Vladimir N Uversky

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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	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). <i>Autophagy</i> , 2016 , 12, 1-222	10.2	3838
995	Why are "natively unfolded" proteins unstructured under physiologic conditions?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000 , 41, 415-27	4.2	1690
994	Natively unfolded proteins: a point where biology waits for physics. <i>Protein Science</i> , 2002 , 11, 739-56	6.3	1470
993	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
992	Classification of intrinsically disordered regions and proteins. <i>Chemical Reviews</i> , 2014 , 114, 6589-631	68.1	1141
991	Intrinsically disordered proteins in human diseases: introducing the D2 concept. <i>Annual Review of Biophysics</i> , 2008 , 37, 215-46	21.1	1018
990	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
989	Flexible nets. The roles of intrinsic disorder in protein interaction networks. <i>FEBS Journal</i> , 2005 , 272, 5129-48	5.7	895
988	Understanding protein non-folding. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010 , 1804, 1231-64	4	875
987	Evidence for a partially folded intermediate in alpha-synuclein fibril formation. <i>Journal of Biological Chemistry</i> , 2001 , 276, 10737-44	5.4	831
986	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
985	Metal-triggered structural transformations, aggregation, and fibrillation of human alpha-synuclein. A possible molecular NK between Parkinson's disease and heavy metal exposure. <i>Journal of Biological Chemistry</i> , 2001 , 276, 44284-96	5.4	791
984	What does it mean to be natively unfolded?. FEBS Journal, 2002, 269, 2-12		766
983	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
982	Function and structure of inherently disordered proteins. <i>Current Opinion in Structural Biology</i> , 2008 , 18, 756-64	8.1	746
981	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
980	DisProt: the Database of Disordered Proteins. <i>Nucleic Acids Research</i> , 2007 , 35, D786-93	20.1	631

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979	Analysis of molecular recognition features (MoRFs). <i>Journal of Molecular Biology</i> , 2006 , 362, 1043-59	6.5	579
978	Intrinsic disorder and functional proteomics. <i>Biophysical Journal</i> , 2007 , 92, 1439-56	2.9	571
977	Coupled folding and binding with alpha-helix-forming molecular recognition elements. <i>Biochemistry</i> , 2005 , 44, 12454-70	3.2	541
976	Intrinsic disorder in transcription factors. <i>Biochemistry</i> , 2006 , 45, 6873-88	3.2	518
975	Introducing protein intrinsic disorder. <i>Chemical Reviews</i> , 2014 , 114, 6561-88	68.1	487
974	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
973	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
972	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
971	Intrinsic disorder is a common feature of hub proteins from four eukaryotic interactomes. <i>PLoS Computational Biology</i> , 2006 , 2, e100	5	435
970	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
969	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
968	Comparing and combining predictors of mostly disordered proteins. <i>Biochemistry</i> , 2005 , 44, 1989-2000	3.2	416
967	The unfoldomics decade: an update on intrinsically disordered proteins. <i>BMC Genomics</i> , 2008 , 9 Suppl 2, S1	4.5	408
966	Esynuclein misfolding and Parkinson's disease. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2012 , 1822, 261-85	6.9	406
965	D₽₽ database of disordered protein predictions. <i>Nucleic Acids Research</i> , 2013 , 41, D508-16	20.1	398
964	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
963	Characterization of molecular recognition features, MoRFs, and their binding partners. <i>Journal of Proteome Research</i> , 2007 , 6, 2351-66	5.6	386
962	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

961	Unusual biophysics of intrinsically disordered proteins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013 , 1834, 932-51	4	377
960	Neuropathology, biochemistry, and biophysics of alpha-synuclein aggregation. <i>Journal of Neurochemistry</i> , 2007 , 103, 17-37	6	373
959	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
958	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
957	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
956	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
955	Assessing protein disorder and induced folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 62, 24-45	4.2	347
954	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
953	Predicting intrinsic disorder in proteins: an overview. <i>Cell Research</i> , 2009 , 19, 929-49	24.7	328
952	Intrinsically disordered proteins from A to Z. <i>International Journal of Biochemistry and Cell Biology</i> , 2011 , 43, 1090-103	5.6	322
951	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
950	What macromolecular crowding can do to a protein. <i>International Journal of Molecular Sciences</i> , 2014 , 15, 23090-140	6.3	318
949	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
948	Probing the mechanism of insulin fibril formation with insulin mutants. <i>Biochemistry</i> , 2001 , 40, 8397-409	93.2	282
947	Composition Profiler: a tool for discovery and visualization of amino acid composition differences. <i>BMC Bioinformatics</i> , 2007 , 8, 211	3.6	276
946	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
945	Mining alpha-helix-forming molecular recognition features with cross species sequence alignments. <i>Biochemistry</i> , 2007 , 46, 13468-77	3.2	270
944	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

