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What does it mean to be natively unfolded?

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795	Equilibrium unfolding and conformational plasticity of troponin I and T. <i>FEBS Journal</i> , 2002 , 269, 5484-91		12
794	Natively unfolded proteins: a point where biology waits for physics. 2002 , 11, 739-56		1470
793	Polycation-induced oligomerization and accelerated fibrillation of human alpha-synuclein in vitro. 2003 , 12, 702-7		109
792	The inactivating factor of glutamine synthetase, IF7, is a "natively unfolded" protein. 2003 , 12, 1443-54		36
791	Local protein unfolding and pathogenesis of polyglutamine-expansion diseases. 2003 , 51, 68-73		11
790	The intracellular domain of the <i>Drosophila</i> cholinesterase-like neural adhesion protein, gliotactin, is natively unfolded. 2003 , 53, 758-67		52
789	Natively unfolded C-terminal domain of caldesmon remains substantially unstructured after the effective binding to calmodulin. 2003 , 53, 855-62		88
788	A protein-chameleon: conformational plasticity of alpha-synuclein, a disordered protein involved in neurodegenerative disorders. 2003 , 21, 211-34		391
787	Biophysical constraints for protein structure prediction. 2003 , 2, 37-42		50

786	DSC studies of a family of natively disordered fragments from Escherichia coli thioredoxin: surface burial in intrinsic coils. 2003 , 42, 3349-58	9
785	Polyproline type II conformation in the C-terminal domain of the nuclear pore complex protein gp210. 2003 , 42, 3519-26	8
784	Conformational behavior and aggregation of alpha-synuclein in organic solvents: modeling the effects of membranes. 2003 , 42, 2720-30	231
783	Flexibility of Monomeric and Dimeric HIV-1 Protease 2003 , 107, 3068-3079	37
782	The N-terminal domain of p53 is natively unfolded. 2003 , 332, 1131-41	203
781	Volumetric properties of proteins. 2003 , 32, 207-35	273
780	Zinc ions promote the interaction between heparin and heparin cofactor II. 2003 , 541, 121-5	18
779	The PIR domain of Grb14 is an intrinsically unstructured protein: implication in insulin signaling. 2003 , 554, 240-6	19
778	Comparative studies on the properties of the extrinsic manganese-stabilizing protein from higher plants and of a synthetic peptide of its C-terminus. 2003 , 1604, 95-104	7
777	Myelin basic protein has multiple calmodulin-binding sites. 2003 , 308, 313-9	30
776	Molecular mechanisms of amyloidosis. 2003 , 349, 583-96	1335
775	New insight into the solution structures of wheat gluten proteins from Raman optical activity. 2003 , 42, 5665-73	69
774	Cofactor binding modulates the conformational stabilities and unfolding patterns of NAD(+)-dependent DNA ligases from Escherichia coli and Thermus scotoductus. 2003 , 278, 49945-53	19
773	Transition from natively unfolded to folded state induced by desiccation in an anhydrobiotic nematode protein. 2003 , 278, 12977-84	166
772	Structural disorder and modular organization in Paramyxovirinae N and P. 2003 , 84, 3239-3252	141
771	Structural analysis of Bacillus subtilis SPP1 phage helicase loader protein G39P. 2003 , 278, 15304-12	9
770	Mutagenesis reveals a specific role for Cox17p in copper transport to cytochrome oxidase. 2003 , 278, 30875-80	31
769	Malleable conformation of the elastic PEVK segment of titin: non-co-operative interconversion of polyproline II helix, beta-turn and unordered structures. 2003 , 374, 687-95	47

768	The C-terminal domain of the measles virus nucleoprotein is intrinsically disordered and folds upon binding to the C-terminal moiety of the phosphoprotein. 2003 , 278, 18638-48	223
767	Disorder in the nuclear pore complex: the FG repeat regions of nucleoporins are natively unfolded. 2003 , 100, 2450-5	384
766	Dynamic targeting of microtubules by TPPP/p25 affects cell survival. 2004 , 117, 6249-59	64
765	TC-1 is a novel tumorigenic and natively disordered protein associated with thyroid cancer. 2004 , 64, 2766-73	59
764	The YefM antitoxin defines a family of natively unfolded proteins: implications as a novel antibacterial target. 2004 , 279, 8252-61	71
763	pH and cation-induced thermodynamic stability of human hyaluronan binding protein 1 regulates its hyaluronan affinity. 2004 , 279, 23061-72	8
762	The von Hippel-Lindau tumor suppressor protein is a molten globule under native conditions: implications for its physiological activities. 2004 , 279, 17190-6	30
761	Reformable intramolecular cross-linking of the N-terminal domain of heparin cofactor II: effects on enzyme inhibition. <i>FEBS Journal</i> , 2004 , 271, 4275-83	11
760	An unstructured initiation site is required for efficient proteasome-mediated degradation. 2004 , 11, 830-7	354
759	Classification and knowledge discovery in protein databases. 2004 , 37, 224-39	64
758	Protein flexibility and intrinsic disorder. 2004 , 13, 71-80	269
757	Fast and faster: a designed variant of the B-domain of protein A folds in 3 microsec. 2004 , 13, 847-53	53
756	Thermal and alkaline denaturation of bovine beta-casein. 2004 , 23, 389-402	45
755	Myelin basic protein-diverse conformational states of an intrinsically unstructured protein and its roles in myelin assembly and multiple sclerosis. 2004 , 35, 503-42	199
754	Protein conformational transitions coupled to binding in molecular recognition of unstructured proteins: deciphering the effect of intermolecular interactions on computational structure prediction of the p27Kip1 protein bound to the cyclin A-cyclin-dependent kinase 2 complex. 2005 , 58, 706-16	14
753	Protein conformational transitions coupled to binding in molecular recognition of unstructured proteins: hierarchy of structural loss from all-atom Monte Carlo simulations of p27Kip1 unfolding-unbinding and structural determinants of the binding mechanism. 2004 , 75, 420-33	6
752	Conformational constraints for amyloid fibrillation: the importance of being unfolded. 2004 , 1698, 131-53	817
751	Recombinant EWS-FLI1 oncoprotein activates transcription. 2004 , 43, 13579-89	52

750	Yeast cox17 solution structure and Copper(I) binding. 2004 , 279, 53584-92	91
749	The HPV16 E7 viral oncoprotein self-assembles into defined spherical oligomers. 2004 , 43, 3310-7	54
748	Unfolded proteins and protein folding studied by NMR. 2004 , 104, 3607-22	541
747	SAXS study of the PIR domain from the Grb14 molecular adaptor: a natively unfolded protein with a transient structure primer?. 2004 , 87, 4056-64	43
746	The MAP2/Tau family of microtubule-associated proteins. 2005 , 6, 204	492
745	Biophysical characterization of Gir2, a highly acidic protein of <i>Saccharomyces cerevisiae</i> with anomalous electrophoretic behavior. 2004 , 314, 229-34	32
744	POPP the question: what do LEA proteins do?. 2004 , 9, 13-7	337
743	Natively unfolded tubulin polymerization promoting protein TPPP/p25 is a common marker of alpha-synucleinopathies. 2004 , 17, 155-62	124
742	Electron paramagnetic resonance spectroscopy and molecular modelling of the interaction of myelin basic protein (MBP) with calmodulin (CaM)-diversity and conformational adaptability of MBP CaM-targets. 2004 , 148, 353-69	28
741	Double-stranded DNA stimulates the fibrillation of alpha-synuclein in vitro and is associated with the mature fibrils: an electron microscopy study. 2004 , 344, 929-38	56
740	No need to be HAMLET or BAMLET to interact with histones: binding of monomeric alpha-lactalbumin to histones and basic poly-amino acids. 2004 , 43, 5575-82	42
739	Raman spectroscopic characterization of secondary structure in natively unfolded proteins: alpha-synuclein. 2004 , 126, 2399-408	338
738	Role of protein-water interactions and electrostatics in alpha-synuclein fibril formation. 2004 , 43, 3289-300	170
737	Adenylation-dependent conformation and unfolding pathways of the NAD ⁺ -dependent DNA ligase from the thermophile <i>Thermus scotoductus</i> . 2004 , 86, 1089-104	25
736	Defects in assembly of cytochrome oxidase: roles in mitochondrial disease. 2004 , 123-148	7
735	Stability of HAMLET--a kinetically trapped alpha-lactalbumin oleic acid complex. 2005 , 14, 329-40	55
734	Amyloid fibril formation by bovine milk kappa-casein and its inhibition by the molecular chaperones alphaS- and beta-casein. 2005 , 44, 17027-36	167
733	Plasma membrane phosphoinositide organization by protein electrostatics. 2005 , 438, 605-11	707

732	EspB from enterohaemorrhagic Escherichia coli is a natively partially folded protein. 2005 , 272, 756-68	18
731	Crystal structure of a subtilisin-like serine proteinase from a psychrotrophic Vibrio species reveals structural aspects of cold adaptation. 2005 , 272, 832-45	71
730	Flexible nets. The roles of intrinsic disorder in protein interaction networks. 2005 , 272, 5129-48	895
729	HIF-1alpha and p53: the ODD couple?. 2005 , 30, 426-9	53
728	Showing your ID: intrinsic disorder as an ID for recognition, regulation and cell signaling. 2005 , 18, 343-84	660
727	NMR of unfolded proteins. 2005 , 117, 3-21	13
726	Implication of C-terminal deletion on the structure and stability of bovine beta-casein. 2005 , 24, 431-44	27
725	Structure and activity of the photosystem II manganese-stabilizing protein: role of the conserved disulfide bond. 2005 , 85, 359-72	22
724	Role of trehalose and heat in the structure of the C-terminal activation domain of the heat shock transcription factor. 2005 , 58, 826-35	16
723	Protein flexibility and rigidity predicted from sequence. 2005 , 61, 115-26	129
722	Exploiting heterogeneous sequence properties improves prediction of protein disorder. 2005 , 61 Suppl 7, 176-82	423
721	Intrinsic unstructuredness and abundance of PEST motifs in eukaryotic proteomes. 2006 , 62, 309-15	79
720	Assessing protein disorder and induced folding. 2006 , 62, 24-45	347
719	PII structure in the model peptides for unfolded proteins: studies on ubiquitin fragments and several alanine-rich peptides containing QQQ, SSS, FFF, and VVV. 2006 , 63, 312-21	18
718	Structure/function of KRAB repression domains: structural properties of KRAB modules inferred from hydrodynamic, circular dichroism, and FTIR spectroscopic analyses. 2006 , 62, 604-16	10
717	Mass spectrometric analysis of the interactions between CP12, a chloroplast protein, and metal ions: a possible regulatory role within a PRK/GAPDH/CP12 complex. 2005 , 19, 3379-88	24
716	A Microscopic Study of Disorder-Order Transitions in Molecular Recognition of Unstructured Proteins: Hierarchy of Structural Loss and the Transition State Determination from Monte Carlo Simulations of P27KIP1 Protein Coupled Unfolding and Unbinding. 2005 , 199-230	
715	G protein-coupled receptors show unusual patterns of intrinsic unfolding. 2005 , 18, 103-10	40

7 ¹⁴	Calcium-binding crystallins from <i>Yersinia pestis</i> . Characterization of two single betagamma-crystallin domains of a putative exported protein. 2005 , 280, 1209-16	37
7 ¹³	Stability constraints and protein evolution: the role of chain length, composition and disulfide bonds. 2005 , 18, 405-15	45
7 ¹²	NMR chemical shift and relaxation measurements provide evidence for the coupled folding and binding of the p53 transactivation domain. 2005 , 33, 2061-77	75
7 ¹¹	Optimizing long intrinsic disorder predictors with protein evolutionary information. 2005 , 3, 35-60	346
7 ¹⁰	The YoeB toxin is a folded protein that forms a physical complex with the unfolded YefM antitoxin. Implications for a structural-based differential stability of toxin-antitoxin systems. 2005 , 280, 30063-72	29
7 ⁰⁹	"Natively unfolded" VPg is essential for <i>Sesbania mosaic virus</i> serine protease activity. 2005 , 280, 30291-300	41
7 ⁰⁸	Energetics of structural transitions of the addiction antitoxin MazE: is a programmed bacterial cell death dependent on the intrinsically flexible nature of the antitoxins?. 2005 , 280, 17397-407	22
7 ⁰⁷	Essential amino acids of the hantaan virus N protein in its interaction with RNA. 2005 , 79, 10032-9	40
7 ⁰⁶	Secondary structure and dynamics of an intrinsically unstructured linker domain. 2005 , 23, 113-24	19
7 ⁰⁵	Statistical studies of flexible nonhomogeneous polypeptide chains. 2005 , 6, 3010-7	
7 ⁰⁴	Inhibition of heparin-induced tau filament formation by phenothiazines, polyphenols, and porphyrins. 2005 , 280, 7614-23	409
7 ⁰³	Characterization of segments from the central region of BRCA1: an intrinsically disordered scaffold for multiple protein-protein and protein-DNA interactions?. 2005 , 345, 275-87	141
7 ⁰²	The pairwise energy content estimated from amino acid composition discriminates between folded and intrinsically unstructured proteins. 2005 , 347, 827-39	767
7 ⁰¹	Nucleoporin domain topology is linked to the transport status of the nuclear pore complex. 2005 , 351, 784-98	62
7 ⁰⁰	Binding of natively unfolded HIF-1alpha ODD domain to p53. 2005 , 17, 11-21	85
699	The interplay between structure and function in intrinsically unstructured proteins. 2005 , 579, 3346-54	563
698	Intracellular processing of the Sendai virus C' protein leads to the generation of a Y protein module: structure-functional implications. 2005 , 579, 5685-90	4
697	Protein disorder: conformational distribution of the flexible linker in a chimeric double cellulase. 2005 , 88, 2823-32	72

