , 10, e13136	3.1	1
972	An Ayurgenomics Approach: Prakriti-Based Drug Discovery and Development for Personalized Care.. <i>Frontiers in Pharmacology</i> , 2022 , 13, 866827	5.6	
971	Design and Analysis of a Mutant form of the Ice-Binding Protein from <i>Choristoneura fumiferana</i> .. <i>Protein Journal</i> , 2022 , 1	3.9	0
970	Brain Metabolite, Myo-inositol, Inhibits Catalase Activity: A Mechanism of the Distortion of the Antioxidant Defense System in Alzheimer's disease.. <i>ACS Omega</i> , 2022 , 7, 12690-12700	3.9	1
969	Liquid-liquid phase separation as an organizing principle of intracellular space: overview of the evolution of the cell compartmentalization concept.. <i>Cellular and Molecular Life Sciences</i> , 2022 , 79, 251	10.3	9
968	Would New SARS-CoV-2 Variants Change the War against COVID-19?. <i>Epidemiologia</i> , 2022 , 3, 229-237	2.8	0
967	Associations and DiseaseDisease Interactions of COVID-19 with Congenital and Genetic Disorders: A Comprehensive Review. <i>Viruses</i> , 2022 , 14, 910	6.2	1
966	What Is Parvalbumin for?. <i>Biomolecules</i> , 2022 , 12, 656	5.9	2
965	Theater in the Self-Cleaning Cell: Intrinsically Disordered Proteins or Protein Regions Acting with Membranes in Autophagy. <i>Membranes</i> , 2022 , 12, 457	3.8	0
964	Shell Disorder Models Detect That Omicron Has Harder Shells with Attenuation but Is Not a Descendant of the Wuhan-Hu-1 SARS-CoV-2. <i>Biomolecules</i> , 2022 , 12, 631	5.9	1
963	Ibuprofen Favors Binding of Amyloid- β Peptide to Its Depot, Serum Albumin. <i>International Journal of Molecular Sciences</i> , 2022 , 23, 6168	6.3	1
962	BIAPSS: A Comprehensive Physicochemical Analyzer of Proteins Undergoing LiquidLiquid Phase Separation. <i>International Journal of Molecular Sciences</i> , 2022 , 23, 6204	6.3	4

961	Natural container for drug storage and delivery: chimeric GFP with embedded xenogenic peptide. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 4192-4197	3.6	
960	On the potential role of exosomes in the COVID-19 reinfection/reactivation opportunity. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 5831-5842	3.6	37
959	Specific cytokines of interleukin-6 family interact with S100 proteins.. <i>Cell Calcium</i> , 2021 , 101, 102520	4	1
958	Emergence of unique SARS-CoV-2 ORF10 variants and their impact on protein structure and function. <i>International Journal of Biological Macromolecules</i> , 2021 , 194, 128-143	7.9	2
957	The gut metabolite, trimethylamine N-oxide inhibits protein folding by affecting cis-trans isomerization and induces cell cycle arrest.. <i>Cellular and Molecular Life Sciences</i> , 2021 , 79, 12	10.3	1
956	The protein disorder cycle.. <i>Biophysical Reviews</i> , 2021 , 13, 1155-1162	3.7	3
955	Protective Face Masks: Current Status and Future Trends. <i>ACS Applied Materials & Interfaces</i> , 2021 , 13, 56725-56751	9.5	16
954	Functional impact of titin (TTN) mutations in ocular surface squamous neoplasia. <i>International Journal of Biological Macromolecules</i> , 2021 , 195, 93-93	7.9	0
953	Structural and functional significance of the amino acid differences ValThr, SerAla, AsnSer, and AlaSer in 3C-like proteinases from SARS-CoV-2 and SARS-CoV. <i>International Journal of Biological Macromolecules</i> , 2021 , 193, 2113-2113	7.9	1
952	Protein folding, misfolding, and un/non-folding: overview of the SP16 Session at the 20 IUPAB congress, 45 Annual Meeting of SBBf, and 50 Annual Meeting of SBBq.. <i>Biophysical Reviews</i> , 2021 , 13, 879-882	3.7	0
951	Are the functions of milk exosomes restricted to their protein cargoes?. <i>Biomedicine and Pharmacotherapy</i> , 2021 , 146, 112540	7.5	
950	Non-specific porins of Gram-negative bacteria as proteins containing intrinsically disordered regions with amyloidogenic potential. <i>Progress in Molecular Biology and Translational Science</i> , 2021 , 183, 75-99	4	0
949	Directed regulation of the human microbiome: contribution to the solution of the demographic problem in Russia. <i>Journal Biomed</i> , 2021 , 17, 99-105	0.4	
948	The signal peptide of the amyloid precursor protein forms amyloid-like aggregates and enhances A β 42 aggregation. <i>Cell Reports Physical Science</i> , 2021 , 2, 100599	6.1	0
947	Structural and functional properties of thermolabile bacteriocin produced by the <i>Limosilactobacillus fermentum</i> IIE MD-150 strain. <i>Journal Biomed</i> , 2021 , 17, 114-117	0.4	
946	Bioinformatics-Based Identification of Selective Cationic Amphipatic Antibacterial Peptides: Aurein 1.2 Variants Case. <i>Current Proteomics</i> , 2021 , 18, 505-518	0.7	
945	DispHScan: A Multi-Sequence Web Tool for Predicting Protein Disorder as a Function of pH. <i>Biomolecules</i> , 2021 , 11,	5.9	1
944	Inhibition and disruption of amyloid formation by the antibiotic levofloxacin: A new direction for antibiotics in an era of multi-drug resistance. <i>Archives of Biochemistry and Biophysics</i> , 2021 , 714, 109077	4.1	1

943	The latitude hypothesis, vitamin D, and SARS-CoV-2. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 6168-6170	3.6	4
942	The structural basis of accelerated host cell entry by SARS-CoV-2. <i>FEBS Journal</i> , 2021 , 288, 5010-5020	5.7	73
941	The Participation of the Intrinsically Disordered Regions of the bHLH-PAS Transcription Factors in Disease Development. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	1
940	Comprehensive Intrinsic Disorder Analysis of 6108 Viral Proteomes: From the Extent of Intrinsic Disorder Penetrance to Functional Annotation of Disordered Viral Proteins. <i>Journal of Proteome Research</i> , 2021 , 20, 2704-2713	5.6	4
939	ER Stress in Cardiometabolic Diseases: From Molecular Mechanisms to Therapeutics. <i>Endocrine Reviews</i> , 2021 , 42, 839-871	27.2	18
938	On the Role of Normal Aging Processes in the Onset and Pathogenesis of Diseases Associated with the Abnormal Accumulation of Protein Aggregates. <i>Biochemistry (Moscow)</i> , 2021 , 86, 275-289	2.9	2
937	The highly flexible disordered regions of the SARS-CoV-2 nucleocapsid N protein within the 1-248 residue construct: sequence-specific resonance assignments through NMR. <i>Biomolecular NMR Assignments</i> , 2021 , 15, 219-227	0.7	7
936	Predicting Associations of miRNAs and Candidate Gastric Cancer Genes for Nanomedicine. <i>Nanomaterials</i> , 2021 , 11,	5.4	2
935	Small heat shock protein 22 kDa can modulate the aggregation and liquid-liquid phase separation behavior of tau. <i>Protein Science</i> , 2021 , 30, 1350-1359	6.3	9
934	Simple and efficient protocol for immunoglobulin Y purification from chicken egg yolk. <i>Poultry Science</i> , 2021 , 100, 100956	3.9	3
933	Prevalence and functionality of intrinsic disorder in human FG-nucleoporins. <i>International Journal of Biological Macromolecules</i> , 2021 , 175, 156-170	7.9	8
932	Natural resources to control COVID-19: could lactoferrin amend SARS-CoV-2 infectivity?. <i>PeerJ</i> , 2021 , 9, e11303	3.1	5
931	Insights into the evolutionary forces that shape the codon usage in the viral genome segments encoding intrinsically disordered protein regions. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	3
930	Carbon-Based Nanomaterials: Promising Antiviral Agents to Combat COVID-19 in the Microbial-Resistant Era. <i>ACS Nano</i> , 2021 , 15, 8069-8086	16.7	59
929	Photo-dependent membrane-less organelles formed from plant phyB and PIF6 proteins in mammalian cells. <i>International Journal of Biological Macromolecules</i> , 2021 , 176, 325-331	7.9	5
928	The QpH1 plasmid is a virulence factor for colonizing bone marrow-derived murine macrophages. <i>Journal of Bacteriology</i> , 2021 ,	3.5	3
927	Structural leitmotif and functional variations of the structural catalytic core in (chymo)trypsin-like serine/cysteine fold proteinases. <i>International Journal of Biological Macromolecules</i> , 2021 , 179, 601-609	7.9	2
926	Structures of MERS-CoV macro domain in aqueous solution with dynamics: Impacts of parallel tempering simulation techniques and CHARMM36m and AMBER99SB force field parameters. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021 , 89, 1289-1299	4.2	0

925	Recent Developments in the Field of Intrinsically Disordered Proteins: Intrinsic Disorder-Based Emergence in Cellular Biology in Light of the Physiological and Pathological Liquid-Liquid Phase Transitions. <i>Annual Review of Biophysics</i> , 2021 , 50, 135-156	21.1	23
924	The Role of Non-Specific Interactions in Canonical and ALT-Associated PML-Bodies Formation and Dynamics. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	4
923	Chemical synthesis of peptidoglycan mimetic-disaccharide-tetrapeptide conjugate and its hydrolysis by bacteriophage T5, RB43 and RB49 L-alanyl-D-glutamate peptidases. <i>PeerJ</i> , 2021 , 9, e11480 ^{3.1}		
922	Serotonin Promotes Serum Albumin Interaction with the Monomeric Amyloid β Peptide. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	4
921	An emerging role for BAG3 in gynaecological malignancies. <i>British Journal of Cancer</i> , 2021 , 125, 789-797	8.7	2
920	A unique view of SARS-CoV-2 through the lens of ORF8 protein. <i>Computers in Biology and Medicine</i> , 2021 , 133, 104380	7	23
919	Understanding structural malleability of the SARS-CoV-2 proteins and relation to the comorbidities. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	2
918	Notable sequence homology of the ORF10 protein introspects the architecture of SARS-CoV-2. <i>International Journal of Biological Macromolecules</i> , 2021 , 181, 801-809	7.9	25
917	Analysis of the dark proteome of Chandipura virus reveals maximum propensity for intrinsic disorder in phosphoprotein. <i>Scientific Reports</i> , 2021 , 11, 13253	4.9	3
916	Networks of Networks: An Essay on Multi-Level Biological Organization. <i>Frontiers in Genetics</i> , 2021 , 12, 706260	4.5	7
915	Tudor staphylococcal nuclease is a docking platform for stress granule components and is essential for SnRK1 activation in Arabidopsis. <i>EMBO Journal</i> , 2021 , 40, e105043	13	4
914	Computational studies on phylogeny and drug designing using molecular simulations for COVID-19. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 1-10	3.6	4
913	Structural Modeling of the Treponema pallidum Outer Membrane Protein Repertoire: a Road Map for Deconvolution of Syphilis Pathogenesis and Development of a Syphilis Vaccine. <i>Journal of Bacteriology</i> , 2021 , 203, e0008221	3.5	3
912	COVID-19 Vaccines and Thrombosis-Roadblock or Dead-End Street?. <i>Biomolecules</i> , 2021 , 11,	5.9	13
911	Dancing with Trojan horses: an interplay between the extracellular vesicles and viruses. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 3034-3060	3.6	15
910	Phenotypic suppression caused by resonance with light-dark cycles indicates the presence of a 24-hours oscillator in yeast and suggests a new role of intrinsically disordered protein regions as internal mediators. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 2490-2501	3.6	6
909	In Vitro N-Terminal Acetylation of Bacterially Expressed Parvalbumins by N-Terminal Acetyltransferases from Escherichia coli. <i>Applied Biochemistry and Biotechnology</i> , 2021 , 193, 1365-1378	3.2	0
908	Structural facets of POU2F1 in light of the functional annotations and sequence-structure patterns. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 1093-1105	3.6	0

907	Functional characterization of an unknown soybean intrinsically disordered protein in vitro and in Escherichia coli. <i>International Journal of Biological Macromolecules</i> , 2021 , 166, 538-549	7.9	0
906	A multitude of signaling pathways associated with Alzheimer's disease and their roles in AD pathogenesis and therapy. <i>Medicinal Research Reviews</i> , 2021 , 41, 2689-2745	14.4	3
905	Understanding COVID-19 via comparative analysis of dark proteomes of SARS-CoV-2, human SARS and bat SARS-like coronaviruses. <i>Cellular and Molecular Life Sciences</i> , 2021 , 78, 1655-1688	10.3	51
904	IDPology of the living cell: intrinsic disorder in the subcellular compartments of the human cell. <i>Cellular and Molecular Life Sciences</i> , 2021 , 78, 2371-2385	10.3	6
903	Bioinformatics analysis of correlation between protein function and intrinsic disorder. <i>International Journal of Biological Macromolecules</i> , 2021 , 167, 446-456	7.9	1
902	Comparative analysis of the active sites of orthologous endolysins of the Escherichia lytic bacteriophages T5, RB43, and RB49. <i>International Journal of Biological Macromolecules</i> , 2021 , 166, 1096-1105	7.9	1
901	Severe acute respiratory syndrome coronavirus 2 infection reaches the human nervous system: How?. <i>Journal of Neuroscience Research</i> , 2021 , 99, 750-777	4.4	20
900	Questions concerning the proximal origin of SARS-CoV-2. <i>Journal of Medical Virology</i> , 2021 , 93, 1204-1206	6.7	31
899	Shell disorder and the HIV vaccine mystery: lessons from the legendary Oswald Avery. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 1-10	3.6	2
898	Mobility and disorder in antibody and antigen binding sites do not prevent immunochemical recognition. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2021 , 56, 149-156	8.7	5
897	Multifunctionality and intrinsic disorder of royal jelly proteome. <i>Proteomics</i> , 2021 , 21, e2000237	4.8	4
896	Bioinformatics-based Identification of Proteins Expressed by Arthropod- borne Viruses Transmitted by Aedes Aegypti Mosquito. <i>Current Proteomics</i> , 2021 , 18, 81-94	0.7	1
895	Secondary structure dependence of amyloid- β (1-40) on simulation techniques and force field parameters. <i>Chemical Biology and Drug Design</i> , 2021 , 97, 1100-1108	2.9	3
894	Baicalein inhibits heparin-induced Tau aggregation by initializing non-toxic Tau oligomer formation. <i>Cell Communication and Signaling</i> , 2021 , 19, 16	7.5	9
893	On the Prevalence and Potential Functionality of an Intrinsic Disorder in the MERS-CoV Proteome. <i>Viruses</i> , 2021 , 13,	6.2	2
892	On the irrationality of rational design of an HIV vaccine in light of protein intrinsic disorder. <i>Archives of Virology</i> , 2021 , 166, 1283-1296	2.6	4
891	The Finite Size Effects and Two-State Paradigm of Protein Folding. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	1
890	Classification of Chromosomal DNA Sequences Using Hybrid Deep Learning Architectures. <i>Current Bioinformatics</i> , 2021 , 15, 1130-1136	4.7	6

889	The viral capsid as novel nanomaterials for drug delivery. <i>Future Science OA</i> , 2021 , 7, FSO744	2.7	3
888	What's in the BAGs? Intrinsic disorder angle of the multifunctionality of the members of a family of chaperone regulators. <i>Journal of Cellular Biochemistry</i> , 2021 ,	4.7	1
887	Per aspera ad chaos: a personal journey to the wonderland of intrinsic disorder. <i>Biochemical Journal</i> , 2021 , 478, 3015-3024	3.8	4
886	Effects of different solutes on the physical chemical properties of aqueous solutions via rearrangement of hydrogen bonds in water. <i>Journal of Molecular Liquids</i> , 2021 , 335, 116288	6	1
885	Interface-based design of the favipiravir-binding site in SARS-CoV-2 RNA-dependent RNA polymerase reveals mutations conferring resistance to chain termination. <i>FEBS Letters</i> , 2021 , 595, 2366-2382	3.8	7
884	Association Analysis of Genetic Variants of Sodium Taurocholate Co-Transporting Polypeptide NTCP Gene (SLC10A1) and HBV Infection Status in a Cohort of Egyptian Patients. <i>Gastroenterology Insights</i> , 2021 , 12, 384-393	2.1	
883	Mechanisms of amyloid proteins aggregation and their inhibition by antibodies, small molecule inhibitors, nano-particles and nano-bodies. <i>International Journal of Biological Macromolecules</i> , 2021 , 186, 580-590	7.9	6
882	Evaluation of ThT augmentation and RLS inner filter effect caused by highly fluorescent coumarin derivative and establishing it as true inhibitor of amyloid fibrillation. <i>Archives of Biochemistry and Biophysics</i> , 2021 , 709, 108981	4.1	2
881	Autoimmunity roots of the thrombotic events after COVID-19 vaccination. <i>Autoimmunity Reviews</i> , 2021 , 20, 102941	13.6	9
880	S-Protein of the Probiotic Strain <i>Lactobacillus crispatus</i> 2029 Prevents the Growth of Permeability of the Caco-2 Monolayer of Human Enterocytes Induced by Intestinal Infections. <i>Journal Biomed</i> , 2021 , 17, 79-83	0.4	
879	Evolutionary Signatures Governing the Codon Usage Bias in Coronaviruses and Their Implications for Viruses Infecting Various Bat Species. <i>Viruses</i> , 2021 , 13,	6.2	4
878	Targeting autophagy in ischemic stroke: From molecular mechanisms to clinical therapeutics. <i>Pharmacology & Therapeutics</i> , 2021 , 225, 107848	13.9	18
877	Periodically aperiodic pattern of SARS-CoV-2 mutations underpins the uncertainty of its origin and evolution. <i>Environmental Research</i> , 2021 , 204, 112092	7.9	1
876	Potential Molecular Mechanisms of Rare Anti-Tumor Immune Response by SARS-CoV-2 in Isolated Cases of Lymphomas. <i>Viruses</i> , 2021 , 13,	6.2	1
875	Liquid-liquid phase separation as a common organizing principle of intracellular space and biomembranes providing dynamic adaptive responses. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2021 , 1868, 119102	4.9	16
874	The mechanism behind flaring/triggering of autoimmunity disorders associated with COVID-19. <i>Autoimmunity Reviews</i> , 2021 , 20, 102909	13.6	4
873	Intrinsic Disorder in Human RNA-Binding Proteins. <i>Journal of Molecular Biology</i> , 2021 , 433, 167229	6.5	4
872	S-layer protein 2 of vaginal <i>Lactobacillus crispatus</i> 2029 enhances growth, differentiation, VEGF production and barrier functions in intestinal epithelial cell line Caco-2. <i>International Journal of Biological Macromolecules</i> , 2021 , 189, 410-419	7.9	1

