

CITATION REPORT

List of articles citing

Intrinsically unstructured proteins: re-assessing the protein structure-function paradigm

DOI: 10.1006/jmbi.1999.3110

Journal of Molecular Biology, 1999, 293, 321-31.

Source: <https://exaly.com/paper-pdf/30914275/citation-report.pdf>

Version: 2024-04-27

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

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

#	Paper	IF	Citations
2332	Folding minimal sequences: the lower bound for sequence complexity of globular proteins. 1999 , 462, 363-7		57
2331	Alpha-amylase inhibitors selected from a combinatorial library of a cellulose binding domain scaffold. 2000 , 41, 316-22		42
2330	Why are "natively unfolded" proteins unstructured under physiologic conditions?. 2000 , 41, 415-27		1690
2329	Autoinhibition and activation mechanisms of the Wiskott-Aldrich syndrome protein. 2000 , 404, 151-8		616
2328	FAT: a novel domain in PIK-related kinases. 2000 , 25, 225-7		243
2327	Nuclear receptors arose from pre-existing protein modules during evolution. 2000 , 25, 227-8		38
2326	Structural genomics: an overview. 2000 , 73, 289-95		35
2325	Sequence-specific 1H, 15N and 13C resonance assignments of the inhibitory prodomain of human furin. 2000 , 16, 275-6		4
2324	Homology modeling and molecular dynamics simulations of lymphotactin. 2000 , 9, 2192-9		2
2323	Post-translational hydroxylation at the N-terminus of the prion protein reveals presence of PPII structure in vivo. 2000 , 19, 5324-31		48
2322	A census of glutamine/asparagine-rich regions: implications for their conserved function and the prediction of novel prions. 2000 , 97, 11910-5		382
2321	Potential use of non-classical pathways for the transport of macromolecular drugs. 2000 , 9, 2039-50		13
2320	Mutational and structural analyses of the ribonucleotide reductase inhibitor Sml1 define its Rnr1 interaction domain whose inactivation allows suppression of mec1 and rad53 lethality. 2000 , 20, 9076-83		75
2319	Isolation and characterization of cDNAs expressed in the early stages of flavonol-induced pollen germination in petunia. 2000 , 123, 699-710		70
2318	A functional R domain from cystic fibrosis transmembrane conductance regulator is predominantly unstructured in solution. 2000 , 97, 5657-62		90
2317	Speeding molecular recognition by using the folding funnel: the fly-casting mechanism. 2000 , 97, 8868-73		847
2316	Proteomics of <i>Mycoplasma genitalium</i> : identification and characterization of unannotated and atypical proteins in a small model genome. 2000 , 28, 3075-82		24

2315	An essential phosphorylation-site domain of human cdc25C interacts with both 14-3-3 and cyclins. 2000 , 275, 28849-57		29
2314	Artificial Neural Networks in Medicine and Biology. 2000 ,		10
2313	Ligand-induced stabilization of PPARgamma monitored by NMR spectroscopy: implications for nuclear receptor activation. <i>Journal of Molecular Biology</i> , 2000 , 298, 187-94	6.5	140
2312	A view of dynamics changes in the molten globule-native folding step by quasielastic neutron scattering. <i>Journal of Molecular Biology</i> , 2000 , 301, 525-36	6.5	53
2311	The virtuoso of versatility: POU proteins that flex to fit. <i>Journal of Molecular Biology</i> , 2000 , 302, 1023-396.5		195
2310	Identification of the phospholipid-binding site of human beta(2)-glycoprotein I domain V by heteronuclear magnetic resonance. <i>Journal of Molecular Biology</i> , 2000 , 304, 927-39	6.5	43
2309	Expression and purification of dynamin II domains and initial studies on structure and function. 2000 , 20, 314-23		16
2308	Flipping the switch: the structural basis for signaling through the CRIB motif. 2000 , 102, 403-6		67
2307	Interaction of the Escherichia coli replication terminator protein (Tus) with DNA: a model derived from DNA-binding studies of mutant proteins by surface plasmon resonance. 2000 , 39, 11989-99		135
2306	Thermal behavior of proteins: heat-resistant proteins and their heat-induced secondary structural changes. 2000 , 39, 14839-46		80
2305	Biophysical characterization of elongin C from Saccharomyces cerevisiae. 2000 , 39, 11137-46		8
2304	Structural differences between Saccharomyces cerevisiae ribosomal stalk proteins P1 and P2 support their functional diversity. 2000 , 39, 8935-43		21
2303	Inhibitory activity and structural characterization of a C-terminal peptide fragment derived from the prosegment of the proprotein convertase PC7. 2000 , 39, 2868-77		26
2302	Characterizing the function of unstructured proteins: Simulations of charged polymers under confinement. 2001 , 115, 4909-4918		16
2301	Current topics in RNA-protein recognition: control of specificity and biological function through induced fit and conformational capture. 2001 , 40, 7947-56		297
2300	NMR structural and dynamic characterization of the acid-unfolded state of apomyoglobin provides insights into the early events in protein folding. 2001 , 40, 3561-71		203
2299	PAS domain receptor photoactive yellow protein is converted to a molten globule state upon activation. 2001 , 276, 20821-3		48
2298	Effects of macromolecular crowding on the intrinsically disordered proteins c-Fos and p27(Kip1). 2001 , 2, 538-40		87

2297	Nuclear magnetic resonance methods for elucidation of structure and dynamics in disordered states. 2001 , 339, 258-70		137
2296	Structure and dynamics of the alpha-lactalbumin molten globule: fluorescence studies using proteins containing a single tryptophan residue. 2001 , 40, 7228-38		56
2295	Structure-activity relationships in flexible protein domains: regulation of rho GTPases by RhoGDI and D4 GDI. <i>Journal of Molecular Biology</i> , 2001 , 305, 121-35	6.5	55
2294	Characterization of NMR relaxation-active motions of a partially folded A-state analogue of ubiquitin. <i>Journal of Molecular Biology</i> , 2001 , 305, 1085-97	6.5	26
2293	Dramatic stabilization of an SH3 domain by a single substitution: roles of the folded and unfolded states. <i>Journal of Molecular Biology</i> , 2001 , 307, 913-28	6.5	73
2292	Phosphorylation-induced structural changes in the amyloid precursor protein cytoplasmic tail detected by NMR. <i>Journal of Molecular Biology</i> , 2001 , 307, 871-84	6.5	126
2291	Conformational properties of alpha-synuclein in its free and lipid-associated states. <i>Journal of Molecular Biology</i> , 2001 , 307, 1061-73	6.5	838
2290	Backbone dynamics of Escherichia coli thioesterase/protease I: evidence of a flexible active-site environment for a serine protease. <i>Journal of Molecular Biology</i> , 2001 , 307, 1075-90	6.5	40
2289	Calculation of ensembles of structures representing the unfolded state of an SH3 domain. <i>Journal of Molecular Biology</i> , 2001 , 308, 1011-32	6.5	184
2288	Structure of the C-terminal RNA-binding domain of hnRNP D0 (AUF1), its interactions with RNA and DNA, and change in backbone dynamics upon complex formation with DNA. <i>Journal of Molecular Biology</i> , 2001 , 311, 973-88	6.5	35
2287	Defining the molecular basis of Arf and Hdm2 interactions. <i>Journal of Molecular Biology</i> , 2001 , 314, 263-275		112
2286	Structure and properties of a dimeric N-terminal fragment of human ubiquitin. <i>Journal of Molecular Biology</i> , 2001 , 314, 773-87	6.5	14
2285	Fold predictions for bacterial genomes. 2001 , 134, 219-31		22
2284	Linked folding and anion binding of the Bacillus subtilis ribonuclease P protein. 2001 , 40, 2777-89		85
2283	Molecular biology of HMGA proteins: hubs of nuclear function. 2001 , 277, 63-81		443
2282	The human genome: an immuno-centric view of evolutionary strategies. 2001 , 22, 227-9		8
2281	Zinc and copper bind to unique sites of histatin 5. 2001 , 491, 76-80		59
2280	Trimethylamine-N-oxide-induced folding of alpha-synuclein. 2001 , 509, 31-5		146

2279	Protein folding: binding of conformationally fluctuating building blocks via population selection. 2001 , 36, 399-433	52
2278	Beta-lactoglobulin molten globule induced by high pressure. 2001 , 49, 3236-43	89
2277	Three-dimensional structure and dynamics of a brain specific growth inhibitory factor: metallothionein-3. 2001 , 40, 11433-41	84
2276	Clusterin, a binding protein with a molten globule-like region. 2001 , 40, 11828-40	96
2275	Solution structure determination and mutational analysis of the papillomavirus E6 interacting peptide of E6AP. 2001 , 40, 1293-9	54
2274	Disorder-to-order transition of the active site of human class Pi glutathione transferase, GST P1-1. 2001 , 40, 11660-9	27
2273	Expression of the Oct-1 transcription factor and characterization of its interactions with the Bob1 coactivator. 2001 , 40, 6580-8	29
2272	Dynamics of the Mrf-2 DNA-binding domain free and in complex with DNA. 2001 , 40, 9142-50	31
2271	Human flap endonuclease-1: conformational change upon binding to the flap DNA substrate and location of the Mg ²⁺ binding site. 2001 , 40, 3208-14	23
2270	Domain architecture of a high mobility group A-type bacterial transcriptional factor. 2001 , 276, 41566-75	35
2269	Protein anatomy: structure and function of peptide fragments corresponding to the secondary structure units of barnase. 2001 , 129, 971-7	1
2268	Low-complexity regions in Plasmodium falciparum proteins. 2001 , 11, 218-29	97
2267	Structural consequences of site-directed mutagenesis in flexible protein domains: NMR characterization of the L(55,56)S mutant of RhoGDI. 2001 , 268, 2253-60	7
2266	Alternate routes to conformational specificity in a Greek key beta barrel protein. 2001 , 268, 4653-63	2
2265	Structure of the C-terminal sterile alpha-motif (SAM) domain of human p73 alpha. 2001 , 57, 545-51	27
2264	NMR spin relaxation methods for characterization of disorder and folding in proteins. 2001 , 19, 3-12	43
2263	Intrinsically disordered protein. 2001 , 19, 26-59	1747
2262	Structured disorder and conformational selection. 2001 , 44, 418-27	173

2261	A conserved helix-unfolding motif in the naturally unfolded proteins. 2001 , 44, 479-83	22
2260	Integrated graphical analysis of protein sequence features predicted from sequence composition. 2001 , 45, 262-73	34
2259	Sequence complexity of disordered protein. 2001 , 42, 38-48	1295
2258	Exploring the energy landscape of a beta hairpin in explicit solvent. 2001 , 42, 345-54	330
2257	Structure determination of membrane-associated proteins from nuclear magnetic resonance data. 2001 , 288, 1-15	19
2256	Recognition between flexible protein molecules: induced and assisted folding. 2001 , 14, 42-61	134
2255	Backbone dynamics of the natively unfolded pro-peptide of subtilisin by heteronuclear NMR relaxation studies. 2001 , 20, 233-49	61
2254	Identification of intrinsic order and disorder in the DNA repair protein XPA. 2001 , 10, 560-71	101
2253	Solution structure and backbone dynamics of the DNA-binding domain of mouse Sox-5. 2001 , 10, 83-98	18
2252	Folding units in calcium vector protein of amphioxus: Structural and functional properties of its amino- and carboxy-terminal halves. 2001 , 10, 771-8	14
2251	pH-induced conformational transitions of a molten-globule-like state of the inhibitory prodomain of furin: implications for zymogen activation. 2001 , 10, 934-42	26
2250	Energy landscape of a peptide consisting of alpha-helix, 3(10)-helix, beta-turn, beta-hairpin, and other disordered conformations. 2001 , 10, 1160-71	74
2249	Phosphorylation disrupts the central helix in Op18/stathmin and suppresses binding to tubulin. 2001 , 2, 505-10	48
2248	Quantitative protein stability measurement in vivo. 2001 , 8, 879-82	138
2247	The protein trinity—linking function and disorder. 2001 , 19, 805-6	485
2246	A tour of structural genomics. 2001 , 2, 801-9	131
2245	HMGI/Y proteins: flexible regulators of transcription and chromatin structure. 2001 , 1519, 13-29	265
2244	Plasticity of secondary structure in the N-terminal region of beta-dystroglycan. 2001 , 1546, 114-21	16