696	NMR relaxation studies on the hydrate layer of intrinsically unstructured proteins. 2005 , 88, 2030-7	72
695	Uncovering the unfoldome: enriching cell extracts for unstructured proteins by acid treatment. 2005 , 4, 1610-8	59
694	Coupled folding and binding with alpha-helix-forming molecular recognition elements. 2005 , 44, 12454-70	541
693	Conformation of the backbone in unfolded proteins. 2006 , 106, 1877-97	229
692	Beta-silks: enhancing and controlling aggregation. 2006 , 73, 17-53	34
691	Abundance of intrinsic disorder in protein associated with cardiovascular disease. 2006 , 45, 10448-60	152
690	Structural and Conformational Prerequisites of Amyloidogenesis. 2006 , 1-20	4
689	Predicting Disordered Regions in Proteins Based on Decision Trees of Reduced Amino Acid Composition. 2006 , 13, 1579-1590	1
688	Low resolution structure of the human alpha4 protein (IgBP1) and studies on the stability of alpha4 and of its yeast ortholog Tap42. 2006 , 1764, 724-34	15
687	Tubulin polymerization promoting proteins (TPPPs): members of a new family with distinct structures and functions. 2006 , 45, 13818-26	72
686	Protein intrinsic disorder and human papillomaviruses: increased amount of disorder in E6 and E7 oncoproteins from high risk HPVs. 2006 , 5, 1829-42	117
685	Conservation of intrinsic disorder in protein domains and families: II. functions of conserved disorder. 2006 , 5, 888-98	107
684	Assessing induced folding of an intrinsically disordered protein by site-directed spin-labeling electron paramagnetic resonance spectroscopy. 2006 , 110, 20596-608	92
683	Conservation of intrinsic disorder in protein domains and families: I. A database of conserved predicted disordered regions. 2006 , 5, 879-87	99
682	Intrinsically disordered structure of Bacillus pasteurii UreG as revealed by steady-state and time-resolved fluorescence spectroscopy. 2006 , 45, 8918-30	42
681	Salmon calcitonin and amyloid beta: two peptides with amyloidogenic capacity adopt different conformational manifolds in their unfolded states. 2006 , 45, 2810-9	27
680	The alpha-synuclein mutation E46K promotes aggregation in cultured cells. 2006 , 197, 515-20	86
679	Characterization of intra-molecular distances and site-specific dynamics in chemically unfolded barstar: evidence for denaturant-dependent non-random structure. 2006 , 359, 174-89	37

678	DNA recognition by the brinker repressor--an extreme case of coupling between binding and folding. 2006 , 361, 659-72	32
677	Analysis of molecular recognition features (MoRFs). 2006 , 362, 1043-59	579
676	Changes in nucleoporin domain topology in response to chemical effectors. 2006 , 363, 39-50	30
675	The alkali molten globule state of horse ferricytochrome c: observation of cold denaturation. 2006 , 364, 483-95	33
674	Fibrillogenic and non-fibrillogenic ensembles of SDS-bound human alpha-synuclein. 2006 , 364, 1061-72	70
673	Inhibition of cGMP-dependent protein kinase by the regulatory subunit of photoreceptor cGMP phosphodiesterase. 2006 , 401, 252-5	3
672	Efficient high level expression of peptides and proteins as fusion proteins with the N-terminal domain of L9: application to the villin headpiece helical subdomain. 2006 , 47, 234-40	10
671	Calmodulin signaling: analysis and prediction of a disorder-dependent molecular recognition. 2006 , 63, 398-410	86
670	Intrinsically unstructured N-terminal domain of bZIP transcription factor HY5. 2006 , 65, 856-66	28
669	Role of intrinsic disorder in transient interactions of hub proteins. 2007 , 66, 761-5	127
668	Prediction of natively unfolded regions in protein chains. 2006 , 40, 298-304	18
667	Vanilla mosaic virus isolates from French Polynesia and the Cook Islands are Dasheen mosaic virus strains that exclusively infect vanilla. 2006 , 151, 905-19	14
666	Interaction of alpha-synuclein and dopamine metabolites in the pathogenesis of Parkinson's disease: a case for the selective vulnerability of the substantia nigra. 2006 , 112, 115-26	68
665	Structural disorder within the replicative complex of measles virus: functional implications. 2006 , 344, 94-110	81
664	Length-dependent prediction of protein intrinsic disorder. 2006 , 7, 208	630
663	Nanoimaging for protein misfolding and related diseases. 2006 , 99, 52-70	39
662	Serine/arginine-rich splicing factors belong to a class of intrinsically disordered proteins. 2006 , 34, 305-12	87
661	Spritz: a server for the prediction of intrinsically disordered regions in protein sequences using kernel machines. 2006 , 34, W164-8	108

660	Prediction of amyloidogenic and disordered regions in protein chains. 2006 , 2, e177	138
659	Predicting disordered regions in proteins based on decision trees of reduced amino acid composition. 2006 , 13, 1723-34	8
658	The disordered amino-terminus of SIMPL interacts with members of the 70-kDa heat-shock protein family. 2006 , 25, 704-14	9
657	Common attributes of native-state structures of proteins, disordered proteins, and amyloid. 2006 , 103, 6883-8	44
656	Trend of amino acid composition of proteins of different taxa. 2006 , 4, 597-608	60
655	Calcium-dependent regulation of NEMO nuclear export in response to genotoxic stimuli. 2007 , 27, 497-509	30
654	Intrinsic disorder and autonomous domain function in the multifunctional nuclear protein, MeCP2. 2007 , 282, 15057-64	97
653	Intrinsic disorder in the C-terminal domain of the Shaker voltage-activated K ⁺ channel modulates its interaction with scaffold proteins. 2007 , 104, 13022-7	49
652	A natively unfolded yeast prion monomer adopts an ensemble of collapsed and rapidly fluctuating structures. 2007 , 104, 2649-54	259
651	Desiccation and zinc binding induce transition of tomato abscisic acid stress ripening 1, a water stress- and salt stress-regulated plant-specific protein, from unfolded to folded state. 2007 , 143, 617-28	75
650	Expected packing density allows prediction of both amyloidogenic and disordered regions in protein chains. 2007 , 19, 285225	6
649	Quantitative characterization of protein nanostructures using atomic force microscopy. 2007 , 2007, 6609-12	6
648	Rapid evolution exposes the boundaries of domain structure and function in natively unfolded FG nucleoporins. 2007 , 6, 272-82	69
647	Synuclein-gamma targeting peptide inhibitor that enhances sensitivity of breast cancer cells to antimicrotubule drugs. 2007 , 67, 626-33	48
646	Polyelectrostatic interactions of disordered ligands suggest a physical basis for ultrasensitivity. 2007 , 104, 9650-5	186
645	One-step purification of bacterially expressed recombinant transducin alpha-subunit and isotopically labeled PDE6 gamma-subunit for NMR analysis. 2007 , 51, 187-97	16
644	DNA induces folding in alpha-synuclein: understanding the mechanism using chaperone property of osmolytes. 2007 , 464, 57-69	59
643	Fluorescence as a method to reveal structures and membrane-interactions of amyloidogenic proteins. 2007 , 1768, 1862-85	228

642	Looking into live cells with in-cell NMR spectroscopy. 2007 , 158, 244-53	119
641	Sulfate acts as phosphate analog on the monomeric catalytic fragment of the CPx-ATPase CopB from <i>Sulfolobus solfataricus</i> . 2007 , 369, 368-85	20
640	Dissecting the non-specific and specific components of the initial folding reaction of barstar by multi-site FRET measurements. 2007 , 370, 385-405	47
639	Copper- and iron-induced differential fibril formation in alpha-synuclein: TEM study. 2007 , 424, 78-82	81
638	Functional anthology of intrinsic disorder. 1. Biological processes and functions of proteins with long disordered regions. 2007 , 6, 1882-98	455
637	Myosin XVA. 2008 , 441-467	1
636	Distinguishing Lewy body dementias from Alzheimer's disease. 2007 , 7, 1499-516	22
635	The N-terminal module of HPV16 E7 is an intrinsically disordered domain that confers conformational and recognition plasticity to the oncoprotein. 2007 , 46, 10405-12	48
634	The carboxy-terminal domain of heat-shock factor 1 is largely unfolded but can be induced to collapse into a compact, partially structured state. 2007 , 46, 3405-15	17
633	The BG21 isoform of Golli myelin basic protein is intrinsically disordered with a highly flexible amino-terminal domain. 2007 , 46, 9700-12	16
632	Fesselin is a natively unfolded protein. 2007 , 6, 3648-54	11
631	Caulollins from <i>Caulobacter crescentus</i> , a pair of partially unstructured proteins of betagamma-crystallin superfamily, gain structure upon binding calcium. 2007 , 46, 12298-307	25
630	Mining alpha-helix-forming molecular recognition features with cross species sequence alignments. 2007 , 46, 13468-77	270
629	Domain 2 of nonstructural protein 5A (NS5A) of hepatitis C virus is natively unfolded. 2007 , 46, 11550-8	78
628	Unfolding pathway of the dimeric and tetrameric forms of phosphofructokinase-2 from <i>Escherichia coli</i> . 2007 , 46, 6141-8	11
627	Functional anthology of intrinsic disorder. 2. Cellular components, domains, technical terms, developmental processes, and coding sequence diversities correlated with long disordered regions. 2007 , 6, 1899-916	215
626	Characterization of molecular recognition features, MoRFs, and their binding partners. 2007 , 6, 2351-66	386
625	Conformation of the EPEC Tir protein in solution: investigating the impact of serine phosphorylation at positions 434/463. 2007 , 93, 586-96	15

624	Macromolecular crowding induces a molten globule state in the C-terminal domain of histone H1. 2007 , 93, 2170-7	46
623	Intrinsic disorder in the Protein Data Bank. 2007 , 24, 325-42	116
622	Self-organization versus Watchmaker: ambiguity of molecular recognition and design charts of cellular circuitry. 2007 , 20, 205-14	22
621	pH-induced structural transitions of caseins. 2007 , 87, 191-9	49
620	Modelling of the ABL and ARG proteins predicts two functionally critical regions that are natively unfolded. 2007 , 67, 1-11	4
619	Dynamic alpha-helices: conformations that do not conform. 2007 , 68, 109-22	15
618	Identifying long-range structure in the intrinsically unstructured transactivation domain of p53. 2007 , 67, 526-30	42
617	The N- and C-termini of the human Nogo molecules are intrinsically unstructured: bioinformatics, CD, NMR characterization, and functional implications. 2007 , 68, 100-8	35
616	Investigating the structural stability of the Tup1-interaction domain of Ssn6: evidence for a conformational change on the complex. 2008 , 70, 72-82	13
615	Intrinsically disordered protein from a pathogenic mesophile <i>Mycobacterium tuberculosis</i> adopts structured conformation at high temperature. 2008 , 71, 1123-33	14
614	Huntingtin interacting protein HYPK is intrinsically unstructured. 2008 , 71, 1686-98	26
613	Neuropathology, biochemistry, and biophysics of alpha-synuclein aggregation. 2007 , 103, 17-37	373
612	Interactions between a non glycosylated human proline-rich protein and flavan-3-ols are affected by protein concentration and polyphenol/protein ratio. 2007 , 55, 4895-901	106
611	Dynamic behavior of an intrinsically unstructured linker domain is conserved in the face of negligible amino acid sequence conservation. 2007 , 65, 277-88	71
610	Mechanistic aspects of Parkinson's disease: alpha-synuclein and the biomembrane. 2007 , 47, 285-99	90
609	Dynamics of well-folded and natively disordered proteins in solution: a time-of-flight neutron scattering study. 2008 , 37, 573-82	60
608	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> . 2008 , 25, 563-76	13
607	Modeling the accessible conformations of the intrinsically unstructured transactivation domain of p53. 2008 , 71, 587-98	38