871	Implications derived from S-protein variants of SARS-CoV-2 from six continents. <i>International Journal of Biological Macromolecules</i> , 2021 , 191, 934-955	7.9	1
870	The role of amyloids in Alzheimer's and Parkinson's diseases. <i>International Journal of Biological Macromolecules</i> , 2021 , 190, 44-55	7.9	6
869	Intrinsically disordered proteins: Chronology of a discovery. <i>Biophysical Chemistry</i> , 2021 , 279, 106694	3.5	3
868	Feasibility of the vaccine development for SARS-CoV-2 and other viruses using the shell disorder analysis. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2021 , 26, 143-153	1.3	1
867	Peptidoglycan-Free Bacterial Ghosts Confer Enhanced Protection against Infection.. <i>Vaccines</i> , 2021 , 10,	5.3	1
866	Circulating extracellular vesicles and rheumatoid arthritis: a proteomic analysis.. <i>Cellular and Molecular Life Sciences</i> , 2021 , 79, 1	10.3	2
865	Possible Transmission Flow of SARS-CoV-2 Based on ACE2 Features. <i>Molecules</i> , 2020 , 25,	4.8	21
864	Intrinsic disorder perspective of an interplay between the renin-angiotensin-aldosterone system and SARS-CoV-2. <i>Infection, Genetics and Evolution</i> , 2020 , 85, 104510	4.5	6
863	Deciphering the structural intricacy in virulence effectors for proton-motive force mediated unfolding in type-III protein secretion. <i>International Journal of Biological Macromolecules</i> , 2020 , 159, 18-33	7.9	2
862	Japanese encephalitis virus - exploring the dark proteome and disorder-function paradigm. <i>FEBS Journal</i> , 2020 , 287, 3751-3776	5.7	11
861	Intrinsic disorder-based design of stable globular proteins. <i>Progress in Molecular Biology and Translational Science</i> , 2020 , 174, 157-186	4	0
860	Intrinsic Disorder in Tetratricopeptide Repeat Proteins. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	2
859	Intrinsic disorder in protein sense-antisense recognition. <i>Journal of Molecular Recognition</i> , 2020 , 33, e28686	6.8	3
858	Unstructured Biology of Proteins from Ubiquitin-Proteasome System: Roles in Cancer and Neurodegenerative Diseases. <i>Biomolecules</i> , 2020 , 10,	5.9	9
857	Shell disorder analysis predicts greater resilience of the SARS-CoV-2 (COVID-19) outside the body and in body fluids. <i>Microbial Pathogenesis</i> , 2020 , 144, 104177	3.8	46
856	Folding and structural polymorphism of p53 C-terminal domain: One peptide with many conformations. <i>Archives of Biochemistry and Biophysics</i> , 2020 , 684, 108342	4.1	17
855	NBCZone: Universal three-dimensional construction of eleven amino acids near the catalytic nucleophile and base in the superfamily of (chymo)trypsin-like serine fold proteases. <i>International Journal of Biological Macromolecules</i> , 2020 , 153, 399-411	7.9	4
854	Sequential and Asynchronous Strengthening of the Influence of Temperature on the Endo- and Exocytosis of Insulin in the Isolated Vertebrata Hepatocytes: Summing up Previous Studies. <i>Current Protein and Peptide Science</i> , 2020 , 21, 22-35	2.8	

853	An in-vitro elucidation of inhibitory potential of carminic acid: Possible therapeutic approach for neurodegenerative diseases. <i>Journal of Molecular Liquids</i> , 2020 , 303, 112692	6	9
852	Mouse S100G protein exhibits properties characteristic of a calcium sensor. <i>Cell Calcium</i> , 2020 , 87, 102185	1.5	2
851	Interfacial tension and mechanism of liquid-liquid phase separation in aqueous media. <i>Physical Chemistry Chemical Physics</i> , 2020 , 22, 4574-4580	3.6	9
850	S-layer protein 2 of <i>Lactobacillus crispatus</i> 2029, its structural and immunomodulatory characteristics and roles in protective potential of the whole bacteria against foodborne pathogens. <i>International Journal of Biological Macromolecules</i> , 2020 , 150, 400-412	7.9	9
849	Nipah shell disorder, modes of infection, and virulence. <i>Microbial Pathogenesis</i> , 2020 , 141, 103976	3.8	10
848	Intrinsically Disordered Proteins 2020 , 587-612		4
847	Serum albumin-mediated strategy for the effective targeting of SARS-CoV-2. <i>Medical Hypotheses</i> , 2020 , 140, 109790	3.8	19
846	Intrinsically disordered proteins of viruses: Involvement in the mechanism of cell regulation and pathogenesis. <i>Progress in Molecular Biology and Translational Science</i> , 2020 , 174, 1-78	4	22
845	New technologies to analyse protein function: an intrinsic disorder perspective. <i>F1000Research</i> , 2020 , 9,	3.6	9
844	RELT stains prominently in B-cell lymphomas and binds the hematopoietic transcription factor MDF1C. <i>Biochemistry and Biophysics Reports</i> , 2020 , 24, 100868	2.2	0
843	Targeting the NTPase site of Zika virus NS3 helicase for inhibitor discovery. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 38, 4827-4837	3.6	9
842	Granulins modulate liquid-liquid phase separation and aggregation of the prion-like C-terminal domain of the neurodegeneration-associated protein TDP-43. <i>Journal of Biological Chemistry</i> , 2020 , 295, 2506-2519	5.4	11
841	Nucleation-dependent amyloid fibrillation of human GRASP55 in aqueous solution. <i>European Biophysics Journal</i> , 2020 , 49, 133-143	1.9	5
840	The dark side of Alzheimer's disease: unstructured biology of proteins from the amyloid cascade signaling pathway. <i>Cellular and Molecular Life Sciences</i> , 2020 , 77, 4163-4208	10.3	15
839	Folding perspectives of an intrinsically disordered transactivation domain and its single mutation breaking the folding propensity. <i>International Journal of Biological Macromolecules</i> , 2020 , 155, 1359-1372	7.9	6
838	Chemical complementarity between immune receptor CDR3s and IDH1 mutants correlates with increased survival for lower grade glioma. <i>Oncogene</i> , 2020 , 39, 1773-1783	9.2	9
837	Understanding the penetrance of intrinsic protein disorder in rotavirus proteome. <i>International Journal of Biological Macromolecules</i> , 2020 , 144, 892-908	7.9	16
836	Epitope region identification challenges of intrinsically disordered proteins in neurodegenerative diseases: Secondary structure dependence of β -synuclein on simulation techniques and force field parameters. <i>Chemical Biology and Drug Design</i> , 2020 , 96, 659-667	2.9	6

835	Comprehensive analysis of the molecular docking of small molecule inhibitors to the A β peptide and its Osaka-mutant: insights into the molecular mechanisms of A β peptide inhibition. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 38, 4536-4566	3.6	3
834	Liquid-liquid phase separation and fibrillation of the prion protein modulated by a high-affinity DNA aptamer. <i>FASEB Journal</i> , 2020 , 34, 365-385	0.9	22
833	Expanding the understanding of the heterogeneous nature of melanoma with bioinformatics and disorder-based proteomics. <i>International Journal of Biological Macromolecules</i> , 2020 , 150, 1281-1293	7.9	3
832	DeepAdd: Protein function prediction from k-mer embedding and additional features. <i>Computational Biology and Chemistry</i> , 2020 , 89, 107379	3.6	3
831	Biophysical characterization of intrinsically disordered human Golgi matrix protein GRASP65. <i>International Journal of Biological Macromolecules</i> , 2020 , 162, 1982-1993	7.9	4
830	A Novel Strategy for the Development of Vaccines for SARS-CoV-2 (COVID-19) and Other Viruses Using AI and Viral Shell Disorder. <i>Journal of Proteome Research</i> , 2020 , 19, 4355-4363	5.6	6
829	Plasminogen Activator. <i>Biomolecules</i> , 2020 , 10,	5.9	4
828	Liquid-Liquid Phase Separation by Intrinsically Disordered Protein Regions of Viruses: Roles in Viral Life Cycle and Control of Virus-Host Interactions. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	25
827	Drug Discovery Targeting the Disorder-To-Order Transition Regions through the Conformational Diversity Mimicking and Statistical Analysis. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	2
826	Hsp22 with an N-Terminal Domain Truncation Mediates a Reduction in Tau Protein Levels. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	3
825	Loops linking secondary structure elements affect the stability of the molten globule intermediate state of apomyoglobin. <i>FEBS Letters</i> , 2020 , 594, 3293-3304	3.8	1
824	Linear Relationships between Partition Coefficients of Different Organic Compounds and Proteins in Aqueous Two-Phase Systems of Various Polymer and Ionic Compositions. <i>Polymers</i> , 2020 , 12,	4.5	1
823	Shell Disorder Analysis Suggests That Pangolins Offered a Window for a Silent Spread of an Attenuated SARS-CoV-2 Precursor among Humans. <i>Journal of Proteome Research</i> , 2020 , 19, 4543-4552	5.6	17
822	Disorder and cysteines in proteins: A design for orchestration of conformational see-saw and modulatory functions. <i>Progress in Molecular Biology and Translational Science</i> , 2020 , 174, 331-373	4	4
821	Papain-like cysteine proteinase zone (PCP-zone) and PCP structural catalytic core (PCP-SCC) of enzymes with cysteine proteinase fold. <i>International Journal of Biological Macromolecules</i> , 2020 , 165, 1438-1446	7.9	2
820	On the roles of calcium and zinc ions in the formation of a catalytically active form of the metalloenzyme, l-alanyl-d-glutamate peptidase of the bacteriophage T5 (EndoT5). <i>International Journal of Biological Macromolecules</i> , 2020 , 164, 2711-2716	7.9	2
819	The exquisite structural biophysics of the Golgi Reassembly and Stacking Proteins. <i>International Journal of Biological Macromolecules</i> , 2020 , 164, 3632-3644	7.9	2
818	Household pets and SARS-CoV2 transmissibility in the light of the ACE2 intrinsic disorder status. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 1-4	3.6	3

817	On the origin of matrix mechanism in protocells and key problems of molecular biology. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 1-12	3.6	
816	The Pathophysiological Significance of Fibulin-3. <i>Biomolecules</i> , 2020 , 10,	5.9	5
815	Zooming into the Dark Side of Human Annexin-S100 Complexes: Dynamic Alliance of Flexible Partners. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	8
814	Intrinsic Disorder in Human Proteins Encoded by Core Duplicon Gene Families. <i>Journal of Physical Chemistry B</i> , 2020 , 124, 8050-8070	3.4	0
813	Insulin fibrillation: toward strategies for attenuating the process. <i>Chemical Communications</i> , 2020 , 56, 11354-11373	5.8	19
812	Interferon Beta Activity Is Modulated via Binding of Specific S100 Proteins. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	2
811	DeepA-RBPBS: A hybrid convolution and recurrent neural network combined with attention mechanism for predicting RBP binding site. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 1-9	3.6	1
810	Outer Membrane Vesicles as Potential Vaccine Candidates in Protecting against Plague. <i>Biomolecules</i> , 2020 , 10,	5.9	1
809	Bacteriostatic and Bactericidal Activities of Camel Lactoferrins Against Salmonella enterica Serovar Typhi. <i>Probiotics and Antimicrobial Proteins</i> , 2020 , 12, 18-31	5.5	12
808	Analyzing aggregation propensities of clinically relevant PTEN mutants: a new culprit in pathogenesis of cancer and other PTENopathies. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 38, 2253-2266	3.6	2
807	Can a retro-polypeptide fold into a globule?. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 38, 2763-2767	3.6	
806	Codon selection reduces GC content bias in nucleic acids encoding for intrinsically disordered proteins. <i>Cellular and Molecular Life Sciences</i> , 2020 , 77, 149-160	10.3	2
805	Disorder in milk proteins: adipophilin and TIP47, important constituents of the milk fat globule membrane. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 38, 1214-1229	3.6	1
804	Single-cell RNA-Seq: a next generation sequencing tool for a high-resolution view of the individual cell. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 38, 3730-3735	3.6	0
803	Structural and functional analysis of "non-smelly" proteins. <i>Cellular and Molecular Life Sciences</i> , 2020 , 77, 2423-2440	10.3	6
802	Current Challenges and Limitations in the Studies of Intrinsically Disordered Proteins in Neurodegenerative Diseases by Computer Simulations. <i>Current Alzheimer Research</i> , 2020 , 17, 805-818	3	6
801	Functions of short lifetime biological structures at large: the case of intrinsically disordered proteins. <i>Briefings in Functional Genomics</i> , 2020 , 19, 60-68	4.9	11
800	Analyzing IDPs in Interactomes. <i>Methods in Molecular Biology</i> , 2020 , 2141, 895-945	1.4	7

799	Many-to-one binding by intrinsically disordered protein regions. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2020 , 25, 159-170	1.3	5
798	Modulating Insulin Fibrillation Using Engineered B-Chains with Mutated C-Termini. <i>Biophysical Journal</i> , 2019 , 117, 1626-1641	2.9	8
797	Molecular basis of the inhibition and disaggregation of thermally-induced amyloid fibrils of human serum albumin by an anti-Parkinson's drug, benserazide hydrochloride. <i>Journal of Molecular Liquids</i> , 2019 , 278, 553-567	6	18
796	Structure Determination by Single-Particle Cryo-Electron Microscopy: Only the Sky (and Intrinsic Disorder) is the Limit. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	30
795	Supramolecular Fuzziness of Intracellular Liquid Droplets: Liquid-Liquid Phase Transitions, Membrane-Less Organelles, and Intrinsic Disorder. <i>Molecules</i> , 2019 , 24,	4.8	18
794	Intrinsically Disordered Proteins and Their Mysterious[(Meta)Physics. <i>Frontiers in Physics</i> , 2019 , 7,	3.9	188
793	Alanine Scanning Effects on the Biochemical and Biophysical Properties of Intrinsically Disordered Proteins: A Case Study of the Histidine to Alanine Mutations in Amyloid- β . <i>Journal of Chemical Information and Modeling</i> , 2019 , 59, 871-884	6.1	7
792	Effects of his-tags on physical properties of parvalbumins. <i>Cell Calcium</i> , 2019 , 77, 1-7	4	3
791	Intrinsic Disorder-Based Emergence in Cellular Biology: Physiological and Pathological Liquid-Liquid Phase Transitions in Cells. <i>Polymers</i> , 2019 , 11,	4.5	33
790	Ferroptosis - An iron- and disorder-dependent programmed cell death. <i>International Journal of Biological Macromolecules</i> , 2019 , 135, 1052-1069	7.9	23
789	The Structural and Functional Diversity of Intrinsically Disordered Regions in Transmembrane Proteins. <i>Journal of Membrane Biology</i> , 2019 , 252, 273-292	2.3	8
788	Protein intrinsic disorder and structure-function continuum. <i>Progress in Molecular Biology and Translational Science</i> , 2019 , 166, 1-17	4	44
787	HIV Vaccine Mystery and Viral Shell Disorder. <i>Biomolecules</i> , 2019 , 9,	5.9	25
786	Stochasticity of Biological Soft Matter: Emerging Concepts in Intrinsically Disordered Proteins and Biological Phase Separation. <i>Trends in Biochemical Sciences</i> , 2019 , 44, 716-728	10.3	53
785	Network mapping of the conformational heterogeneity of SOD1 by deploying statistical cluster analysis of FTIR spectra. <i>Cellular and Molecular Life Sciences</i> , 2019 , 76, 4145-4154	10.3	3
784	Effect of Cu and Zn ions on human serum albumin interaction with plasma unsaturated fatty acids. <i>International Journal of Biological Macromolecules</i> , 2019 , 131, 505-509	7.9	3
783	Structural and Dynamical Order of a Disordered Protein: Molecular Insights into Conformational Switching of PAGE4 at the Systems Level. <i>Biomolecules</i> , 2019 , 9,	5.9	11
782	Cyclized NDGA modifies dynamic β -nuclein monomers preventing aggregation and toxicity. <i>Scientific Reports</i> , 2019 , 9, 2937	4.9	20

781	Synergistic Killing of Pathogenic Escherichia coli Using Camel Lactoferrin from Different Saudi Camel Clans and Various Antibiotics. <i>Protein Journal</i> , 2019 , 38, 479-496	3.9	2
780	Analyzing the structural and functional roles of residues from the 'black' and 'gray' clusters of human S100P protein. <i>Cell Calcium</i> , 2019 , 80, 46-55	4	2
779	On the Need to Develop Guidelines for Characterizing and Reporting Intrinsic Disorder in Proteins. <i>Proteomics</i> , 2019 , 19, e1800415	4.8	3
778	Intrinsic Disorder-Based Design of Stable Globular Proteins. <i>Biomolecules</i> , 2019 , 10,	5.9	4
777	Multi-functionality of proteins involved in GPCR and G protein signaling: making sense of structure-function continuum with intrinsic disorder-based proteoforms. <i>Cellular and Molecular Life Sciences</i> , 2019 , 76, 4461-4492	10.3	28
776	An interplay of structure and intrinsic disorder in the functionality of peptidylarginine deiminases, a family of key autoimmunity-related enzymes. <i>Cellular and Molecular Life Sciences</i> , 2019 , 76, 4635-4662	10.3	16
775	Intrinsically disordered proteins in various hypotheses on the pathogenesis of Alzheimer's and Parkinson's diseases. <i>Progress in Molecular Biology and Translational Science</i> , 2019 , 166, 145-223	4	11
774	5-Aminolevulinate synthase catalysis: The catcher in heme biosynthesis. <i>Molecular Genetics and Metabolism</i> , 2019 , 128, 178-189	3.7	14
773	Introduction to intrinsically disordered proteins and regions 2019 , 1-34		7
772	Small Heat Shock Proteins, Big Impact on Protein Aggregation in Neurodegenerative Disease. <i>Frontiers in Pharmacology</i> , 2019 , 10, 1047	5.6	53
771	Zika and Flavivirus Shell Disorder: Virulence and Fetal Morbidity. <i>Biomolecules</i> , 2019 , 9,	5.9	17
770	Development of a MEL Cell-Derived Allograft Mouse Model for Cancer Research. <i>Cancers</i> , 2019 , 11,	6.6	1
769	Biophysical Elucidation of Amyloid Fibrillation Inhibition and Prevention of Secondary Nucleation by Cholic Acid: An Unexplored Function of Cholic Acid. <i>ACS Chemical Neuroscience</i> , 2019 , 10, 4704-4715	5.7	9
768	Intrinsic Disorder of the BAF Complex: Roles in Chromatin Remodeling and Disease Development. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	7
767	Bioinformatics characterisation of the (mutated) proteins related to Andersen-Tawil syndrome. <i>Mathematical Biosciences and Engineering</i> , 2019 , 16, 2532-2548	2.1	2
766	Nanoparticle formulations in the diagnosis and therapy of Alzheimer's disease. <i>International Journal of Biological Macromolecules</i> , 2019 , 130, 515-526	7.9	54
765	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	4
764	Rational discovery of antimetastatic agents targeting the intrinsically disordered region of MBD2. <i>Science Advances</i> , 2019 , 5, eaav9810	14.3	12

763	Characterization of an Extensive Interface on Vitronectin for Binding to Plasminogen Activator Inhibitor-1: Adoption of Structure in an Intrinsically Disordered Region. <i>Biochemistry</i> , 2019 , 58, 5117-5134 ²	3.2	3
762	Evolutionary Analyses of Sequence and Structure Space Unravel the Structural Facets of SOD1. <i>Biomolecules</i> , 2019 , 9,	5.9	3
761	Life in Phases: Intra- and Inter- Molecular Phase Transitions in Protein Solutions. <i>Biomolecules</i> , 2019 , 9,	5.9	20
760	Binding of LcrV protein from <i>Yersinia pestis</i> to human T-cells induces apoptosis, which is completely blocked by specific antibodies. <i>International Journal of Biological Macromolecules</i> , 2019 , 122, 1062-1070	7.9	5
759	Effects of amino acids on solvent properties of water. <i>Journal of Molecular Liquids</i> , 2019 , 277, 123-131	6	6
758	Does Intrinsic Disorder in Proteins Favor Their Interaction with Lipids?. <i>Proteomics</i> , 2019 , 19, e1800098	4.8	11
757	Molecular docking of A β peptide and its Iowa DN mutant using small molecule inhibitors: Possible mechanisms of A β peptide inhibition. <i>International Journal of Biological Macromolecules</i> , 2019 , 127, 250-270	7.9	17
756	Effect of C-terminal His-tag and purification routine on the activity and structure of the metalloenzyme, l-alanyl-d-glutamate peptidase of the bacteriophage T5. <i>International Journal of Biological Macromolecules</i> , 2019 , 124, 810-818	7.9	5
755	Perturbation of water structure by water-polymer interactions probed by FTIR and polarized Raman spectroscopy. <i>Journal of Molecular Liquids</i> , 2019 , 275, 463-473	6	15
754	Structural disorder in the proteome and interactome of Alkhurma virus (ALKV). <i>Cellular and Molecular Life Sciences</i> , 2019 , 76, 577-608	10.3	13
753	Effects of sodium chloride and sodium perchlorate on properties and partition behavior of solutes in aqueous dextran-polyethylene glycol and polyethylene glycol-sodium sulfate two-phase systems. <i>Journal of Chromatography A</i> , 2019 , 1583, 28-38	4.5	12
752	Molecular dynamics analysis of the effects of GTP, GDP and benzimidazole derivative on structural dynamics of a cell division protein FtsZ from. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019 , 37, 4361-4373	3.6	8
751	Repeated repeat problems: Combinatorial effect of C9orf72-derived dipeptide repeat proteins. <i>International Journal of Biological Macromolecules</i> , 2019 , 127, 136-145	7.9	8
750	Folding of poly-amino acids and intrinsically disordered proteins in overcrowded milieu induced by pH change. <i>International Journal of Biological Macromolecules</i> , 2019 , 125, 244-255	7.9	7
749	Predicting Functions of Disordered Proteins with MoRFPred. <i>Methods in Molecular Biology</i> , 2019 , 1851, 337-352	1.4	11
748	A multiparametric analysis of the synergistic impact of anti-Parkinson's drugs on the fibrillation of human serum albumin. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019 , 1867, 275-285	4	8
747	On the Regularities of the Polar Profiles of Proteins Related to Ebola Virus Infection and their Functional Domains. <i>Cell Biochemistry and Biophysics</i> , 2018 , 76, 411-431	3.2	3
746	The Use of Human, Bovine, and Camel Milk Albumins in Anticancer Complexes with Oleic Acid. <i>Protein Journal</i> , 2018 , 37, 203-215	3.9	17