2243	Predicting properties of intrinsically unstructured proteins. 2001 , 76, 131-73	59
2242	Protein functional epitopes: hot spots, dynamics and combinatorial libraries. 2001 , 11, 364-9	107
2241	Structural transformations accompanying the assembly of bacteriophage P22 portal protein rings in vitro. 2001 , 276, 6779-88	23
2240	Human p8 is a HMG-I/Y-like protein with DNA binding activity enhanced by phosphorylation. 2001 , 276, 2742-51	95
2239	Site-specific molecular design and its relevance to pharmacogenomics and chemical biology. 2001 , 1, 38-47	4
2238	Actin filament cross-linking by MARCKS: characterization of two actin-binding sites within the phosphorylation site domain. 2001 , 276, 22351-8	61
2237	A chemical inhibitor of N-WASP reveals a new mechanism for targeting protein interactions. 2001 , 98, 10624-9	82
2236	Molecular interactions of the Gbeta binding domain of the Ste20p/PAK family of protein kinases. An isolated but fully functional Gbeta binding domain from Ste20p is only partially folded as shown by heteronuclear NMR spectroscopy. 2001 , 276, 41205-12	12
2235	Regulation of the cystic fibrosis transmembrane conductance regulator Cl ⁻ channel by its R domain. 2001 , 276, 7689-92	90
2234	Folding and signaling share the same pathway in a photoreceptor. 2001 , 98, 9062-7	39
2233	Disordered to ordered folding in the regulation of diphtheria toxin repressor activity. 2001 , 98, 11259-64	40
2232	Formation and implications of a ternary complex of profilin, thymosin beta 4, and actin. 2001 , 276, 45555-63	36
2231	ProDDO: a database of disordered proteins from the Protein Data Bank (PDB). 2001 , 17, 379-80	12
2230	Probing conformational changes in the estrogen receptor: evidence for a partially unfolded intermediate facilitating ligand binding and release. 2001 , 15, 421-8	60
2229	Interactions of the 18.5-kDa isoform of myelin basic protein with Ca(2+)-calmodulin: in vitro studies using fluorescence microscopy and spectroscopy. 2002 , 80, 395-406	22
2228	Delineation of the high-affinity single-stranded telomeric DNA-binding domain of <i>Saccharomyces cerevisiae</i> Cdc13. 2002 , 30, 4305-13	42
2227	Identification of a substrate recognition site on Ubc9. 2002 , 277, 21740-8	99
2226	Conclusive evidence that the major T-cell antigens of the <i>Mycobacterium tuberculosis</i> complex ESAT-6 and CFP-10 form a tight, 1:1 complex and characterization of the structural properties of ESAT-6, CFP-10, and the ESAT-6*CFP-10 complex. Implications for pathogenesis and virulence. 2002 , 277, 21598-603	252

2225	The solution structure of acyl carrier protein from <i>Mycobacterium tuberculosis</i> . 2002 , 277, 15874-80	102
2224	An alanine-zipper structure determined by long range intermolecular interactions. 2002 , 277, 48708-13	14
2223	Does fusion of domains from unrelated proteins affect their folding pathways and the structural changes involved in their function? A case study with the diphtheria toxin T domain. 2002 , 15, 383-91	26
2222	Structural plasticity in influenza virus protein NS2 (NEP). 2002 , 277, 7108-17	23
2221	The ubiquitous nature of RNA chaperone proteins. 2002 , 72, 223-68	142
2220	Conformational analysis of the androgen receptor amino-terminal domain involved in transactivation. Influence of structure-stabilizing solutes and protein-protein interactions. 2002 , 277, 20079-86	102
2219	Characterization of the structure and dynamics of a near-native equilibrium intermediate in the unfolding pathway of an all beta-barrel protein. 2002 , 277, 47507-16	15
2218	Cross-talk unfolded: MARCKS proteins. 2002 , 362, 1-12	261
2217	Cross-talk unfolded: MARCKS proteins. 2002 , 362, 1-12	204
2216	Protein kinase A enhances, whereas glycogen synthase kinase-3 beta inhibits, the activity of the exon 2-encoded transactivator domain of heterogeneous nuclear ribonucleoprotein D in a hierarchical fashion. 2002 , 363, 127-36	18
2215	Protein kinase A enhances, whereas glycogen synthase kinase-3 β inhibits, the activity of the exon 2-encoded transactivator domain of heterogeneous nuclear ribonucleoprotein D in a hierarchical fashion. 2002 , 363, 127-136	19
2214	Unfolded proteins studied by Raman optical activity. 2002 , 62, 51-90	90
2213	Solid State NMR Studies of Uniformly Isotopically Enriched Proteins. 2002 , 103-120	1
2212	Engineering of metallothionein-3 neuroinhibitory activity into the inactive isoform metallothionein-1. 2002 , 277, 37023-8	52
2211	Stress-induced aggregation profiles of GST-alpha-synuclein fusion proteins: role of the C-terminal acidic tail of alpha-synuclein in protein thermosolubility and stability. 2002 , 41, 4137-46	46
2210	Interactions of cytoplasmic dynein light chains Tctex-1 and LC8 with the intermediate chain IC74. 2002 , 41, 4302-11	89
2209	Functional consequences of preorganized helical structure in the intrinsically disordered cell-cycle inhibitor p27(Kip1). 2002 , 41, 752-9	131
2208	Effect of zinc and temperature on the conformation of the gamma subunit of retinal phosphodiesterase: a natively unfolded protein. 2002 , 1, 149-59	57

2207	Structural and functional implications of C-terminal regions of alpha-synuclein. 2002 , 41, 13782-90		127
2206	Transcription activation by ultrabithorax I β protein requires a predicted alpha-helical region. 2002 , 41, 2774-85		21
2205	Insights into the structure and dynamics of unfolded proteins from nuclear magnetic resonance. 2002 , 62, 311-40		183
2204	Long-range interactions within a nonnative protein. 2002 , 295, 1719-22		548
2203	Extended conformation of mammalian translation elongation factor 1A in solution. 2002 , 41, 15342-9		32
2202	Distribution of molecular size within an unfolded state ensemble using small-angle X-ray scattering and pulse field gradient NMR techniques. <i>Journal of Molecular Biology</i> , 2002 , 316, 101-12	6.5	158
2201	Base flexibility in HIV-2 TAR RNA mapped by solution (15)N, (13)C NMR relaxation. <i>Journal of Molecular Biology</i> , 2002 , 317, 263-78	6.5	70
2200	Effect of tandem rare codon substitution and vector-host combinations on the expression of the EBV gp110 C-terminal domain in <i>Escherichia coli</i> . 2002 , 24, 470-80		14
2199	Toward a taxonomy of the denatured state: small angle scattering studies of unfolded proteins. 2002 , 62, 241-62		133
2198	Intrinsic disorder and protein function. 2002 , 41, 6573-82		1462
2197	General framework for studying the dynamics of folded and nonfolded proteins by NMR relaxation spectroscopy and MD simulation. 2002 , 124, 4522-34		172
2196	Equilibrium and stop-flow kinetic studies of fluorescently labeled DNA substrates with DNA repair proteins XPA and replication protein A. 2002 , 41, 131-43		22
2195	Molecular mechanics of cardiac titin's PEVK and N2B spring elements. 2002 , 277, 11549-58		113
2194	Analysis of protein-carbohydrate interaction at the lower size limit of the protein part (15-mer peptide) by NMR spectroscopy, electrospray ionization mass spectrometry, and molecular modeling. 2002 , 41, 9707-17		29
2193	Identification and functions of usefully disordered proteins. 2002 , 62, 25-49		303
2192	Molecular Modeling and Simulation. 2002 ,		318
2191	Methionine oxidation inhibits fibrillation of human alpha-synuclein in vitro. 2002 , 517, 239-44		182
2190	The regions of securin and cyclin B proteins recognized by the ubiquitination machinery are natively unfolded. 2002 , 527, 303-8		34

2189	Structural dynamics of the membrane translocation domain of colicin E9 and its interaction with TolB. <i>Journal of Molecular Biology</i> , 2002 , 318, 787-804	6.5	37
2188	Functional interactions of nucleocapsid protein of feline immunodeficiency virus and cellular prion protein with the viral RNA. <i>Journal of Molecular Biology</i> , 2002 , 318, 149-59	6.5	35
2187	Metal-dependent folding and stability of nuclear hormone receptor DNA-binding domains. <i>Journal of Molecular Biology</i> , 2002 , 319, 87-106	6.5	36
2186	Kinetic studies and structural models of the association of E. coli sigma(70) RNA polymerase with the lambdaP(R) promoter: large scale conformational changes in forming the kinetically significant intermediates. <i>Journal of Molecular Biology</i> , 2002 , 319, 649-71	6.5	102
2185	Truncation of amino-terminal tail stimulates activity of human endonuclease III (hNTH1). <i>Journal of Molecular Biology</i> , 2002 , 321, 265-76	6.5	45
2184	Loopy proteins appear conserved in evolution. <i>Journal of Molecular Biology</i> , 2002 , 322, 53-64	6.5	168
2183	Cooperative interactions and a non-native buried Trp in the unfolded state of an SH3 domain. <i>Journal of Molecular Biology</i> , 2002 , 322, 163-78	6.5	63
2182	p53 contains large unstructured regions in its native state. <i>Journal of Molecular Biology</i> , 2002 , 322, 917-215		214
2181	Intrinsic disorder in cell-signaling and cancer-associated proteins. <i>Journal of Molecular Biology</i> , 2002 , 323, 573-84	6.5	967
2180	Transient structure formation in unfolded acyl-coenzyme A-binding protein observed by site-directed spin labelling. <i>Journal of Molecular Biology</i> , 2002 , 324, 349-57	6.5	80
2179	Solution studies and structural model of the extracellular domain of the human amyloid precursor protein. 2002 , 83, 3513-24		24
2178	Effects of the osmolyte trimethylamine-N-oxide on conformation, self-association, and two-dimensional crystallization of myelin basic protein. 2002 , 139, 13-26		41
2177	Is polyproline II a major backbone conformation in unfolded proteins?. 2002 , 62, 163-240		250
2176	Dehydrins. 2002 , 3, 155-171		43
2175	The Protein Trinity: Structure/Function Relationships That Include Intrinsic Disorder. 2002 , 2, 49-50		5
2174	Intrinsically unstructured proteins. 2002 , 27, 527-33		1663
2173	Coupling of folding and binding for unstructured proteins. 2002 , 12, 54-60		1121
2172	Complexity and simplicity of ligand-macromolecule interactions: the energy landscape perspective. 2002 , 12, 197-203		99