606	Apo-parvalbumin as an intrinsically disordered protein. 2008 , 72, 822-36	46
605	A robust approach for analyzing a heterogeneous structural ensemble. 2008 , 73, 918-28	8
604	Mapping alpha-helical induced folding within the intrinsically disordered C-terminal domain of the measles virus nucleoprotein by site-directed spin-labeling EPR spectroscopy. 2008 , 73, 973-88	93
603	Processing conditions for the formation of spider silk microspheres. 2008 , 1, 413-6	93
602	Interaction with Al and Zn induces structure formation and aggregation in natively unfolded caseins. 2008 , 93, 36-43	16
601	Study of thermally and chemically unfolded conformations of bovine serum albumin by means of dynamic light scattering. 2008 , 28, 594-600	36
600	To be folded or to be unfolded?. 2004 , 13, 2871-7	63
599	Exploring CP12 binding proteins revealed aldolase as a new partner for the phosphoribulokinase/glyceraldehyde 3-phosphate dehydrogenase/CP12 complex--purification and kinetic characterization of this enzyme from <i>Chlamydomonas reinhardtii</i> . 2008 , 275, 1248-59	32
598	Multienzyme docking in hybrid megasynthetases. 2008 , 4, 75-81	70
597	The unfoldomics decade: an update on intrinsically disordered proteins. 2008 , 9 Suppl 2, S1	408
596	Intrinsic disorder in scaffold proteins: getting more from less. 2008 , 98, 85-106	213
595	Effect of temperature on self-assembly of bovine beta-casein above and below isoelectric pH. Structural analysis by cryogenic-transmission electron microscopy and small-angle X-ray scattering. 2008 , 24, 3020-9	59
594	Structural features of the full-length adaptor protein GADS in solution determined using small-angle X-ray scattering. 2008 , 94, 1766-72	5
593	Biophysical characterization of the unstructured cytoplasmic domain of the human neuronal adhesion protein neuroligin 3. 2008 , 95, 1928-44	34
592	Domain conformation of tau protein studied by solution small-angle X-ray scattering. 2008 , 47, 10345-53	142
591	Intrinsic disorder in pathogenic and non-pathogenic microbes: discovering and analyzing the unfoldomes of early-branching eukaryotes. 2008 , 4, 328-40	101
590	A comparative analysis of viral matrix proteins using disorder predictors. 2008 , 5, 126	51
589	Human regulatory protein Ki-1/57 has characteristics of an intrinsically unstructured protein. 2008 , 7, 4465-74	20

588	Guiding protein aggregation with macromolecular crowding. 2008 , 47, 8993-9006	138
587	Self-assembly of bovine beta-casein below the isoelectric pH. 2008 , 56, 2192-8	60
586	Partially folded bovine pancreatic trypsin inhibitor analogues attain fully native structures when co-crystallized with S195A rat trypsin. 2008 , 375, 812-23	1
585	Solution conformation, backbone dynamics and lipid interactions of the intrinsically unstructured malaria surface protein MSP2. 2008 , 379, 105-21	52
584	Conformational properties of the aggregation precursor state of HypF-N. 2008 , 379, 554-67	44
583	Intrinsically disordered human C/EBP homologous protein regulates biological activity of colon cancer cells during calcium stress. 2008 , 380, 313-26	17
582	Denatured-state energy landscapes of a protein structural database reveal the energetic determinants of a framework model for folding. 2008 , 381, 1184-201	17
581	Intrinsic structural disorder of DF31, a Drosophila protein of chromatin decondensation and remodeling activities. 2008 , 7, 2291-9	16
580	Late Embryogenesis Abundant Proteins. 2008 , 211-255	86
579	The natively unfolded character of tau and its aggregation to Alzheimer-like paired helical filaments. 2008 , 47, 10526-39	177
578	Effect of methionine oxidation on the structural properties, conformational stability, and aggregation of immunoglobulin light chain LEN. 2008 , 47, 8665-77	30
577	The intrinsically disordered RNR inhibitor Sml1 is a dynamic dimer. 2008 , 47, 13428-37	45
576	Prevalence of intrinsic disorder in the intracellular region of human single-pass type I proteins: the case of the notch ligand Delta-4. 2008 , 7, 2496-506	35
575	Site-directed mutagenesis of conserved C-terminal tyrosine and tryptophan residues of PsbO, the photosystem II manganese-stabilizing protein, alters its activity and fluorescence properties. 2008 , 47, 6490-8	12
574	Starmaker exhibits properties of an intrinsically disordered protein. 2008 , 9, 2118-25	22
573	The intrinsically disordered cytoplasmic domain of the T cell receptor zeta chain binds to the nef protein of simian immunodeficiency virus without a disorder-to-order transition. 2008 , 47, 12942-4	45
572	The folding kinetics of the SDS-induced molten globule form of reduced cytochrome c. 2008 , 47, 5450-9	21
571	Structural characterization of the native NH ₂ -terminal transactivation domain of the human androgen receptor: a collapsed disordered conformation underlies structural plasticity and protein-induced folding. 2008 , 47, 3360-9	78

570	Brucella abortus MFP: a trimeric coiled-coil protein with membrane fusogenic activity. 2008 , 47, 8165-75	6
569	Amyloid fibril formation by bovine milk alpha s2-casein occurs under physiological conditions yet is prevented by its natural counterpart, alpha s1-casein. 2008 , 47, 3926-36	88
568	An unusual intrinsically disordered protein from the model legume Lotus japonicus stabilizes proteins in vitro. 2008 , 283, 31142-52	32
567	RNA chaperoning and intrinsic disorder in the core proteins of Flaviviridae. 2008 , 36, 712-25	116
566	Organization of the core structure of the postsynaptic density. 2008 , 105, 4453-8	198
565	Evidence for a coiled-coil interaction mode of disordered proteins from bacterial type III secretion systems. 2008 , 283, 34062-8	35
564	Mechanism of low density lipoprotein (LDL) release in the endosome: implications of the stability and Ca ²⁺ affinity of the fifth binding module of the LDL receptor. 2008 , 283, 22670-9	39
563	Two microtubule-associated proteins of Arabidopsis MAP65s promote antiparallel microtubule bundling. 2008 , 19, 4534-44	98
562	Virulence factor of potato virus Y, genome-attached terminal protein VPg, is a highly disordered protein. 2008 , 283, 213-221	51
561	The threat of instability: neurodegeneration predicted by protein destabilization and aggregation propensity. 2008 , 6, e193	18
560	Amyloidogenesis of natively unfolded proteins. 2008 , 5, 260-87	147
559	Life inside a thin section: tomography. 2008 , 28, 9321-7	38
558	Bovine viral diarrhea virus core is an intrinsically disordered protein that binds RNA. 2008 , 82, 1294-304	36
557	The retinal cGMP phosphodiesterase gamma-subunit - a chameleon. 2008 , 9, 611-25	14
556	TOP-IDP-scale: a new amino acid scale measuring propensity for intrinsic disorder. 2008 , 15, 956-63	266
555	Hsp70 chaperones and type I PRMTs are sequestered at intranuclear inclusions caused by polyalanine expansions in PABPN1. 2009 , 4, e6418	34
554	Pup, a prokaryotic ubiquitin-like protein, is an intrinsically disordered protein. 2009 , 422, 207-15	83
553	CP12 from Chlamydomonas reinhardtii, a permanent specific "chaperone-like" protein of glyceraldehyde-3-phosphate dehydrogenase. 2009 , 284, 12735-44	33

552	Protein dynamics: from molecules, to interactions, to biology. 2009 , 10, 1360-8	3
551	Vaccine potentials of an intrinsically unstructured fragment derived from the blood stage-associated Plasmodium falciparum protein PFF0165c. 2009 , 77, 5701-9	41
550	Unfoldomics of human diseases: linking protein intrinsic disorder with diseases. 2009 , 10 Suppl 1, S7	199
549	CDF it all: consensus prediction of intrinsically disordered proteins based on various cumulative distribution functions. 2009 , 583, 1469-74	99
548	Intrinsic disorder explains diverse nuclear roles of chromatin remodeling proteins. 2009 , 22, 1-8	38
547	Study of the interactions between a proline-rich protein and a flavan-3-ol by NMR: residual structures in the natively unfolded protein provides anchorage points for the ligands. 2009 , 91, 745-56	51
546	Interaction of the adenoviral IVa2 protein with a truncated viral DNA packaging sequence. 2009 , 140, 78-90	9
545	Thermally induced structural changes of intrinsically disordered small heat shock protein Hsp22. 2009 , 145, 79-85	32
544	Disorder-to-order conformational transitions in protein structure and its relationship to disease. 2009 , 330, 105-20	26
543	Intrinsically disordered proteins and their environment: effects of strong denaturants, temperature, pH, counter ions, membranes, binding partners, osmolytes, and macromolecular crowding. 2009 , 28, 305-25	235
542	Order propensity of an intrinsically disordered protein, the cyclin-dependent-kinase inhibitor Sic1. 2009 , 76, 731-46	58
541	Dematin exhibits a natively unfolded core domain and an independently folded headpiece domain. 2009 , 18, 629-36	10
540	The acidic domains of the Toc159 chloroplast preprotein receptor family are intrinsically disordered protein domains. 2009 , 10, 35	31
539	Scale-free flow of life: on the biology, economics, and physics of the cell. 2009 , 6, 6	39
538	A recombinant polypeptide extends the in vivo half-life of peptides and proteins in a tunable manner. 2009 , 27, 1186-90	272
537	Intrinsic disorder and coiled-coil formation in prostate apoptosis response factor 4. 2009 , 276, 3710-28	22
536	Solution structure and dynamics of the chimeric SH3 domains, SHH- and SHA-"Bergeracs". 2009 , 1794, 1813-22	13
535	The rod-shaped conformation of Starmaker. 2009 , 1794, 1616-24	15

534	Human full-length Securin is a natively unfolded protein. 2005 , 14, 1410-8	47
533	Intrinsic Disorder in Proteins Associated with Neurodegenerative Diseases. 2009 , 21-75	6
532	In vitro activity of the EWS oncogene transcriptional activation domain. 2009 , 48, 2849-57	7
531	The K-segment of maize DHN1 mediates binding to anionic phospholipid vesicles and concomitant structural changes. 2009 , 150, 1503-14	166
530	Heterologous expression, isotopic-labeling and immuno-characterization of Cin1, a novel protein secreted by the phytopathogenic fungus <i>Venturia inaequalis</i> . 2009 , 65, 140-7	3
529	At low concentrations, 3,4-dihydroxyphenylacetic acid (DOPAC) binds non-covalently to alpha-synuclein and prevents its fibrillation. 2009 , 388, 597-610	43
528	Modular organization of rabies virus phosphoprotein. 2009 , 388, 978-96	93
527	Prokaryotic ubiquitin-like protein pup is intrinsically disordered. 2009 , 392, 208-17	91
526	Tropoelastin as a thermodynamically unfolded premolten globule protein: The effect of trimethylamine N-oxide on structure and coacervation. 2009 , 487, 79-84	28
525	Kinetics of contact formation and end-to-end distance distributions of swollen disordered peptides. 2009 , 96, 1515-28	40
524	Binding-induced folding transitions in calpastatin subdomains A and C. 2003 , 12, 2327-36	28
523	Organization and dynamics of tryptophan residues in erythroid spectrin: novel structural features of denatured spectrin revealed by the wavelength-selective fluorescence approach. 2003 , 12, 2389-403	51
522	Intrinsic disorder in Viral Proteins Genome-Linked: experimental and predictive analyses. 2009 , 6, 23	55
521	Protein intrinsic disorder and influenza virulence: the 1918 H1N1 and H5N1 viruses. 2009 , 6, 69	64
520	Asp157 is required for the function of PsbO, the photosystem II manganese stabilizing protein. 2009 , 48, 11920-8	19
519	Nucleocapsid structure and function. 2009 , 329, 103-28	53
518	Biophysics of Parkinson's disease: structure and aggregation of alpha-synuclein. 2009 , 10, 483-99	250
517	References. 2009 , 265-312	

516	Probing early events in ferrous cytochrome c folding with time-resolved natural and magnetic circular dichroism spectroscopies. 2009 , 10, 464-75	14
515	Function of PsbO, the photosystem II manganese-stabilizing protein: probing the role of aspartic acid 157. 2010 , 49, 6042-51	14
514	DANGLE: A Bayesian inferential method for predicting protein backbone dihedral angles and secondary structure. 2010 , 202, 223-33	179
513	Comparative sequence analysis of CP12, a small protein involved in the formation of a Calvin cycle complex in photosynthetic organisms. 2010 , 103, 183-94	47
512	The protein kingdom extended: ordered and intrinsically disordered proteins, their folding, supramolecular complex formation, and aggregation. 2010 , 102, 73-84	157
511	Structural diversity in free and bound states of intrinsically disordered protein phosphatase 1 regulators. 2010 , 18, 1094-103	94
510	Bayesian statistical modelling of human protein interaction network incorporating protein disorder information. 2010 , 11, 46	13
509	The double mutation Δ 6MW241F in PsbO, the photosystem II manganese stabilizing protein, yields insights into the evolution of its structure and function. 2010 , 584, 4009-14	7
508	Circular Dichroism of Intrinsically Disordered Proteins. 2010 , 303-321	15
507	Analytical Ultracentrifugation, a Useful Tool to Probe Intrinsically Disordered Proteins. 2010 , 431-449	6
506	Dynamic and Static Light Scattering. 2010 , 477-524	3
505	Analyzing Intrinsically Disordered Proteins by Size Exclusion Chromatography. 2010 , 525-544	2
504	Conformational Behavior of Intrinsically Disordered Proteins: Effects of Strong Denaturants, Temperature, PH, Counterions, and Macromolecular Crowding. 2010 , 545-568	
503	The Structural Biology of IDPs inside Cells. 2010 , 37-58	
502	Detecting Disordered Regions in Proteins by Limited Proteolysis. 2010 , 569-626	7
501	Large-Scale Identification of Intrinsically Disordered Proteins. 2010 , 671-693	
500	Purification of Intrinsically Disordered Proteins. 2010 , 695-704	3
499	Determining Structural Ensembles for Intrinsically Disordered Proteins. 2010 , 107-129	1