745	Deciphering the dark proteome of Chikungunya virus. <i>Scientific Reports</i> , 2018 , 8, 5822	4.9	32
744	Arrestins: structural disorder creates rich functionality. <i>Protein and Cell</i> , 2018 , 9, 986-1003	7.2	16
743	Alpha-synuclein inhibits Snx3-retromer-mediated retrograde recycling of iron transporters in <i>S. cerevisiae</i> and <i>C. elegans</i> models of Parkinson's disease. <i>Human Molecular Genetics</i> , 2018 , 27, 1514-1532	5.6	20
742	Structural Impact of Phosphorylation and Dielectric Constant Variation on Synaptotagmin's IDR. <i>Biophysical Journal</i> , 2018 , 114, 550-561	2.9	8
741	Phase equilibria, solvent properties, and protein partitioning in aqueous polyethylene glycol-600-trimethylamine N-oxide and polyethylene glycol-600-choline chloride two-phase systems. <i>Journal of Chromatography A</i> , 2018 , 1535, 154-161	4.5	13
740	In Aqua Veritas: The Indispensable yet Mostly Ignored Role of Water in Phase Separation and Membrane-less Organelles. <i>Biochemistry</i> , 2018 , 57, 2437-2451	3.2	40
739	Conserved Functional Dynamics: I Like to Move It, Move It!. <i>Structure</i> , 2018 , 26, 371-373	5.2	2
738	Mbd2-CP2c loop drives adult-type globin gene expression and definitive erythropoiesis. <i>Nucleic Acids Research</i> , 2018 , 46, 4933-4949	20.1	5
737	Molecular dynamics analysis of the structural and dynamic properties of the functionally enhanced hepta-variant of mouse 5-aminolevulinate synthase. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018 , 36, 152-165	3.6	4
736	Effect of human heat shock protein HspB6 on the solvent features of water in aqueous solutions. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018 , 36, 1520-1528	3.6	11
735	Intrinsically Disordered Regions in Serum Albumin: What Are They For?. <i>Cell Biochemistry and Biophysics</i> , 2018 , 76, 39-57	3.2	12
734	Dissecting physical structure of calreticulin, an intrinsically disordered Ca-buffering chaperone from endoplasmic reticulum. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018 , 36, 1617-1636	3.6	8
733	Virucidal activity of cell-penetrating peptides of viral origin. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018 , 36, 1739-1746	3.6	5
732	Intrinsic Disorder, Protein-Protein Interactions, and Disease. <i>Advances in Protein Chemistry and Structural Biology</i> , 2018 , 110, 85-121	5.3	66
731	Intrinsically Disordered Proteome of Human Membrane-Less Organelles. <i>Proteomics</i> , 2018 , 18, e1700193	4.8	109
730	Potential functions of LEA proteins from the brine shrimp <i>Artemia franciscana</i> - anhydrobiosis meets bioinformatics. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018 , 36, 3291-3309	3.6	17
729	Intrinsically disordered proteins in crowded milieu: when chaos prevails within the cellular gumbo. <i>Cellular and Molecular Life Sciences</i> , 2018 , 75, 3907-3929	10.3	48
728	Intrinsic Disorder and Posttranslational Modifications: The Darker Side of the Biological Dark Matter. <i>Frontiers in Genetics</i> , 2018 , 9, 158	4.5	111

727	Modified binodal model describes phase separation in aqueous two-phase systems in terms of the effects of phase-forming components on the solvent features of water. <i>Journal of Chromatography A</i> , 2018 , 1567, 226-232	4.5	4
726	Insights into the Molecular Mechanisms of Alzheimer's and Parkinson's Diseases with Molecular Simulations: Understanding the Roles of Artificial and Pathological Missense Mutations in Intrinsically Disordered Proteins Related to Pathology. <i>International Journal of Molecular Sciences</i> , 2018 , 19, 3333-3346	6.3	37
725	Anti-Correlation between the Dynamics of the Active Site Loop and C-Terminal Tail in Relation to the Homodimer Asymmetry of the Mouse Erythroid 5-Aminolevulinate Synthase. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	5
724	Prediction of Disordered Regions and Their Roles in the Anti-Pathogenic and Immunomodulatory Functions of Butyrophilins. <i>Molecules</i> , 2018 , 23,	4.8	4
723	Variability of Some Milk-Associated Genes and Proteins in Several Breeds of Saudi Arabian Camels. <i>Protein Journal</i> , 2018 , 37, 333-352	3.9	1
722	Elucidating the Inhibitory Potential of Designed Peptides Against Amyloid Fibrillation and Amyloid Associated Cytotoxicity. <i>Frontiers in Chemistry</i> , 2018 , 6, 311	5	24
721	Understanding the interactability of chikungunya virus proteins molecular recognition feature analysis.. <i>RSC Advances</i> , 2018 , 8, 27293-27303	3.7	18
720	The solvent side of proteinaceous membrane-less organelles in light of aqueous two-phase systems. <i>International Journal of Biological Macromolecules</i> , 2018 , 117, 1224-1251	7.9	30
719	Neurodegenerative Diseases as Protein Folding Disorders 2018 , 243-267		
718	Chemical modifications of insulin: Finding a compromise between stability and pharmaceutical performance. <i>International Journal of Pharmaceutics</i> , 2018 , 547, 450-468	6.5	19
717	Disorder in Milk Proteins: Lactadherin Multifunctionality and Structure. <i>Current Protein and Peptide Science</i> , 2018 , 19, 983-997	2.8	11
716	Repeat Problems: Combinatorial Effect of C9orf72-Derived Dipeptide Repeat Proteins. <i>FASEB Journal</i> , 2018 , 32, 526.3	0.9	
715	β-synuclein inhibits Snx3-retromer-mediated retrograde recycling of iron transporters in a S. cerevisiae model of Parkinson's disease. <i>FASEB Journal</i> , 2018 , 32, 795.12	0.9	0
714	A Statistical Approach to Detect Intrinsically Disordered Proteins Associated with Uterine Leiomyoma. <i>Protein and Peptide Letters</i> , 2018 , 25, 483-491	1.9	1
713	Stabilizing proteins to prevent conformational changes required for amyloid fibril formation. <i>Journal of Cellular Biochemistry</i> , 2018 , 120, 2642	4.7	15
712	In silico evaluation of the resistance of the T790M variant of epidermal growth factor receptor kinase to cancer drug Erlotinib. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018 , 36, 4209-4219	3.6	10
711	Not all AMLETs are made equal: complexes of cow and camel lactalbumin with oleic acid show different structure and stability. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018 , 36, 4405-4412	3.6	2
710	Molecular Recognition Features in Zika Virus Proteome. <i>Journal of Molecular Biology</i> , 2018 , 430, 2372-2388	3.8	46

709	High-level intrinsic disorder explains the universality of CLIP binding to diverse MHC class II variants. <i>Cellular and Molecular Immunology</i> , 2018 , 15, 76-78	15.4	1
708	Immunogenicity and Protective Activity of a Chimeric Protein Based on the Domain III of the Tick-Borne Encephalitis Virus E Protein and the OmpF Porin of Incorporated into the TI-Complex. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	2
707	Effect of an Intrinsically Disordered Plant Stress Protein on the Properties of Water. <i>Biophysical Journal</i> , 2018 , 115, 1696-1706	2.9	15
706	Intrinsically Disordered Proteins: The Dark Horse of the Dark Proteome. <i>Proteomics</i> , 2018 , 18, e1800061	4.8	39
705	Taxonomic Landscape of the Dark Proteomes: Whole-Proteome Scale Interplay Between Structural Darkness, Intrinsic Disorder, and Crystallization Propensity. <i>Proteomics</i> , 2018 , 18, e1800243	4.8	23
704	Functionally Aberrant Mutant KCNQ1 With Intermediate Heterozygous and Homozygous Phenotypes. <i>Canadian Journal of Cardiology</i> , 2018 , 34, 1174-1184	3.8	1
703	Flexibility of the Sec13/31 cage is influenced by the Sec31 C-terminal disordered domain. <i>Journal of Structural Biology</i> , 2018 , 204, 250-260	3.4	6
702	Comprehensive analysis of the roles of 'black' and 'gray' clusters in structure and function of rat β -parvalbumin. <i>Cell Calcium</i> , 2018 , 75, 64-78	4	7
701	On the relationship between the conserved 'black' and 'gray' structural clusters and intrinsic disorder in parvalbumins. <i>International Journal of Biological Macromolecules</i> , 2018 , 120, 1055-1062	7.9	5
700	Recombinant Fusion Protein Joining E Protein Domain III of Tick-Borne Encephalitis Virus and HSP70 of as an Antigen for the TI-Complexes. <i>Biomolecules</i> , 2018 , 8,	5.9	1
699	Born This Way: Using Intrinsic Disorder to Map the Connections between SLITRKs, TSHR, and Male Sexual Orientation. <i>Proteomics</i> , 2018 , 18, e1800307	4.8	0
698	Structure-Function Relationships in the Oligomeric NADPH-Dependent Assimilatory Sulfite Reductase. <i>Biochemistry</i> , 2018 , 57, 3764-3772	3.2	5
697	Dissection of the deep-blue autofluorescence changes accompanying amyloid fibrillation. <i>Archives of Biochemistry and Biophysics</i> , 2018 , 651, 13-20	4.1	31
696	Interleukin-11 binds specific EF-hand proteins via their conserved structural motifs. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017 , 35, 78-91	3.6	18
695	Effects of low urea concentrations on protein-water interactions. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017 , 35, 207-218	3.6	5
694	Abundance and functional roles of intrinsic disorder in the antimicrobial peptides of the NK-lysin family. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017 , 35, 836-856	3.6	8
693	Evidence for the residual tertiary structure in the urea-unfolded form of bacteriophage T5 endolysin. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017 , 35, 1331-1338	3.6	6
692	Protein intrinsic disorder-based liquid-liquid phase transitions in biological systems: Complex coacervates and membrane-less organelles. <i>Advances in Colloid and Interface Science</i> , 2017 , 239, 97-114	14.3	126

691	Effects of osmolytes on solvent features of water in aqueous solutions. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017 , 35, 1055-1068	3.6	23
690	Effects of the Hofmeister series of sodium salts on the solvent properties of water. <i>Physical Chemistry Chemical Physics</i> , 2017 , 19, 5254-5261	3.6	22
689	Data on evolution of intrinsically disordered regions of the human kinome and contribution of FAK1 IDRs to cytoskeletal remodeling. <i>Data in Brief</i> , 2017 , 10, 315-324	1.2	1
688	Not an exception to the rule: the functional significance of intrinsically disordered protein regions in enzymes. <i>Molecular BioSystems</i> , 2017 , 13, 463-469		30
687	Effects of Intrinsic and Extrinsic Factors on Aggregation of Physiologically Important Intrinsically Disordered Proteins. <i>International Review of Cell and Molecular Biology</i> , 2017 , 329, 145-185	6	14
686	On the potential of using peculiarities of the protein intrinsic disorder distribution in mitochondrial cytochrome to identify the source of animal meats. <i>Intrinsically Disordered Proteins</i> , 2017 , 5, e1264350		1
685	The Calreticulin control of human stress erythropoiesis is impaired by JAK2V617F in polycythemia vera. <i>Experimental Hematology</i> , 2017 , 50, 53-76	3.1	9
684	Purification, biochemical, and structural characterization of a novel fibrinolytic enzyme from <i>Mucor subtilissimus</i> UCP 1262. <i>Bioprocess and Biosystems Engineering</i> , 2017 , 40, 1209-1219	3.7	21
683	Tyrosine Regulates β -Sheet Structure Formation in Amyloid- β : A New Clustering Algorithm for Disordered Proteins. <i>Journal of Chemical Information and Modeling</i> , 2017 , 57, 1342-1358	6.1	19
682	DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , 2017 , 45, D219-D227	20.1	182
681	Quarterly intrinsic disorder digest (April-May-June, 2014). <i>Intrinsically Disordered Proteins</i> , 2017 , 5, e1287505		
680	Intrinsic disorder here, there, and everywhere, and nowhere to escape from it. <i>Cellular and Molecular Life Sciences</i> , 2017 , 74, 3065-3067	10.3	21
679	Comprehensive review of methods for prediction of intrinsic disorder and its molecular functions. <i>Cellular and Molecular Life Sciences</i> , 2017 , 74, 3069-3090	10.3	122
678	Intrinsically Disordered Proteins as Important Players during Desiccation Stress of Soybean Radicles. <i>Journal of Proteome Research</i> , 2017 , 16, 2393-2409	5.6	10
677	Disulfide bonds and disorder in granulin-3: An unusual handshake between structural stability and plasticity. <i>Protein Science</i> , 2017 , 26, 1759-1772	6.3	10
676	Computational Prediction of Intrinsic Disorder in Proteins. <i>Current Protocols in Protein Science</i> , 2017 , 88, 2.16.1-2.16.14	3.1	37
675	PTEN proteoforms in biology and disease. <i>Cellular and Molecular Life Sciences</i> , 2017 , 74, 2783-2794	10.3	54
674	Simultaneous quantification of protein order and disorder. <i>Nature Chemical Biology</i> , 2017 , 13, 339-342	11.7	83

673	Isoniazid inhibits human erythroid 5-aminolevulinate synthase: Molecular mechanism and tolerance study with four X-linked protoporphyria patients. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2017 , 1863, 428-439	6.9	11
672	The effects of crowding agents Dextran-70k and PEG-8k on actin structure and unfolding reaction. <i>Journal of Molecular Structure</i> , 2017 , 1140, 46-51	3.4	7
671	Divergent Anticancer Activity of Free and Formulated Camel Milk β -Lactalbumin. <i>Cancer Investigation</i> , 2017 , 35, 610-623	2.1	25
670	The roles of intrinsic disorder-based liquid-liquid phase transitions in the "Dr. Jekyll-Mr. Hyde" behavior of proteins involved in amyotrophic lateral sclerosis and frontotemporal lobar degeneration. <i>Autophagy</i> , 2017 , 13, 2115-2162	10.2	35
669	Role of solvent properties of water in crowding effects induced by macromolecular agents and osmolytes. <i>Molecular BioSystems</i> , 2017 , 13, 2551-2563		32
668	How accurate are your simulations? Effects of confined aqueous volume and AMBER FF99SB and CHARMM22/CMAP force field parameters on structural ensembles of intrinsically disordered proteins: Amyloid- β in water. <i>Intrinsically Disordered Proteins</i> , 2017 , 5, e1377813		27
667	Paradoxes and wonders of intrinsic disorder: Stability of instability. <i>Intrinsically Disordered Proteins</i> , 2017 , 5, e1327757		16
666	Flexibility of the "rigid" classics or rugged bottom of the folding funnels of myoglobin, lysozyme, RNase A, chymotrypsin, cytochrome c, and carboxypeptidase A1. <i>Intrinsically Disordered Proteins</i> , 2017 , 5, e1355205		1
665	Photophysical Properties of Fluorescent Probe Thioflavin T in Crowded Milieu. <i>Journal of Spectroscopy</i> , 2017 , 2017, 1-10	1.5	8
664	Carbonyl-based blue autofluorescence of proteins and amino acids. <i>PLoS ONE</i> , 2017 , 12, e0176983	3.7	39
663	Structure and Conformational Properties of d-Glucose/d-Galactose-Binding Protein in Crowded Milieu. <i>Molecules</i> , 2017 , 22,	4.8	7
662	Functional Analysis of Human Hub Proteins and Their Interactors Involved in the Intrinsic Disorder-Enriched Interactions. <i>International Journal of Molecular Sciences</i> , 2017 , 18,	6.3	60
661	Cancer/Testis Antigens: "Smart" Biomarkers for Diagnosis and Prognosis of Prostate and Other Cancers. <i>International Journal of Molecular Sciences</i> , 2017 , 18,	6.3	21
660	Looking at the recent advances in understanding β -synuclein and its aggregation through the proteoform prism. <i>F1000Research</i> , 2017 , 6, 525	3.6	34
659	In search for globally disordered apo-parvalbumins: Case of parvalbumin β 1 from coho salmon. <i>Cell Calcium</i> , 2017 , 67, 53-64	4	10
658	The effect of phosphorylation on the salt-tolerance-related functions of the soybean protein PM18, a member of the group-3 LEA protein family. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017 , 1865, 1291-1303	4	10
657	Peculiarities of thermal denaturation of OmpF porin from <i>Yersinia ruckeri</i> . <i>Molecular BioSystems</i> , 2017 , 13, 1854-1862		3
656	Functionality of intrinsic disorder in tumor necrosis factor- α and its receptors. <i>FEBS Journal</i> , 2017 , 284, 3589-3618	5.7	5

655	The relationship between folding and activity in UreG, an intrinsically disordered enzyme. <i>Scientific Reports</i> , 2017 , 7, 5977	4.9	26
654	BMP-2 and BMP-9 binding specificities with ALK-3 in aqueous solution with dynamics. <i>Journal of Molecular Graphics and Modelling</i> , 2017 , 77, 181-188	2.8	2
653	Functional roles of intrinsic disorder in CRISPR-associated protein Cas9. <i>Molecular BioSystems</i> , 2017 , 13, 1770-1780		4
652	How to manipulate partition behavior of proteins in aqueous two-phase systems: Effect of trimethylamine N-oxide (TMAO). <i>Fluid Phase Equilibria</i> , 2017 , 449, 217-224	2.5	5
651	Intrinsically disordered proteins in overcrowded milieu: Membrane-less organelles, phase separation, and intrinsic disorder. <i>Current Opinion in Structural Biology</i> , 2017 , 44, 18-30	8.1	353
650	Intrinsic disorder in proteins involved in amyotrophic lateral sclerosis. <i>Cellular and Molecular Life Sciences</i> , 2017 , 74, 1297-1318	10.3	32
649	Comparative Analysis of the Antiviral Activity of Camel, Bovine, and Human Lactoperoxidases Against Herpes Simplex Virus Type 1. <i>Applied Biochemistry and Biotechnology</i> , 2017 , 182, 294-310	3.2	24
648	How to Predict Disorder in a Protein of Interest. <i>Methods in Molecular Biology</i> , 2017 , 1484, 137-158	1.4	11
647	Prediction of Disordered RNA, DNA, and Protein Binding Regions Using DisoRDPbind. <i>Methods in Molecular Biology</i> , 2017 , 1484, 187-203	1.4	44
646	Physicochemical sequence characteristics that influence S-palmitoylation propensity. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017 , 35, 2337-2350	3.6	13
645	Protective effects of carnosine on dehydroascorbate-induced structural alteration and opacity of lens crystallins: important implications of carnosine pleiotropic functions to combat cataractogenesis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017 , 35, 1766-1784	3.6	11
644	Effect of natural polymorphism on structure and function of the Yersinia pestis outer membrane porin F (OmpF protein): a computational study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017 , 35, 2588-2603	3.6	3
643	What are the structural features that drive partitioning of proteins in aqueous two-phase systems?. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017 , 1865, 113-120	4	14
642	Structural pliability adjacent to the kinase domain highlights contribution of FAK1 IDRs to cytoskeletal remodeling. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017 , 1865, 43-54	4	2
641	Challenging drug target for Parkinson's disease: Pathological complex of the chameleon TPPP/p25 and alpha-synuclein proteins. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2017 , 1863, 310-323	6.9	14
640	Osmolyte-Like Stabilizing Effects of Low GdnHCl Concentrations on d-Glucose/d-Galactose-Binding Protein. <i>International Journal of Molecular Sciences</i> , 2017 , 18,	6.3	1
639	A Comprehensive Survey of the Roles of Highly Disordered Proteins in Type 2 Diabetes. <i>International Journal of Molecular Sciences</i> , 2017 , 18,	6.3	23
638	Identification and Initial Characterization of the Effectors of an Anther Smut Fungus and Potential Host Target Proteins. <i>International Journal of Molecular Sciences</i> , 2017 , 18,	6.3	9