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943	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
942	"Domain" Coil-Globule Transition in Homopolymers. <i>Macromolecules</i> , 1995 , 28, 7519-7524	5.5	260
941	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
940	Nuclear localization of alpha-synuclein and its interaction with histones. <i>Biochemistry</i> , 2003 , 42, 8465-7	13.2	255
939	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
938	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
937	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
936	Is Congo red an amyloid-specific dye?. <i>Journal of Biological Chemistry</i> , 2001 , 276, 22715-21	5.4	239
935	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
934	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
933	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
932	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
931	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
930	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
929	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
928	Intrinsic disorder in scaffold proteins: getting more from less. <i>Progress in Biophysics and Molecular Biology</i> , 2008 , 98, 85-106	4.7	213
927	Accelerated alpha-synuclein fibrillation in crowded milieu. FEBS Letters, 2002, 515, 99-103	3.8	209
926	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

925	Early events in the fibrillation of monomeric insulin. Journal of Biological Chemistry, 2005, 280, 42669-7	'5 _{5.4}	203
924	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
923	Unfoldomics of human diseases: linking protein intrinsic disorder with diseases. <i>BMC Genomics</i> , 2009 , 10 Suppl 1, S7	4.5	199
922	Rational drug design via intrinsically disordered protein. <i>Trends in Biotechnology</i> , 2006 , 24, 435-42	15.1	199
921	Close encounters of the third kind: disordered domains and the interactions of proteins. <i>BioEssays</i> , 2009 , 31, 328-35	4.1	197
920	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
919	Intrinsically Disordered Proteins and Their Mysterious (Meta) Physics. Frontiers in Physics, 2019, 7,	3.9	188
918	Pathological unfoldomics of uncontrolled chaos: intrinsically disordered proteins and human diseases. <i>Chemical Reviews</i> , 2014 , 114, 6844-79	68.1	186
917	Conformational prerequisites for alpha-lactalbumin fibrillation. <i>Biochemistry</i> , 2002 , 41, 12546-51	3.2	186
916	Intrinsic disorder-based protein interactions and their modulators. <i>Current Pharmaceutical Design</i> , 2013 , 19, 4191-213	3.3	185
915	"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
914	DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , 2017 , 45, D219-D227	20.1	182
913	Do viral proteins possess unique biophysical features?. <i>Trends in Biochemical Sciences</i> , 2009 , 34, 53-9	10.3	182
912	Partially folded intermediates in insulin fibrillation. <i>Biochemistry</i> , 2003 , 42, 11404-16	3.2	182
911	Methionine oxidation inhibits fibrillation of human alpha-synuclein in vitro. FEBS Letters, 2002, 517, 239	9- 4 .&	182
910	Rifampicin inhibits alpha-synuclein fibrillation and disaggregates fibrils. <i>Chemistry and Biology</i> , 2004 , 11, 1513-21		176
909	The mysterious unfoldome: structureless, underappreciated, yet vital part of any given proteome. <i>Journal of Biomedicine and Biotechnology</i> , 2010 , 2010, 568068		173
908	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

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907	Role of protein-water interactions and electrostatics in alpha-synuclein fibril formation. <i>Biochemistry</i> , 2004 , 43, 3289-300	3.2	170
906	Accelerated neurodegeneration through chaperone-mediated oligomerization of tau. <i>Journal of Clinical Investigation</i> , 2013 , 123, 4158-69	15.9	169
905	Intrinsic disorder in proteins associated with neurodegenerative diseases. <i>Frontiers in Bioscience - Landmark</i> , 2009 , 14, 5188-238	2.8	169
904	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
903	Alpha-synuclein misfolding and neurodegenerative diseases. <i>Current Protein and Peptide Science</i> , 2008 , 9, 507-40	2.8	163
902	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
901	Malleable machines take shape in eukaryotic transcriptional regulation. <i>Nature Chemical Biology</i> , 2008 , 4, 728-37	11.7	161
900	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
899	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
898	Distinct \Bsheet structure in protein aggregates determined by ATR-FTIR spectroscopy. <i>Biochemistry</i> , 2013 , 52, 5176-83	3.2	154
897	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
896	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
895	Abundance of intrinsic disorder in protein associated with cardiovascular disease. <i>Biochemistry</i> , 2006 , 45, 10448-60	3.2	152
894	Mysterious oligomerization of the amyloidogenic proteins. <i>FEBS Journal</i> , 2010 , 277, 2940-53	5.7	151
893	Certain metals trigger fibrillation of methionine-oxidized alpha-synuclein. <i>Journal of Biological Chemistry</i> , 2003 , 278, 27630-5	5.4	151
892	Amyloidogenesis of natively unfolded proteins. <i>Current Alzheimer Research</i> , 2008 , 5, 260-87	3	147
891	Trimethylamine-N-oxide-induced folding of alpha-synuclein. FEBS Letters, 2001, 509, 31-5	3.8	146
890	Structural characteristics of alpha-synuclein oligomers stabilized by the flavonoid baicalein. <i>Journal of Molecular Biology</i> , 2008 , 383, 214-23	6.5	145