2171	Protein surface salt bridges and paths for DNA wrapping. 2002 , 12, 311-9	64
2170	Did evolution leap to create the protein universe?. 2002 , 12, 409-16	41
2169	Evolutionary rate heterogeneity in proteins with long disordered regions. 2002 , 55, 104-10	341
2168	A Raman optical activity study of rheomorphism in caseins, synucleins and tau. New insight into the structure and behaviour of natively unfolded proteins. 2002 , 269, 148-56	181
2167	What does it mean to be natively unfolded?. 2002 , 269, 2-12	766
2166	Casein structure, self-assembly and gelation. 2002 , 7, 456-461	252
2165	Equilibrium unfolding and conformational plasticity of troponin I and T. 2002 , 269, 5484-91	12
2164	Intrinsic structural disorder and sequence features of the cell cycle inhibitor p57Kip2. 2002 , 46, 1-7	62
2163	Dynamic and structural analysis of isotropically distributed molecular ensembles. 2002 , 46, 177-89	37
2162	Principles of docking: An overview of search algorithms and a guide to scoring functions. 2002 , 47, 409-43	954
2161	Structural modeling of ataxin-3 reveals distant homology to adaptins. 2003 , 50, 355-70	27
2160	Functional organization of the yeast proteome by systematic analysis of protein complexes. 2002 , 415, 141-7	4018
2159	Mutual synergistic folding in recruitment of CBP/p300 by p160 nuclear receptor coactivators. 2002 , 415, 549-53	373
2158	A residue-specific view of the association and dissociation pathway in protein-DNA recognition. 2002 , 9, 193-7	27
2157	The N-terminal domain of the phosphoprotein of Morbilliviruses belongs to the natively unfolded class of proteins. 2002 , 296, 251-62	87
2156	Recovery of paramyxovirus simian virus 5 with a V protein lacking the conserved cysteine-rich domain: the multifunctional V protein blocks both interferon-beta induction and interferon signaling. 2002 , 303, 15-32	161
2155	Identification of protein functions from a molecular surface database, eF-site. 2002 , 2, 9-22	94
2154	Role for NMR in structural genomics. 2002 , 2, 155-69	28

2153	Natively unfolded proteins: a point where biology waits for physics. 2002 , 11, 739-56	1470
2152	Clathrin light and heavy chain interface: alpha-helix binding superhelix loops via critical tryptophans. 2002 , 21, 6072-82	42
2151	Efficient expression of isotopically labeled peptides for high resolution NMR studies: application to the Cdc42/Rac binding domains of virulent kinases in <i>Candida albicans</i> . 2003 , 26, 317-26	16
2150	Detection of nano-second internal motion and determination of overall tumbling times independent of the time scale of internal motion in proteins from NMR relaxation data. 2003 , 27, 291-312	16
2149	Transcription Factor Oct-1: Plasticity and Multiplicity of Functions. 2003 , 37, 637-648	24
2148	Polycation-induced oligomerization and accelerated fibrillation of human alpha-synuclein in vitro. 2003 , 12, 702-7	109
2147	Improved amino acid flexibility parameters. 2003 , 12, 1060-72	137
2146	Structure of Cdc42 in a complex with the GTPase-binding domain of the cell polarity protein, Par6. 2003 , 22, 1125-33	137
2145	Protein folding revisited. A polypeptide chain at the folding-misfolding-nonfolding cross-roads: which way to go?. 2003 , 60, 1852-71	271
2144	Protein aggregation and aggregate toxicity: new insights into protein folding, misfolding diseases and biological evolution. 2003 , 81, 678-99	1272
2143	Are there temperature-dependent structural transitions in the "intrinsically unstructured" protein prothymosin alpha?. 2003 , 31, 586-94	9
2142	Extended disordered proteins: targeting function with less scaffold. 2003 , 28, 81-5	286
2141	Conformational diversity and protein evolution--a 60-year-old hypothesis revisited. 2003 , 28, 361-8	439
2140	Crystallography: embracing conformational flexibility in proteins. 2003 , 11, 735-6	6
2139	Drug discovery and p53. 2003 , 8, 347-55	81
2138	Protein disorder prediction: implications for structural proteomics. 2003 , 11, 1453-9	964
2137	Order, disorder, and flexibility: prediction from protein sequence. 2003 , 11, 1316-7	49
2136	Analysis of two large functionally uncharacterized regions in the <i>Methanopyrus kandleri</i> AV19 genome. 2003 , 4, 12	8

2135	Mathematical modeling suggests cooperative interactions between a disordered polyvalent ligand and a single receptor site. 2003 , 13, 1669-78	72
2134	Allovalency: a case of molecular entanglement. 2003 , 13, R876-8	8
2133	Negative design for improved therapeutic proteins. 2003 , 21, 425-7	5
2132	Folding for binding or binding for folding?. 2003 , 21, 423-5	19
2131	Intrinsically unstructured proteins evolve by repeat expansion. 2003 , 25, 847-55	222
2130	The physics and bioinformatics of binding and folding-an energy landscape perspective. 2003 , 68, 333-49	109
2129	The functional benefits of protein disorder. 2003 , 666-667, 361-371	68
2128	Characterization of sub-nanosecond dynamics of the molten globule state of β -lactalbumin using quasielastic neutron scattering and molecular dynamics simulations. 2003 , 292, 435-443	16
2127	Local protein unfolding and pathogenesis of polyglutamine-expansion diseases. 2003 , 51, 68-73	11
2126	Flavors of protein disorder. 2003 , 52, 573-84	291
2125	The intracellular domain of the <i>Drosophila</i> cholinesterase-like neural adhesion protein, gliotactin, is natively unfolded. 2003 , 53, 758-67	52
2124	Natively unfolded C-terminal domain of caldesmon remains substantially unstructured after the effective binding to calmodulin. 2003 , 53, 855-62	88
2123	Prediction of disordered regions in proteins from position specific score matrices. 2003 , 53 Suppl 6, 573-8	175
2122	Predicting intrinsic disorder from amino acid sequence. 2003 , 53 Suppl 6, 566-72	364
2121	Proteomic signatures: amino acid and oligopeptide compositions differentiate among phyla. 2004 , 54, 20-40	117
2120	Sequence-based study of two related proteins with different folding behaviors. 2004 , 54, 8-12	3
2119	A double-take on MAPs. 2003 , 10, 314-6	6
2118	Prized malaria drug target nailed. 2003 , 10, 316-8	13

2117	Crystal structure of a MARCKS peptide containing the calmodulin-binding domain in complex with Ca ²⁺ -calmodulin. 2003 , 10, 226-31	93
2116	From genomics to proteomics. 2003 , 422, 193-7	734
2115	Thermally induced structural changes in glycinin, the 11S globulin of soya bean (<i>Glycine max</i>)--an in situ spectroscopic study. 2003 , 1648, 105-14	51
2114	A protein-chameleon: conformational plasticity of alpha-synuclein, a disordered protein involved in neurodegenerative disorders. 2003 , 21, 211-34	391
2113	DSC studies of a family of natively disordered fragments from <i>Escherichia coli</i> thioredoxin: surface burial in intrinsic coils. 2003 , 42, 3349-58	9
2112	Molecular recognition of the human coactivator CBP by the HIV-1 transcriptional activator Tat. 2003 , 42, 910-6	35
2111	Amino acid residues of <i>Escherichia coli</i> acyl carrier protein involved in heterologous protein interactions. 2003 , 42, 167-76	39
2110	Conformational dynamics of partially denatured myoglobin studied by time-resolved electrospray mass spectrometry with online hydrogen-deuterium exchange. 2003 , 42, 5896-905	52
2109	Zinc-mediated helix capping in a triple-helical protein. 2003 , 42, 5657-64	10
2108	Native state proline isomerization: an intrinsic molecular switch. 2003 , 42, 9515-24	218
2107	Structural characterization by NMR of the natively unfolded extracellular domain of beta-dystroglycan: toward the identification of the binding epitope for alpha-dystroglycan. 2003 , 42, 13717-24	14
2106	Side chain dynamics in unfolded protein states: an NMR based ² H spin relaxation study of delta ¹³ C. 2003 , 125, 1748-58	43
2105	A novel complexity measure for comparative analysis of protein sequences from complete genomes. 2003 , 20, 657-68	14
2104	Structural characterization of yeast acidic ribosomal P proteins forming the P1A-P2B heterocomplex. 2003 , 42, 3399-408	33
2103	Conformational behavior and aggregation of alpha-synuclein in organic solvents: modeling the effects of membranes. 2003 , 42, 2720-30	231
2102	Role of water mediated interactions in protein-protein recognition landscapes. 2003 , 125, 9170-8	158
2101	The binding of maize DHN1 to lipid vesicles. Gain of structure and lipid specificity. 2003 , 131, 309-16	276
2100	Conformation of a group 2 late embryogenesis abundant protein from soybean. Evidence of poly (L-proline)-type II structure. 2003 , 131, 963-75	101

2099	The N-terminal domain of p53 is natively unfolded. <i>Journal of Molecular Biology</i> , 2003 , 332, 1131-41	6.5	203
2098	Antibody multispecificity mediated by conformational diversity. 2003 , 299, 1362-7		605
2097	Volumetric properties of proteins. 2003 , 32, 207-35		273
2096	Computational simulation of the statistical properties of unfolded proteins. <i>Journal of Molecular Biology</i> , 2003 , 326, 1615-33	6.5	107
2095	Towards an understanding of the poliovirus replication complex: the solution structure of the soluble domain of the poliovirus 3A protein. <i>Journal of Molecular Biology</i> , 2003 , 330, 225-34	6.5	53
2094	Mutual induced fit binding of <i>Xenopus</i> ribosomal protein L5 to 5S rRNA. <i>Journal of Molecular Biology</i> , 2003 , 330, 979-92	6.5	34
2093	A protein-DNA binding mechanism proceeds through multi-state or two-state parallel pathways. <i>Journal of Molecular Biology</i> , 2003 , 331, 89-99	6.5	34
2092	<i>Thermotoga maritima</i> IscU. Structural characterization and dynamics of a new class of metallochaperone. <i>Journal of Molecular Biology</i> , 2003 , 331, 907-24	6.5	54
2091	Structural basis for recognition and catalysis by the bifunctional dCTP deaminase and dUTPase from <i>Methanococcus jannaschii</i> . <i>Journal of Molecular Biology</i> , 2003 , 331, 885-96	6.5	22
2090	Nitration inhibits fibrillation of human alpha-synuclein in vitro by formation of soluble oligomers. 2003 , 542, 147-52		132
2089	The PIR domain of Grb14 is an intrinsically unstructured protein: implication in insulin signaling. 2003 , 554, 240-6		19
2088	Are non-functional, unfolded proteins ('junk proteins') common in the genome?. 2003 , 554, 237-9		20
2087	Biochemical analysis of hyalin gelation: an essential step in the assembly of the sea urchin extraembryonic matrix, the hyaline layer. 2003 , 414, 279-86		3
2086	The small protein CP12: a protein linker for supramolecular complex assembly. 2003 , 42, 8163-70		95
2085	New insight into the solution structures of wheat gluten proteins from Raman optical activity. 2003 , 42, 5665-73		69
2084	Abstracts Albany 2003 The 13th Conversation. 2003 , 20, 829-958		
2083	The closely related estrogen-regulated trefoil proteins TFF1 and TFF3 have markedly different hydrodynamic properties, overall charge, and distribution of surface charge. 2003 , 42, 8250-9		28
2082	HMGA proteins: flexibility finds a nuclear niche?. 2003 , 81, 185-95		34