637	Real Time Monitoring of Children, and Adults with Mental Disabilities Using a Low-Cost Non-Invasive Electronic Device. <i>Micromachines</i> , 2017 , 8,	3.3	1
636	Intrinsic Disorder in Proteins with Pathogenic Repeat Expansions. <i>Molecules</i> , 2017 , 22,	4.8	33
635	Calreticulin: Challenges Posed by the Intrinsically Disordered Nature of Calreticulin to the Study of Its Function. <i>Frontiers in Cell and Developmental Biology</i> , 2017 , 5, 96	5.7	11
634	Human cyclophilin 40 unravels neurotoxic amyloids. <i>PLoS Biology</i> , 2017 , 15, e2001336	9.7	29
633	The polar profile of ancient proteins: a computational extrapolation from prebiotics to paleobiochemistry. <i>Acta Biochimica Polonica</i> , 2017 , 64, 117-122	2	2
632	Diagnostic and prognostic relevance of CP2c and YY1 expression in hepatocellular carcinoma. <i>Oncotarget</i> , 2017 , 8, 24389-24400	3.3	14
631	In Vitro Exploration of the Anti-HCV Potential of the Synthetic Spacer Peptides Derived from Human, Bovine, and Camel Lactoferrins. <i>Protein and Peptide Letters</i> , 2017 , 24, 909-921	1.9	4
630	When Good Goes Awry: The Aggregation of Protein Therapeutics. <i>Protein and Peptide Letters</i> , 2017 , 24, 340-347	1.9	8
629	Highly Disordered Proteins in Prostate Cancer. <i>Current Protein and Peptide Science</i> , 2017 , 18, 453-481	2.8	8
628	Parvalbumin as a Pleomorphic Protein. <i>Current Protein and Peptide Science</i> , 2017 , 18, 780-794	2.8	16
627	Electronegativity and intrinsic disorder of preeclampsia-related proteins. <i>Acta Biochimica Polonica</i> , 2017 , 64, 99-111	2	
626	Intrinsic Disorder in Male Sex Determination: Disorderedness of Proteins from the Sry Transcriptional Network. <i>Current Protein and Peptide Science</i> , 2017 , 18, 482-514	2.8	
625	Protein unfolding in crowded milieu: what crowding can do to a protein undergoing unfolding?. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016 , 34, 2155-70	3.6	23
624	Pseudocatalytic Antiaggregation Activity of Antibodies: Immunoglobulins can Influence β -Synuclein Aggregation at Substoichiometric Concentrations. <i>Molecular Neurobiology</i> , 2016 , 53, 1949-1958	6.2	9
623	Nickel impact on human health: An intrinsic disorder perspective. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016 , 1864, 1714-1731	4	98
622	Substitutions of Amino Acids with Large Number of Contacts in the Native State Have no Effect on the Rates of Protein Folding. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016 , 1864, 1809-1817	4.17	2
621	Baicalein inhibits β -Synuclein oligomer formation and prevents progression of β -Synuclein accumulation in a rotenone mouse model of Parkinson's disease. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2016 , 1862, 1883-90	6.9	49
620	The unfolding pathways of the native and molten globule states of 5-aminolevulinate synthase. <i>Biochemical and Biophysical Research Communications</i> , 2016 , 480, 321-327	3.4	2

619	Looking at the carcinogenicity of human insulin analogues via the intrinsic disorder prism. <i>Scientific Reports</i> , 2016 , 6, 23320	4.9	6
618	Intrinsic disorder in biomarkers of insulin resistance, hypoadiponectinemia, and endothelial dysfunction among the type 2 diabetic patients. <i>Intrinsically Disordered Proteins</i> , 2016 , 4, e1171278		5
617	Virucidal activity of human α - and β -defensins against hepatitis C virus genotype 4. <i>Molecular BioSystems</i> , 2016 , 12, 2785-97		6
616	Interleukin-11: A Multifunctional Cytokine with Intrinsically Disordered Regions. <i>Cell Biochemistry and Biophysics</i> , 2016 , 74, 285-96	3.2	12
615	Protein folding and stability in the presence of osmolytes. <i>Biophysics (Russian Federation)</i> , 2016 , 61, 185-192	4.9	5
614	Disordered nucleome: Abundance of intrinsic disorder in the DNA- and RNA-binding proteins in 1121 species from Eukaryota, Bacteria and Archaea. <i>Proteomics</i> , 2016 , 16, 1486-98	4.8	66
613	Resolving the ambiguity: Making sense of intrinsic disorder when PDB structures disagree. <i>Protein Science</i> , 2016 , 25, 676-88	6.3	34
612	Mechanistic study of the inhibitory activity of Geum urbanum extract against β -Synuclein fibrillation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016 , 1864, 1160-1169	4	15
611	Structural differences between amyloid beta oligomers. <i>Biochemical and Biophysical Research Communications</i> , 2016 , 477, 700-705	3.4	47
610	Role of solvent properties of aqueous media in macromolecular crowding effects. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016 , 34, 92-103	3.6	43
609	Intrinsically disordered proteins in PubMed: what can the tip of the iceberg tell us about what lies below?. <i>RSC Advances</i> , 2016 , 6, 11513-11521	3.7	12
608	Paradoxes and wonders of intrinsic disorder: Complexity of simplicity. <i>Intrinsically Disordered Proteins</i> , 2016 , 4, e1135015		31
607	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). <i>Autophagy</i> , 2016 , 12, 1-222	10.2	3838
606	Molecular recognition features (MoRFs) in three domains of life. <i>Molecular BioSystems</i> , 2016 , 12, 697-710		95
605	High Fluorescence Anisotropy of Thioflavin T in Aqueous Solution Resulting from Its Molecular Rotor Nature. <i>Analytical Chemistry</i> , 2016 , 88, 718-24	7.8	28
604	Interrelationship between partition behavior of organic compounds and proteins in aqueous dextran-polyethylene glycol and polyethylene glycol-sodium sulfate two-phase systems. <i>Journal of Chromatography A</i> , 2016 , 1443, 21-5	4.5	8
603	Quarterly intrinsic disorder digest (January-February-March, 2014). <i>Intrinsically Disordered Proteins</i> , 2016 , 4, e1153395		1
602	Dancing Protein Clouds: The Strange Biology and Chaotic Physics of Intrinsically Disordered Proteins. <i>Journal of Biological Chemistry</i> , 2016 , 291, 6681-8	5.4	128

601	Solvent interaction analysis as a proteomic approach to structure-based biomarker discovery and clinical diagnostics. <i>Expert Review of Proteomics</i> , 2016 , 13, 9-17	4.2	9
600	A hyperbranched dopamine-containing PEG-based polymer for the inhibition of β -synuclein fibrillation. <i>Biochemical and Biophysical Research Communications</i> , 2016 , 469, 830-5	3.4	19
599	Analytical applications of partitioning in aqueous two-phase systems: Exploring protein structural changes and protein-partner interactions in vitro and in vivo by solvent interaction analysis method. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016 , 1864, 622-44	4	32
598	(Intrinsically disordered) splice variants in the proteome: implications for novel drug discovery. <i>Genes and Genomics</i> , 2016 , 38, 577-594	2.1	8
597	Antimicrobial potentials and structural disorder of human and animal defensins. <i>Cytokine and Growth Factor Reviews</i> , 2016 , 28, 95-111	17.9	45
596	Erythropoietin and co.: intrinsic structure and functional disorder. <i>Molecular BioSystems</i> , 2016 , 13, 56-72		15
595	Intrinsic Disorder in Transmembrane Proteins: Roles in Signaling and Topology Prediction. <i>PLoS ONE</i> , 2016 , 11, e0158594	3.7	35
594	β -Lactalbumin: Of Camels and Cows. <i>Protein and Peptide Letters</i> , 2016 , 23, 1072-1080	1.9	13
593	Disorder in Milk Proteins: β -Lactalbumin. Part A. Structural Properties and Conformational Behavior. <i>Current Protein and Peptide Science</i> , 2016 , 17, 352-67	2.8	8
592	Disorder in Milk Proteins: β -Lactalbumin. Part B. A Multifunctional Whey Protein Acting as an Oligomeric Molten Globular "Oil Container" in the Anti-Tumorigenic Drugs, Lipotides. <i>Current Protein and Peptide Science</i> , 2016 , 17, 612-28	2.8	9
591	Disorder in Milk Proteins: β -Lactalbumin. Part C. Peculiarities of Metal Binding. <i>Current Protein and Peptide Science</i> , 2016 , 17, 735-745	2.8	10
590	Disorder in Milk Proteins: β -Lactalbumin. Part A. Structural Properties and Conformational Behavior. <i>Current Protein and Peptide Science</i> , 2016 , 17, 352-367	2.8	9
589	Untapped Potential of Disordered Proteins in Current Druggable Human Proteome. <i>Current Drug Targets</i> , 2016 , 17, 1198-205	3	45
588	Unfoldomics of prostate cancer: on the abundance and roles of intrinsically disordered proteins in prostate cancer. <i>Asian Journal of Andrology</i> , 2016 , 18, 662-72	2.8	5
587	A widely employed germ cell marker is an ancient disordered protein with reproductive functions in diverse eukaryotes. <i>ELife</i> , 2016 , 5,	8.9	35
586	Structure and stability of recombinant bovine odorant-binding protein: II. Unfolding of the monomeric forms. <i>PeerJ</i> , 2016 , 4, e1574	3.1	2
585	Structure and stability of recombinant bovine odorant-binding protein: III. Peculiarities of the wild type bOBP unfolding in crowded milieu. <i>PeerJ</i> , 2016 , 4, e1642	3.1	3
584	Structure and stability of recombinant bovine odorant-binding protein: I. Design and analysis of monomeric mutants. <i>PeerJ</i> , 2016 , 4, e1933	3.1	4

583	Simple approach for ranking structure determining residues. <i>PeerJ</i> , 2016 , 4, e2136	3.1	2
582	Unfoldomes and Unfoldomics: Introducing Intrinsically Disordered Proteins 2016 , 125-150		1
581	Polymorphism of the Cysteine Protease YopT from <i>Yersinia pestis</i> . <i>Protein and Peptide Letters</i> , 2016 , 23, 379-85	1.9	
580	Classifying lipoproteins based on their polar profiles. <i>Acta Biochimica Polonica</i> , 2016 , 63, 235-41	2	
579	Structure and function relationships of proteins based on polar profile: a review. <i>Acta Biochimica Polonica</i> , 2016 , 63, 229-33	2	4
578	Order, Disorder, and Everything in Between. <i>Molecules</i> , 2016 , 21,	4.8	56
577	Intrinsically Disordered Side of the Zika Virus Proteome. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016 , 6, 144	5.9	65
576	Peculiarities of the Super-Folder GFP Folding in a Crowded Milieu. <i>International Journal of Molecular Sciences</i> , 2016 , 17,	6.3	8
575	p53 Proteoforms and Intrinsic Disorder: An Illustration of the Protein Structure-Function Continuum Concept. <i>International Journal of Molecular Sciences</i> , 2016 , 17,	6.3	102
574	<i>Yersinia pestis</i> Caf1 Protein: Effect of Sequence Polymorphism on Intrinsic Disorder Propensity, Serological Cross-Reactivity and Cross-Protectivity of Isoforms. <i>PLoS ONE</i> , 2016 , 11, e0162308	3.7	3
573	Prothymosin- Δ Variants Elicit Anti-HIV-1 Response via TLR4 Dependent and Independent Pathways. <i>PLoS ONE</i> , 2016 , 11, e0156486	3.7	7
572	Two Isoforms of <i>Yersinia pestis</i> Plasminogen Activator Pla: Intraspecies Distribution, Intrinsic Disorder Propensity, and Contribution to Virulence. <i>PLoS ONE</i> , 2016 , 11, e0168089	3.7	5
571	Expression, Purification, and Characterization of Interleukin-11 Orthologues. <i>Molecules</i> , 2016 , 21,	4.8	2
570	Autophagy-related intrinsically disordered proteins in intra-nuclear compartments. <i>Molecular BioSystems</i> , 2016 , 12, 2798-817		24
569	Chicken cathelicidins as potent intrinsically disordered biocides with antimicrobial activity against infectious pathogens. <i>Developmental and Comparative Immunology</i> , 2016 , 65, 8-24	3.2	10
568	Structure and dynamics of the retro-form of the bacteriophage T5 endolysin. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016 , 1864, 1281-91	4	6
567	Native globular actin has a thermodynamically unstable quasi-stationary structure with elements of intrinsic disorder. <i>FEBS Journal</i> , 2016 , 283, 438-45	5.7	6
566	Intrinsic disorder in spondins and some of their interacting partners. <i>Intrinsically Disordered Proteins</i> , 2016 , 4, e1255295		7

565	Understanding the roles of intrinsic disorder in subunits of hemoglobin and the disease process of sickle cell anemia. <i>Intrinsically Disordered Proteins</i> , 2016 , 4, e1248273		4
564	How disordered is my protein and what is its disorder for? A guide through the "dark side" of the protein universe. <i>Intrinsically Disordered Proteins</i> , 2016 , 4, e1259708		66
563	Comparison of the intrinsic disorder propensities of the RuBisCO activase enzyme from the motile and non-motile oceanic green microalgae. <i>Intrinsically Disordered Proteins</i> , 2016 , 4, e1253526		3
562	Genes encoding intrinsic disorder in Eukaryota have high GC content. <i>Intrinsically Disordered Proteins</i> , 2016 , 4, e1262225		16
561	Macromolecular crowders and osmolytes modulate the structural and catalytic properties of alkaline molten globular 5-aminolevulinate synthase. <i>RSC Advances</i> , 2016 , 6, 114541-114552	3.7	2
560	Why physicochemical properties of aqueous solutions of various compounds are linearly interrelated. <i>Journal of Molecular Liquids</i> , 2016 , 221, 116-123	6	15
559	Biocidal activity of chicken defensin-9 against microbial pathogens. <i>Biochemistry and Cell Biology</i> , 2016 , 94, 176-87	3.6	9
558	Functional correlations of respiratory syncytial virus proteins to intrinsic disorder. <i>Molecular BioSystems</i> , 2016 , 12, 1507-26		13
557	Troponins, intrinsic disorder, and cardiomyopathy. <i>Biological Chemistry</i> , 2016 , 397, 731-51	4.5	15
556	Murine erythroid 5-aminolevulinate synthase: Truncation of a disordered N-terminal extension is not detrimental for catalysis. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016 , 1864, 441-524		5
555	Correlating Flavivirus virulence and levels of intrinsic disorder in shell proteins: protective roles vs. immune evasion. <i>Molecular BioSystems</i> , 2016 , 12, 1881-91		25
554	A simplified method for the purification of an intrinsically disordered coagulant protein from defatted Moringa oleifera seeds. <i>Process Biochemistry</i> , 2016 , 51, 1085-1091	4.8	28
553	Hydrophobicity-dependent effects of polymers on different protein conformations. <i>RSC Advances</i> , 2016 , 6, 42971-42983	3.7	3
552	Significant antibacterial activity and synergistic effects of camel lactoferrin with antibiotics against methicillin-resistant Staphylococcus aureus (MRSA). <i>Research in Microbiology</i> , 2016 , 167, 480-91	4	31
551	Analysis of the distribution of organic compounds and drugs between biological tissues in the framework of solute partitioning in aqueous two-phase systems. <i>Molecular BioSystems</i> , 2016 , 12, 3567-3575		4
550	Effects of osmolytes on protein-solvent interactions in crowded environment: Analyzing the effect of TMAO on proteins in crowded solutions. <i>Archives of Biochemistry and Biophysics</i> , 2015 , 570, 66-74	4.1	18
549	Unreported intrinsic disorder in proteins: Disorder emergency room. <i>Intrinsically Disordered Proteins</i> , 2015 , 3, e1010999		3
548	Analyzing the effects of protecting osmolytes on solute-water interactions by solvatochromic comparison method: I. Small organic compounds. <i>RSC Advances</i> , 2015 , 5, 59812-59822	3.7	24

547	Analyzing the effects of protecting osmolytes on solute-water interactions by solvatochromic comparison method: II. Globular proteins. <i>RSC Advances</i> , 2015 , 5, 59780-59791	3.7	20
546	Human consensus interferons: Bridging the natural and artificial cytokines with intrinsic disorder. <i>Cytokine and Growth Factor Reviews</i> , 2015 , 26, 637-45	17.9	4
545	Structural, morphological, and functional diversity of amyloid oligomers. <i>FEBS Letters</i> , 2015 , 589, 2640-83.8	120	
544	Protein Misfolding in Lipid-Mimetic Environments. <i>Advances in Experimental Medicine and Biology</i> , 2015 , 855, 33-66	3.6	10
543	Potential antiviral activities of camel, bovine, and human lactoperoxidases against hepatitis C virus genotype 4. <i>RSC Advances</i> , 2015 , 5, 60441-60452	3.7	12
542	The multifaceted roles of intrinsic disorder in protein complexes. <i>FEBS Letters</i> , 2015 , 589, 2498-506	3.8	92
541	Paradoxes and wonders of intrinsic disorder: Prevalence of exceptionality. <i>Intrinsically Disordered Proteins</i> , 2015 , 3, e1065029		9
540	Effects of Polymer Hydrophobicity on Protein Structure and Aggregation Kinetics in Crowded Milieu. <i>Biochemistry</i> , 2015 , 54, 2957-66	3.2	30
539	High-resolution NMR structure of a Zn ²⁺ -containing form of the bacteriophage T5 L-alanyl-D-glutamate peptidase. <i>RSC Advances</i> , 2015 , 5, 41041-41049	3.7	9
538	Responses of proteins to different ionic environment are linearly interrelated. <i>Journal of Chromatography A</i> , 2015 , 1387, 32-41	4.5	17
537	Effects of osmolytes on protein-solvent interactions in crowded environments: study of sucrose and trehalose effects on different proteins by solvent interaction analysis. <i>RSC Advances</i> , 2015 , 5, 27154-27162	3.7	16
536	Hidden disorder propensity of the N-terminal segment of universal adapter protein 14-3-3 is manifested in its monomeric form: Novel insights into protein dimerization and multifunctionality. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015 , 1854, 492-504	4	15
535	Identification of intrinsically disordered regions in PTEN and delineation of its function via a network approach. <i>Methods</i> , 2015 , 77-78, 69-74	4.6	10
534	Digested disorder, Quarterly intrinsic disorder digest (October-November-December, 2013). <i>Intrinsically Disordered Proteins</i> , 2015 , 3, e984569		2
533	Pliable natural biocide: Jaburetox is an intrinsically disordered insecticidal and fungicidal polypeptide derived from jack bean urease. <i>FEBS Journal</i> , 2015 , 282, 1043-64	5.7	23
532	The intrinsic disorder alphabet. III. Dual personality of serine. <i>Intrinsically Disordered Proteins</i> , 2015 , 3, e1027032		20
531	Biophysical Methods to Investigate Intrinsically Disordered Proteins: Avoiding an "Elephant and Blind Men" Situation. <i>Advances in Experimental Medicine and Biology</i> , 2015 , 870, 215-60	3.6	26
530	Intrinsically disordered proteins in the nucleus of human cells. <i>Biochemistry and Biophysics Reports</i> , 2015 , 1, 33-51	2.2	37