498	Site-Directed Spin Labeling EPR Spectroscopy. 2010 , 131-169	3
497	Understanding protein non-folding. 2010 , 1804, 1231-64	875
496	Aquifex aeolicus FlgM protein exhibits a temperature-dependent disordered nature. 2010 , 1804, 1457-66	7
495	Order without design. 2010 , 7, 12	12
494	Functional dissection of an intrinsically disordered protein: understanding the roles of different domains of Knr4 protein in protein-protein interactions. 2010 , 19, 1376-85	10
493	Modularity of intrinsic disorder in the human proteome. 2010 , 78, 212-21	80
492	Identification, analysis, and prediction of protein ubiquitination sites. 2010 , 78, 365-80	424
491	UV and X-ray structural studies of a 101-residue long Tat protein from a HIV-1 primary isolate and of its mutated, detoxified, vaccine candidate. 2010 , 78, 1441-56	25
490	Two-state conformational equilibrium in the Par-4 leucine zipper domain. 2010 , 78, 2433-49	8
489	Prevalence of intrinsic disorder in the hepatitis C virus ARFP/Core+1/S protein. 2010 , 277, 774-89	13
488	Inhibition of mitochondrial fusion by α -synuclein is rescued by PINK1, Parkin and DJ-1. 2010 , 29, 3571-89	375
487	Structural disorder within Henipavirus nucleoprotein and phosphoprotein: from predictions to experimental assessment. 2010 , 5, e11684	63
486	Syncytial phenotype of C-terminally truncated herpes simplex virus type 1 gB is associated with diminished membrane interactions. 2010 , 84, 4923-35	33
485	The C terminus of the Alb3 membrane insertase recruits cpSRP43 to the thylakoid membrane. 2010 , 285, 5954-62	72
484	Perturbed amelogenin secondary structure leads to uncontrolled aggregation in amelogenesis imperfecta mutant proteins. 2010 , 285, 40593-603	27
483	The dissociated form of kappa-casein is the precursor to its amyloid fibril formation. 2010 , 429, 251-60	42
482	N-terminal domains of DELLA proteins are intrinsically unstructured in the absence of interaction with GID1/gibberellic acid receptors. 2010 , 285, 11557-71	55
481	DNA search efficiency is modulated by charge composition and distribution in the intrinsically disordered tail. 2010 , 107, 21004-9	99

480	The mysterious unfoldome: structureless, underappreciated, yet vital part of any given proteome. 2010 , 2010, 568068	173
479	The SCHOOL of nature: II. Protein order, disorder and oligomericity in transmembrane signaling. 2010 , 1, 89-102	14
478	Targeting intrinsically disordered proteins in neurodegenerative and protein dysfunction diseases: another illustration of the D(2) concept. 2010 , 7, 543-64	100
477	Conformations of phenylalanine in the tripeptides AFA and GFG probed by combining MD simulations with NMR, FTIR, polarized Raman, and VCD spectroscopy. 2010 , 114, 3965-78	22
476	Cellular stress and protein misfolding during aging. 2010 , 648, 107-17	16
475	Structure and interactions of fish type III antifreeze protein in solution. 2010 , 99, 609-18	17
474	Calcium-induced folding and stabilization of the intrinsically disordered RTX domain of the CyaA toxin. 2010 , 99, 3744-53	54
473	Extracellular Chaperones. 2010 , 1	1
472	A natively unfolded β -crystallin domain from <i>Hahella chejuensis</i> . 2010 , 49, 9746-55	19
471	Self-association of the adenoviral L4-22K protein. 2010 , 49, 9830-8	5
470	Off-pathway status for the alkali molten globule of horse ferricytochrome C. 2010 , 49, 7764-73	15
469	Searching DNA via a "Monkey Bar" mechanism: the significance of disordered tails. 2010 , 396, 674-84	119
468	Characterization of the regions involved in the calcium-induced folding of the intrinsically disordered RTX motifs from the bordetella pertussis adenylate cyclase toxin. 2010 , 397, 534-49	55
467	Solution structure of the N-terminal transactivation domain of ERM modified by SUMO-1. 2010 , 399, 104-10	14
466	Conformation and thermodynamic stability of pre-molten and molten globule states of mammalian cytochromes-c. 2011 , 3, 327-38	16
465	Mixed micellization between natural and synthetic block copolymers: β -casein and Lutrol F-127. 2011 , 13, 3153-60	18
464	Extracellular chaperones. 2013 , 328, 241-68	19
463	Protein Folding Landscapes in the Living Cell. 2011 , 2, 314-319	40

462	Conformational changes of trialanine induced by direct interactions between alanine residues and alcohols in binary mixtures of water with glycerol and ethanol. 2011 , 133, 12728-39	29
461	Compaction properties of an intrinsically disordered protein: Sic1 and its kinase-inhibitor domain. 2011 , 100, 2243-52	53
460	The role of the LH subdomain in the function of the Cip/Kip cyclin-dependent kinase regulators. 2011 , 100, 2486-94	13
459	Intrinsically Disordered Chaperones and Neurodegeneration. 2011 , 1-63	1
458	Solvent Interactions with Proteins and Other Macromolecules. 2011 , 277-360	1
457	Flexible nets of malleable guardians: intrinsically disordered chaperones in neurodegenerative diseases. 2011 , 111, 1134-66	59
456	The chaperone action of bovine milk β 1- and β 2-caseins and their associated form β -casein. 2011 , 510, 42-52	46
455	Intrinsically disordered proteins from A to Z. 2011 , 43, 1090-103	322
454	Molecular mechanisms of the anomalous thermal aggregation of green fluorescent protein. 2011 , 1814, 1930-9	14
453	Senescence-associated barley NAC (NAM, ATAF1,2, CUC) transcription factor interacts with radical-induced cell death 1 through a disordered regulatory domain. 2011 , 286, 35418-35429	67
452	Intrinsic disorder in S100 proteins. 2011 , 7, 2164-80	21
451	The evidence of large-scale DNA-induced compaction in the mycobacterial chromosomal ParB. 2011 , 413, 901-7	12
450	Assays for β synuclein aggregation. 2011 , 53, 295-305	80
449	Sequential melting of two hydrophobic clusters within the green fluorescent protein GFP-cycle3. 2011 , 50, 7735-44	13
448	Interaction of Sesbania mosaic virus movement protein with VPg and P10: implication to specificity of genome recognition. 2011 , 6, e15609	17
447	Reduced stability and increased dynamics in the human proliferating cell nuclear antigen (PCNA) relative to the yeast homolog. 2011 , 6, e16600	20
446	Disorder predictors also predict backbone dynamics for a family of disordered proteins. 2011 , 6, e29207	10
445	Do Viral Proteins Possess Unique Features?. 2011 , 1-34	4

- 444 Intrinsic Disorder in Genome-Linked Viral Proteins VPgs of Potyviruses. **2011**, 277-312
- 443 Structural Disorder in Matrix Proteins of HIV-Related Viruses. **2011**, 143-167
- 442 Making Order in the Intrinsically Disordered Regions of HIV-1 Vif Protein. **2011**, 201-221 1
- 441 Structural Disorder in Proteins of the Rhabdoviridae Replication Complex. **2011**, 115-141
- 440 Beyond the random coil: stochastic conformational switching in intrinsically disordered proteins. **2011**, 19, 566-76 87
- 439 Disordered TPPP/p25 binds GTP and displays Mg²⁺-dependent GTPase activity. **2011**, 585, 803-8 24
- 438 Role of metal ions in aggregation of intrinsically disordered proteins in neurodegenerative diseases. **2011**, 3, 1163-80 88
- 437 The intracellular distal tail of the Na⁺/H⁺ exchanger NHE1 is intrinsically disordered: implications for NHE1 trafficking. **2011**, 50, 3469-80 50
- 436 Zn²⁺-induced rearrangement of the disordered TPPP/p25 affects its microtubule assembly and GTPase activity. **2011**, 50, 9568-78 20
- 435 Multitude of binding modes attainable by intrinsically disordered proteins: a portrait gallery of disorder-based complexes. **2011**, 40, 1623-34 199
- 434 Intrinsic disorder of Drosophila melanogaster hormone receptor 38 N-terminal domain. **2011**, 79, 376-92 13
- 433 Fractal dimension of an intrinsically disordered protein: small-angle X-ray scattering and computational study of the bacteriophage λ N protein. **2011**, 20, 1955-70 33
- 432 Intrinsically unstructured proteins and neurodegenerative diseases: conformational promiscuity at its best. **2011**, 63, 478-88 13
- 431 Amino acids with hydrogen-bonding side chains have an intrinsic tendency to sample various turn conformations in aqueous solution. **2011**, 17, 6789-97 42
- 430 Temperature dependence of calcium and magnesium induced caseinate precipitation in H₂O and D₂O. **2011**, 126, 8-14 30
- 429 Intrinsically disordered proteins may escape unwanted interactions via functional misfolding. **2011**, 1814, 693-712 52
- 428 PsbO, the manganese-stabilizing protein: analysis of the structure-function relations that provide insights into its role in photosystem II. **2011**, 104, 179-90 50
- 427 Outer membrane targeting of secretin PulD protein relies on disordered domain recognition by a dedicated chaperone. **2011**, 286, 38833-43 34

426	Characterization of the interactions between the nucleoprotein and the phosphoprotein of Henipavirus. 2011 , 286, 13583-602	51
425	Effect of Src kinase phosphorylation on disordered C-terminal domain of N-methyl-D-aspartic acid (NMDA) receptor subunit GluN2B protein. 2011 , 286, 29904-12	36
424	ATP binding to hemoglobin response gene 1 protein is necessary for regulation of the mating type locus in <i>Candida albicans</i> . 2011 , 286, 13914-24	1
423	Folding, assembly, and aggregation of recombinant murine amelogenins with T21I and P41T point mutations. 2011 , 194, 284-90	11
422	Quantitative analyses of cryptochrome-mBMAL1 interactions: mechanistic insights into the transcriptional regulation of the mammalian circadian clock. 2011 , 286, 22414-25	35
421	Dissecting amelogenin protein nanospheres: characterization of metastable oligomers. 2011 , 286, 34643-53	54
420	Competing interactions stabilize pro- and anti-aggregant conformations of human Tau. 2011 , 286, 20512-24	35
419	A three-part signal governs differential processing of Gli1 and Gli3 proteins by the proteasome. 2011 , 286, 39051-8	29
418	Calcium-induced folding of intrinsically disordered repeat-in-toxin (RTX) motifs via changes of protein charges and oligomerization states. 2011 , 286, 16997-7004	41
417	CSpritz: accurate prediction of protein disorder segments with annotation for homology, secondary structure and linear motifs. 2011 , 39, W190-6	66
416	Assembly of a filamin four-domain fragment and the influence of splicing variant-1 on the structure. 2011 , 286, 26921-30	13
415	Anchoring intrinsically disordered proteins to multiple targets: lessons from N-terminus of the p53 protein. 2011 , 12, 1410-30	19
414	Mutual synergistic protein folding in split intein. 2012 , 32, 433-42	15
413	ESpritz: accurate and fast prediction of protein disorder. 2012 , 28, 503-9	317
412	NOT THAT RIGID MIDGETS AND NOT SO FLEXIBLE GIANTS: ON THE ABUNDANCE AND ROLES OF INTRINSIC DISORDER IN SHORT AND LONG PROTEINS. 2012 , 20, 471-511	16
411	Frontmatter. 2012 , i-xxii	
410	Secondary Structure and Dynamics of a Family of Disordered Proteins. 2012 , 221-238	
409	Intrinsically disordered proteins: lessons from colicins. 2012 , 40, 1534-8	7