2081	GlobPlot: Exploring protein sequences for globularity and disorder. 2003 , 31, 3701-8	752
2080	NORSp: Predictions of long regions without regular secondary structure. 2003 , 31, 3833-5	107
2079	The oligomerization domain of VP3, the scaffolding protein of infectious bursal disease virus, plays a critical role in capsid assembly. 2003 , 77, 6438-49	61
2078	Structural disorder and modular organization in Paramyxovirinae N and P. 2003 , 84, 3239-3252	141
2077	Structural analysis of Bacillus subtilis SPP1 phage helicase loader protein G39P. 2003 , 278, 15304-12	9
2076	Isolation and characterization of T4 bacteriophage gp17 terminase, a large subunit multimer with enhanced ATPase activity. 2003 , 278, 4618-27	61
2075	Multiple sclerosis: an important role for post-translational modifications of myelin basic protein in pathogenesis. 2003 , 2, 453-62	144
2074	Recognition of the intrinsically flexible addiction antidote MazE by a dromedary single domain antibody fragment. Structure, thermodynamics of binding, stability, and influence on interactions with DNA. 2003 , 278, 14101-11	30
2073	Simulating disorder-order transitions in molecular recognition of unstructured proteins: where folding meets binding. 2003 , 100, 5148-53	95
2072	De novo designed cyclic-peptide heme complexes. 2003 , 100, 13140-5	45
2071	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
2070	The amino-terminal extensions of the longer Sendai virus C proteins modulate pY701-Stat1 and bulk Stat1 levels independently of interferon signaling. 2003 , 77, 2321-9	51
2069	Crystal structure of the intrinsically flexible addiction antidote MazE. 2003 , 278, 28252-7	99
2068	Extraordinarily slow binding of guanosine to the Tetrahymena group I ribozyme: implications for RNA preorganization and function. 2003 , 100, 2300-5	37
2067	Thermodynamics of the Op18/stathmin-tubulin interaction. 2003 , 278, 38926-34	38
2066	Cellular and behavioral effects of D2 dopamine receptor hydrophobic eigenmode-targeted peptide ligands. 2003 , 28 Suppl 1, S98-107	7
2065	Exploring the entire conformational space of proteins by high-pressure NMR. 2003 , 75, 927-936	37
2064	Thymosin beta 4 interactions. 2003 , 66, 297-316	14

2063	The androgen receptor transactivation domain: the interplay between protein conformation and protein-protein interactions. 2003 , 31, 1042-6	21
2062	Interactions of LC8 with N-terminal segments of the intermediate chain of cytoplasmic dynein. 2003 , 3, 647-54	5
2061	. 2004 ,	10
2060	Hydrogen-exchange strategies applied to energetics of intermediate processes in protein folding. 2004 , 380, 328-49	18
2059	HMGA proteins: multifaceted players in nuclear function. 2004 , 155-180	
2058	Coupled folding-binding versus docking: a lattice model study. 2004 , 120, 3983-9	20
2057	The role of structural disorder in the function of RNA and protein chaperones. 2004 , 18, 1169-75	456
2056	Bioinformatics for Geneticists. 2004 , 5, 209-210	
2055	Protein Structure Prediction: Bioinformatics Approach. 2004 , 5, 207-209	
2054	Interaction of SDS with Na ⁺ /K ⁺ -ATPase: SDS-solubilized enzyme retains partial structure and function. 2004 , 279, 29832-40	11
2053	Disorder in a target for the smad2 mad homology 2 domain and its implications for binding and specificity. 2004 , 279, 40707-14	19
2052	Coupling of folding and binding of thymosin beta4 upon interaction with monomeric actin monitored by nuclear magnetic resonance. 2004 , 279, 23637-45	81
2051	The structural basis of the TIM10 chaperone assembly. 2004 , 279, 18959-66	50
2050	TC-1 is a novel tumorigenic and natively disordered protein associated with thyroid cancer. 2004 , 64, 2766-73	59
2049	Novel membrane protein shrew-1 targets to cadherin-mediated junctions in polarized epithelial cells. 2004 , 15, 397-406	37
2048	Identifying DNA-binding proteins using structural motifs and the electrostatic potential. 2004 , 32, 4732-41	87
2047	Emergence of new regulatory mechanisms in the Benson-Calvin pathway via protein-protein interactions: a glyceraldehyde-3-phosphate dehydrogenase/CP12/phosphoribulokinase complex. 2004 , 55, 1245-54	96
2046	Rapid refinement of crystallographic protein construct definition employing enhanced hydrogen/deuterium exchange MS. 2004 , 101, 751-6	137

2045	Novel sensors of the regulatory switch on the regulatory light chain of smooth muscle Myosin. 2004 , 279, 39905-14	19
2044	Comparative analysis of protein unfoldedness in human housekeeping and non-housekeeping proteins. 2004 , 20, 2904-10	17
2043	Human septin-septin interactions as a prerequisite for targeting septin complexes in the cytosol. 2004 , 382, 783-91	42
2042	Preferred peptide backbone conformations in the unfolded state revealed by the structure analysis of alanine-based (AXA) tripeptides in aqueous solution. 2004 , 101, 10054-9	106
2041	Integrating folding kinetics and protein function: biphasic kinetics and dual binding specificity in a WW domain. 2004 , 101, 3432-7	61
2040	High affinity streptococcal binding to human fibronectin requires specific recognition of sequential F1 modules. 2004 , 279, 39017-25	56
2039	Identification of specific functional subdomains within the linker histone H10 C-terminal domain. 2004 , 279, 8701-7	107
2038	Reformable intramolecular cross-linking of the N-terminal domain of heparin cofactor II: effects on enzyme inhibition. 2004 , 271, 4275-83	11
2037	The molecular basis of fibronectin-mediated bacterial adherence to host cells. 2004 , 52, 631-41	214
2036	Structural characterization of the human Nogo-A functional domains. Solution structure of Nogo-40, a Nogo-66 receptor antagonist enhancing injured spinal cord regeneration. 2004 , 271, 3512-22	15
2035	Regulation of the c-Abl and Bcr-Abl tyrosine kinases. 2004 , 5, 33-44	380
2034	Natively unfolded domains in endocytosis: hooks, lines and linkers. 2004 , 5, 1046-52	70
2033	Long live structural biology. 2004 , 11, 293-5	25
2032	p27 binds cyclin-CDK complexes through a sequential mechanism involving binding-induced protein folding. 2004 , 11, 358-64	250
2031	The solution structure of type III effector protein AvrPto reveals conformational and dynamic features important for plant pathogenesis. 2004 , 12, 1257-68	43
2030	Combining prediction, computation and experiment for the characterization of protein disorder. 2004 , 14, 570-6	113
2029	Protein flexibility and intrinsic disorder. 2004 , 13, 71-80	269
2028	The C-terminal domain of full-length E. coli SSB is disordered even when bound to DNA. 2004 , 13, 1942-7	115

2027	The effect of an ionic detergent on the natively unfolded beta-dystroglycan ectodomain and on its interaction with alpha-dystroglycan. 2004 , 13, 2437-45	5
2026	A mobile loop order-disorder transition modulates the speed of chaperonin cycling. 2004 , 13, 2139-48	16
2025	Modelling of third cytoplasmic loop of bovine rhodopsin by multicanonical molecular dynamics. 2004 , 23, 59-68	7
2024	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
2023	Antibodies as specific chaperones. 2004 , 69, 1233-8	16
2022	Protein NMR in biomedical research. 2004 , 61, 580-599	60
2021	Automatic target selection for structural genomics on eukaryotes. 2004 , 56, 188-200	58
2020	Sequence patterns associated with disordered regions in proteins. 2005 , 58, 144-50	61
2019	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
2018	The ribbon of hydrogen bonds in globular proteins. IV. The example of the papain family. 2004 , 73, 178-91	
2017	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
2016	Structural biology of hepatitis C virus. 2004 , 39, 5-19	495
2015	Rifampicin inhibits alpha-synuclein fibrillation and disaggregates fibrils. 2004 , 11, 1513-21	176
2014	Conformational constraints for amyloid fibrillation: the importance of being unfolded. 2004 , 1698, 131-53	817
2013	Charge sequence coding in statistical modeling of unfolded proteins. 2004 , 1702, 1-8	6
2012	2003 Fred Beamish Award Lecture ? Exploring the dynamics of biological systems by mass spectrometry. 2004 , 82, 1565-1580	2
2011	Design and characterization of helical peptides that inhibit the E6 protein of papillomavirus. 2004 , 43, 7421-31	63
2010	Toward an integrated model of protein-DNA recognition as inferred from NMR studies on the Lac repressor system. 2004 , 104, 3567-86	65

2009	Tripeptides with ionizable side chains adopt a perturbed polyproline II structure in water. 2004 , 43, 613-21	65
2008	The LEF-1 high-mobility group domain undergoes a disorder-to-order transition upon formation of a complex with cognate DNA. 2004 , 43, 8725-34	57
2007	Yeast cox17 solution structure and Copper(I) binding. 2004 , 279, 53584-92	91
2006	The bZIP region of the plant transcription factor opaque-2 forms stable homodimers in solution and retains its helical structure upon subunit dissociation. 2004 , 43, 4862-8	12
2005	Forced folding and structural analysis of metastable proteins. 2004 , 126, 9498-9	64
2004	Crystal structures of the catalytic domains of pseudouridine synthases RluC and RluD from Escherichia coli. 2004 , 43, 4454-63	23
2003	IA3, an aspartic proteinase inhibitor from Saccharomyces cerevisiae, is intrinsically unstructured in solution. 2004 , 43, 4071-81	31
2002	Limited proteolysis of human growth hormone at low pH: isolation, characterization, and complementation of the two biologically relevant fragments 1-44 and 45-191. 2004 , 43, 6576-86	25
2001	Charge and hydrophobicity patterning along the sequence predicts the folding mechanism and aggregation of proteins: a computational approach. 2004 , 3, 1243-53	42
2000	The N-terminal domain of the Drosophila histone mRNA binding protein, SLBP, is intrinsically disordered with nascent helical structure. 2004 , 43, 9390-400	17
1999	Myelin basic protein?diverse conformational states of an intrinsically unstructured protein and its roles in myelin assembly and multiple sclerosis. 2004 ,	
1998	Overview of protein structural and functional folds. 2004 , Chapter 17, Unit 17.1	6
1997	Unfolded proteins and protein folding studied by NMR. 2004 , 104, 3607-22	541
1996	Helix formation and the unfolded state of a 52-residue helical protein. 2004 , 13, 177-89	18
1995	Modulation of the structural integrity of helix F in apomyoglobin by single amino acid replacements. 2004 , 13, 1572-85	27
1994	Energy Landscape Analysis of Protein Dimers. 2004 , 44, 281-297	18
1993	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
1992	Kinetics of protein-DNA interaction: facilitated target location in sequence-dependent potential. 2004 , 87, 4021-35	415