529	Human Erythroid 5-Aminolevulinate Synthase Mutations Associated with X-Linked Protoporphyria Disrupt the Conformational Equilibrium and Enhance Product Release. <i>Biochemistry</i> , 2015 , 54, 5617-31	3.2	16
528	Analysis of partitioning of organic compounds and proteins in aqueous polyethylene glycol-sodium sulfate aqueous two-phase systems in terms of solute-solvent interactions. <i>Journal of Chromatography A</i> , 2015 , 1415, 1-10	4.5	28
527	Intrinsically disordered proteins as crucial constituents of cellular aqueous two phase systems and coacervates. <i>FEBS Letters</i> , 2015 , 589, 15-22	3.8	153
526	Intrinsic disorder mediates hepatitis C virus core-host cell protein interactions. <i>Protein Science</i> , 2015 , 24, 221-35	6.3	34
525	Proteins without unique 3D structures: biotechnological applications of intrinsically unstable/disordered proteins. <i>Biotechnology Journal</i> , 2015 , 10, 356-66	5.6	19
524	Exceptionally abundant exceptions: comprehensive characterization of intrinsic disorder in all domains of life. <i>Cellular and Molecular Life Sciences</i> , 2015 , 72, 137-51	10.3	234
523	Beyond the excluded volume effects: mechanistic complexity of the crowded milieu. <i>Molecules</i> , 2015 , 20, 1377-409	4.8	118
522	Unstructural biology of the Dengue virus proteins. <i>FEBS Journal</i> , 2015 , 282, 3368-94	5.7	43
521	Identifying Similar Patterns of Structural Flexibility in Proteins by Disorder Prediction and Dynamic Programming. <i>International Journal of Molecular Sciences</i> , 2015 , 16, 13829-49	6.3	5
520	"In-plant" NMR: analysis of the intact plant <i>Vesicularia dubyana</i> by high resolution NMR spectroscopy. <i>Molecules</i> , 2015 , 20, 4359-68	4.8	3
519	Solvent Properties of Water in Aqueous Solutions of Elastin-Like Polypeptide. <i>International Journal of Molecular Sciences</i> , 2015 , 16, 13528-47	6.3	17
518	Hot, Hotter, and Hottest Trends in Synuclein Research. <i>Current Protein and Peptide Science</i> , 2015 , 16, 682-7	2.8	5
517	Identification of proteins associated with amyloidosis by polarity index method. <i>Acta Biochimica Polonica</i> , 2015 , 62, 41-55	2	3
516	Intrinsically disordered proteins and their (disordered) proteomes in neurodegenerative disorders. <i>Frontiers in Aging Neuroscience</i> , 2015 , 7, 18	5.3	109
515	Shell disorder, immune evasion and transmission behaviors among human and animal retroviruses. <i>Molecular BioSystems</i> , 2015 , 11, 2312-23		17
514	Detection of links between Ebola nucleocapsid and virulence using disorder analysis. <i>Molecular BioSystems</i> , 2015 , 11, 2337-44		15
513	Effect of sodium chloride on solute-solvent interactions in aqueous polyethylene glycol-sodium sulfate two-phase systems. <i>Journal of Chromatography A</i> , 2015 , 1425, 51-61	4.5	11
512	In various protein complexes, disordered protomers have large per-residue surface areas and area of protein-, DNA- and RNA-binding interfaces. <i>FEBS Letters</i> , 2015 , 589, 2561-9	3.8	30

511	Role of monomer arrangement in the amyloid self-assembly. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015 , 1854, 218-28	4	14
510	Functional roles of transiently and intrinsically disordered regions within proteins. <i>FEBS Journal</i> , 2015 , 282, 1182-9	5.7	121
509	Disorder in milk proteins: caseins, intrinsically disordered colloids. <i>Current Protein and Peptide Science</i> , 2015 , 16, 228-42	2.8	28
508	Disorder in milk proteins: structure, functional disorder, and biocidal potentials of lactoperoxidase. <i>Current Protein and Peptide Science</i> , 2015 , 16, 352-65	2.8	17
507	Intrinsically disordered caldesmon binds calmodulin via the "buttons on a string" mechanism. <i>PeerJ</i> , 2015 , 3, e1265	3.1	7
506	Compartmentalization and Functionality of Nuclear Disorder: Intrinsic Disorder and Protein-Protein Interactions in Intra-Nuclear Compartments. <i>International Journal of Molecular Sciences</i> , 2015 , 17,	6.3	78
505	A creature with a hundred waggly tails: intrinsically disordered proteins in the ribosome. <i>Cellular and Molecular Life Sciences</i> , 2014 , 71, 1477-504	10.3	98
504	A putative role of the Sup35p C-terminal domain in the cytoskeleton organization during yeast mitosis. <i>Molecular BioSystems</i> , 2014 , 10, 925-40		4
503	Structural features important for differences in protein partitioning in aqueous dextran-polyethylene glycol two-phase systems of different ionic compositions. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 694-704	4	20
502	Disordered proteinaceous machines. <i>Chemical Reviews</i> , 2014 , 114, 6806-43	68.1	92
501	Pathological unfoldomics of uncontrolled chaos: intrinsically disordered proteins and human diseases. <i>Chemical Reviews</i> , 2014 , 114, 6844-79	68.1	186
500	Structural disorder in viral proteins. <i>Chemical Reviews</i> , 2014 , 114, 6880-911	68.1	133
499	Introducing protein intrinsic disorder. <i>Chemical Reviews</i> , 2014 , 114, 6561-88	68.1	487
498	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
497	The crowd you're in with: effects of different types of crowding agents on protein aggregation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 346-57	4	66
496	Identification of Atg3 as an intrinsically disordered polypeptide yields insights into the molecular dynamics of autophagy-related proteins in yeast. <i>Autophagy</i> , 2014 , 10, 1093-104	10.2	26
495	The intrinsically disordered structural platform of the plant defence hub protein RPM1-interacting protein 4 provides insights into its mode of action in the host-pathogen interface and evolution of the nitrate-induced domain protein family. <i>FEBS Journal</i> , 2014 , 281, 3955-79	5.7	27
494	The intrinsic disorder status of the human hepatitis C virus proteome. <i>Molecular BioSystems</i> , 2014 , 10, 1345-63		52

493 Fundamentals of Protein Folding **2014**, 1-61

492	Toward a common aggregation mechanism for a β -barrel protein family: insights derived from a stable dimeric species. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 1599-607	4	7
491	Screening the anti infectivity potentials of native N- and C-lobes derived from the camel lactoferrin against hepatitis C virus. <i>BMC Complementary and Alternative Medicine</i> , 2014 , 14, 219	4.7	33
490	Catalytically active alkaline molten globular enzyme: Effect of pH and temperature on the structural integrity of 5-aminolevulinate synthase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 2145-54	4	15
489	Potential lactoferrin activity against pathogenic viruses. <i>Comptes Rendus - Biologies</i> , 2014 , 337, 581-95	1.4	58
488	Classification of intrinsically disordered regions and proteins. <i>Chemical Reviews</i> , 2014 , 114, 6589-631	68.1	1141
487	Conditionally and transiently disordered proteins: awakening cryptic disorder to regulate protein function. <i>Chemical Reviews</i> , 2014 , 114, 6779-805	68.1	136
486	Dancing retro: solution structure and micelle interactions of the retro-SH3-domain, retro-SHH-'Bergerac'. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014 , 32, 257-72	3.6	7
485	Molecular Mechanisms of Protein Misfolding 2014 , 1-14		
484	Presence and utility of intrinsically disordered regions in kinases. <i>Molecular BioSystems</i> , 2014 , 10, 2876-88		22
483	Intrinsic disorder in proteins involved in the innate antiviral immunity: another flexible side of a molecular arms race. <i>Journal of Molecular Biology</i> , 2014 , 426, 1322-50	6.5	27
482	The structural and functional signatures of proteins that undergo multiple events of post-translational modification. <i>Protein Science</i> , 2014 , 23, 1077-93	6.3	226
481	Intracellular processing of disease-associated β -synuclein in the human brain suggests prion-like cell-to-cell spread. <i>Neurobiology of Disease</i> , 2014 , 69, 76-92	7.5	78
480	Wrecked regulation of intrinsically disordered proteins in diseases: pathogenicity of deregulated regulators. <i>Frontiers in Molecular Biosciences</i> , 2014 , 1, 6	5.6	68
479	Improving protein order-disorder classification using charge-hydropathy plots. <i>BMC Bioinformatics</i> , 2014 , 15 Suppl 17, S4	3.6	38
478	Intrinsic disorder in the BK channel and its interactome. <i>PLoS ONE</i> , 2014 , 9, e94331	3.7	14
477	The triple power of $\Delta\alpha$ protein intrinsic disorder in degenerative diseases. <i>Frontiers in Bioscience - Landmark</i> , 2014 , 19, 181-258	2.8	62
476	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

475	What macromolecular crowding can do to a protein. <i>International Journal of Molecular Sciences</i> , 2014 , 15, 23090-140	6.3	318
474	Digested disorder: Quarterly intrinsic disorder digest (July-August-September, 2013). <i>Intrinsically Disordered Proteins</i> , 2014 , 2, e27833		5
473	Actinous enigma or enigmatic actin: Folding, structure, and functions of the most abundant eukaryotic protein. <i>Intrinsically Disordered Proteins</i> , 2014 , 2, e34500		10
472	Unreported intrinsic disorder in proteins: Building connections to the literature on IDPs. <i>Intrinsically Disordered Proteins</i> , 2014 , 2, e970499		7
471	Probiotic Properties of <i>Lactobacillus crispatus</i> 2,029: Homeostatic Interaction with Cervicovaginal Epithelial Cells and Antagonistic Activity to Genitourinary Pathogens. <i>Probiotics and Antimicrobial Proteins</i> , 2014 , 6, 165-76	5.5	30
470	Amino acid/water interactions study: a new amino acid scale. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014 , 32, 959-68	3.6	34
469	DRM1 and DRM2 expression regulation: potential role of splice variants in response to stress and environmental factors in Arabidopsis. <i>Molecular Genetics and Genomics</i> , 2014 , 289, 317-32	3.1	24
468	Identifying novel cell cycle proteins in Apicomplexa parasites through co-expression decision analysis. <i>PLoS ONE</i> , 2014 , 9, e97625	3.7	8
467	Disordered interactome of human papillomavirus. <i>Current Pharmaceutical Design</i> , 2014 , 20, 1274-92	3.3	17
466	Structural heterogeneity and multifunctionality of lactoferrin. <i>Current Protein and Peptide Science</i> , 2014 , 15, 778-97	2.8	34
465	Prediction of intrinsic disorder in proteins using MFDp2. <i>Methods in Molecular Biology</i> , 2014 , 1137, 147-62	4.4	32
464	Amino acid code for protein folding, misfolding, and non-folding. <i>Amino Acids, Peptides and Proteins</i> , 2014 , 192-236	2.7	3
463	Unusual biophysics of intrinsically disordered proteins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013 , 1834, 932-51	4	377
462	High throughput characterization of structural differences between closely related proteins in solution. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013 , 1834, 583-92	4	25
461	Interplay between estrogen receptor and AKT in estradiol-induced alternative splicing. <i>BMC Medical Genomics</i> , 2013 , 6, 21	3.7	19
460	Modulating the intrinsic disorder in the cytoplasmic domain alters the biological activity of the N-methyl-D-aspartate-sensitive glutamate receptor. <i>Journal of Biological Chemistry</i> , 2013 , 288, 22506-15	5.4	26
459	Under-folded proteins: Conformational ensembles and their roles in protein folding, function, and pathogenesis. <i>Biopolymers</i> , 2013 , 99, 870-87	2.2	33
458	Distinct β -sheet structure in protein aggregates determined by ATR-FTIR spectroscopy. <i>Biochemistry</i> , 2013 , 52, 5176-83	3.2	154

457	Solvent interaction analysis of intrinsically disordered proteins in aqueous two-phase systems. <i>Molecular BioSystems</i> , 2013 , 9, 3068-79		14
456	Intrinsically disordered regions of p53 family are highly diversified in evolution. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013 , 1834, 725-38	4	58
455	Protein intrinsic disorder in the acetylome of intracellular and extracellular <i>Toxoplasma gondii</i> . <i>Molecular BioSystems</i> , 2013 , 9, 645-57		39
454	The PTEN Long N-tail is intrinsically disordered: increased viability for PTEN therapy. <i>Molecular BioSystems</i> , 2013 , 9, 2877-88		38
453	Utilization of protein intrinsic disorder knowledge in structural proteomics. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013 , 1834, 487-98	4	46
452	Exploring the binding diversity of intrinsically disordered proteins involved in one-to-many binding. <i>Protein Science</i> , 2013 , 22, 258-73	6.3	132
451	RAPID: fast and accurate sequence-based prediction of intrinsic disorder content on proteomic scale. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013 , 1834, 1671-80	4	35
450	The UBE2E proteins as conjugating dispersers: extending function with extended extensions. <i>Journal of Molecular Biology</i> , 2013 , 425, 4067-70	6.5	3
449	Stochastic machines as a colocalization mechanism for scaffold protein function. <i>FEBS Letters</i> , 2013 , 587, 1587-91	3.8	33
448	Effect of salt additives on protein partition in polyethylene glycol-sodium sulfate aqueous two-phase systems. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013 , 1834, 2859-66	4	31
447	MultIDIMensionality of IDIMs: intrinsic disorder in autoinhibition. <i>Structure</i> , 2013 , 21, 315-6	5.2	4
446	A decade and a half of protein intrinsic disorder: biology still waits for physics. <i>Protein Science</i> , 2013 , 22, 693-724	6.3	341
445	Sequence microheterogeneity of parvalbumin, the major fish allergen. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013 , 1834, 1607-14	4	7
444	The Effects of Mutations on Protein Function: A Comparative Study of Three Databases of Mutations in Humans. <i>Israel Journal of Chemistry</i> , 2013 , 53, 217-226	3.4	2
443	Resilience of death: intrinsic disorder in proteins involved in the programmed cell death. <i>Cell Death and Differentiation</i> , 2013 , 20, 1257-67	12.7	62
442	The most important thing is the tail: multitudinous functionalities of intrinsically disordered protein termini. <i>FEBS Letters</i> , 2013 , 587, 1891-901	3.8	95
441	Imbalance of Hsp70 family variants fosters tau accumulation. <i>FASEB Journal</i> , 2013 , 27, 1450-9	0.9	84
440	Targeting the chameleon: a focused look at β -nuclein and its roles in neurodegeneration. <i>Molecular Neurobiology</i> , 2013 , 47, 446-59	6.2	17

439	Agrochemicals, β -synuclein, and Parkinson's disease. <i>Molecular Neurobiology</i> , 2013 , 47, 598-612	6.2	24
438	Distribution and cluster analysis of predicted intrinsically disordered protein Pfam domains. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e25724		9
437	Digested disorder: Quarterly intrinsic disorder digest (January/February/March, 2013). <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e25496		8
436	The alphabet of intrinsic disorder: II. Various roles of glutamic acid in ordered and intrinsically disordered proteins. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e24684		54
435	Structural characterizations of phosphorylatable residues in transmembrane proteins from. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e25713		5
434	Understanding the molecular mechanisms underlying complex cancer genome rearrangements. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e25954		
433	Hypothesis: The unfolding power of protein dielectricity. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e25725		3
432	Digested disorder: Quarterly intrinsic disorder digest (April-May-June, 2013). <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e27454		6
431	Biophysical Characterization of β -synuclein and Rotenone Interaction. <i>Biomolecules</i> , 2013 , 3, 703-32	5.9	22
430	What's in a name? Why these proteins are intrinsically disordered: Why these proteins are intrinsically disordered. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e24157		171
429	Intrinsic disorder in PTEN and its interactome confers structural plasticity and functional versatility. <i>Scientific Reports</i> , 2013 , 3, 2035	4.9	59
428	Multifarious roles of intrinsic disorder in proteins illustrate its broad impact on plant biology. <i>Plant Cell</i> , 2013 , 25, 38-55	11.6	103
427	Extracting structural information from charge-state distributions of intrinsically disordered proteins by non-denaturing electrospray-ionization mass spectrometry. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e25068		22
426	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
425	Intrinsic disorder in pathogen effectors: protein flexibility as an evolutionary hallmark in a molecular arms race. <i>Plant Cell</i> , 2013 , 25, 3153-7	11.6	48
424	Disorder in the lifetime of a protein. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e26782		2
423	Alteration of tropomyosin-binding properties of tropomodulin-1 affects its capping ability and localization in skeletal myocytes. <i>Journal of Biological Chemistry</i> , 2013 , 288, 4899-907	5.4	11
422	Rapid evolutionary dynamics of structural disorder as a potential driving force for biological divergence in flaviviruses. <i>Genome Biology and Evolution</i> , 2013 , 5, 504-13	3.9	23

421	Accelerated neurodegeneration through chaperone-mediated oligomerization of tau. <i>Journal of Clinical Investigation</i> , 2013 , 123, 4158-69	15.9	169
420	Ordered disorder of the astrocytic dystrophin-associated protein complex in the norm and pathology. <i>PLoS ONE</i> , 2013 , 8, e73476	3.7	10
419	Intrinsic disorder-based protein interactions and their modulators. <i>Current Pharmaceutical Design</i> , 2013 , 19, 4191-213	3.3	185
418	DPP database of disordered protein predictions. <i>Nucleic Acids Research</i> , 2013 , 41, D508-16	20.1	398
417	On the intrinsic disorder status of the major players in programmed cell death pathways. <i>F1000Research</i> , 2013 , 2, 190	3.6	18
416	Prediction of Intrinsic Disorder in MERS-CoV/HCoV-EMC Supports a High Oral-Fecal Transmission. <i>PLOS Currents</i> , 2013 , 5,		48
415	Actinidia DRM1--an intrinsically disordered protein whose mRNA expression is inversely correlated with spring budbreak in kiwifruit. <i>PLoS ONE</i> , 2013 , 8, e57354	3.7	17
414	The case for intrinsically disordered proteins playing contributory roles in molecular recognition without a stable 3D structure. <i>F1000 Biology Reports</i> , 2013 , 5, 1		70
413	Looking at microbial metabolism by high-resolution (2)H-NMR spectroscopy. <i>PeerJ</i> , 2013 , 1, e101	3.1	1
412	Malleable ribonucleoprotein machine: protein intrinsic disorder in the <i>Saccharomyces cerevisiae</i> spliceosome. <i>PeerJ</i> , 2013 , 1, e2	3.1	30
411	Mapping Conformational Dynamics in Unfolded Polypeptide Chains Using Short Model Peptides by NMR Spectroscopy 2012 , 187-219		
410	Secondary Structure and Dynamics of a Family of Disordered Proteins 2012 , 221-238		
409	Binding stoichiometry and affinity of fluorescent dyes to proteins in different structural states. <i>Methods in Molecular Biology</i> , 2012 , 895, 441-60	1.4	14
408	Denaturant-induced conformational transitions in intrinsically disordered proteins. <i>Methods in Molecular Biology</i> , 2012 , 896, 197-213	1.4	3
407	Intrinsically disordered proteins and novel strategies for drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2012 , 7, 475-88	6.2	78
406	Size-exclusion chromatography in structural analysis of intrinsically disordered proteins. <i>Methods in Molecular Biology</i> , 2012 , 896, 179-94	1.4	35
405	Insights in the (un)structural organization of <i>Bacillus pasteurii</i> UreG, an intrinsically disordered GTPase enzyme. <i>Molecular BioSystems</i> , 2012 , 8, 220-8		40
404	High-throughput characterization of intrinsic disorder in proteins from the Protein Structure Initiative. <i>Journal of Structural Biology</i> , 2012 , 180, 201-15	3.4	31

403	Thermodynamic and Kinetic Models for Aggregation of Intrinsically Disordered Proteins 2012 , 413-440		1
402	More than just tails: intrinsic disorder in histone proteins. <i>Molecular BioSystems</i> , 2012 , 8, 1886-901		87
401	SPINE-D: accurate prediction of short and long disordered regions by a single neural-network based method. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012 , 29, 799-813	3.6	126
400	The roles of intrinsic disorder in orchestrating the Wnt-pathway. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012 , 29, 843-61	3.6	37
399	Fibrillation mechanism of a model intrinsically disordered protein revealed by 2D correlation deep UV resonance Raman spectroscopy. <i>Biomacromolecules</i> , 2012 , 13, 1503-9	6.9	18
398	Sweeping away protein aggregation with entropic bristles: intrinsically disordered protein fusions enhance soluble expression. <i>Biochemistry</i> , 2012 , 51, 7250-62	3.2	78
397	Disordered competitive recruiter: fast and foldable. <i>Journal of Molecular Biology</i> , 2012 , 418, 267-8	6.5	20
396	α-synuclein misfolding and Parkinson's disease. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2012 , 1822, 261-85	6.9	406
395	Oxidative Stress and Protein Oxidation 2012 , 1-214		2
394	SS-Stabilizing Proteins Rationally: Intrinsic Disorder-Based Design of Stabilizing Disulphide Bridges in GFP. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012 , 29, 815-24	3.6	21
393	Why are we Interested in the Unfolded Peptides and Proteins? 2012 , 1-54		4
392	Protein intrinsic disorder and induced pluripotent stem cells. <i>Molecular BioSystems</i> , 2012 , 8, 134-50		32
391	Protein Disorder and Human Genetic Disease 2012 ,		2
390	Multiparametric analysis of intrinsically disordered proteins: looking at intrinsic disorder through compound eyes. <i>Analytical Chemistry</i> , 2012 , 84, 2096-104	7.8	70
389	Influence of serum proteins on conformation of prostate-specific antigen. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012 , 29, 1051-64	3.6	16
388	Modifiers of Protein Aggregation From Nonspecific to Specific Interactions 2012 , 441-478		2
387	Peculiarities of copper binding to alpha-synuclein. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012 , 29, 825-42	3.6	26
386	Analyzing thioflavin T binding to amyloid fibrils by an equilibrium microdialysis-based technique. <i>PLoS ONE</i> , 2012 , 7, e30724	3.7	54