408	Denaturant-induced conformational transitions in intrinsically disordered proteins. 2012 , 896, 197-213	3
407	Intrinsically disordered proteins and novel strategies for drug discovery. 2012 , 7, 475-88	78
406	Disordered Protein Diffusion under Crowded Conditions. 2012 , 3, 2703-2706	42
405	Sequence repeats and protein structure. 2012 , 86, 050901	2
404	Sedimentation velocity analytical ultracentrifugation for intrinsically disordered proteins. 2012 , 896, 91-105	13
403	Size-exclusion chromatography in structural analysis of intrinsically disordered proteins. 2012 , 896, 179-94	35
402	Immobilization of proteins for single-molecule fluorescence resonance energy transfer measurements of conformation and dynamics. 2012 , 896, 3-20	21
401	Novel insights through the integration of structural and functional genomics data with protein networks. 2012 , 179, 320-6	16
400	Compaction and binding properties of the intrinsically disordered C-terminal domain of Henipavirus nucleoprotein as unveiled by deletion studies. 2012 , 8, 392-410	38
399	Understanding the structural ensembles of a highly extended disordered protein. 2012 , 8, 308-19	31
398	The roles of intrinsic disorder in orchestrating the Wnt-pathway. 2012 , 29, 843-61	37
397	Hydrophobic moments, shape, and packing in disordered proteins. 2012 , 116, 6326-35	13
396	Triaspertate: a model system for conformationally flexible DDD motifs in proteins. 2012 , 116, 5160-71	16
395	Dynamic and static light scattering of intrinsically disordered proteins. 2012 , 896, 137-61	18
394	Microtubule assembly-derived by dimerization of TPPP/p25. Evaluation of thermodynamic parameters for multiple equilibrium system from ITC data. 2012 , 1820, 785-94	11
393	Biophysical studies with AICD-47 reveal unique binding behavior characteristic of an unfolded domain. 2012 , 425, 201-6	2
392	3.9 Intrinsically Disordered Proteins. 2012 , 170-211	0
391	Why are we Interested in the Unfolded Peptides and Proteins?. 2012 , 1-54	4

390	Using chemical shifts to assess transient secondary structure and generate ensemble structures of intrinsically disordered proteins. 2012 , 895, 139-52	11
389	Circular dichroism techniques for the analysis of intrinsically disordered proteins and domains. 2012 , 895, 387-404	60
388	Conformational propensities and residual structures in unfolded peptides and proteins. 2012 , 8, 122-33	53
387	Lateral self-assembly of 18.5-kDa myelin basic protein (MBP) charge component-C1 on membranes. 2012 , 1818, 2636-47	18
386	Novel ATPase activity of the polyprotein intermediate, Viral Protein genome-linked-Nuclear Inclusion-a protease, of Pepper vein banding potyvirus. 2012 , 427, 113-8	9
385	Solution model of the intrinsically disordered polyglutamine tract-binding protein-1. 2012 , 102, 1608-16	13
384	Multiparametric analysis of intrinsically disordered proteins: looking at intrinsic disorder through compound eyes. 2012 , 84, 2096-104	70
383	Influence of serum proteins on conformation of prostate-specific antigen. 2012 , 29, 1051-64	16
382	Intrinsically disordered regions as affinity tuners in protein-DNA interactions. 2012 , 8, 47-57	147
381	Inherent structural disorder and dimerisation of murine norovirus NS1-2 protein. 2012 , 7, e30534	24
380	Free cysteine modulates the conformation of human C/EBP homologous protein. 2012 , 7, e34680	3
379	Characterization of molten globule PopB in absence and presence of its chaperone PcrH. 2012 , 31, 401-16	9
378	Evolution of immunity: no development without risk. 2012 , 52, 176-81	5
377	Length-dependent compaction of intrinsically disordered proteins. 2012 , 586, 70-3	24
376	Intrinsic disorder in cell signaling and gene transcription. 2012 , 348, 457-65	87
375	Biomineralization mechanisms: a new paradigm for crystal nucleation in organic matrices. 2013 , 93, 307-15	89
374	Unusual biophysics of intrinsically disordered proteins. 2013 , 1834, 932-51	377
373	Intrinsic disorder of the bacterial cell division protein ZipA: coil-to-brush conformational transition. 2013 , 27, 3363-75	18

372	Interaction between DNA and chromosomal proteins HMGB1 and H1 studied by IR/VCD spectroscopy. 2013 , 1044, 167-172	10
371	[Self-association and secondary structure of beta-casein]. 2013 , 39, 411-7	16
370	Water in the formation of biogenic minerals: peeling away the hydration layers. 2013 , 183, 278-303	45
369	Modulating the intrinsic disorder in the cytoplasmic domain alters the biological activity of the N-methyl-D-aspartate-sensitive glutamate receptor. 2013 , 288, 22506-15	26
368	Under-folded proteins: Conformational ensembles and their roles in protein folding, function, and pathogenesis. 2013 , 99, 870-87	33
367	The importance of size and disorder in the cryoprotective effects of dehydrins. 2013 , 163, 1376-86	73
366	Interactions of bovine serum albumin with biological buffers, TES, TAPS, and TAPSO in aqueous solutions. 2013 , 48, 1686-1696	23
365	Solvent interaction analysis of intrinsically disordered proteins in aqueous two-phase systems. 2013 , 9, 3068-79	14
364	The arginine-rich RNA-binding motif of HIV-1 Rev is intrinsically disordered and folds upon RRE binding. 2013 , 105, 1004-17	36
363	Protein intrinsic disorder in the acetylome of intracellular and extracellular <i>Toxoplasma gondii</i> . 2013 , 9, 645-57	39
362	Interactions of <i>Thellungiella salsuginea</i> dehydrins TsDHN-1 and TsDHN-2 with membranes at cold and ambient temperatures-surface morphology and single-molecule force measurements show phase separation, and reveal tertiary and quaternary associations. 2013 , 1828, 967-80	27
361	RAPID: fast and accurate sequence-based prediction of intrinsic disorder content on proteomic scale. 2013 , 1834, 1671-80	35
360	Biochemical and structural studies of the oligomerization domain of the Nipah virus phosphoprotein: evidence for an elongated coiled-coil homotrimer. 2013 , 446, 162-72	19
359	Polypeptide chain collapse and protein folding. 2013 , 531, 24-33	45
358	The contribution of intrinsic disorder prediction to the elucidation of protein function. 2013 , 23, 467-72	43
357	A decade and a half of protein intrinsic disorder: biology still waits for physics. 2013 , 22, 693-724	341
356	Interaction between κ -casein micelles and imidazolium-based ionic liquid surfactant. 2013 , 9, 3671	28
355	Effects of solvent and alkaline earth metals on the heat-induced precipitation process of sodium caseinate. 2013 , 136, 266-72	13

354	The intrinsically disordered C-terminal region of Arabidopsis thaliana TCP8 transcription factor acts both as a transactivation and self-assembly domain. 2013 , 9, 2282-95	25
353	Assessing induced folding within the intrinsically disordered C-terminal domain of the Henipavirus nucleoproteins by site-directed spin labeling EPR spectroscopy. 2013 , 31, 453-71	30
352	Ligand-controlled assembly of hexamers, dihexamers, and linear multihexamer structures by the engineered acylated insulin degludec. 2013 , 52, 295-309	56
351	The most important thing is the tail: multitudinous functionalities of intrinsically disordered protein termini. 2013 , 587, 1891-901	95
350	FlgM proteins from different bacteria exhibit different structural characteristics. 2013 , 1834, 808-16	6
349	Structural disorder and local order of hNopp140. 2013 , 1834, 342-50	22
348	Analysis of a single β -synuclein fibrillation by the interaction with a protein nanopore. 2013 , 85, 8254-61	54
347	Digested disorder: Quarterly intrinsic disorder digest (January/February/March, 2013). 2013 , 1, e25496	8
346	Extracting structural information from charge-state distributions of intrinsically disordered proteins by non-denaturing electrospray-ionization mass spectrometry. 2013 , 1, e25068	22
345	Conformations of intrinsically disordered proteins are influenced by linear sequence distributions of oppositely charged residues. 2013 , 110, 13392-7	493
344	Structural divergence is more extensive than sequence divergence for a family of intrinsically disordered proteins. 2013 , 81, 1686-98	11
343	Disorder in the lifetime of a protein. 2013 , 1, e26782	2
342	Conformational dissection of a viral intrinsically disordered domain involved in cellular transformation. 2013 , 8, e72760	14
341	Ordered disorder of the astrocytic dystrophin-associated protein complex in the norm and pathology. 2013 , 8, e73476	10
340	Sequence complexity of amyloidogenic regions in intrinsically disordered human proteins. 2014 , 9, e89781	15
339	Intrinsically disordered and pliable Starmaker-like protein from medaka (<i>Oryzias latipes</i>) controls the formation of calcium carbonate crystals. 2014 , 9, e114308	25
338	The TFE-induced transient native-like structure of the intrinsically disordered Ω domain of Escherichia coli RNA polymerase. 2014 , 43, 581-94	7
337	What macromolecular crowding can do to a protein. 2014 , 15, 23090-140	318

336	A comparative study of Whi5 and retinoblastoma proteins: from sequence and structure analysis to intracellular networks. 2013 , 4, 315	10
335	Actinous enigma or enigmatic actin: Folding, structure, and functions of the most abundant eukaryotic protein. 2014 , 2, e34500	10
334	Conformational modulation and hydrodynamic radii of CP12 protein and its complexes probed by fluorescence correlation spectroscopy. 2014 , 281, 3206-17	13
333	Hug1 is an intrinsically disordered protein that inhibits ribonucleotide reductase activity by directly binding Rnr2 subunit. 2014 , 42, 13174-85	14
332	Disorder and function: a review of the dehydrin protein family. 2014 , 5, 576	176
331	The staphylococcal elastin-binding protein regulates zinc-dependent growth/biofilm formation. 2014 , 156, 155-62	12
330	Direct binding of the Alu binding protein dimer SRP9/14 to 40S ribosomal subunits promotes stress granule formation and is regulated by Alu RNA. 2014 , 42, 11203-17	19
329	Local order in the unfolded state: conformational biases and nearest neighbor interactions. 2014 , 4, 725-73	47
328	Folding and self-association of atTic20 in lipid membranes: implications for understanding protein transport across the inner envelope membrane of chloroplasts. 2014 , 15, 29	5
327	Alternate splicing of dysferlin C2A confers Ca ²⁺ -dependent and Ca ²⁺ -independent binding for membrane repair. 2014 , 22, 104-15	37
326	Novel unfolding sequence of banana lectin: Folded, unfolded and natively unfolded-like monomeric states in guanidine hydrochloride. 2014 , 99, 138-45	3
325	Insights into the Binding of Intrinsically Disordered Proteins from Molecular Dynamics Simulation. 2014 , 4, 182-198	50
324	Botulinum neurotoxin: unique folding of enzyme domain of the most-poisonous poison. 2014 , 32, 804-15	12
323	Glyceraldehyde-3-phosphate dehydrogenase is regulated by ferredoxin-NADP reductase in the diatom <i>Asterionella formosa</i> . 2014 , 203, 414-423	22
322	Disordered proteinaceous machines. 2014 , 114, 6806-43	92
321	Structural disorder in viral proteins. 2014 , 114, 6880-911	133
320	Introducing protein intrinsic disorder. 2014 , 114, 6561-88	487
319	Identification of Atg3 as an intrinsically disordered polypeptide yields insights into the molecular dynamics of autophagy-related proteins in yeast. 2014 , 10, 1093-104	26

318	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. 2014 , 281, 3955-79	27
317	Evolutionarily conserved and conformationally constrained short peptides might serve as DNA recognition elements in intrinsically disordered regions. 2014 , 10, 1469-80	3
316	Calcium, acylation, and molecular confinement favor folding of Bordetella pertussis adenylate cyclase CyaA toxin into a monomeric and cytotoxic form. 2014 , 289, 30702-30716	34
315	Fundamentals of Protein Folding. 2014 , 1-61	
314	Entropy reduction in unfolded peptides (and proteins) due to conformational preferences of amino acid residues. 2014 , 16, 22527-36	10
313	Sodium dodecyl sulfate monomers induce XAO peptide polyproline II to α -helix transition. 2014 , 118, 10565-75	9
312	Stimuli-sensitive intrinsically disordered protein brushes. 2014 , 5, 5145	51
311	Three-dimensional protein structure prediction: Methods and computational strategies. 2014 , 53PB, 251-276	107
310	Purification and biophysical characterization of the CapA membrane protein FTT0807 from Francisella tularensis. 2014 , 53, 1958-70	8
309	Temperature-dependent dynamics of dry and hydrated β -casein studied by quasielastic neutron scattering. 2014 , 118, 10821-9	11
308	Conditionally and transiently disordered proteins: awakening cryptic disorder to regulate protein function. 2014 , 114, 6779-805	136
307	Chagas disease: a homology model for the three-dimensional structure of the Trypanosoma cruzi ribosomal P0 antigenic protein. 2014 , 43, 361-6	3
306	Physicochemical properties of cells and their effects on intrinsically disordered proteins (IDPs). 2014 , 114, 6661-714	301
305	Dancing retro: solution structure and micelle interactions of the retro-SH3-domain, retro-SHH-'Bergerac'. 2014 , 32, 257-72	7
304	Chimera-induced folding: implications for amyloidosis. 2014 , 15, 2992-3001	
303	Identification of motives mediating alternative functions of the neomorphic moonlighting TPPP/p25. 2014 , 1842, 547-57	17
302	Intrinsic disorder in proteins involved in the innate antiviral immunity: another flexible side of a molecular arms race. 2014 , 426, 1322-50	27
301	Dynamics and rigidity in an intrinsically disordered protein, β -casein. 2014 , 118, 7317-26	39