1991	Natively disordered proteins: functions and predictions. 2004 , 3, 105-13		117
1990	Membrane localization and flexibility of a lipidated ras peptide studied by molecular dynamics simulations. 2004 , 126, 15277-86		64
1989	Automated protein structure homology modeling: a progress report. 2004 , 5, 405-16		93
1988	Reduced amino acid alphabet is sufficient to accurately recognize intrinsically disordered protein. 2004 , 576, 348-52		102
1987	Biophysical characterization of Gir2, a highly acidic protein of <i>Saccharomyces cerevisiae</i> with anomalous electrophoretic behavior. 2004 , 314, 229-34		32
1986	The C-terminal domain of measles virus nucleoprotein belongs to the class of intrinsically disordered proteins that fold upon binding to their physiological partner. 2004 , 99, 157-67		139
1985	Computational methods for generating models of denatured and partially folded proteins. 2004 , 34, 144-50		16
1984	Mining the structural genomics pipeline: identification of protein properties that affect high-throughput experimental analysis. <i>Journal of Molecular Biology</i> , 2004 , 336, 115-30	6.5	126
1983	Prediction and functional analysis of native disorder in proteins from the three kingdoms of life. <i>Journal of Molecular Biology</i> , 2004 , 337, 635-45	6.5	1625
1982	Distinct properties of the two putative "globular domains" of the yeast linker histone, Hho1p. <i>Journal of Molecular Biology</i> , 2004 , 337, 1123-35	6.5	19
1981	Preformed structural elements feature in partner recognition by intrinsically unstructured proteins. <i>Journal of Molecular Biology</i> , 2004 , 338, 1015-26	6.5	448
1980	Surface-decoration of microtubules by human tau. <i>Journal of Molecular Biology</i> , 2004 , 339, 539-53	6.5	109
1979	Conformational flexibility in recombinant measles virus nucleocapsids visualised by cryo-negative stain electron microscopy and real-space helical reconstruction. <i>Journal of Molecular Biology</i> , 2004 , 340, 319-31	6.5	80
1978	Structural characterization of unfolded states of apomyoglobin using residual dipolar couplings. <i>Journal of Molecular Biology</i> , 2004 , 340, 1131-42	6.5	157
1977	Estimating the prevalence of protein sequences adopting functional enzyme folds. <i>Journal of Molecular Biology</i> , 2004 , 341, 1295-315	6.5	36
1976	Analysis of ordered and disordered protein complexes reveals structural features discriminating between stable and unstable monomers. <i>Journal of Molecular Biology</i> , 2004 , 341, 1327-41	6.5	144
1975	DNA binding and bending by HMG boxes: energetic determinants of specificity. <i>Journal of Molecular Biology</i> , 2004 , 343, 371-93	6.5	102
1974	Raman optical activity demonstrates poly(L-proline) II helix in the N-terminal region of the ovine prion protein: implications for function and misfunction. <i>Journal of Molecular Biology</i> , 2004 , 343, 467-76	6.5	69

1973	Solution structure and heparin interaction of human hepatoma-derived growth factor. <i>Journal of Molecular Biology</i> , 2004 , 343, 1365-77	6.5	42
1972	Bacteriophage T4: structure, assembly, and initiation infection studied in three dimensions. 2004 , 63, 287-352		12
1971	An evolution of minimalist models for protein folding: from the behavior of protein-like polymers to protein function. 2004 , 2, 127-133		
1970	Tau paired helical filaments from Alzheimer's disease brain and assembled in vitro are based on beta-structure in the core domain. 2004 , 43, 1694-703		172
1969	Role of protein-water interactions and electrostatics in alpha-synuclein fibril formation. 2004 , 43, 3289-300		170
1968	The importance of intrinsic disorder for protein phosphorylation. 2004 , 32, 1037-49		1043
1967	Designing human m1 muscarinic receptor-targeted hydrophobic eigenmode matched peptides as functional modulators. 2004 , 86, 1308-31		6
1966	Conformation of prion protein repeat peptides probed by FRET measurements and molecular dynamics simulations. 2004 , 86, 2467-83		55
1965	Deriving Function From Structure. 2005 , 801-829		1
1964	Studying Protein Folding and Aggregation by Laser Light Scattering. 673-709		8
1963	Prediction in 1D: Secondary Structure, Membrane Helices, and Accessibility. 2005 , 559-587		7
1962	Challenges in NMR-based structural genomics. 2005 , 350, 12-27		7
1961	Dynamical binding of proline-rich peptides to their recognition domains. 2005 , 1754, 232-8		14
1960	Compensating increases in protein backbone flexibility occur when the Dead ringer AT-rich interaction domain (ARID) binds DNA: a nitrogen-15 relaxation study. 2005 , 14, 1140-50		6
1959	Stability of HAMLET--a kinetically trapped alpha-lactalbumin oleic acid complex. 2005 , 14, 329-40		55
1958	Urea-induced denaturation of apolipoprotein serum amyloid A reveals marginal stability of hexamer. 2005 , 14, 1811-7		13
1957	The intrinsically disordered C-terminal domain of the measles virus nucleoprotein interacts with the C-terminal domain of the phosphoprotein via two distinct sites and remains predominantly unfolded. 2005 , 14, 1975-92		125
1956	What is the biological significance of the brain-specific tubulin-polymerization promoting protein (TPPP/p25)?. 2005 , 57, 765-8		7

1955	The histone H1 C-terminal domain binds to the apoptotic nuclease, DNA fragmentation factor (DFF40/CAD) and stimulates DNA cleavage. 2005 , 44, 7871-8	52
1954	Computational Methods for Predicting Protein-Protein Interactions. 2005 , 89-114	2
1953	Intrinsically unstructured proteins and their functions. 2005 , 6, 197-208	2985
1952	EspB from enterohaemorrhagic Escherichia coli is a natively partially folded protein. 2005 , 272, 756-68	18
1951	Protein dissection enhances the amyloidogenic properties of alpha-lactalbumin. 2005 , 272, 2176-88	32
1950	Flexible nets. The roles of intrinsic disorder in protein interaction networks. 2005 , 272, 5129-48	895
1949	Structural disorder throws new light on moonlighting. 2005 , 30, 484-9	381
1948	Natively unfolded proteins. 2005 , 15, 35-41	612
1947	SQ/TQ cluster domains: concentrated ATM/ATR kinase phosphorylation site regions in DNA-damage-response proteins. 2005 , 27, 397-407	151
1946	Computational Analysis of Modular Protein Architectures. 2005 , 439-476	2
1945	Showing your ID: intrinsic disorder as an ID for recognition, regulation and cell signaling. 2005 , 18, 343-84	660
1944	Solution NMR studies of an intrinsically unstructured protein within a dilute, 75 kDa eukaryotic protein assembly; probing the practical limits for efficiently assigning polypeptide backbone resonances. 2005 , 6, 2242-6	13
1943	Disordered RNA chaperone proteins: from functions to disease. 2005 , 62, 1409-17	64
1942	NMR of unfolded proteins. 2005 , 117, 3-21	13
1941	Describing partially unfolded states of proteins from sparse NMR data. 2005 , 33, 175-86	16
1940	Accurate Prediction of Protein Disordered Regions by Mining Protein Structure Data. 2005 , 11, 213-222	163
1939	Structure of Mycobacterium smegmatis single-stranded DNA-binding protein and a comparative study involving homologous SSBs: biological implications of structural plasticity and variability in quaternary association. 2005 , 61, 1140-8	28
1938	A C-terminal segment of the V1R vasopressin receptor is unstructured in the crystal structure of its chimera with the maltose-binding protein. 2005 , 61, 341-5	9

1937	Comparison of cell-based and cell-free protocols for producing target proteins from the <i>Arabidopsis thaliana</i> genome for structural studies. 2005 , 59, 633-43	52
1936	Addressing the intrinsic disorder bottleneck in structural proteomics. 2005 , 59, 444-53	69
1935	Protein flexibility and rigidity predicted from sequence. 2005 , 61, 115-26	129
1934	Origin of the sequence-dependent polyproline II structure in unfolded peptides. 2005 , 61, 769-76	15
1933	Exploiting heterogeneous sequence properties improves prediction of protein disorder. 2005 , 61 Suppl 7, 176-82	423
1932	Intrinsic unstructuredness and abundance of PEST motifs in eukaryotic proteomes. 2006 , 62, 309-15	79
1931	Assessing protein disorder and induced folding. 2006 , 62, 24-45	347
1930	Natively unfolded regions of the vertebrate fibrinogen molecule. 2006 , 63, 391-7	30
1929	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
1928	Efficient synthesis and comparative studies of the arginine and Nomega,Nomega-dimethylarginine forms of the human nucleolin glycine/arginine rich domain. 2005 , 11, 17-28	25
1927	Early-stage folding in proteins (in silico) sequence-to-structure relation. 2005 , 2005, 65-79	16
1926	Conformation and Dynamics of Nonnative States of Proteins studied by NMR Spectroscopy. 737-808	5
1925	The Life Cycle of P53: A Key Target in Drug Development. 2005 , 157-172	2
1924	Significance of the first transcribed nucleoside of capped RNA for ligand-induced folding of the cap-binding complex. 2005 , 17, S1495-S1502	
1923	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	
1922	The native metastability and misfolding of serine protease inhibitors. 2005 , 12, 477-81	7
1921	FoldIndex: a simple tool to predict whether a given protein sequence is intrinsically unfolded. 2005 , 21, 3435-8	776
1920	Correlation between evolutionary structural development and protein folding. 2005 , 102, 18950-5	15

1919	Predicted and measured disorder in peripherin/rds, a retinal tetraspanin. 2005 , 12, 677-86	22
1918	High solubility of random-sequence proteins consisting of five kinds of primitive amino acids. 2005 , 18, 279-84	58
1917	G protein-coupled receptors show unusual patterns of intrinsic unfolding. 2005 , 18, 103-10	40
1916	Variable control of Ets-1 DNA binding by multiple phosphates in an unstructured region. 2005 , 309, 142-5	204
1915	Heme binding by the N-terminal fragment 1-44 of human growth hormone. 2005 , 44, 16079-89	8
1914	Single-molecule study of protein-protein and protein-DNA interaction dynamics. 2005 , 305, 385-414	7
1913	NMR chemical shift and relaxation measurements provide evidence for the coupled folding and binding of the p53 transactivation domain. 2005 , 33, 2061-77	75
1912	Multiple time scale dynamics of distance fluctuations in a semiflexible polymer: a one-dimensional generalized Langevin equation treatment. 2005 , 123, 204903	37
1911	Optimizing long intrinsic disorder predictors with protein evolutionary information. 2005 , 3, 35-60	346
1910	FrankSum: new feature selection method for protein function prediction. 2005 , 15, 259-75	24
1909	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
1908	How to Use Protein 1- D Structure Predicted by PROFphd. 2005 , 875-901	14
1907	Interactions of TolB with the translocation domain of colicin E9 require an extended TolB box. 2005 , 187, 6733-41	25
1906	Proteomics and Protein-Protein Interactions. 2005 ,	10
1905	Common effects of acidic activators on large-scale chromatin structure and transcription. 2005 , 25, 958-68	56
1904	Biochemical and NMR mapping of the interface between CREB-binding protein and ligand binding domains of nuclear receptor: beyond the LXXLL motif. 2005 , 280, 5682-92	15
1903	Characterization of wild-type recombinant Bet v 1a as a candidate vaccine against birch pollen allergy. 2005 , 136, 239-49	45
1902	DisProt: a database of protein disorder. 2005 , 21, 137-40	205