385	Free cysteine modulates the conformation of human C/EBP homologous protein. <i>PLoS ONE</i> , 2012 , 7, e34680	3.7	3
384	An intrinsically disordered region of the acetyltransferase p300 with similarity to prion-like domains plays a role in aggregation. <i>PLoS ONE</i> , 2012 , 7, e48243	3.7	24
383	Orderly order in protein intrinsic disorder distribution: disorder in 3500 proteomes from viruses and the three domains of life. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012 , 30, 137-49	3.6	370
382	Protein intrinsic disorder as a flexible armor and a weapon of HIV-1. <i>Cellular and Molecular Life Sciences</i> , 2012 , 69, 1211-59	10.3	82
381	A new trend in the experimental methodology for the analysis of the thioflavin T binding to amyloid fibrils. <i>Molecular Neurobiology</i> , 2012 , 45, 488-98	6.2	46
380	Interactions between the C-terminus of Kv1.5 and Kv β regulate pyridine nucleotide-dependent changes in channel gating. <i>Pflugers Archiv European Journal of Physiology</i> , 2012 , 463, 799-818	4.6	31
379	Length-dependent compaction of intrinsically disordered proteins. <i>FEBS Letters</i> , 2012 , 586, 70-3	3.8	24
378	Common features at the start of the neurodegeneration cascade. <i>PLoS Biology</i> , 2012 , 10, e1001335	9.7	52
377	Disease-associated mutations disrupt functionally important regions of intrinsic protein disorder. <i>PLoS Computational Biology</i> , 2012 , 8, e1002709	5	95
376	MoRFPred, a computational tool for sequence-based prediction and characterization of short disorder-to-order transitioning binding regions in proteins. <i>Bioinformatics</i> , 2012 , 28, i75-83	7.2	254
375	HSF transcription factor family, heat shock response, and protein intrinsic disorder. <i>Current Protein and Peptide Science</i> , 2012 , 13, 86-103	2.8	79
374	Accurate prediction of protein structural classes using functional domains and predicted secondary structure sequences. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012 , 29, 623-33	3.6	15
373	NOT THAT RIGID MIDGETS AND NOT SO FLEXIBLE GIANTS: ON THE ABUNDANCE AND ROLES OF INTRINSIC DISORDER IN SHORT AND LONG PROTEINS. <i>Journal of Biological Systems</i> , 2012 , 20, 471-511	1.6	16
372	Understanding Viral Transmission Behavior via Protein Intrinsic Disorder Prediction: Coronaviruses. <i>Journal of Pathogens</i> , 2012 , 2012, 738590	1.9	32
371	Local flexibility facilitates oxidization of buried methionine residues. <i>Protein and Peptide Letters</i> , 2012 , 19, 688-97	1.9	21
370	Self-Assembling Alanine-Rich Peptides of Biomedical and Biotechnological Relevance 2012 , 307-350		2
369	Structural Elements Regulating Interactions in the Early Stages of Fibrillogenesis: A Human Calcitonin Model System 2012 , 351-388		1
368	Computational Studies of Folding and Assembly of Amyloidogenic Proteins 2012 , 479-527		

367	Intrinsic Flexibility of Nucleic Acid Chaperone Proteins from Pathogenic RNA Viruses 2012 , 279-306		
366	Binding Promiscuity of Unfolded Peptides 2012 , 239-277		0
365	Molecular profiling: an essential technology enabling personalized medicine in breast cancer. <i>Current Drug Targets</i> , 2012 , 13, 541-54	3	5
364	Oligomers of β -Synuclein in the Pathogenesis of Parkinson's Disease 2012 , 189-216		
363	Intrinsic protein disorder and protein-protein interactions. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2012 , 116-27	1.3	42
362	Subclassifying disordered proteins by the CH-CDF plot method. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2012 , 128-39	1.3	29
361	SUBCLASSIFYING DISORDERED PROTEINS BY THE CH-CDF PLOT METHOD 2011 ,		11
360	Intrinsically Disordered Chaperones and Neurodegeneration 2011 , 1-63		1
359	Redox Regulation of Protein Misfolding, Synaptic Damage, and Neuronal Loss in Neurodegenerative Diseases 2011 , 65-99		
358	Chaperone and Anti-Chaperone Properties of Synuclein: Implications for Development, Aging, and Neurodegenerative Disease 2011 , 139-177		
357	Emerging Area: TorsinA, a Novel ATP-Dependent Factor Linked to Dystonia 2011 , 359-383		1
356	Intrinsic disorder of the extracellular matrix. <i>Molecular BioSystems</i> , 2011 , 7, 3353-65		46
355	Flexible nets of malleable guardians: intrinsically disordered chaperones in neurodegenerative diseases. <i>Chemical Reviews</i> , 2011 , 111, 1134-66	68.1	59
354	Intrinsically disordered proteins from A to Z. <i>International Journal of Biochemistry and Cell Biology</i> , 2011 , 43, 1090-103	5.6	322
353	Molecular mechanisms of the anomalous thermal aggregation of green fluorescent protein. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011 , 1814, 1930-9	4	14
352	Intrinsic disorder in S100 proteins. <i>Molecular BioSystems</i> , 2011 , 7, 2164-80		21
351	Sequential melting of two hydrophobic clusters within the green fluorescent protein GFP-cycle3. <i>Biochemistry</i> , 2011 , 50, 7735-44	3.2	13
350	Modulating α -synuclein misfolding and fibrillation in vitro by agrochemicals. <i>Research and Reports in Biology</i> , 2011 , 43		1

- 349 Analyzing and mapping sweat metabolomics by high-resolution NMR spectroscopy. *PLoS ONE*, **2011**, 6, e28824 3.7 61
- 348 Do Viral Proteins Possess Unique Features? **2011**, 1-34 4
- 347 Intrinsically Disordered Domains of Sesbania Mosaic Virus Encoded Proteins **2011**, 257-276
- 346 Intrinsic Disorder in Genome-Linked Viral Proteins VPgs of Potyviruses **2011**, 277-312
- 345 Core-Lations Between Intrinsic Disorder and Multifaceted Activities in Hepatitis C Virus and Related Viruses **2011**, 375-407
- 344 The NS5A Domain II of HCV: Conservation of Intrinsic Disorder in Several Genotypes **2011**, 409-424 1
- 343 Bacteriophage Φ N Protein Disorder-Order Transitions upon Interactions with RNA or Proteins **2011**, 425-444
- 342 Structural Disorder within the Nucleoprotein and Phosphoprotein from Measles, Nipah, and Hendra Viruses **2011**, 47-94 5
- 341 Structural Disorder within Sendai Virus Nucleoprotein and Phosphoprotein **2011**, 95-114
- 340 Structural Disorder in Matrix Proteins of HIV-Related Viruses **2011**, 143-167
- 339 Making Order in the Intrinsically Disordered Regions of HIV-1 Vif Protein **2011**, 201-221 1
- 338 Order from Disorder: Structure, Function, and Dynamics of the HIV-1 Transactivator of Transcription **2011**, 223-256
- 337 Characterization of the non-fibrillar β -synuclein oligomers. *Protein and Peptide Letters*, **2011**, 18, 230-40 1.9 40
- 336 INTRINSIC PROTEIN DISORDER AND PROTEIN-PROTEIN INTERACTIONS **2011**, 5
- 335 N-Terminal Extension Region of Hordeivirus Movement TGB1 Protein Consists of Two Domains with Different Content of Disordered Structure **2011**, 445-471
- 334 Structural Disorder in Proteins of the Rhabdoviridae Replication Complex **2011**, 115-141
- 333 Functional Role of Structural Disorder in Capsid Proteins **2011**, 35-46 2
- 332 Structural Disorder in Proteins from Influenza Virus **2011**, 169-200

331	Intrinsic Disorder in the Human Papillomavirus E7 Protein 2011 , 313-346		2
330	The Semliki Forest Virus Capsid Protease is Disordered and Yet Displays Catalytic Activity 2011 , 347-373		
329	Regions of intrinsic disorder help identify a novel nuclear localization signal in <i>Toxoplasma gondii</i> histone acetyltransferase TgGCN5-B. <i>Molecular and Biochemical Parasitology</i> , 2011 , 175, 192-5	1.9	18
328	Role of metal ions in aggregation of intrinsically disordered proteins in neurodegenerative diseases. <i>Metallomics</i> , 2011 , 3, 1163-80	4.5	88
327	Multitude of binding modes attainable by intrinsically disordered proteins: a portrait gallery of disorder-based complexes. <i>Chemical Society Reviews</i> , 2011 , 40, 1623-34	58.5	199
326	A functionally required unfoldome from the plant kingdom: intrinsically disordered N-terminal domains of GRAS proteins are involved in molecular recognition during plant development. <i>Plant Molecular Biology</i> , 2011 , 77, 205-23	4.6	99
325	In-silico prediction of disorder content using hybrid sequence representation. <i>BMC Bioinformatics</i> , 2011 , 12, 245	3.6	37
324	Abundance and functional roles of intrinsic disorder in allergenic proteins and allergen representative peptides. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 2595-606	4.2	5
323	Systematic analysis of tropomodulin/tropomyosin interactions uncovers fine-tuned binding specificity of intrinsically disordered proteins. <i>Journal of Molecular Recognition</i> , 2011 , 24, 647-55	2.6	31
322	Intrinsically disordered proteins may escape unwanted interactions via functional misfolding. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011 , 1814, 693-712	4	52
321	Differential occurrence of protein intrinsic disorder in the cytoplasmic signaling domains of cell receptors. <i>Self/nonself</i> , 2011 , 2, 55-72		22
320	Effects of HMGN variants on the cellular transcription profile. <i>Nucleic Acids Research</i> , 2011 , 39, 4076-87	20.1	29
319	Predictive Power Estimation Algorithm (PPEA)--a new algorithm to reduce overfitting for genomic biomarker discovery. <i>PLoS ONE</i> , 2011 , 6, e24233	3.7	5
318	Protein tandem repeats ¶the more perfect, the less structured. <i>FEBS Journal</i> , 2010 , 277, 2673-2682	5.7	90
317	Mysterious oligomerization of the amyloidogenic proteins. <i>FEBS Journal</i> , 2010 , 277, 2940-53	5.7	151
316	SPA: Short peptide analyzer of intrinsic disorder status of short peptides. <i>Genes To Cells</i> , 2010 , 15, 635-46	6.3	7
315	Effects of Various Flavonoids on the α -Synuclein Fibrillation Process. <i>Parkinson's Disease</i> , 2010 , 2010, 650794	2.6	67
314	Fluorescence quantum yield of thioflavin T in rigid isotropic solution and incorporated into the amyloid fibrils. <i>PLoS ONE</i> , 2010 , 5, e15385	3.7	131

313	Oncogenic partnerships: EWS-FLI1 protein interactions initiate key pathways of Ewing's sarcoma. <i>Clinical Cancer Research</i> , 2010 , 16, 4077-83	12.9	107
312	N-terminal domains of DELLA proteins are intrinsically unstructured in the absence of interaction with GID1/gibberellic acid receptors. <i>Journal of Biological Chemistry</i> , 2010 , 285, 11557-71	5.4	55
311	A bimodal distribution of two distinct categories of intrinsically disordered structures with separate functions in FG nucleoporins. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 2205-24	7.6	232
310	The mysterious unfoldome: structureless, underappreciated, yet vital part of any given proteome. <i>Journal of Biomedicine and Biotechnology</i> , 2010 , 2010, 568068		173
309	Retro-MoRFs: identifying protein binding sites by normal and reverse alignment and intrinsic disorder prediction. <i>International Journal of Molecular Sciences</i> , 2010 , 11, 3725-47	6.3	35
308	Viral disorder or disordered viruses: do viral proteins possess unique features?. <i>Protein and Peptide Letters</i> , 2010 , 17, 932-51	1.9	96
307	Metalloproteomics and metal toxicology of β -synuclein. <i>Metallomics</i> , 2010 , 2, 378-92	4.5	79
306	Targeting intrinsically disordered proteins in neurodegenerative and protein dysfunction diseases: another illustration of the D(2) concept. <i>Expert Review of Proteomics</i> , 2010 , 7, 543-64	4.2	100
305	Unique physical properties and interactions of the domains of methylated DNA binding protein 2. <i>Biochemistry</i> , 2010 , 49, 4395-410	3.2	77
304	Proteomic identification of Hsc70 as a mediator of RGS9-2 degradation by in vivo interactome analysis. <i>Journal of Proteome Research</i> , 2010 , 9, 1510-21	5.6	13
303	Drugs for 'protein clouds': targeting intrinsically disordered transcription factors. <i>Current Opinion in Pharmacology</i> , 2010 , 10, 782-8	5.1	132
302	Methionine oxidation stabilizes non-toxic oligomers of alpha-synuclein through strengthening the auto-inhibitory intra-molecular long-range interactions. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2010 , 1802, 322-30	6.9	75
301	Characterization of intrinsically disordered proteins with electrospray ionization mass spectrometry: conformational heterogeneity of alpha-synuclein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 714-22	4.2	73
300	Analysis of the metabolites in apical area of Allium cepa roots by high resolution NMR spectroscopy method. <i>Protein and Peptide Letters</i> , 2010 , 17, 86-91	1.9	6
299	Calbindin-D28K acts as a calcium-dependent chaperone suppressing β -synuclein fibrillation in vitro. <i>Open Life Sciences</i> , 2010 , 5, 11-20	1.2	2
298	The protein kingdom extended: ordered and intrinsically disordered proteins, their folding, supramolecular complex formation, and aggregation. <i>Progress in Biophysics and Molecular Biology</i> , 2010 , 102, 73-84	4.7	157
297	Seven lessons from one IDP structural analysis. <i>Structure</i> , 2010 , 18, 1069-71	5.2	11
296	IDPs and Protein Degradation in the Cell 2010 , 1-36		3

295	Circular Dichroism of Intrinsically Disordered Proteins 2010 , 303-321	15
294	Fluorescence Spectroscopy of Intrinsically Disordered Proteins 2010 , 323-344	
293	Hydration of Intrinsically Disordered Proteins from Wide-Line NMR 2010 , 345-368	5
292	Single-Molecule Spectroscopy of Unfolded Proteins 2010 , 369-389	2
291	Monitoring the Conformational Equilibria of Monomeric Intrinsically Disordered Proteins by Single-Molecule Force Spectroscopy 2010 , 391-430	1
290	Analytical Ultracentrifugation, a Useful Tool to Probe Intrinsically Disordered Proteins 2010 , 431-449	6
289	Structural Insights into Intrinsically Disordered Proteins by Small-Angle X-Ray Scattering 2010 , 451-476	5
288	Dynamic and Static Light Scattering 2010 , 477-524	3
287	Analyzing Intrinsically Disordered Proteins by Size Exclusion Chromatography 2010 , 525-544	2
286	Conformational Behavior of Intrinsically Disordered Proteins: Effects of Strong Denaturants, Temperature, PH, Counterions, and Macromolecular Crowding 2010 , 545-568	
285	The Structural Biology of IDPs inside Cells 2010 , 37-58	
284	Detecting Disordered Regions in Proteins by Limited Proteolysis 2010 , 569-626	7
283	Mass Spectrometry Tools for the Investigation of Structural Disorder and Conformational Transitions in Proteins 2010 , 627-652	
282	Recombinant Production of Intrinsically Disordered Proteins for Biophysical and Structural Characterization 2010 , 653-670	1
281	Large-Scale Identification of Intrinsically Disordered Proteins 2010 , 671-693	
280	Purification of Intrinsically Disordered Proteins 2010 , 695-704	3
279	Nuclear Magnetic Resonance Spectroscopy Applied to (Intrinsically) Disordered Proteins 2010 , 59-87	1
278	Atomic-Level Characterization of Disordered Protein Ensembles Using NMR Residual Dipolar Couplings 2010 , 89-106	1

277	Determining Structural Ensembles for Intrinsically Disordered Proteins 2010 , 107-129		1
276	Site-Directed Spin Labeling EPR Spectroscopy 2010 , 131-169		3
275	The Structure of Unfolded Peptides and Proteins Explored by Vibrational Spectroscopy 2010 , 171-224		4
274	Intrinsically Disordered Proteins and Induced Folding Studied by Fourier Transform Infrared Spectroscopy 2010 , 225-252		2
273	Genetically Engineered Polypeptides as a Model of Intrinsically Disordered Fibrillogenic Proteins: Deep UV Resonance Raman Spectroscopic Study 2010 , 253-302		2
272	PONDR-FIT: a meta-predictor of intrinsically disordered amino acids. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010 , 1804, 996-1010	4	749
271	Understanding protein non-folding. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010 , 1804, 1231-64	4	875
270	Archaic chaos: intrinsically disordered proteins in Archaea. <i>BMC Systems Biology</i> , 2010 , 4 Suppl 1, S1	3.5	99
269	Functional dissection of an intrinsically disordered protein: understanding the roles of different domains of Knr4 protein in protein-protein interactions. <i>Protein Science</i> , 2010 , 19, 1376-85	6.3	10
268	Analysis of Ca ²⁺ /Mg ²⁺ selectivity in alpha-lactalbumin and Ca(2+)-binding lysozyme reveals a distinct Mg(2+)-specific site in lysozyme. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 2609-24	4.2	8
267	Protein tandem repeats - the more perfect, the less structured. <i>FEBS Journal</i> , 2010 , 277, 2673-82	5.7	58
266	Quantitative interactome analysis of RGS9-2 degradation mechanisms in mammalian brain.. <i>FASEB Journal</i> , 2010 , 24, 523.2	0.9	
265	Replacement of aromatic amino acids based on their consensus temporal order suggests that ancient proteins tend to be intrinsically disordered. <i>FASEB Journal</i> , 2010 , 24, 901.2	0.9	
264	α-Synuclein and Metals 2010 , 169-191		
263	Intrinsic disorder in proteins associated with neurodegenerative diseases. <i>Frontiers in Bioscience - Landmark</i> , 2009 , 14, 5188-238	2.8	169
262	Cryoenzymology: enzyme action in slow motion. <i>Current Protein and Peptide Science</i> , 2009 , 10, 408-15	2.8	2
261	Accelerated fibrillation of alpha-synuclein induced by the combined action of macromolecular crowding and factors inducing partial folding. <i>Current Alzheimer Research</i> , 2009 , 6, 252-60	3	30
260	Influence of sequence changes and environment on intrinsically disordered proteins. <i>PLoS Computational Biology</i> , 2009 , 5, e1000497	5	37