300	Coiled-coil deformations in crystal structures: the measles virus phosphoprotein multimerization domain as an illustrative example. 2014 , 70, 1589-603	24
299	Why are the truncated cyclin Es more effective CDK2 activators than the full-length isoforms?. 2014 , 53, 4612-24	15
298	Dual life of TPPP/p25 evolved in physiological and pathological conditions. 2014 , 42, 1762-7	10
297	The inverted free energy landscape of an intrinsically disordered peptide by simulations and experiments. 2015 , 5, 15449	84
296	Overview on Sobemoviruses and a Proposal for the Creation of the Family Sobemoviridae. 2015 , 7, 3076-115	37
295	Fairy "tails": flexibility and function of intrinsically disordered extensions in the photosynthetic world. 2015 , 2, 23	20
294	Amyloid misfolding, aggregation, and the early onset of protein deposition diseases: insights from AFM experiments and computational analyses. 2015 , 2, 190-210	12
293	Protein dynamics: from rattling in a cage to structural relaxation. 2015 , 11, 4984-98	87
292	Disorder-to-order transition in the CyaA toxin RTX domain: implications for toxin secretion. 2014 , 7, 1-20	33
291	Intrinsically disordered cytoplasmic domains of two cytokine receptors mediate conserved interactions with membranes. 2015 , 468, 495-506	47
290	Insights into the Hendra virus NTAIL-XD complex: Evidence for a parallel organization of the helical MoRE at the XD surface stabilized by a combination of hydrophobic and polar interactions. 2015 , 1854, 1038-53	13
289	In various protein complexes, disordered protomers have large per-residue surface areas and area of protein-, DNA- and RNA-binding interfaces. 2015 , 589, 2561-9	30
288	Insights into the coiled-coil organization of the Hendra virus phosphoprotein from combined biochemical and SAXS studies. 2015 , 477, 42-55	8
287	Functional assessment of intrinsic disorder central domains of BRCA1. 2015 , 33, 2469-78	6
286	Structural characterization of MG and pre-MG states of proteins by MD simulations, NMR, and other techniques. 2015 , 33, 2267-84	43
285	Protein intrinsic disorder in Arabidopsis NAC transcription factors: transcriptional activation by ANAC013 and ANAC046 and their interactions with RCD1. 2015 , 465, 281-94	36
284	Analyzing the effects of protecting osmolytes on solute-water interactions by solvatochromic comparison method: II. Globular proteins. 2015 , 5, 59780-59791	20
283	Structural Characterization of Phosducin and Its Complex with the 14-3-3 Protein. 2015 , 290, 16246-60	18

282	Single-molecule spectroscopy of protein conformational dynamics in live eukaryotic cells. 2015 , 12, 773-9	170
281	Redefining the Chaperone Mechanism of sHsps: Not Just Holdase Chaperones. 2015 , 179-195	5
280	Amyloid-like fibrils formed from intrinsically disordered caseins: physicochemical and nanomechanical properties. 2015 , 11, 5898-904	38
279	The multifaceted roles of intrinsic disorder in protein complexes. 2015 , 589, 2498-506	92
278	New insight into the structure and function of Hfq C-terminus. 2015 , 35,	40
277	Transition Metal Induced Conformational Change of Heme Proteins. 2015 , 48, 324-330	5
276	Intrinsic disorder of human Yin Yang 1 protein. 2015 , 83, 1284-96	14
275	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. 2015 , 1854, 492-504	15
274	Alternative splicing modulates Kv channel clustering through a molecular ball and chain mechanism. 2015 , 6, 6488	14
273	Pliable natural biocide: Jaburetox is an intrinsically disordered insecticidal and fungicidal polypeptide derived from jack bean urease. 2015 , 282, 1043-64	23
272	Biophysical Methods to Investigate Intrinsically Disordered Proteins: Avoiding an "Elephant and Blind Men" Situation. 2015 , 870, 215-60	26
271	Emerging Roles of Disordered Sequences in RNA-Binding Proteins. 2015 , 40, 662-672	144
270	Structural and Functional Insights into the Cryoprotection of Membranes by the Intrinsically Disordered Dehydrins. 2015 , 290, 26900-26913	32
269	Targeting the interface of the pathological complex of β synuclein and TPPP/p25. 2015 , 1852, 2653-61	10
268	Calcium ion binding properties and the effect of phosphorylation on the intrinsically disordered Starmaker protein. 2015 , 54, 6525-34	20
267	Unfoldome variation upon plant-pathogen interactions: strawberry infection by <i>Colletotrichum acutatum</i> . 2015 , 89, 49-65	2
266	Dynamics of the intrinsically disordered C-terminal domain of the nipah virus nucleoprotein and interaction with the x domain of the phosphoprotein as unveiled by NMR spectroscopy. 2015 , 16, 268-76	22
265	Effect of temperature on the conformation of natively unfolded protein 4E-BP1 in aqueous and mixed solutions containing trifluoroethanol and hexafluoroisopropanol. 2015 , 34, 18-28	5

264	Low complexity and disordered regions of proteins have different structural and amino acid preferences. 2015 , 11, 585-94	23
263	Buffers more than buffering agent: introducing a new class of stabilizers for the protein BSA. 2015 , 17, 1114-33	27
262	Proteins without unique 3D structures: biotechnological applications of intrinsically unstable/disordered proteins. 2015 , 10, 356-66	19
261	Peculiarities of the Super-Folder GFP Folding in a Crowded Milieu. 2016 , 17,	8
260	p53 Proteoforms and Intrinsic Disorder: An Illustration of the Protein Structure-Function Continuum Concept. 2016 , 17,	102
259	Expression, Purification, and Characterization of Interleukin-11 Orthologues. 2016 , 21,	2
258	Chicken cathelicidins as potent intrinsically disordered biocides with antimicrobial activity against infectious pathogens. 2016 , 65, 8-24	10
257	Probing conformational propensities of histidine in different protonation states of the unblocked glycyL-histidyl-glycine peptide by vibrational and NMR spectroscopy. 2016 , 47, 1063-1072	16
256	Structural and thermodynamic characterisation of L94F mutant of horse cytochrome c. 2016 , 92, 202-212	12
255	Structural effects of amphiphilic protein/gold nanoparticle hybrid based nanozyme on peroxidase-like activity and silver-mediated inhibition. 2016 , 6, 112435-112444	21
254	Relevance of Intrinsic Disorder in Protein Structure and Function. 2016 , 29-72	1
253	Intrinsic disorder in spondins and some of their interacting partners. 2016 , 4, e1255295	7
252	Comparison of the intrinsic disorder propensities of the RuBisCO activase enzyme from the motile and non-motile oceanic green microalgae. 2016 , 4, e1253526	3
251	Molecular chaperone accumulation as a function of stress evidences adaptation to high hydrostatic pressure in the piezophilic archaeon <i>Thermococcus barophilus</i> . 2016 , 6, 29483	22
250	<i>Mycobacterium tuberculosis</i> copper-regulated protein SocB is an intrinsically disordered protein that folds upon interaction with a synthetic phospholipid bilayer. 2016 , 84, 193-200	3
249	Troponins, intrinsic disorder, and cardiomyopathy. 2016 , 397, 731-51	15
248	Characterizing the denatured state ensemble of ubiquitin under native conditions using replica exchange molecular dynamics. 2016 , 6, 95584-95589	1
247	Biomimetic mineralization of collagen. 2016 , 187-232	5

246	The contribution of alpha synuclein to neuronal survival and function - Implications for Parkinson's disease. 2016 , 137, 331-59	124
245	Large-scale analysis of intrinsic disorder flavors and associated functions in the protein sequence universe. 2016 , 25, 2164-2174	34
244	Tau and tauopathies. 2016 , 126, 238-292	292
243	Gibberellin hormone signal perception: down-regulating DELLA repressors of plant growth and development. 2016 , 153-188	20
242	TGF- β 1 autocrine signalling and enamel matrix components. 2016 , 6, 33644	19
241	New structural insights into Golgi Reassembly and Stacking Protein (GRASP) in solution. 2016 , 6, 29976	15
240	Intrinsic disorder in biomarkers of insulin resistance, hypoadiponectinemia, and endothelial dysfunction among the type 2 diabetic patients. 2016 , 4, e1171278	5
239	Structured and Unstructured Binding of an Intrinsically Disordered Protein as Revealed by Atomistic Simulations. 2016 , 138, 8742-51	30
238	Paradoxes and wonders of intrinsic disorder: Complexity of simplicity. 2016 , 4, e1135015	31
237	Molecular recognition features (MoRFs) in three domains of life. 2016 , 12, 697-710	95
236	Fuzzy regions in an intrinsically disordered protein impair protein-protein interactions. 2016 , 283, 576-94	29
235	Dancing Protein Clouds: The Strange Biology and Chaotic Physics of Intrinsically Disordered Proteins. 2016 , 291, 6681-8	128
234	Intrinsic Disorder to Order Transitions in the Scaffold Phosphoprotein P from the Respiratory Syncytial Virus RNA Polymerase Complex. 2016 , 55, 1441-54	9
233	Dynamic Protein Interaction Networks and New Structural Paradigms in Signaling. 2016 , 116, 6424-62	118
232	Antimicrobial potentials and structural disorder of human and animal defensins. 2016 , 28, 95-111	45
231	Protein unfolding in crowded milieu: what crowding can do to a protein undergoing unfolding?. 2016 , 34, 2155-70	23
230	Deciphering the cause of evolutionary variance within intrinsically disordered regions in human proteins. 2017 , 35, 233-249	7
229	Abundance and functional roles of intrinsic disorder in the antimicrobial peptides of the NK-lysin family. 2017 , 35, 836-856	8

228	Folding of intrinsically disordered plant LEA proteins is driven by glycerol-induced crowding and the presence of membranes. 2017 , 284, 919-936	46
227	From Compact to String-The Role of Secondary and Tertiary Structure in Charge-Induced Unzipping of Gas-Phase Proteins. 2017 , 28, 638-646	13
226	Overall Structural Model of NS5A Protein from Hepatitis C Virus and Modulation by Mutations Confering Resistance of Virus Replication to Cyclosporin A. 2017 , 56, 3029-3048	22
225	Intrinsically Disordered Proteins as Important Players during Desiccation Stress of Soybean Radicles. 2017 , 16, 2393-2409	10
224	The Henipavirus V protein is a prevalently unfolded protein with a zinc-finger domain involved in binding to DDB1. 2017 , 13, 2254-2267	10
223	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. 2017 , 13, 2115-2162	35
222	Control of transcriptional activity by design of charge patterning in the intrinsically disordered RAM region of the Notch receptor. 2017 , 114, E9243-E9252	62
221	Paradoxes and wonders of intrinsic disorder: Stability of instability. 2017 , 5, e1327757	16
220	NMR spectroscopic studies of a TAT-derived model peptide in imidazolium-based ILs: influence on chemical shifts and the cis/trans equilibrium state. 2017 , 19, 24115-24125	4
219	In search for globally disordered apo-parvalbumins: Case of parvalbumin β 1 from coho salmon. 2017 , 67, 53-64	10
218	Structural properties of the intrinsically disordered, multiple calcium ion-binding otolith matrix macromolecule-64 (OMM-64). 2017 , 1865, 1358-1371	10
217	The effect of phosphorylation on the salt-tolerance-related functions of the soybean protein PM18, a member of the group-3 LEA protein family. 2017 , 1865, 1291-1303	10
216	CRISPR-induced null alleles show that protects reproduction after cold exposure. 2017 , 220, 3344-3354	9
215	Functionality of intrinsic disorder in tumor necrosis factor- α and its receptors. 2017 , 284, 3589-3618	5
214	Rapid-Acting and Human Insulins: Hexamer Dissociation Kinetics upon Dilution of the Pharmaceutical Formulation. 2017 , 34, 2270-2286	19
213	Current Understanding of Neurodegenerative Diseases Associated With the Protein Tau. 2017 , 92, 1291-1303	31
212	The Two-State Prehensile Tail of the Antibacterial Toxin Colicin N. 2017 , 113, 1673-1684	10
211	Eukaryotic transcription factors: paradigms of protein intrinsic disorder. 2017 , 474, 2509-2532	75