1901	Nonlinear protein degradation and the function of genetic circuits. 2005 , 102, 9559-64	138
1900	Structure and kinetics of a transient antibody binding intermediate reveal a kinetic discrimination mechanism in antigen recognition. 2005 , 102, 12730-5	81
1899	CaSPredictor: a new computer-based tool for caspase substrate prediction. 2005 , 21 Suppl 1, i169-76	47
1898	The Proteomics Protocols Handbook. 2005 ,	204
1897	Identification and characterization of tandem repeats in exon III of dopamine receptor D4 (DRD4) genes from different mammalian species. 2005 , 24, 795-804	10
1896	Essential amino acids of the hantaan virus N protein in its interaction with RNA. 2005 , 79, 10032-9	40
1895	Feature Selection Based on Physicochemical Properties of Redefined N-term Region and C-term Regions for Predicting Disorder. 2005 ,	1
1894	Intracellularly truncated human alpha2B-adrenoceptors: stable and functional GPCRs for structural studies. 2005 , 25, 99-124	3
1893	Histone structure and nucleosome stability. 2005 , 2, 719-29	179
1892	Clusters in an intrinsically disordered protein create a protein-binding site: the TolB-binding region of colicin E9. 2005 , 44, 11496-507	24
1891	Nature of the cytochrome c molten globule. 2005 , 127, 15370-1	28
1890	Structural properties of the promiscuous VP16 activation domain. 2005 , 44, 827-39	57
1889	A Neural Network for Predicting Protein Disorder using Amino Acid Hydropathy Values. 2005 ,	1
1888	Secondary structure and dynamics of an intrinsically unstructured linker domain. 2005 , 23, 113-24	19
1887	Statistical studies of flexible nonhomogeneous polypeptide chains. 2005 , 6, 3010-7	
1886	Primary contact sites in intrinsically unstructured proteins: the case of calpastatin and microtubule-associated protein 2. 2005 , 44, 3955-64	88
1885	Reversible dimerization of acid-denatured ACBP controlled by helix A4. 2005 , 44, 1375-84	15
1884	A structural model for unfolded proteins from residual dipolar couplings and small-angle x-ray scattering. 2005 , 102, 17002-7	357

1883	Probing single-molecule protein conformational dynamics. 2005 , 38, 557-65		81
1882	The preferred conformation of the tripeptide Ala-Phe-Ala in water is an inverse gamma-turn: implications for protein folding and drug design. 2005 , 44, 14170-8		34
1881	Thermodynamic characterization of the osmolyte- and ligand-folded states of Bacillus subtilis ribonuclease P protein. 2005 , 44, 13014-26		12
1880	Alternative binding modes of proline-rich peptides binding to the GYF domain. 2005 , 44, 6404-15		9
1879	New reverse micelle surfactant systems optimized for high-resolution NMR spectroscopy of encapsulated proteins. 2005 , 21, 10632-7		24
1878	Thermodynamics of a protein acylation: activation of Escherichia coli hemolysin toxin. 2005 , 44, 1329-37		10
1877	Reconciling observations of sequence-specific conformational propensities with the generic polymeric behavior of denatured proteins. 2005 , 44, 11369-80		90
1876	Protein Structural Flexibility: Molecular Motions. 2005 ,		
1875	Induced alpha-helix structure in the aryl hydrocarbon receptor transactivation domain modulates protein-protein interactions. 2005 , 44, 734-43		22
1874	Characterization of segments from the central region of BRCA1: an intrinsically disordered scaffold for multiple protein-protein and protein-DNA interactions?. <i>Journal of Molecular Biology</i> , 2005 , 345, 275-87	6.5	141
1873	N and C-terminal sub-regions in the c-Myc transactivation region and their joint role in creating versatility in folding and binding. <i>Journal of Molecular Biology</i> , 2005 , 346, 175-89	6.5	23
1872	Molecular recognition via coupled folding and binding in a TPR domain. <i>Journal of Molecular Biology</i> , 2005 , 346, 717-32	6.5	79
1871	The pairwise energy content estimated from amino acid composition discriminates between folded and intrinsically unstructured proteins. <i>Journal of Molecular Biology</i> , 2005 , 347, 827-39	6.5	767
1870	Evidence for structural plasticity of heavy chain complementarity-determining region 3 in antibody-ssDNA recognition. <i>Journal of Molecular Biology</i> , 2005 , 347, 965-78	6.5	25
1869	The GB1 amyloid fibril: recruitment of the peripheral beta-strands of the domain swapped dimer into the polymeric interface. <i>Journal of Molecular Biology</i> , 2005 , 348, 687-98	6.5	39
1868	Molecular basis for the specificity of p27 toward cyclin-dependent kinases that regulate cell division. <i>Journal of Molecular Biology</i> , 2005 , 349, 764-73	6.5	58
1867	Disordered p27Kip1 exhibits intrinsic structure resembling the Cdk2/cyclin A-bound conformation. <i>Journal of Molecular Biology</i> , 2005 , 353, 1118-28	6.5	90
1866	Binding of natively unfolded HIF-1alpha ODD domain to p53. 2005 , 17, 11-21		85

1865	Tau aggregation is driven by a transition from random coil to beta sheet structure. 2005 , 1739, 158-66	249
1864	Gir2 is an intrinsically unstructured protein that is present in <i>Saccharomyces cerevisiae</i> as a group of heterogeneously electrophoretic migrating forms. 2005 , 332, 450-5	15
1863	Acid- and pressure-induced (un)folding of yeast glutathione reductase: competition between protein oligomerization and aggregation. 2005 , 37, 1890-9	4
1862	The interplay between structure and function in intrinsically unstructured proteins. 2005 , 579, 3346-54	563
1861	Expression and characterization of N-terminal domain of Epstein-Barr virus latent membrane protein 2A in <i>Escherichia coli</i> . 2005 , 41, 9-17	3
1860	Aggregation as bacterial inclusion bodies does not imply inactivation of enzymes and fluorescent proteins. 2005 , 4, 27	217
1859	Protein disorder: conformational distribution of the flexible linker in a chimeric double cellulase. 2005 , 88, 2823-32	72
1858	NMR relaxation studies on the hydrate layer of intrinsically unstructured proteins. 2005 , 88, 2030-7	72
1857	Potentials of mean force for the interaction of blocked alanine dipeptide molecules in water and gas phase from MD simulations. 2005 , 89, 1433-45	11
1856	Probing conformational disorder in neurotensin by two-dimensional solid-state NMR and comparison to molecular dynamics simulations. 2005 , 89, 2113-20	46
1855	pH dependence of amide chemical shifts in natively disordered polypeptides detects medium-range interactions with ionizable residues. 2005 , 89, 3293-302	15
1854	Pathways to Amyloid Fibril Formation: Partially Folded Intermediates in the Fibrillation of Natively Unfolded Proteins. 246-273	1
1853	Structural details on mdm2-p53 interaction. 2005 , 280, 38795-802	109
1852	Comparing and combining predictors of mostly disordered proteins. 2005 , 44, 1989-2000	416
1851	Rapid assessment of protein structural stability and fold validation via NMR. 2005 , 394, 142-75	16
1850	Natively Disordered Proteins. 275-357	54
1849	Tertiary contact formation in alpha-synuclein probed by electron transfer. 2005 , 127, 16388-9	61
1848	Stability and DNA binding ability of the DNA binding domains of interferon regulatory factors 1 and 3. 2005 , 44, 14202-9	13

1847	Uncovering the unfoldome: enriching cell extracts for unstructured proteins by acid treatment. 2005 , 4, 1610-8	59
1846	Coupled folding and binding with alpha-helix-forming molecular recognition elements. 2005 , 44, 12454-70	541
1845	Flexible peptides and cytoplasmic gels. 2005 , 6, 106	5
1844	Conformation of the backbone in unfolded proteins. 2006 , 106, 1877-97	229
1843	Disorder and sequence repeats in hub proteins and their implications for network evolution. 2006 , 5, 2985-95	273
1842	Abundance of intrinsic disorder in protein associated with cardiovascular disease. 2006 , 45, 10448-60	152
1841	Surface adhesins of Staphylococcus aureus. 2006 , 51, 187-224	197
1840	The role of protein dynamics in increasing binding affinity for an engineered protein-protein interaction established by H/D exchange mass spectrometry. 2006 , 45, 8488-98	33
1839	Intrinsic disorder in transcription factors. 2006 , 45, 6873-88	518
1838	Structural and Conformational Prerequisites of Amyloidogenesis. 2006 , 1-20	4
1837	Coupling ligand recognition to protein folding in an engineered variant of rabbit ileal lipid binding protein. 2006 , 4623-5	14
1836	The intrinsically unstructured domain of PC4 modulates the activity of the structured core through inter- and intramolecular interactions. 2006 , 45, 5067-81	18
1835	FoldUnfold: web server for the prediction of disordered regions in protein chain. 2006 , 22, 2948-9	124
1834	Intrinsically disordered C-terminal segments of voltage-activated potassium channels: a possible fishing rod-like mechanism for channel binding to scaffold proteins. 2006 , 22, 1546-50	32
1833	sgTarget: a target selection resource for structural genomics. 2006 , 34, W225-30	4
1832	Long-lived conformational isomerism of protein dimers: the role of the free energy of subunit association. 2006 , 91, 2826-32	6
1831	Tubulin polymerization promoting proteins (TPPPs): members of a new family with distinct structures and functions. 2006 , 45, 13818-26	72
1830	Protein intrinsic disorder and human papillomaviruses: increased amount of disorder in E6 and E7 oncoproteins from high risk HPVs. 2006 , 5, 1829-42	117

1829	New Views of Protein Structure: Implications for Potential New Protein Structure-Function Relationships. 2006 , 1-18		1
1828	Proteomic studies of the intrinsically unstructured mammalian proteome. 2006 , 5, 2839-48		57
1827	Alpha-synuclein structures probed by 5-fluorotryptophan fluorescence and 19F NMR spectroscopy. 2006 , 110, 7058-61		29
1826	Conservation of intrinsic disorder in protein domains and families: II. functions of conserved disorder. 2006 , 5, 888-98		107
1825	Absolute net charge and the biological activity of oligopeptides. 2006 , 46, 2183-90		4
1824	Configurational entropies of lipids in pure and mixed bilayers from atomic-level and coarse-grained molecular dynamics simulations. 2006 , 110, 15602-14		55
1823	Prevalent structural disorder in E. coli and S. cerevisiae proteomes. 2006 , 5, 1996-2000		102
1822	The DNA-binding domain of the ultraspiracle drives deformation of the response element whereas the DNA-binding domain of the ecdysone receptor is responsible for a slight additional change of the preformed structure. 2006 , 45, 668-75		9
1821	Micelle-induced folding of spinach thylakoid soluble phosphoprotein of 9 kDa and its functional implications. 2006 , 45, 15633-43		14
1820	Determinants of specificity of MDM2 for the activation domains of p53 and p65: proline27 disrupts the MDM2-binding motif of p53. 2006 , 45, 11945-57		63
1819	Conservation of intrinsic disorder in protein domains and families: I. A database of conserved predicted disordered regions. 2006 , 5, 879-87		99
1818	Disordered domains and high surface charge confer hubs with the ability to interact with multiple proteins in interaction networks. 2006 , 580, 2041-5		217
1817	Hyperphosphorylation of tau induces local polyproline II helix. 2006 , 45, 5527-37		71
1816	Intrinsically disordered loops inserted into the structural domains of human proteins. <i>Journal of Molecular Biology</i> , 2006 , 355, 845-57	6.5	29
1815	The denatured state under native conditions: a non-native-like collapsed state of N-PGK. <i>Journal of Molecular Biology</i> , 2006 , 357, 365-72	6.5	25
1814	Characterization of intra-molecular distances and site-specific dynamics in chemically unfolded barstar: evidence for denaturant-dependent non-random structure. <i>Journal of Molecular Biology</i> , 2006 , 359, 174-89	6.5	37
1813	Tetramerization of the LexA repressor in solution: implications for gene regulation of the E.coli SOS system at acidic pH. <i>Journal of Molecular Biology</i> , 2006 , 359, 1059-74	6.5	22
1812	Human transcription factors contain a high fraction of intrinsically disordered regions essential for transcriptional regulation. <i>Journal of Molecular Biology</i> , 2006 , 359, 1137-49	6.5	206