259	Do viral proteins possess unique biophysical features?. <i>Trends in Biochemical Sciences</i> , 2009 , 34, 53-9	10.3	182
258	Protein disorder in the human diseasome: unfoldomics of human genetic diseases. <i>BMC Genomics</i> , 2009 , 10 Suppl 1, S12	4.5	105
257	Unfoldomics of human diseases: linking protein intrinsic disorder with diseases. <i>BMC Genomics</i> , 2009 , 10 Suppl 1, S7	4.5	199
256	CDF it all: consensus prediction of intrinsically disordered proteins based on various cumulative distribution functions. <i>FEBS Letters</i> , 2009 , 583, 1469-74	3.8	99
255	Metal-controlled interdomain cooperativity in parvalbumins. <i>Cell Calcium</i> , 2009 , 46, 163-75	4	18
254	Close encounters of the third kind: disordered domains and the interactions of proteins. <i>BioEssays</i> , 2009 , 31, 328-35	4.1	197
253	Intrinsically disordered proteins and their environment: effects of strong denaturants, temperature, pH, counter ions, membranes, binding partners, osmolytes, and macromolecular crowding. <i>Protein Journal</i> , 2009 , 28, 305-25	3.9	235
252	Order propensity of an intrinsically disordered protein, the cyclin-dependent-kinase inhibitor Sic1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 76, 731-46	4.2	58
251	Smoking and Parkinson's disease: does nicotine affect alpha-synuclein fibrillation?. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009 , 1794, 282-90	4	65
250	Solution structure and dynamics of the chimeric SH3 domains, SHH- and SHA-"Bergeracs". <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009 , 1794, 1813-22	4	13
249	Molecular mechanisms underlying the flavonoid-induced inhibition of alpha-synuclein fibrillation. <i>Biochemistry</i> , 2009 , 48, 8206-24	3.2	106
248	Intrinsic Disorder in Proteins Associated with Neurodegenerative Diseases. <i>Focus on Structural Biology</i> , 2009 , 21-75		6
247	Exploring the molecular design of protein interaction sites with molecular dynamics simulations and free energy calculations. <i>Biochemistry</i> , 2009 , 48, 399-414	3.2	46
246	At low concentrations, 3,4-dihydroxyphenylacetic acid (DOPAC) binds non-covalently to alpha-synuclein and prevents its fibrillation. <i>Journal of Molecular Biology</i> , 2009 , 388, 597-610	6.5	43
245	Intrinsic disorder in Viral Proteins Genome-Linked: experimental and predictive analyses. <i>Virology Journal</i> , 2009 , 6, 23	6.1	55
244	Protein intrinsic disorder and influenza virulence: the 1918 H1N1 and H5N1 viruses. <i>Virology Journal</i> , 2009 , 6, 69	6.1	64
243	Analysis of structured and intrinsically disordered regions of transmembrane proteins. <i>Molecular BioSystems</i> , 2009 , 5, 1688-1702		55
242	Predicting intrinsic disorder in proteins: an overview. <i>Cell Research</i> , 2009 , 19, 929-49	24.7	328

241	Biophysics of Parkinson's disease: structure and aggregation of alpha-synuclein. <i>Current Protein and Peptide Science</i> , 2009 , 10, 483-99	2.8	250
240	Mechanisms and consequences of protein aggregation: the role of folding intermediates. <i>Current Protein and Peptide Science</i> , 2009 , 10, 456-63	2.8	11
239	Unfoldomics of human genetic diseases: illustrative examples of ordered and intrinsically disordered members of the human diseasome. <i>Protein and Peptide Letters</i> , 2009 , 16, 1533-47	1.9	52
238	Acid denaturation and anion-induced folding of globular proteins: multitude of equilibrium partially folded intermediates. <i>Current Protein and Peptide Science</i> , 2009 , 10, 447-55	2.8	13
237	Tony Fink (1943-2008): scientist, teacher and artist. <i>Current Protein and Peptide Science</i> , 2009 , 10, 395-6	2.8	
236	Malleable machines take shape in eukaryotic transcriptional regulation. <i>Nature Chemical Biology</i> , 2008 , 4, 728-37	11.7	161
235	Potato virus A genome-linked protein VPg is an intrinsically disordered molten globule-like protein with a hydrophobic core. <i>Virology</i> , 2008 , 377, 280-8	3.6	59
234	Flexible nets: disorder and induced fit in the associations of p53 and 14-3-3 with their partners. <i>BMC Genomics</i> , 2008 , 9 Suppl 1, S1	4.5	425
233	The unfoldomics decade: an update on intrinsically disordered proteins. <i>BMC Genomics</i> , 2008 , 9 Suppl 2, S1	4.5	408
232	Short Linear Motifs recognized by SH2, SH3 and Ser/Thr Kinase domains are conserved in disordered protein regions. <i>BMC Genomics</i> , 2008 , 9 Suppl 2, S26	4.5	54
231	Protein intrinsic disorder toolbox for comparative analysis of viral proteins. <i>BMC Genomics</i> , 2008 , 9 Suppl 2, S4	4.5	53
230	Function and structure of inherently disordered proteins. <i>Current Opinion in Structural Biology</i> , 2008 , 18, 756-64	8.1	746
229	Intrinsic disorder in scaffold proteins: getting more from less. <i>Progress in Biophysics and Molecular Biology</i> , 2008 , 98, 85-106	4.7	213
228	Intrinsically disordered proteins in human diseases: introducing the D2 concept. <i>Annual Review of Biophysics</i> , 2008 , 37, 215-46	21.1	1018
227	Thioflavin T as a molecular rotor: fluorescent properties of thioflavin T in solvents with different viscosity. <i>Journal of Physical Chemistry B</i> , 2008 , 112, 15893-902	3.4	256
226	Intrinsic disorder in pathogenic and non-pathogenic microbes: discovering and analyzing the unfoldomes of early-branching eukaryotes. <i>Molecular BioSystems</i> , 2008 , 4, 328-40		101
225	Biochemistry. Controlled chaos. <i>Science</i> , 2008 , 322, 1340-1	33.3	59
224	A comparative analysis of viral matrix proteins using disorder predictors. <i>Virology Journal</i> , 2008 , 5, 126	6.1	51

223	Guiding protein aggregation with macromolecular crowding. <i>Biochemistry</i> , 2008 , 47, 8993-9006	3.2	138
222	Intrinsically disordered human C/EBP homologous protein regulates biological activity of colon cancer cells during calcium stress. <i>Journal of Molecular Biology</i> , 2008 , 380, 313-26	6.5	17
221	The effect of membranes on the in vitro fibrillation of an amyloidogenic light-chain variable-domain SMA. <i>Journal of Molecular Biology</i> , 2008 , 381, 989-99	6.5	21
220	Structural characteristics of alpha-synuclein oligomers stabilized by the flavonoid baicalein. <i>Journal of Molecular Biology</i> , 2008 , 383, 214-23	6.5	145
219	Effect of methionine oxidation on the structural properties, conformational stability, and aggregation of immunoglobulin light chain LEN. <i>Biochemistry</i> , 2008 , 47, 8665-77	3.2	30
218	Protein disorder is positively correlated with gene expression in Escherichia coli. <i>Journal of Proteome Research</i> , 2008 , 7, 2234-45	5.6	26
217	Prevalence of intrinsic disorder in the intracellular region of human single-pass type I proteins: the case of the notch ligand Delta-4. <i>Journal of Proteome Research</i> , 2008 , 7, 2496-506	5.6	35
216	Amyloidogenesis of natively unfolded proteins. <i>Current Alzheimer Research</i> , 2008 , 5, 260-87	3	147
215	Malleable machines in transcription regulation: the mediator complex. <i>PLoS Computational Biology</i> , 2008 , 4, e1000243	5	91
214	Fluorescent proteins as biomarkers and biosensors: throwing color lights on molecular and cellular processes. <i>Current Protein and Peptide Science</i> , 2008 , 9, 338-69	2.8	117
213	Alpha-synuclein misfolding and neurodegenerative diseases. <i>Current Protein and Peptide Science</i> , 2008 , 9, 507-40	2.8	163
212	TOP-IDP-scale: a new amino acid scale measuring propensity for intrinsic disorder. <i>Protein and Peptide Letters</i> , 2008 , 15, 956-63	1.9	266
211	Concerted action of metals and macromolecular crowding on the fibrillation of alpha-synuclein. <i>Protein and Peptide Letters</i> , 2008 , 15, 1079-85	1.9	20
210	Structure-function analysis of Knr4/Smi1, a newly member of intrinsically disordered proteins family, indispensable in the absence of a functional PKC1-SLT2 pathway in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2008 , 25, 563-76	3.4	13
209	Apo-parvalbumin as an intrinsically disordered protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 72, 822-36	4.2	46
208	Understanding the role of Arg96 in structure and stability of green fluorescent protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 73, 539-51	4.2	13
207	Hen egg white lysozyme fibrillation: a deep-UV resonance Raman spectroscopic study. <i>Journal of Biophotonics</i> , 2008 , 1, 215-29	3.1	58
206	Dynamics of oligomer formation by denatured carbonic anhydrase II. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008 , 1784, 834-42	4	7

205	Assessing Conservation of Disordered Regions in Proteins. <i>The Open Proteomics Journal</i> , 2008 , 1, 46-53		13
204	Interaction of Yersinia pestis Virulence Factors with IL-1R/TLR Recognition System 2008 , 215-225		
203	Mining alpha-helix-forming molecular recognition features with cross species sequence alignments. <i>Biochemistry</i> , 2007 , 46, 13468-77	3.2	270
202	Attachment of LcrV from Yersinia pestis at dual binding sites to human TLR-2 and human IFN-gamma receptor. <i>Journal of Proteome Research</i> , 2007 , 6, 2222-31	5.6	21
201	Functional anthology of intrinsic disorder. 2. Cellular components, domains, technical terms, developmental processes, and coding sequence diversities correlated with long disordered regions. <i>Journal of Proteome Research</i> , 2007 , 6, 1899-916	5.6	215
200	A computational investigation of allostery in the catabolite activator protein. <i>Journal of the American Chemical Society</i> , 2007 , 129, 15668-76	16.4	62
199	DisProt: the Database of Disordered Proteins. <i>Nucleic Acids Research</i> , 2007 , 35, D786-93	20.1	631
198	Characterization of molecular recognition features, MoRFs, and their binding partners. <i>Journal of Proteome Research</i> , 2007 , 6, 2351-66	5.6	386
197	Intrinsic disorder and functional proteomics. <i>Biophysical Journal</i> , 2007 , 92, 1439-56	2.9	571
196	Intrinsic disorder in the Protein Data Bank. <i>Journal of Biomolecular Structure and Dynamics</i> , 2007 , 24, 325-42	3.6	116
195	Nanoimaging in protein-misfolding and -conformational diseases. <i>Nanomedicine</i> , 2007 , 2, 615-43	5.6	12
194	Neuropathology, biochemistry, and biophysics of alpha-synuclein aggregation. <i>Journal of Neurochemistry</i> , 2007 , 103, 17-37	6	373
193	Composition Profiler: a tool for discovery and visualization of amino acid composition differences. <i>BMC Bioinformatics</i> , 2007 , 8, 211	3.6	276
192	Recoverin as a redox-sensitive protein. <i>Journal of Proteome Research</i> , 2007 , 6, 1855-63	5.6	16
191	Expression and localization of RGS9-2/G 5/R7BP complex in vivo is set by dynamic control of its constitutive degradation by cellular cysteine proteases. <i>Journal of Neuroscience</i> , 2007 , 27, 14117-27	6.6	56
190	Multiple aromatic side chains within a disordered structure are critical for transcription and transforming activity of EWS family oncoproteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 479-84	11.5	81
189	Synuclein-gamma targeting peptide inhibitor that enhances sensitivity of breast cancer cells to antimicrotubule drugs. <i>Cancer Research</i> , 2007 , 67, 626-33	10.1	48
188	ThT as an instrument for testing and investigation of amyloid and amyloid-like fibrils 2007 ,		5

187	Functional anthology of intrinsic disorder. 1. Biological processes and functions of proteins with long disordered regions. <i>Journal of Proteome Research</i> , 2007 , 6, 1882-98	5.6	455
186	Functional anthology of intrinsic disorder. 3. Ligands, post-translational modifications, and diseases associated with intrinsically disordered proteins. <i>Journal of Proteome Research</i> , 2007 , 6, 1917-32	5.6	322
185	Spectral properties of thioflavin T in solvents with different dielectric properties and in a fibril-incorporated form. <i>Journal of Proteome Research</i> , 2007 , 6, 1392-401	5.6	166
184	Prediction of intrinsic disorder and its use in functional proteomics. <i>Methods in Molecular Biology</i> , 2007 , 408, 69-92	1.4	32
183	α-Synuclein Aggregation and Parkinson's Disease 2007 , 61-110		2
182	Rational drug design via intrinsically disordered protein. <i>Trends in Biotechnology</i> , 2006 , 24, 435-42	15.1	199
181	Nanoimaging for protein misfolding and related diseases. <i>Journal of Cellular Biochemistry</i> , 2006 , 99, 52-70	4.7	39
180	New Views of Protein Structure: Applications to the Caseins: Protein Structure and Functionality. <i>ACS Symposium Series</i> , 2006 , 52-70	0.4	21
179	Intrinsic disorder is a common feature of hub proteins from four eukaryotic interactomes. <i>PLoS Computational Biology</i> , 2006 , 2, e100	5	435
178	Local flexibility in molecular function paradigm. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 1212-23	7.6	38
177	The disordered amino-terminus of SIMPL interacts with members of the 70-kDa heat-shock protein family. <i>DNA and Cell Biology</i> , 2006 , 25, 704-14	3.6	9
176	Alternative splicing in concert with protein intrinsic disorder enables increased functional diversity in multicellular organisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 8390-5	11.5	358
175	Abundance of intrinsic disorder in protein associated with cardiovascular disease. <i>Biochemistry</i> , 2006 , 45, 10448-60	3.2	152
174	Intrinsic disorder in transcription factors. <i>Biochemistry</i> , 2006 , 45, 6873-88	3.2	518
173	Structural and Conformational Prerequisites of Amyloidogenesis 2006 , 1-20		4
172	Protein intrinsic disorder and human papillomaviruses: increased amount of disorder in E6 and E7 oncoproteins from high risk HPVs. <i>Journal of Proteome Research</i> , 2006 , 5, 1829-42	5.6	117
171	New Views of Protein Structure: Implications for Potential New Protein Structure-Function Relationships. <i>ACS Symposium Series</i> , 2006 , 1-18	0.4	1
170	Conservation of intrinsic disorder in protein domains and families: II. functions of conserved disorder. <i>Journal of Proteome Research</i> , 2006 , 5, 888-98	5.6	107

169	Conformational properties of the SDS-bound state of alpha-synuclein probed by limited proteolysis: unexpected rigidity of the acidic C-terminal tail. <i>Biochemistry</i> , 2006 , 45, 11523-31	3.2	49
168	Lipid-binding activity of intrinsically unstructured cytoplasmic domains of multichain immune recognition receptor signaling subunits. <i>Biochemistry</i> , 2006 , 45, 15731-9	3.2	93
167	Nanotools for megaproblems: probing protein misfolding diseases using nanomedicine modus operandi. <i>Journal of Proteome Research</i> , 2006 , 5, 2505-22	5.6	24
166	Conservation of intrinsic disorder in protein domains and families: I. A database of conserved predicted disordered regions. <i>Journal of Proteome Research</i> , 2006 , 5, 879-87	5.6	99
165	Analysis of molecular recognition features (MoRFs). <i>Journal of Molecular Biology</i> , 2006 , 362, 1043-59	6.5	579
164	Calmodulin signaling: analysis and prediction of a disorder-dependent molecular recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 63, 398-410	4.2	86
163	Role of lysine versus arginine in enzyme cold-adaptation: modifying lysine to homo-arginine stabilizes the cold-adapted alpha-amylase from <i>Pseudoalteromonas haloplanktis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 64, 486-501	4.2	55
162	Assessing protein disorder and induced folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 62, 24-45	4.2	347
161	Structure-related statistical singularities along protein sequences: a correlation study. <i>Journal of Chemical Information and Modeling</i> , 2005 , 45, 183-9	6.1	25
160	Improving solubility of <i>Shewanella oneidensis</i> MR-1 and <i>Clostridium thermocellum</i> JW-20 proteins expressed into <i>Escherichia coli</i> . <i>Journal of Proteome Research</i> , 2005 , 4, 1942-51	5.6	38
159	Agrin binds alpha-synuclein and modulates alpha-synuclein fibrillation. <i>Glycobiology</i> , 2005 , 15, 1320-31	5.8	61
158	Early events in the fibrillation of monomeric insulin. <i>Journal of Biological Chemistry</i> , 2005 , 280, 42669-75	5.4	203
157	Conversion of human alpha-lactalbumin to an apo-like state in the complexes with basic poly-amino acids: toward understanding of the molecular mechanism of antitumor action of HAMLET. <i>Journal of Proteome Research</i> , 2005 , 4, 564-9	5.6	18
156	Forcing nonamyloidogenic beta-synuclein to fibrillate. <i>Biochemistry</i> , 2005 , 44, 9096-107	3.2	95
155	Protein interactions and misfolding analyzed by AFM force spectroscopy. <i>Journal of Molecular Biology</i> , 2005 , 354, 1028-42	6.5	107
154	Effects of nitration on the structure and aggregation of alpha-synuclein. <i>Molecular Brain Research</i> , 2005 , 134, 84-102		127
153	Domain coupling in a multimodular cellobiohydrolase CbhA from <i>Clostridium thermocellum</i> . <i>FEBS Letters</i> , 2005 , 579, 4367-73	3.8	6
152	Comparing and combining predictors of mostly disordered proteins. <i>Biochemistry</i> , 2005 , 44, 1989-2000	3.2	416

151	Uncovering the unfoldome: enriching cell extracts for unstructured proteins by acid treatment. <i>Journal of Proteome Research</i> , 2005 , 4, 1610-8	5.6	59
150	Coupled folding and binding with alpha-helix-forming molecular recognition elements. <i>Biochemistry</i> , 2005 , 44, 12454-70	3.2	541
149	Methionine oxidation, alpha-synuclein and Parkinson's disease. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005 , 1703, 157-69	4	134
148	Protein dissection enhances the amyloidogenic properties of alpha-lactalbumin. <i>FEBS Journal</i> , 2005 , 272, 2176-88	5.7	32
147	Flexible nets. The roles of intrinsic disorder in protein interaction networks. <i>FEBS Journal</i> , 2005 , 272, 5129-48	5.7	895
146	A GLYmmer of insight into fibril formation. <i>Structure</i> , 2005 , 13, 1090-2	5.2	6
145	Lysozyme fibrillation: deep UV Raman spectroscopic characterization of protein structural transformation. <i>Biopolymers</i> , 2005 , 79, 58-61	2.2	44
144	Showing your ID: intrinsic disorder as an ID for recognition, regulation and cell signaling. <i>Journal of Molecular Recognition</i> , 2005 , 18, 343-84	2.6	660
143	How to improve nature: study of the electrostatic properties of the surface of alpha-lactalbumin. <i>Protein Engineering, Design and Selection</i> , 2005 , 18, 425-33	1.9	36
142	Intrinsic Disorder is a Common Feature of Hub Proteins from Four Eukaryotic Interactomes. <i>PLoS Computational Biology</i> , 2005 , preprint, e100	5	2
141	Stimulation of insulin fibrillation by urea-induced intermediates. <i>Journal of Biological Chemistry</i> , 2004 , 279, 14999-5013	5.4	85
140	Interactions between immunoglobulin-like and catalytic modules in Clostridium thermocellum cellulosomal cellobiohydrolase CbhA. <i>Protein Engineering, Design and Selection</i> , 2004 , 17, 759-69	1.9	46
139	Neurotoxicant-induced animal models of Parkinson's disease: understanding the role of rotenone, maneb and paraquat in neurodegeneration. <i>Cell and Tissue Research</i> , 2004 , 318, 225-41	4.2	218
138	The effect of macromolecular crowding on protein aggregation and amyloid fibril formation. <i>Journal of Molecular Recognition</i> , 2004 , 17, 456-64	2.6	249
137	Rifampicin inhibits alpha-synuclein fibrillation and disaggregates fibrils. <i>Chemistry and Biology</i> , 2004 , 11, 1513-21		176
136	Conformational constraints for amyloid fibrillation: the importance of being unfolded. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2004 , 1698, 131-53	4	817
135	Charge and hydrophobicity patterning along the sequence predicts the folding mechanism and aggregation of proteins: a computational approach. <i>Journal of Proteome Research</i> , 2004 , 3, 1243-53	5.6	42
134	Comparative studies on the structure and stability of fluorescent proteins EGFP, zFP506, mRFP1, "dimer2", and DsRed1. <i>Biochemistry</i> , 2004 , 43, 14913-23	3.2	73