210	Sauromatum guttatum lectin: Spectral studies, lectin-carbohydrate interaction, molecular cloning and in silico analysis. 2017 , 104, 1267-1279	8
209	Distinct VASP tetramers synergize in the processive elongation of individual actin filaments from clustered arrays. 2017 , 114, E5815-E5824	28
208	Intrinsic disorder in proteins involved in amyotrophic lateral sclerosis. 2017 , 74, 1297-1318	32
207	Erythropoietin and co.: intrinsic structure and functional disorder. 2016 , 13, 56-72	15
206	Biophysical Evidence for Intrinsic Disorder in the C-terminal Tails of the Epidermal Growth Factor Receptor (EGFR) and HER3 Receptor Tyrosine Kinases. 2017 , 292, 597-610	16
205	Structural disorder and induced folding within two cereal, ABA stress and ripening (ASR) proteins. 2017 , 7, 15544	30
204	Potential Roles of Intrinsic Disorder in Maternal-Effect Proteins Involved in the Maintenance of DNA Methylation. 2017 , 18,	3
203	Genome Analysis of Conserved Dehydrin Motifs in Vascular Plants. 2017 , 8, 709	32
202	Intrinsic Disorder in Proteins with Pathogenic Repeat Expansions. 2017 , 22,	33
201	Cancer/Testis Antigens: "Smart" Biomarkers for Diagnosis and Prognosis of Prostate and Other Cancers. 2017 , 18,	21
200	HullRad: Fast Calculations of Folded and Disordered Protein and Nucleic Acid Hydrodynamic Properties. 2018 , 114, 856-869	60
199	Exploring intrinsically disordered proteins in Chlamydomonas reinhardtii. 2018 , 8, 6805	16
198	Prosystemin, a prohormone that modulates plant defense barriers, is an intrinsically disordered protein. 2018 , 27, 620-632	7
197	Intrinsically Disordered Regions in Serum Albumin: What Are They For?. 2018 , 76, 39-57	12
196	Intrinsic Disorder, Protein-Protein Interactions, and Disease. 2018 , 110, 85-121	66
195	Partner-Mediated Polymorphism of an Intrinsically Disordered Protein. 2018 , 430, 2493-2507	13
194	Gibberellin Hormone Signal Perception: Down-Regulating DELLA Repressors of Plant Growth and Development. 2018 , 153-187	7
193	Where differences resemble: sequence-feature analysis in curated databases of intrinsically disordered proteins. 2018 , 2018,	6

192	A Focus on the Beneficial Effects of Alpha Synuclein and a Re-Appraisal of Synucleinopathies. 2018 , 19, 598-611	13
191	Functions of short lifetime biological structures at large: the case of intrinsically disordered proteins. 2020 , 19, 60-68	11
190	Experimental Characterization of Fuzzy Protein Assemblies: Interactions of Paramyxoviral N Domains With Their Functional Partners. 2018 , 611, 137-192	7
189	Using NMR Chemical Shifts to Determine Residue-Specific Secondary Structure Populations for Intrinsically Disordered Proteins. 2018 , 611, 101-136	7
188	Comparison of Peptide Ion Conformers Arising from Non-Helical and Helical Peptides Using Ion Mobility Spectrometry and Gas-Phase Hydrogen/Deuterium Exchange. 2018 , 29, 2402-2412	5
187	Comprehensive analysis of the roles of 'black' and 'gray' clusters in structure and function of rat β -parvalbumin. 2018 , 75, 64-78	7
186	Born This Way: Using Intrinsic Disorder to Map the Connections between SLITRKs, TSHR, and Male Sexual Orientation. 2018 , 18, e1800307	0
185	Structural Diversity of Nucleosomes Characterized by Native Mass Spectrometry. 2018 , 90, 8217-8226	12
184	Intrinsically disordered proteins in crowded milieu: when chaos prevails within the cellular gumbo. 2018 , 75, 3907-3929	48
183	Intrinsic Disorder and Posttranslational Modifications: The Darker Side of the Biological Dark Matter. 2018 , 9, 158	111
182	InSiDDe: A Server for Designing Artificial Disordered Proteins. 2017 , 19,	5
181	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. 2018 , 19,	5
180	Understanding the interactability of chikungunya virus proteins molecular recognition feature analysis.. 2018 , 8, 27293-27303	18
179	Regulation of microtubule plus end dynamics by septin 9. 2019 , 76, 83-91	19
178	Multi-functionality of proteins involved in GPCR and G protein signaling: making sense of structure-function continuum with intrinsic disorder-based proteoforms. 2019 , 76, 4461-4492	28
177	Thermally triggered self-assembly of β -casein amyloid nanofibrils and their nanomechanical properties. 2019 , 179, 121626	5
176	A suite of kinetically superior AEP ligases can cyclise an intrinsically disordered protein. 2019 , 9, 10820	29
175	An arsenal of methods for the experimental characterization of intrinsically disordered proteins - How to choose and combine them?. 2019 , 676, 108055	21

174	The ionic liquid [Cmpy][TfN] induces bound-like structure in the intrinsically disordered protein FlgM. 2019 , 21, 17950-17958	5
173	Introduction to intrinsically disordered proteins and regions. 2019 , 1-34	7
172	Neuronal microtubules and proteins linked to Parkinson's disease: a relevant interaction?. 2019 , 400, 1099-1112	9
171	Intrinsic Disorder of the BAF Complex: Roles in Chromatin Remodeling and Disease Development. 2019 , 20,	7
170	Identifying molecular recognition features in intrinsically disordered regions of proteins by transfer learning. 2020 , 36, 1107-1113	14
169	Supramolecular Fuzziness of Intracellular Liquid Droplets: Liquid-Liquid Phase Transitions, Membrane-Less Organelles, and Intrinsic Disorder. 2019 , 24,	18
168	Intrinsically Disordered Proteins and Their Mysterious[(Meta)Physics. 2019 , 7,	188
167	Intrinsic Disorder-Based Emergence in Cellular Biology: Physiological and Pathological Liquid-Liquid Phase Transitions in Cells. 2019 , 11,	33
166	Ferroptosis - An iron- and disorder-dependent programmed cell death. 2019 , 135, 1052-1069	23
165	Tetramer formation by the caspase-activated fragment of the Par-4 tumor suppressor. 2019 , 286, 4060-4073	4
164	The Structural and Functional Diversity of Intrinsically Disordered Regions in Transmembrane Proteins. 2019 , 252, 273-292	8
163	Protein intrinsic disorder and structure-function continuum. 2019 , 166, 1-17	44
162	The Role of HSP90 Chaperones in Stability and Plasticity of Ontogenesis of Plants under Normal and Stressful Conditions (Arabidopsis thaliana). 2019 , 53, 143-161	6
161	Thermally versus Chemically Denatured Protein States. 2019 , 58, 2519-2523	19
160	Hydrodynamic Behavior of the Intrinsically Disordered Potyvirus Protein VPg, of the Translation Initiation Factor eIF4E and of their Binary Complex. 2019 , 20,	4
159	Functional Heme Binding to the Intrinsically Disordered C-Terminal Region of Bach1, a Transcriptional Repressor. 2019 , 247, 153-159	3
158	Troubleshooting Guide to Expressing Intrinsically Disordered Proteins for Use in NMR Experiments. 2018 , 5, 118	10
157	Disease-modifying therapies for tauopathies: agents in the pipeline. 2019 , 19, 397-408	10

156	Biophysical characterization of heme binding to the intrinsically disordered region of Bach1. 2019 , 48, 361-369	2
155	How Full-Length FVIII Benefits from Its Heterogeneity - Insights into the Role of the B-Domain. 2019 , 36, 77	3
154	Tauopathy. 2019 ,	1
153	Evolutionary conservation of the intrinsic disorder-based Radical-Induced Cell Death1 hub interactome. 2019 , 9, 18927	9
152	Structural Features of Tight-Junction Proteins. 2019 , 20,	42
151	Life in Phases: Intra- and Inter- Molecular Phase Transitions in Protein Solutions. 2019 , 9,	20
150	Tau Biology, Tauopathy, Traumatic Brain Injury, and Diagnostic Challenges. 2019 , 67, 447-467	46
149	First evidence of formation of pre-molten globule state in myoglobin: A macromolecular crowding approach towards protein folding in vivo. 2019 , 126, 1288-1294	26
148	Structural disorder in the proteome and interactome of Alkhurma virus (ALKV). 2019 , 76, 577-608	13
147	Stabilizing proteins to prevent conformational changes required for amyloid fibril formation. 2018 , 120, 2642	15
146	The intrinsically disordered C-terminal F domain of the ecdysteroid receptor from <i>Aedes aegypti</i> exhibits metal ion-binding ability. 2019 , 186, 42-55	2
145	Disorder in milk proteins: adipophilin and TIP47, important constituents of the milk fat globule membrane. 2020 , 38, 1214-1229	1
144	DISOselect: Disorder predictor selection at the protein level. 2020 , 29, 184-200	7
143	Electrostatic interactions in molecular recognition of intrinsically disordered proteins. 2020 , 38, 4883-4894	8
142	Accuracy of protein-level disorder predictions. 2020 , 21, 1509-1522	24
141	Presence and structure-activity relationship of intrinsically disordered regions across mucins. 2020 , 34, 1939-1957	4
140	Hydrodynamic Properties of Biomacromolecules and Macromolecular Complexes: Concepts and Methods. A Tutorial Mini-review. 2020 , 432, 2930-2948	3
139	Ordered structure-forming properties of the intrinsically disordered AB region of hXRRL and its ability to promote liquid-liquid phase separation. 2020 , 198, 105571	6

138	Folding perspectives of an intrinsically disordered transactivation domain and its single mutation breaking the folding propensity. 2020 , 155, 1359-1372	6
137	The Evolution of Unusually Small Amelogenin Genes in Cetaceans; Pseudogenization, X-Y Gene Conversion, and Feeding Strategy. 2020 , 88, 122-135	3
136	Bioinformatic Analysis and Biophysical Characterization Reveal Structural Disorder in G0S2 Protein. 2020 , 5, 25841-25847	3
135	Plasminogen Activator. 2020 , 10,	4
134	Structure-Function Insights of Jaburetox and Soyuretox: Novel Intrinsically Disordered Polypeptides Derived from Plant Ureases. 2020 , 25,	1
133	Roles, Characteristics, and Analysis of Intrinsically Disordered Proteins: A Minireview. 2020 , 10,	3
132	The Anti-Inflammatory Protein TNIP1 Is Intrinsically Disordered with Structural Flexibility Contributed by Its AHD1-UBAN Domain. 2020 , 10,	1
131	Dynamical Behavior and Conformational Selection Mechanism of the Intrinsically Disordered Sic1 Kinase-Inhibitor Domain. 2020 , 10,	1
130	Diversity and genome mapping assessment of disordered and functional domains in trypanosomatids. 2020 , 227, 103919	2
129	Functional Diversity of Non-Histone Chromosomal Protein HmgB1. 2020 , 21,	11
128	Huntingtin Yeast Two-Hybrid Protein K (HYPK): An Intrinsically Unstructured Heat Shock Inducible Protein with Diverse Cellular and Molecular Functions. 2020 , 249-274	
127	The Pathophysiological Significance of Fibulin-3. 2020 , 10,	5
126	Zooming into the Dark Side of Human Annexin-S100 Complexes: Dynamic Alliance of Flexible Partners. 2020 , 21,	8
125	Relevance of Electrostatic Charges in Compactness, Aggregation, and Phase Separation of Intrinsically Disordered Proteins. 2020 , 21,	20
124	The Role of Protein Disorder in Nuclear Transport and in Its Subversion by Viruses. 2020 , 9,	7
123	A protein sequence fitness function for identifying natural and nonnatural proteins. 2020 , 88, 1271-1284	5
122	Japanese encephalitis virus - exploring the dark proteome and disorder-function paradigm. 2020 , 287, 3751-3776	11
121	Physicochemical and structural properties of lunasin revealed by spectroscopic, chromatographic and molecular dynamics approaches. 2020 , 1868, 140440	2

120	Specific Conformational Dynamics and Expansion Underpin a Multi-Step Mechanism for Specific Binding of p27 with Cdk2/Cyclin A. 2020 , 432, 2998-3017	10
119	Aggregation and coacervation with Monte Carlo simulations. 2020 , 170, 505-520	0
118	Functional derivatives of human dentin matrix protein 1 modulate morphology of calcium carbonate crystals. 2020 , 34, 6147-6165	2
117	Protein folding: how, why, and beyond. 2020 , 3-22	
116	Development of disease-modifying drugs for frontotemporal dementia spectrum disorders. 2020 , 16, 213-228	34
115	Probing Surfaces in Dynamic Protein Interactions. 2020 , 432, 2949-2972	8
114	Computational Investigation of Structural Interfaces of Protein Complexes with Short Linear Motifs. 2020 , 19, 3254-3263	1
113	Mouse S100G protein exhibits properties characteristic of a calcium sensor. 2020 , 87, 102185	2
112	Stable casein micelle dispersions at pH 4.5 enabled by propylene glycol alginate following a pH-cycle treatment. 2020 , 233, 115834	10
111	Self-Assembly of Exendin-4-Derived Dual Peptide Agonists is Mediated by Acylation and Correlated to the Length of Conjugated Fatty Acyl Chains. 2020 , 17, 965-978	3
110	Intrinsically Disordered Proteins. 2020 , 587-612	4
109	Exploration of reaction rates of chlorine dioxide with tryptophan residue in oligopeptides and proteins. 2020 , 93, 129-136	4
108	Similar Yet Different-Structural and Functional Diversity among LEA_4 Proteins. 2020 , 21,	6
107	Dancing with Trojan horses: an interplay between the extracellular vesicles and viruses. 2021 , 39, 3034-3060	15
106	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. 2021 , 39, 2490-2501	6
105	IDPology of the living cell: intrinsic disorder in the subcellular compartments of the human cell. 2021 , 78, 2371-2385	6
104	Unraveling protein's structural dynamics: from configurational dynamics to ensemble switching guides functional mesoscale assemblies. 2021 , 66, 129-138	9
103	Tuning intrinsic disorder predictors for virus proteins. 2021 , 7, veaa106	1