1811	Analysis of molecular recognition features (MoRFs). <i>Journal of Molecular Biology</i> , 2006 , 362, 1043-59	6.5	579
1810	Binding-induced stabilization and assembly of the phage P22 tail accessory factor gp4. <i>Journal of Molecular Biology</i> , 2006 , 363, 558-76	6.5	41
1809	Early protein evolution: building domains from ligand-binding polypeptide segments. <i>Journal of Molecular Biology</i> , 2006 , 363, 460-8	6.5	36
1808	Delineation of protein structure classes from multivariate analysis of protein Raman optical activity data. <i>Journal of Molecular Biology</i> , 2006 , 363, 19-26	6.5	51
1807	Characterisation of the conformational properties of urea-unfolded Im7: implications for the early stages of protein folding. <i>Journal of Molecular Biology</i> , 2006 , 364, 824-35	6.5	38
1806	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
1805	RACK1 has the nerve to act: structure meets function in the nervous system. 2006 , 78, 117-34		108
1804	Molecular biology of the morbilliviruses. 2006 , 31-IV		9
1803	The human androgen receptor AF1 transactivation domain: interactions with transcription factor IIF and molten-globule-like structural characteristics. 2006 , 34, 1054-7		28
1802	Functionality and the Evolution of Marginal Stability in Proteins: Inferences from Lattice Simulations. 2006 , 2, 117693430600200		21
1801	Metallothioneins Based in part on the article Metallothioneins by Milan Vař & Jeremias H. R. Kři which appeared in the Encyclopedia of Inorganic Chemistry, First Edition.. 2006 ,		
1800	Honing the in silico toolkit for detecting protein disorder. 2006 , 62, 1260-6		22
1799	Entropy capacity determines protein folding. 2006 , 63, 144-54		24
1798	Calmodulin signaling: analysis and prediction of a disorder-dependent molecular recognition. 2006 , 63, 398-410		86
1797	Intrinsic disorder is a key characteristic in partners that bind 14-3-3 proteins. 2006 , 63, 35-42		87
1796	Role of lysine versus arginine in enzyme cold-adaptation: modifying lysine to homo-arginine stabilizes the cold-adapted alpha-amylase from <i>Pseudoalteromonas haloplanktis</i> . 2006 , 64, 486-501		55
1795	Phosphorylation-induced transient intrinsic structure in the kinase-inducible domain of CREB facilitates its recognition by the KIX domain of CBP. 2006 , 64, 749-57		27
1794	Insights into protein structure and function from disorder-complexity space. 2007 , 66, 16-28		18

1793	Intrinsically unstructured N-terminal domain of bZIP transcription factor HY5. 2006 , 65, 856-66	28
1792	Prediction of peptide structure: how far are we?. 2006 , 65, 889-97	54
1791	Role of intrinsic disorder in transient interactions of hub proteins. 2007 , 66, 761-5	127
1790	Antioxidant compounds have potent anti-fibrillogenic and fibril-destabilizing effects for alpha-synuclein fibrils in vitro. 2006 , 97, 105-15	252
1789	Multilateral in vivo and in vitro protective effects of the novel heat shock protein coinducer, bimoclomol: results of preclinical studies. 2001 , 19, 133-51	33
1788	Optimal ratio between the average conformational entropy and the average energy of interaction between residues for fast protein folding. 2006 , 51, 554-564	
1787	Prediction of natively unfolded regions in protein chains. 2006 , 40, 298-304	18
1786	Coexistence of two protein folding states in the crystal structure of ribosomal protein L20. 2006 , 7, 1013-8	22
1785	Alzheimer's-disease-associated conformation of intrinsically disordered tau protein studied by intrinsically disordered protein liquid-phase competitive enzyme-linked immunosorbent assay. 2006 , 359, 230-7	14
1784	Unraveling the nature of the segmentation clock: Intrinsic disorder of clock proteins and their interaction map. 2006 , 30, 241-8	12
1783	Thermodynamic characterization of interactions between p27(Kip1) and activated and non-activated Cdk2: intrinsically unstructured proteins as thermodynamic tethers. 2006 , 1764, 182-9	25
1782	Comparative analysis of polyphenol oxidase from plant and fungal species. 2006 , 100, 108-23	177
1781	Advances in vibrational spectroscopy as a sensitive probe of peptide and protein structure. 2006 , 42, 98-117	130
1780	The Unfolded Protein State Revisited. 2006 , 235-252	2
1779	According to current textbooks, a well-defined three-dimensional structure is a prerequisite for the function of a protein. Is this correct?. 2006 , 58, 107-9	18
1778	Hydrogen/deuterium-exchange (H/D-Ex) of PPARgamma LBD in the presence of various modulators. 2006 , 15, 1883-92	97
1777	Nm23-H1/NDP kinase folding intermediates and cancer: a hypothesis. 2006 , 38, 265-8	5
1776	The 'interactome' of the Knr4/Smi1, a protein implicated in coordinating cell wall synthesis with bud emergence in <i>Saccharomyces cerevisiae</i> . 2006 , 275, 217-30	28

1775	Structural disorder within the replicative complex of measles virus: functional implications. 2006 , 344, 94-110	81
1774	Apolipoprotein E structure: insights into function. 2006 , 31, 445-54	397
1773	Length-dependent prediction of protein intrinsic disorder. 2006 , 7, 208	630
1772	Protein disorder prediction by condensed PSSM considering propensity for order or disorder. 2006 , 7, 319	78
1771	Carbohydrate chain of ganglioside GM1 as a ligand: identification of the binding strategies of three 15 mer peptides and their divergence from the binding modes of growth-regulatory galectin-1 and cholera toxin. 2005 , 12, 388-402	31
1770	A weakly clustered N terminus inhibits Abeta(1-40) amyloidogenesis. 2006 , 7, 1662-6	11
1769	Nanoimaging for protein misfolding and related diseases. 2006 , 99, 52-70	39
1768	Identification and characterization of homologues of vertebrate beta-thymosin in the marine mollusk <i>Aplysia californica</i> . 2006 , 41, 1030-40	24
1767	p53 transcriptional activation domain: a molecular chameleon?. 2006 , 5, 489-94	30
1766	PROFbval: predict flexible and rigid residues in proteins. 2006 , 22, 891-3	117
1765	Serine/arginine-rich splicing factors belong to a class of intrinsically disordered proteins. 2006 , 34, 305-12	87
1764	Progesterone receptors (PR)-B and -A regulate transcription by different mechanisms: AF-3 exerts regulatory control over coactivator binding to PR-B. 2006 , 20, 2656-70	74
1763	p8 and prothymosin alpha: unity is strength. 2006 , 5, 829-30	15
1762	Spritz: a server for the prediction of intrinsically disordered regions in protein sequences using kernel machines. 2006 , 34, W164-8	108
1761	Spectroscopic approaches to the conformation of tau protein in solution and in paired helical filaments. 2006 , 3, 197-206	47
1760	Role of peripherin/rds in vertebrate photoreceptor architecture and inherited retinal degenerations. 2006 , 253, 131-75	61
1759	Large-scale prediction of protein structure and function from sequence. 2006 , 12, 2067-86	11
1758	Intrinsic disorder is a common feature of hub proteins from four eukaryotic interactomes. 2006 , 2, e100	435

1757	Prediction of amyloidogenic and disordered regions in protein chains. 2006 , 2, e177	138
1756	Water and the Cell. 2006 ,	21
1755	The inverted chevron plot measured by NMR relaxation reveals a native-like unfolding intermediate in acyl-CoA binding protein. 2006 , 103, 6877-82	21
1754	Local flexibility in molecular function paradigm. 2006 , 5, 1212-23	38
1753	The intracellular region of CLC-3 chloride channel is in a partially folded state and a monomer. 2006 , 139, 813-20	2
1752	Dequalinium-induced protofibril formation of alpha-synuclein. 2006 , 281, 3463-72	21
1751	A novel two-dimensional electrophoresis technique for the identification of intrinsically unstructured proteins. 2006 , 5, 265-73	56
1750	The Concept of Protein Mosaics: Physiological Role and Relevance for Prion Disease. 2006 , 3, 171-179	4
1749	Structural study of the H/ACA snoRNP components Nop10p and the 3' hairpin of U65 snoRNA. 2006 , 12, 40-52	31
1748	A network-based analysis of polyanion-binding proteins utilizing yeast protein arrays. 2006 , 5, 2263-78	12
1747	The disordered amino-terminus of SIMPL interacts with members of the 70-kDa heat-shock protein family. 2006 , 25, 704-14	9
1746	Alternative splicing in concert with protein intrinsic disorder enables increased functional diversity in multicellular organisms. 2006 , 103, 8390-5	358
1745	Common attributes of native-state structures of proteins, disordered proteins, and amyloid. 2006 , 103, 6883-8	44
1744	Trend of amino acid composition of proteins of different taxa. 2006 , 4, 597-608	60
1743	Protein Misfolding, Aggregation, and Conformational Diseases. 2007 ,	13
1742	Neutralization of acidic residues in helix II stabilizes the folded conformation of acyl carrier protein and variably alters its function with different enzymes. 2007 , 282, 4494-4503	31
1741	A network-based analysis of polyanion-binding proteins utilizing human protein arrays. 2007 , 282, 10153-63	24
1740	The existence of multiple conformers of interleukin-21 directs engineering of a superpotent analogue. 2007 , 282, 23326-36	29