133	Role of individual methionines in the fibrillation of methionine-oxidized alpha-synuclein. <i>Biochemistry</i> , 2004 , 43, 4621-33	3.2	88
132	Use of the phase diagram method to analyze the protein unfolding-refolding reactions: fishing out the "invisible" intermediates. <i>Journal of Proteome Research</i> , 2004 , 3, 485-94	5.6	120
131	Conformational prerequisites for formation of amyloid fibrils from histones. <i>Journal of Molecular Biology</i> , 2004 , 342, 1305-24	6.5	69
130	No need to be HAMLET or BAMLET to interact with histones: binding of monomeric alpha-lactalbumin to histones and basic poly-amino acids. <i>Biochemistry</i> , 2004 , 43, 5575-82	3.2	42
129	Role of protein-water interactions and electrostatics in alpha-synuclein fibril formation. <i>Biochemistry</i> , 2004 , 43, 3289-300	3.2	170
128	Adenylation-dependent conformation and unfolding pathways of the NAD ⁺ -dependent DNA ligase from the thermophile <i>Thermus scotoductus</i> . <i>Biophysical Journal</i> , 2004 , 86, 1089-104	2.9	25
127	Disorder in the nuclear pore complex: the FG repeat regions of nucleoporins are natively unfolded. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 2450-5	11.5	384
126	Calcium and domain interactions contribute to the thermostability of domains of the multimodular cellobiohydrolase, CbhA, a subunit of the <i>Clostridium thermocellum</i> cellulosome. <i>Biochemical Journal</i> , 2003 , 372, 151-61	3.8	22
125	Polycation-induced oligomerization and accelerated fibrillation of human alpha-synuclein in vitro. <i>Protein Science</i> , 2003 , 12, 702-7	6.3	109
124	Protein folding revisited. A polypeptide chain at the folding-misfolding-nonfolding cross-roads: which way to go?. <i>Cellular and Molecular Life Sciences</i> , 2003 , 60, 1852-71	10.3	271
123	Prediction of the association state of insulin using spectral parameters. <i>Journal of Pharmaceutical Sciences</i> , 2003 , 92, 847-58	3.9	61
122	Ultraviolet illumination-induced reduction of alpha-lactalbumin disulfide bridges. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 51, 498-503	4.2	38
121	Natively unfolded C-terminal domain of caldesmon remains substantially unstructured after the effective binding to calmodulin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53, 855-62	4.2	88
120	Structural and functional adaptations to extreme temperatures in psychrophilic, mesophilic, and thermophilic DNA ligases. <i>Journal of Biological Chemistry</i> , 2003 , 278, 37015-23	5.4	136
119	Partially folded intermediates in insulin fibrillation. <i>Biochemistry</i> , 2003 , 42, 11404-16	3.2	182
118	High stability of Discosoma DsRed as compared to Aequorea EGFP. <i>Biochemistry</i> , 2003 , 42, 7879-84	3.2	89
117	A protein-chameleon: conformational plasticity of alpha-synuclein, a disordered protein involved in neurodegenerative disorders. <i>Journal of Biomolecular Structure and Dynamics</i> , 2003 , 21, 211-34	3.6	391
116	Nuclear localization of alpha-synuclein and its interaction with histones. <i>Biochemistry</i> , 2003 , 42, 8465-71	3.2	255

115	Biophysical constraints for protein structure prediction. <i>Journal of Proteome Research</i> , 2003 , 2, 37-42	5.6	50
114	Structural and functional properties of IL-4delta2, an alternative splice variant of human IL-4. <i>Journal of Proteome Research</i> , 2003 , 2, 273-81	5.6	26
113	Structural transformations of oligomeric intermediates in the fibrillation of the immunoglobulin light chain LEN. <i>Biochemistry</i> , 2003 , 42, 8094-104	3.2	77
112	Recoverin is a zinc-binding protein. <i>Journal of Proteome Research</i> , 2003 , 2, 51-7	5.6	21
111	Conformational behavior and aggregation of alpha-synuclein in organic solvents: modeling the effects of membranes. <i>Biochemistry</i> , 2003 , 42, 2720-30	3.2	231
110	Nitration inhibits fibrillation of human alpha-synuclein in vitro by formation of soluble oligomers. <i>FEBS Letters</i> , 2003 , 542, 147-52	3.8	132
109	Cofactor binding modulates the conformational stabilities and unfolding patterns of NAD(+)-dependent DNA ligases from Escherichia coli and Thermus scotoductus. <i>Journal of Biological Chemistry</i> , 2003 , 278, 49945-53	5.4	19
108	Certain metals trigger fibrillation of methionine-oxidized alpha-synuclein. <i>Journal of Biological Chemistry</i> , 2003 , 278, 27630-5	5.4	151
107	Polymeric aspects of protein folding: a brief overview. <i>Protein and Peptide Letters</i> , 2003 , 10, 239-45	1.9	24
106	Native-like secondary structure of molten globules. <i>BBA - Proteins and Proteomics</i> , 2002 , 1594, 168-77		62
105	Unraveling multistate unfolding of rabbit muscle creatine kinase. <i>BBA - Proteins and Proteomics</i> , 2002 , 1596, 138-55		88
104	What does it mean to be natively unfolded?. <i>FEBS Journal</i> , 2002 , 269, 2-12		766
103	Natively unfolded proteins: a point where biology waits for physics. <i>Protein Science</i> , 2002 , 11, 739-56	6.3	1470
102	The Saccharomyces cerevisiae nucleoporin Nup2p is a natively unfolded protein. <i>Journal of Biological Chemistry</i> , 2002 , 277, 33447-55	5.4	81
101	Elucidation of the molecular mechanism during the early events in immunoglobulin light chain amyloid fibrillation. Evidence for an off-pathway oligomer at acidic pH. <i>Journal of Biological Chemistry</i> , 2002 , 277, 12666-79	5.4	84
100	Effect of association state and conformational stability on the kinetics of immunoglobulin light chain amyloid fibril formation at physiological pH. <i>Journal of Biological Chemistry</i> , 2002 , 277, 12657-65	5.4	62
99	Effect of zinc and temperature on the conformation of the gamma subunit of retinal phosphodiesterase: a natively unfolded protein. <i>Journal of Proteome Research</i> , 2002 , 1, 149-59	5.6	57
98	Structural and functional properties of Yersinia pestis Caf1 capsular antigen and their possible role in fulminant development of primary pneumonic plague. <i>Journal of Proteome Research</i> , 2002 , 1, 307-15	5.6	9

97	Biophysical properties of the synucleins and their propensities to fibrillate: inhibition of alpha-synuclein assembly by beta- and gamma-synucleins. <i>Journal of Biological Chemistry</i> , 2002 , 277, 11970-8	5.4	361
96	Conformational prerequisites for alpha-lactalbumin fibrillation. <i>Biochemistry</i> , 2002 , 41, 12546-51	3.2	186
95	The herbicide paraquat causes up-regulation and aggregation of alpha-synuclein in mice: paraquat and alpha-synuclein. <i>Journal of Biological Chemistry</i> , 2002 , 277, 1641-4	5.4	474
94	Cracking the folding code. Why do some proteins adopt partially folded conformations, whereas other don't?. <i>FEBS Letters</i> , 2002 , 514, 181-3	3.8	32
93	The chicken-egg scenario of protein folding revisited. <i>FEBS Letters</i> , 2002 , 515, 79-83	3.8	55
92	Accelerated alpha-synuclein fibrillation in crowded milieu. <i>FEBS Letters</i> , 2002 , 515, 99-103	3.8	209
91	Methionine oxidation inhibits fibrillation of human alpha-synuclein in vitro. <i>FEBS Letters</i> , 2002 , 517, 239-44	3.8	182
90	Amino acid determinants of alpha-synuclein aggregation: putting together pieces of the puzzle. <i>FEBS Letters</i> , 2002 , 522, 9-13	3.8	79
89	Human alpha-fetoprotein as a Zn(2+)-binding protein. Tight cation binding is not accompanied by global changes in protein structure and stability. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2002 , 1586, 1-10	6.9	6
88	Conformational behavior of human alpha-synuclein is modulated by familial Parkinson's disease point mutations A30P and A53T. <i>NeuroToxicology</i> , 2002 , 23, 553-67	4.4	117
87	Synergistic effects of pesticides and metals on the fibrillation of alpha-synuclein: implications for Parkinson's disease. <i>NeuroToxicology</i> , 2002 , 23, 527-36	4.4	163
86	Heparin and other glycosaminoglycans stimulate the formation of amyloid fibrils from alpha-synuclein in vitro. <i>Biochemistry</i> , 2002 , 41, 1502-11	3.2	286
85	Biophysical characterization of albumin preparations from blood serum of healthy donors and patients with renal diseases. Part I: spectrofluorometric analysis. <i>Medical Science Monitor</i> , 2002 , 8, BR261-5	3.2	2
84	Role of conformational changes in the heme-dependent regulation of human soluble guanylate cyclase. <i>Journal of Inorganic Biochemistry</i> , 2001 , 87, 267-76	4.2	13
83	Denatured collapsed states in protein folding: example of apomyoglobin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 44, 244-54	4.2	91
82	Partially folded conformations in the folding pathway of bovine carbonic anhydrase II: a fluorescence spectroscopic analysis. <i>ChemBioChem</i> , 2001 , 2, 813-21	3.8	115
81	Evidence for a partially folded intermediate in alpha-synuclein fibril formation. <i>Journal of Biological Chemistry</i> , 2001 , 276, 10737-44	5.4	831
80	Metal-triggered structural transformations, aggregation, and fibrillation of human alpha-synuclein. A possible molecular link between Parkinson's disease and heavy metal exposure. <i>Journal of Biological Chemistry</i> , 2001 , 276, 44284-96	5.4	791

79	Stabilization of partially folded conformation during alpha-synuclein oligomerization in both purified and cytosolic preparations. <i>Journal of Biological Chemistry</i> , 2001 , 276, 43495-8	5.4	141
78	Mutating aspartate in the calcium-binding site of alpha-lactalbumin: effects on the protein stability and cation binding. <i>Protein Engineering, Design and Selection</i> , 2001 , 14, 785-9	1.9	18
77	Effect of familial Parkinson's disease point mutations A30P and A53T on the structural properties, aggregation, and fibrillation of human alpha-synuclein. <i>Biochemistry</i> , 2001 , 40, 11604-13	3.2	422
76	Effect of environmental factors on the kinetics of insulin fibril formation: elucidation of the molecular mechanism. <i>Biochemistry</i> , 2001 , 40, 6036-46	3.2	936
75	Probing the mechanism of insulin fibril formation with insulin mutants. <i>Biochemistry</i> , 2001 , 40, 8397-409	3.2	282
74	Human soluble guanylate cyclase: functional expression, purification and structural characterization. <i>Archives of Biochemistry and Biophysics</i> , 2001 , 388, 185-97	4.1	18
73	Pesticides directly accelerate the rate of alpha-synuclein fibril formation: a possible factor in Parkinson's disease. <i>FEBS Letters</i> , 2001 , 500, 105-8	3.8	269
72	Trimethylamine-N-oxide-induced folding of alpha-synuclein. <i>FEBS Letters</i> , 2001 , 509, 31-5	3.8	146
71	Is Congo red an amyloid-specific dye?. <i>Journal of Biological Chemistry</i> , 2001 , 276, 22715-21	5.4	239
70	Structural and functional similarity between Yersinia pestis capsular protein Caf1 and human interleukin-1 beta. <i>Biochemistry</i> , 2001 , 40, 6076-84	3.2	16
69	Effect of salts on the stability and folding of staphylococcal nuclease. <i>Biochemistry</i> , 2001 , 40, 2113-28	3.2	68
68	Secondary Structure of the Homologous Proteins, A A-Fetoprotein and Serum Albumin, from their Circular Dichroism and Infrared Spectra. <i>Protein and Peptide Letters</i> , 2001 , 8, 297-302	1.9	9
67	Why are "natively unfolded" proteins unstructured under physiologic conditions?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000 , 41, 415-27	4.2	1690
66	Structure and function of alpha-fetoprotein: a biophysical overview. <i>BBA - Proteins and Proteomics</i> , 2000 , 1480, 41-56		71
65	Point amino acid substitutions in the Ca ²⁺ -binding sites of recoverin: II. The unusual behavior of the protein upon the binding of calcium ions. <i>Russian Journal of Bioorganic Chemistry</i> , 2000 , 26, 152-156	1	
64	Multisite fluorescence in proteins with multiple tryptophan residues. Apomyoglobin natural variants and site-directed mutants. <i>Journal of Biological Chemistry</i> , 2000 , 275, 36285-94	5.4	23
63	Zn(2+)-mediated structure formation and compaction of the "natively unfolded" human prothymosin alpha. <i>Biochemical and Biophysical Research Communications</i> , 2000 , 267, 663-8	3.4	64
62	Effects of mutations in the calcium-binding sites of recoverin on its calcium affinity: evidence for successive filling of the calcium binding sites. <i>Protein Engineering, Design and Selection</i> , 2000 , 13, 783-90	1.9	36

61	Why are natively unfolded proteins unstructured under physiologic conditions? 2000 , 41, 415		4
60	Why are natively unfolded proteins unstructured under physiologic conditions? 2000 , 41, 415		14
59	Association of partially-folded intermediates of staphylococcal nuclease induces structure and stability. <i>Protein Science</i> , 1999 , 8, 161-73	6.3	49
58	Structure and stability of recombinant protein depend on the extra N-terminal methionine residue: S6 permutein from direct and fusion expression systems. <i>BBA - Proteins and Proteomics</i> , 1999 , 1432, 324-32		5
57	Fine tuning the N-terminus of a calcium binding protein: alpha-lactalbumin. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 37, 65-72	4.2	20
56	Natively unfolded human prothymosin alpha adopts partially folded collapsed conformation at acidic pH. <i>Biochemistry</i> , 1999 , 38, 15009-16	3.2	126
55	Transient dimer in the refolding kinetics of cytochrome c characterized by small-angle X-ray scattering. <i>Biochemistry</i> , 1999 , 38, 15352-9	3.2	68
54	Effect of self-association on the structural organization of partially folded proteins: inactivated actin. <i>Biophysical Journal</i> , 1999 , 77, 2788-800	2.9	41
53	Self-association of 8-anilino-1-naphthalene-sulfonate molecules: spectroscopic characterization and application to the investigation of protein folding. <i>BBA - Proteins and Proteomics</i> , 1998 , 1388, 133-42		37
52	Can grafting of an octapeptide improve the structure of a de novo protein?. <i>FEBS Letters</i> , 1998 , 425, 101-4	3.8	13
51	Hyperphosphorylation induces structural modification of tau-protein. <i>FEBS Letters</i> , 1998 , 439, 21-5	3.8	24
50	Anion-induced folding of Staphylococcal nuclease: characterization of multiple equilibrium partially folded intermediates. <i>Journal of Molecular Biology</i> , 1998 , 278, 879-94	6.5	113
49	Association-induced folding of globular proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998 , 95, 5480-3	11.5	93
48	Effect of natural ligands on the structural properties and conformational stability of proteins. <i>Biochemistry (Moscow)</i> , 1998 , 63, 420-33	2.9	12
47	Structural effect of association on protein molecules in partially folded intermediates. <i>Biochemistry (Moscow)</i> , 1998 , 63, 456-62	2.9	5
46	Structural properties of staphylococcal nuclease in oligomeric A-forms. <i>Biochemistry (Moscow)</i> , 1998 , 63, 463-9	2.9	3
45	Equilibrium unfolding of partially folded staphylococcal nuclease A2- and A3-forms is accompanied by the formation of an intermediate state. <i>Biochemistry (Moscow)</i> , 1998 , 63, 470-5	2.9	2
44	Sequential Compaction of a Random Copolymer of Hydrophilic and Hydrophobic Amino Acid Residues. <i>Macromolecules</i> , 1997 , 30, 7427-7434	5.5	11

43	Ligand-free form of human alpha-fetoprotein: evidence for the molten globule state. <i>FEBS Letters</i> , 1997 , 410, 280-4	3.8	26
42	S6 permutein shows that the unusual target topology is not responsible for the absence of rigid tertiary structure in de novo protein albebetin. <i>FEBS Letters</i> , 1997 , 414, 243-6	3.8	6
41	Rigidity of human alpha-fetoprotein tertiary structure is under ligand control. <i>Biochemistry</i> , 1997 , 36, 13638-45	3.2	91
40	Conformational transitions provoked by organic solvents in beta-lactoglobulin: can a molten globule like intermediate be induced by the decrease in dielectric constant?. <i>Folding & Design</i> , 1997 , 2, 163-72		153
39	Further evidence on the equilibrium "pre-molten globule state": four-state guanidinium chloride-induced unfolding of carbonic anhydrase B at low temperature. <i>Journal of Molecular Biology</i> , 1996 , 255, 215-28	6.5	194
38	Molten globule-like state of cytochrome c under conditions simulating those near the membrane surface. <i>Biochemistry</i> , 1996 , 35, 6058-63	3.2	208
37	Protein engineering of de novo protein with predesigned structure and activity. <i>Applied Biochemistry and Biotechnology</i> , 1996 , 61, 85-96	3.2	2
36	All-or-none solvent-induced transitions between native, molten globule and unfolded states in globular proteins. <i>Folding & Design</i> , 1996 , 1, 117-22		68
35	Use of fluorescence decay times of 8-ANS-protein complexes to study the conformational transitions in proteins which unfold through the molten globule state. <i>Biophysical Chemistry</i> , 1996 , 60, 79-88	3.5	112
34	Circularly permuted dihydrofolate reductase possesses all the properties of the molten globule state, but can resume functional tertiary structure by interaction with its ligands. <i>Protein Science</i> , 1996 , 5, 1844-51	6.3	59
33	The de novo protein with grafted biological function: transferring of interferon blast-transforming activity to albebetin. <i>Protein Engineering, Design and Selection</i> , 1996 , 9, 195-201	1.9	8
32	Structural properties of alpha-fetoprotein from human cord serum: the protein molecule at low pH possesses all the properties of the molten globule. <i>FEBS Letters</i> , 1995 , 364, 165-7	3.8	13
31	"Domain" Coil-Globule Transition in Homopolymers. <i>Macromolecules</i> , 1995 , 28, 7519-7524	5.5	260
30	Kinetic and equilibrium folding intermediates. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 1995 , 348, 35-41	5.8	92
29	Circularly permuted dihydrofolate reductase of E. coli has functional activity and a destabilized tertiary structure. <i>Protein Engineering, Design and Selection</i> , 1994 , 7, 1373-7	1.9	33
28	A new approach to artificial and modified proteins: theory-based design, synthesis in a cell-free system and fast testing of structural properties by radiolabels. <i>Protein Engineering, Design and Selection</i> , 1994 , 7, 1041-52	1.9	5
27	"Partly folded" state, a new equilibrium state of protein molecules: four-state guanidinium chloride-induced unfolding of beta-lactamase at low temperature. <i>Biochemistry</i> , 1994 , 33, 2782-91	3.2	183
26	The molten globule is a third thermodynamical state of protein molecules. <i>FEBS Letters</i> , 1994 , 341, 15-8	3.8	141

25	Comparative stability of dihydrofolate reductase mutants in vitro and in vivo. <i>Protein Engineering, Design and Selection</i> , 1993 , 6, 81-4	1.9	10
24	Use of fast protein size-exclusion liquid chromatography to study the unfolding of proteins which denature through the molten globule. <i>Biochemistry</i> , 1993 , 32, 13288-98	3.2	437
23	Introduction of Ca(2+)-binding amino-acid sequence into the T4 lysozyme. <i>BBA - Proteins and Proteomics</i> , 1993 , 1162, 84-8		3
22	Triple point mutation Asp10-->His, Asn101-->Asp, Arg148-->Ser in T4 phage lysozyme leads to the molten globule. <i>Protein Engineering, Design and Selection</i> , 1992 , 5, 781-3	1.9	5
21	'All-or-none' mechanism of the molten globule unfolding. <i>FEBS Letters</i> , 1992 , 314, 89-92	3.8	81
20	Study of the "molten globule" intermediate state in protein folding by a hydrophobic fluorescent probe. <i>Biopolymers</i> , 1991 , 31, 119-28	2.2	1177
19	Two slow stages in refolding of bovine carbonic anhydrase B are due to proline isomerization. <i>Journal of Molecular Biology</i> , 1990 , 213, 561-8	6.5	50
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1 Role of structural disorder in the multi-functionality of flavivirus proteins. *Expert Review of Proteomics*, 4:2