102	Structural and Functional Characterization of the ABA-Water Deficit Stress Domain from Wheat and Barley: An Intrinsically Disordered Domain behind the Versatile Functions of the Plant Abscisic Acid, Stress and Ripening Protein Family. 2021 , 22,	3
101	Probing Protein Folding with Sequence-Reversed β -Helical Bundles. 2021 , 22,	1
100	Structural Analysis of the cl-Par-4 Tumor Suppressor as a Function of Ionic Environment. 2021 , 11,	1
99	Conformational Dynamics of β Synuclein during the Interaction with Phospholipid Nanodiscs by Millisecond Hydrogen-Deuterium Exchange Mass Spectrometry. 2021 , 32, 1169-1179	2
98	Probing Interdomain Linkers and Protein Supertertiary Structure In Vitro and in Live Cells with Fluorescent Protein Resonance Energy Transfer. 2021 , 433, 166793	6
97	Isolation and Characterization of Human Colon Adenocarcinoma Stem-Like Cells Based on the Endogenous Expression of the Stem Markers. 2021 , 22,	0
96	A Data-Driven Hydrophobicity Scale for Predicting Liquid-Liquid Phase Separation of Proteins. 2021 , 125, 4046-4056	20
95	Conformational buffering underlies functional selection in intrinsically disordered protein regions.	1
94	Immunotherapies for Parkinson's Disease: Progression of Clinical Development. 2021 , 20, 802-813	3
93	RT-PCR Amplification and in-silico Analysis of Water Stress-Responsive Hydrophilic TaDreb, TaDHN and TaWCS20 Genes from Triticum aestivum. 2021 , 47, 218-232	
92	AlphaFold and the amyloid landscape. 2021 , 433, 167059	10
91	The Structural Organization of the HMGB1 Nuclear Protein and Its Effect on the Formation of Ordered Supramolecular Complexes. 2021 , 66, 373-378	2
90	"Janus-Faced" β Synuclein: Role in Parkinson's Disease. 2021 , 9, 673395	3
89	Polyaminoacids in Biomimetic Collagen Mineralization: Roles of Isomerization and Disorder in Polyaspartic and Polyglutamic Acids. 2021 , 22, 2996-3004	4
88	What's in the BAGs? Intrinsic disorder angle of the multifunctionality of the members of a family of chaperone regulators. 2021 ,	1
87	The sequence-ensemble relationship in fuzzy protein complexes. 2021 , 118,	0
86	Expression analysis and molecular modelling of hydrophilin LEA-2-like gene from wheat. 1	1
85	Novel Approaches Used to Examine and Control Neurogenesis in Parkinson's Disease. 2021 , 22,	1

84	Improving the alkaline stability of pepsin through rational protein design using renin, an alkaline-stable aspartic protease, as a structural and functional reference. 2021 , 150, 109871	
83	Intrinsically disordered proteins: Chronology of a discovery. 2021 , 279, 106694	3
82	Non-Bulk-Like Water on Cellular Interfaces. 2006 , 315-324	6
81	α-Synuclein Aggregation and Parkinson's Disease. 2007 , 61-110	2
80	Predicting Conformational Properties of Intrinsically Disordered Proteins from Sequence. 2020 , 2141, 347-389	3
79	Production of Intrinsically Disordered Proteins for Biophysical Studies: Tips and Tricks. 2020 , 2141, 195-209	2
78	Interplay between protein order, disorder and oligomericity in receptor signaling. 2012 , 725, 50-73	6
77	The Structure of Intrinsically Disordered Peptides Implicated in Amyloid Diseases: Insights from Fully Atomistic Simulations. 2012 , 215-227	6
76	Myosins and Hearing. 2020 , 1239, 317-330	9
75	General aspects of neurodegeneration. 2003 , 101-44	80
74	New technologies to analyse protein function: an intrinsic disorder perspective. 2020 , 9,	9
73	Prediction of Intrinsic Disorder in MERS-CoV/HCoV-EMC Supports a High Oral-Fecal Transmission. 2013 , 5,	48
72	Improved disorder prediction by combination of orthogonal approaches. 2009 , 4, e4433	157
71	Solution structure of the QUA1 dimerization domain of pXqua, the Xenopus ortholog of Quaking. 2013 , 8, e57345	3
70	Conformational analysis of isolated domains of Helicobacter pylori CagA. 2013 , 8, e79367	13
69	Intrinsic Disorder of the C-Terminal Domain of Drosophila Methoprene-Tolerant Protein. 2016 , 11, e0162950	7
68	Polyglycine Acts as a Rejection Signal for Protein Transport at the Chloroplast Envelope. 2016 , 11, e0167802	5
67	Role of p27 as a transcriptional regulator. 2018 , 9, 26259-26278	18

66	Overexpression of the extracellular and cytoplasmic domains of the Drosophila adhesion protein, gliotactin. 2004 , 687-689	1
65	Multi-Agent Systems in Three-Dimensional Protein Structure Prediction. 2017 , 241-278	1
64	Unfoldomics of prostate cancer: on the abundance and roles of intrinsically disordered proteins in prostate cancer. 2016 , 18, 662-72	5
63	Intrinsically disordered caldesmon binds calmodulin via the "buttons on a string" mechanism. 2015 , 3, e1265	7
62	Malleable ribonucleoprotein machine: protein intrinsic disorder in the Saccharomyces cerevisiae spliceosome. 2013 , 1, e2	30
61	Amyloid Fibril Formation of Natively Unfolded Proteins. 247	
60	Unfoldomes and Unfoldomics: Introducing Intrinsically Disordered Proteins. 2016 , 125-150	1
59	Conformation of disordered peptides modulated by distributions of charged residues: Case study of random peptides composed of arginines and aspartic acids. 2018 , 67, 058701	1
58	Multi-Agent Systems in Three-Dimensional Protein Structure Prediction. 2019 , 1031-1068	
57	The unfolding of iRFP713 in a crowded milieu. 2019 , 7, e6707	0
56	Novel Cytoskeleton-Associated Proteins in Are Essential for Cell Morphogenesis and Cytokinesis. 2021 , 9,	1
55	fLPS 2.0: rapid annotation of compositionally-biased regions in biological sequences. 2021 , 9, e12363	0
54	Intrinsic Disorder in Plant Transcription Factor Systems: Functional Implications. 2020 , 21,	2
53	Analysis of a Nuclear Intrinsically Disordered Proteome. 2020 , 2175, 181-196	
52	Exploring Protein Intrinsic Disorder with MobiDB. 2020 , 2141, 127-143	0
51	The protein disorder cycle.. 2021 , 13, 1155-1162	3
50	Anti-amyloidogenic effect of artemin on β -synuclein. 2020 , 401, 1143-1151	2
49	Tuning intrinsic disorder predictors for virus proteins.	

48	Conformational dynamics of β -synuclein during the interaction with phospholipid nanodiscs by Millisecond Hydrogen Deuterium Exchange Mass Spectrometry.	
47	At the Interface of Three Nucleic Acids: The Role of RNA-Binding Proteins and Poly(ADP-ribose) in DNA Repair. 2017 , 9, 4-16	6
46	Topological frustration leading to backtracking in a coupled folding-binding process.. 2022 , 24, 2630-2637	
45	Co-opting disorder into order: Intrinsically disordered proteins and the early evolution of complex multicellularity.. 2022 , 201, 29-36	1
44	Experimental Evidence of Intrinsic Disorder and Amyloid Formation by the W Proteins.. 2022 , 23,	1
43	Methods for recombinant production and purification of intrinsically disordered proteins. 2022 , 41-48	
42	Experimental methods to study intrinsically disordered proteins. 2022 , 505-533	2
41	Grape ASR-Silencing Sways Nuclear Proteome, Histone Marks and Interplay of Intrinsically Disordered Proteins.. 2022 , 23,	1
40	What stabilizes pre-folded structures in the intrinsically disordered β -helical binding motifs?.	0
39	Challenges in Discovering Drugs That Target the Protein-Protein Interactions of Disordered Proteins.. 2022 , 23,	3
38	An MP2/Molecular Dynamics study of the solvent effects on the conformational equilibrium of the glycine dipeptide. 2022 , 351, 118557	
37	Poleovirus genomic variation.. 2021 , 7, veab102	3
36	Characterization of recombinant β -subunit of human MUC4 mucin (rMUC4 β). 2021 , 11, 23730	0
35	In vitro evolution of uracil glycosylase towards DnaKJ and GroEL binding evolves different misfolded states.	
34	Distribution of Charged Residues Affects the Average Size and Shape of Intrinsically Disordered Proteins.. 2022 , 12,	0
33	Liquid-liquid phase separation as an organizing principle of intracellular space: overview of the evolution of the cell compartmentalization concept.. 2022 , 79, 251	9
32	Insights into Fluctuations of Structure of Proteins: Significance of Intermediary States in Regulating Biological Functions.. 2022 , 14,	
31	The tauopathies: Neuroimaging characteristics and emerging experimental therapies.. 2022 ,	

30	Structural Insights into the Intrinsically Disordered GPCR C-Terminal Region, Major Actor in Arrestin-GPCR Interaction. 2022 , 12, 617	0
29	Shell Disorder Models Detect That Omicron Has Harder Shells with Attenuation but Is Not a Descendant of the Wuhan-Hu-1 SARS-CoV-2. 2022 , 12, 631	1
28	Randomizing of Oligopeptide Conformations by Nearest Neighbor Interactions between Amino Acid Residues. 2022 , 12, 684	1
27	Intron-Encoded Domain of Herstatin, An Autoinhibitor of Human Epidermal Growth Factor Receptors, Is Intrinsically Disordered.. 2022 , 9, 862910	
26	Exploring Nearest Neighbor Interactions and Their Influence on the Gibbs Energy Landscape of Unfolded Proteins and Peptides. 2022 , 23, 5643	1
25	In vitro Evolution of Uracil Glycosylase Towards DnaKJ and GroEL Binding Evolves Different Misfolded States. 2022 , 434, 167627	
24	The free energy folding penalty accompanying binding of intrinsically disordered helical motifs. 2022 , 31,	0
23	Electronic Polarization at the Interface between the p53 Transactivation Domain and Two Binding Partners.	
22	ThhspA1 is involved in lacA transcriptional regulation of <i>Trametes hirsuta</i> AH28-2 exposed to o-toluidine. 2022 , 161, 103716	
21	The Molten Globule State of a Globular Protein in a Cell Is More or Less Frequent Case Rather than an Exception. 2022 , 27, 4361	1
20	Delineating organizational principles of the endogenous L-A virus by cryo-EM and computational analysis of native cell extracts.	0
19	Lighting up Nobel Prize-winning studies with protein intrinsic disorder. 2022 , 79,	0
18	Conformational buffering underlies functional selection in intrinsically disordered protein regions. 2022 , 29, 781-790	3
17	Global genetic diversity and evolutionary patterns among Potato leafroll virus populations. 13,	0
16	A disordered region retains the full protease inhibitor activity and the capacity to induce CD8+ T cells in vivo of the oral vaccine adjuvant U-Omp19. 2022 , 20, 5098-5114	0
15	A Study on the Nature of SARS-CoV-2 Using the Shell Disorder Models: Reproducibility, Evolution, Spread, and Attenuation. 2022 , 12, 1353	1
14	Looking at the Pathogenesis of the Rabies Lyssavirus Strain Pasteur Vaccins through a Prism of the Disorder-Based Bioinformatics. 2022 , 12, 1436	0
13	Molecular determinants of fibrillation in a viral amyloidogenic domain from combined biochemical and biophysical studies.	2

- 12 Liquid–liquid phase in anhydrobiosis. **2023**, 545-555 ○
- 11 Cross-talk between β -synuclein and the microtubule cytoskeleton in neurodegeneration. **2023**, 359, 114251 ○
- 10 Liquid–liquid phase separation, membrane-less organelles, and biomolecular condensates in cardiovascular disease. **2023**, 663-679 ○
- 9 Stress, membraneless organelles, and liquid–liquid phase separation. **2023**, 505-529 ○
- 8 Intrinsically Disordered Proteins: An Overview. **2022**, 23, 14050 2
- 7 Methods for measuring structural disorder in proteins. **2023**, 149-198 ○
- 6 Structure and disorder: protein functions depend on this new binary transforming lock-and-key into structure-function continuum. **2023**, 127-148 ○
- 5 Coprinopsis cinerea Galectin CGL1 Induces Apoptosis and Inhibits Tumor Growth in Colorectal Cancer Cells. **2023**, 24, 235 ○
- 4 Convergent behavior of extended stalk regions from staphylococcal surface proteins with widely divergent sequence patterns. ○
- 3 Molecular Determinants of Fibrillation in a Viral Amyloidogenic Domain from Combined Biochemical and Biophysical Studies. **2023**, 24, 399 ○
- 2 Pre-Molten, Wet, and Dry Molten Globules en Route to the Functional State of Proteins. **2023**, 24, 2424 ○
- 1 Electronegative clusters modulate folding status and RNA binding of unstructured RNA-binding proteins. ○