889	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
888	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
887	The molten globule is a third thermodynamical state of protein molecules. FEBS Letters, 1994, 341, 15-8	3.8	141
886	Guiding protein aggregation with macromolecular crowding. <i>Biochemistry</i> , 2008 , 47, 8993-9006	3.2	138
885	Conditionally and transiently disordered proteins: awakening cryptic disorder to regulate protein function. <i>Chemical Reviews</i> , 2014 , 114, 6779-805	68.1	136
884	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
883	Methionine oxidation, alpha-synuclein and Parkinson's disease. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005 , 1703, 157-69	4	134
882	Structural disorder in viral proteins. <i>Chemical Reviews</i> , 2014 , 114, 6880-911	68.1	133
881	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
880	Drugs for 'protein clouds': targeting intrinsically disordered transcription factors. <i>Current Opinion in Pharmacology</i> , 2010 , 10, 782-8	5.1	132
879	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
878	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
877	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
876	Effects of nitration on the structure and aggregation of alpha-synuclein. <i>Molecular Brain Research</i> , 2005 , 134, 84-102		127
875	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
874	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
873	Natively unfolded human prothymosin alpha adopts partially folded collapsed conformation at acidic pH. <i>Biochemistry</i> , 1999 , 38, 15009-16	3.2	126
872	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

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871	Functional roles of transiently and intrinsically disordered regions within proteins. <i>FEBS Journal</i> , 2015 , 282, 1182-9	5.7	121
870	Structural, morphological, and functional diversity of amyloid oligomers. FEBS Letters, 2015, 589, 2640-	· 8 3.8	120
869	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
868	Beyond the excluded volume effects: mechanistic complexity of the crowded milieu. <i>Molecules</i> , 2015 , 20, 1377-409	4.8	118
867	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
866	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
865	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
864	Intrinsic disorder in the Protein Data Bank. <i>Journal of Biomolecular Structure and Dynamics</i> , 2007 , 24, 325-42	3.6	116
863	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
862	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
861	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
860	Intrinsic Disorder and Posttranslational Modifications: The Darker Side of the Biological Dark Matter. <i>Frontiers in Genetics</i> , 2018 , 9, 158	4.5	111
859	Intrinsically Disordered Proteome of Human Membrane-Less Organelles. <i>Proteomics</i> , 2018 , 18, e170019	93 4.8	109
858	Intrinsically disordered proteins and their (disordered) proteomes in neurodegenerative disorders. <i>Frontiers in Aging Neuroscience</i> , 2015 , 7, 18	5.3	109
857	Polycation-induced oligomerization and accelerated fibrillation of human alpha-synuclein in vitro. <i>Protein Science</i> , 2003 , 12, 702-7	6.3	109
856	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
855	Protein interactions and misfolding analyzed by AFM force spectroscopy. <i>Journal of Molecular Biology</i> , 2005 , 354, 1028-42	6.5	107
854	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

853	Molecular mechanisms underlying the flavonoid-induced inhibition of alpha-synuclein fibrillation. <i>Biochemistry</i> , 2009 , 48, 8206-24	3.2	106
852	Protein disorder in the human diseasome: unfoldomics of human genetic diseases. <i>BMC Genomics</i> , 2009 , 10 Suppl 1, S12	4.5	105
851	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
850	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
849	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
848	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
847	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
846	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
845	Archaic chaos: intrinsically disordered proteins in Archaea. <i>BMC Systems Biology</i> , 2010 , 4 Suppl 1, S1	3.5	99
844	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
843	Nickel impact on human health: An intrinsic disorder perspective. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016 , 1864, 1714-1731	4	98
842	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
841	Viral disorder or disordered viruses: do viral proteins possess unique features?. <i>Protein and Peptide Letters</i> , 2010 , 17, 932-51	1.9	96
840	Molecular recognition features (MoRFs) in three domains of life. <i>Molecular BioSystems</i> , 2016 , 12, 697-7	10	95
839	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
838	Disease-associated mutations disrupt functionally important regions of intrinsic protein disorder. <i>PLoS Computational Biology</i> , 2012 , 8, e1002709	5	95
837	Forcing nonamyloidogenic beta-synuclein to fibrillate. <i>Biochemistry</i> , 2005 , 44, 9096-107	3.2	95
836	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

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835	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
834	The multifaceted roles of intrinsic disorder in protein complexes. FEBS Letters, 2015, 589, 2498-506	3.8	92
833	Disordered proteinaceous machines. <i>Chemical Reviews</i> , 2014 , 114, 6806-43	68.1	92
832	Kinetic and equilibrium folding intermediates. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 1995 , 348, 35-41	5.8	92
831	Rigidity of human alpha-fetoprotein tertiary structure is under ligand control. <i>Biochemistry</i> , 1997 , 36, 13638-45	3.2	91
830	Malleable machines in transcription regulation: the mediator complex. <i>PLoS Computational Biology</i> , 2008 , 4, e1000243	5	91
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