1739	NMR structural analysis of cadmium sensing by winged helix repressor CmtR. 2007 , 282, 30181-8	36
1738	Inferring function using patterns of native disorder in proteins. 2007 , 3, e162	104
1737	The unstructured C-terminus of the tau subunit of Escherichia coli DNA polymerase III holoenzyme is the site of interaction with the alpha subunit. 2007 , 35, 2813-24	46
1736	Towards proteomic approaches for the identification of structural disorder. 2007 , 8, 173-9	16
1735	p27Kip1 metabolism: a fascinating labyrinth. 2007 , 6, 1053-61	87
1734	Protein structure based strategies for antigen discovery and vaccine development against malaria and other pathogens. 2007 , 7, 259-65	30
1733	Expected packing density allows prediction of both amyloidogenic and disordered regions in protein chains. 2007 , 19, 285225	6
1732	RVCaB, a calcium-binding protein in radish vacuoles, is predominantly an unstructured protein with a polyproline type II helix. 2007 , 142, 201-11	19
1731	Identification of a minimal myosin Va binding site within an intrinsically unstructured domain of melanophilin. 2007 , 282, 21518-28	29
1730	iPDA: integrated protein disorder analyzer. 2007 , 35, W465-72	46
1729	The N-terminal domain of elastin-binding protein of Staphylococcus aureus changes its secondary structure in a membrane-mimetic environment. 2007 , 142, 131-4	9
1728	PrDOS: prediction of disordered protein regions from amino acid sequence. 2007 , 35, W460-4	537
1727	Natively unstructured regions in proteins identified from contact predictions. 2007 , 23, 2376-84	102
1726	DNA binding and phosphorylation induce conformational alterations in the kinase-inducible domain of CREB. Implications for the mechanism of transcription function. 2007 , 282, 19872-83	20
1725	Structure and function of a mitochondrial late embryogenesis abundant protein are revealed by desiccation. 2007 , 19, 1580-9	176
1724	Structural Genomics. 203-220	
1723	Exploring alternative knowledge representations for protein secondary-structure prediction. 2007 , 1, 286-313	3
1722	Mirl is highly upregulated and localized to nuclei during infectious hyphal growth in the rice blast fungus. 2007 , 20, 448-58	23

1721	Protein-Targeting Drug Discovery Guided by Hydrogen/Deuterium Exchange Mass Spectrometry (DXMS). 2007 , 377-398		
1720	Adjuvant activity of polymer microparticles and Montanide ISA 720 on immune responses to Plasmodium falciparum MSP2 long synthetic peptides in mice. 2007 , 25, 877-85		32
1719	Purification of CREB to apparent homogeneity: removal of truncation products and contaminating nucleic acid. 2007 , 55, 406-18		14
1718	Structure and functions of the human amyloid precursor protein: the whole is more than the sum of its parts. 2007 , 82, 11-32		135
1717	Properties, functions, and drug targeting of the multifunctional nucleocapsid protein of the human immunodeficiency virus. 2007 , 55, 299-346		66
1716	What drives proteins into the major or minor grooves of DNA?. <i>Journal of Molecular Biology</i> , 2007 , 365, 1-9	6.5	154
1715	Amyloid fibril formation and disaggregation of fragment 1-29 of apomyoglobin: insights into the effect of pH on protein fibrillogenesis. <i>Journal of Molecular Biology</i> , 2007 , 367, 1237-45	6.5	57
1714	Intrinsically disordered regions of human plasma membrane proteins preferentially occur in the cytoplasmic segment. <i>Journal of Molecular Biology</i> , 2007 , 368, 902-13	6.5	80
1713	The structurally disordered KRAB repression domain is incorporated into a protease resistant core upon binding to KAP-1-RBCC domain. <i>Journal of Molecular Biology</i> , 2007 , 370, 269-89	6.5	20
1712	Bile acid interactions with rabbit ileal lipid binding protein and an engineered helixless variant reveal novel ligand binding properties of a versatile beta-clam shell protein scaffold. <i>Journal of Molecular Biology</i> , 2007 , 371, 1365-77	6.5	18
1711	Crystal structure of conserved domains 1 and 2 of the human DEAD-box helicase DDX3X in complex with the mononucleotide AMP. <i>Journal of Molecular Biology</i> , 2007 , 372, 150-9	6.5	102
1710	Molecular principles of the interactions of disordered proteins. <i>Journal of Molecular Biology</i> , 2007 , 372, 549-61	6.5	220
1709	Construction of intramolecular luciferase complementation probe for detecting specific RNA. 2007 , 18, 956-62		14
1708	Functional anthology of intrinsic disorder. 1. Biological processes and functions of proteins with long disordered regions. 2007 , 6, 1882-98		455
1707	Distribution patterns of small-molecule ligands in the protein universe and implications for origin of life and drug discovery. 2007 , 8, R176		50
1706	Molecular "negativity" may underlie multiple sclerosis: role of the myelin basic protein family in the pathogenesis of MS. 2007 , 79, 149-72		40
1705	Intrinsically Disordered Proteins: An Update. 2007 ,		
1704	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

1703	Fesselin is a natively unfolded protein. 2007 , 6, 3648-54	11
1702	Mining alpha-helix-forming molecular recognition features with cross species sequence alignments. 2007 , 46, 13468-77	270
1701	Domain 2 of nonstructural protein 5A (NS5A) of hepatitis C virus is natively unfolded. 2007 , 46, 11550-8	78
1700	Bioinformatics Research and Development. 2007 ,	3
1699	Effects of zinc binding on the structure and dynamics of the intrinsically disordered protein prothymosin alpha: evidence for metalation as an entropic switch. 2007 , 46, 13120-30	47
1698	UV resonance Raman measurements of poly-L-lysine's conformational energy landscapes: dependence on perchlorate concentration and temperature. 2007 , 111, 7675-80	32
1697	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
1696	DisProt: the Database of Disordered Proteins. 2007 , 35, D786-93	631
1695	Intrinsic disorder as a mechanism to optimize allosteric coupling in proteins. 2007 , 104, 8311-5	326
1694	Signal response of coexisting protein conformers in electrospray mass spectrometry. 2007 , 79, 2499-506	79
1693	Pockets of short-range transient order and restricted topological heterogeneity in the guanidine-denatured state ensemble of GED of dynamin. 2007 , 46, 11819-32	20
1692	Probing the unfolding and refolding processes of carbonic anhydrase 2 using electrospray ionization mass spectrometry combined with pH jump. 2007 , 79, 8342-9	12
1691	Computational Methods for Protein Structure Prediction and Modeling. 2007 ,	5
1690	Monte Carlo study of substrate-induced folding and refolding of lattice proteins. 2007 , 92, 1150-6	19
1689	Intrinsic disorder and functional proteomics. 2007 , 92, 1439-56	571
1688	Intrinsic dynamics of the partly unstructured PX domain from the Sendai virus RNA polymerase cofactor P. 2007 , 93, 2830-44	33
1687	Intrinsic disorder in the Protein Data Bank. 2007 , 24, 325-42	116
1686	Acyl carrier protein: structure-function relationships in a conserved multifunctional protein family. 2007 , 85, 649-62	141

1685	Energy Metabolism in Conformational Diseases. 233-257	3
1684	Structure and Dynamics of Disordered Proteins. 2007 ,	
1683	Abundance of intrinsic disorder in SV-IV, a multifunctional androgen-dependent protein secreted from rat seminal vesicle. 2007 ,	
1682	. 2007 ,	8
1681	. 2007 ,	1
1680	. 2007 ,	16
1679	Structure induction of the T-cell receptor zeta-chain upon lipid binding investigated by NMR spectroscopy. 2007 , 8, 820-7	35
1678	Phosphorylation-induced conformational changes in short peptides probed by fluorescence resonance energy transfer in the 10A domain. 2007 , 8, 567-73	23
1677	Peptide based malaria vaccine development: personal considerations. 2007 , 9, 767-71	6
1676	Minireview: The compact phase in polymers and proteins. 2007 , 384, 122-127	3
1675	Electrospray ionization mass spectra of acyl carrier protein are insensitive to its solution phase conformation. 2007 , 18, 1525-32	8
1674	Identifying long-range structure in the intrinsically unstructured transactivation domain of p53. 2007 , 67, 526-30	42
1673	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
1672	Investigating the structural stability of the Tup1-interaction domain of Ssn6: evidence for a conformational change on the complex. 2008 , 70, 72-82	13
1671	Intrinsic disorder in yeast transcriptional regulatory network. 2007 , 68, 602-5	55
1670	Intrinsically disordered protein from a pathogenic mesophile <i>Mycobacterium tuberculosis</i> adopts structured conformation at high temperature. 2008 , 71, 1123-33	14
1669	Huntingtin interacting protein HYPK is intrinsically unstructured. 2008 , 71, 1686-98	26
1668	Is the intrinsic disorder of proteins the cause of the scale-free architecture of protein-protein interaction networks?. 2007 , 7, 961-4	17

1667	Structured proteins and proteins with intrinsic disorder. 2007 , 41, 262-277	11
1666	CFTR regulatory region interacts with NBD1 predominantly via multiple transient helices. 2007 , 14, 738-45	233
1665	Mechanism of coupled folding and binding of an intrinsically disordered protein. 2007 , 447, 1021-5	852
1664	Neuropathology, biochemistry, and biophysics of alpha-synuclein aggregation. 2007 , 103, 17-37	373
1663	Dynamics of alpha-synuclein aggregation and inhibition of pore-like oligomer development by beta-synuclein. 2007 , 274, 1862-77	139
1662	Structural properties of semenogelin I. 2007 , 274, 4503-10	8
1661	False occurrences of functional motifs in protein sequences highlight evolutionary constraints. 2007 , 8, 68	5
1660	Predicting mostly disordered proteins by using structure-unknown protein data. 2007 , 8, 78	54
1659	Another window into disordered protein function. 2007 , 15, 1026-8	13
1658	The intrinsically disordered TC-1 interacts with Chibby via regions with high helical propensity. 2007 , 16, 2510-8	20
1657	Energetic rationale for an unexpected and abrupt reversal of guanidinium chloride-induced unfolding of peptide deformylase. 2008 , 17, 11-5	4
1656	A new list of functions of the cytoskeleton. 2007 , 59, 127-33	14
1655	Dynamic behavior of an intrinsically unstructured linker domain is conserved in the face of negligible amino acid sequence conservation. 2007 , 65, 277-88	71
1654	A tale of two citrullines--structural and functional aspects of myelin basic protein deimination in health and disease. 2007 , 32, 137-58	116
1653	Maximum entropy reconstruction of joint phi, psi-distribution with a coil-library prior: the backbone conformation of the peptide hormone motilin in aqueous solution from phi and psi-dependent J-couplings. 2007 , 38, 107-23	7
1652	Dynamics of well-folded and natively disordered proteins in solution: a time-of-flight neutron scattering study. 2008 , 37, 573-82	60
1651	DPROT: prediction of disordered proteins using evolutionary information. 2008 , 35, 599-605	10
1650	Knitting and untying the protein network: modulation of protein ensembles as a therapeutic strategy. 2009 , 18, 481-93	18

1649	Residual structure in disordered peptides and unfolded proteins from multivariate analysis and ab initio simulation of Raman optical activity data. 2008 , 70, 823-33	63
1648	Modeling the accessible conformations of the intrinsically unstructured transactivation domain of p53. 2008 , 71, 587-98	38
1647	Apo-parvalbumin as an intrinsically disordered protein. 2008 , 72, 822-36	46
1646	Mechanism of induced folding: Both folding before binding and binding before folding can be realized in staphylococcal nuclease mutants. 2008 , 72, 837-47	44
1645	A robust approach for analyzing a heterogeneous structural ensemble. 2008 , 73, 918-28	8
1644	Protein structure and dynamics studied by mass spectrometry: H/D exchange, hydroxyl radical labeling, and related approaches. 2008 , 43, 1021-36	162
1643	The tubulin polymerization promoting protein, TPPP/p25. 2008 , 60, 637-42	6
1642	DeSUMOylating enzymes--SENPs. 2008 , 60, 734-42	83
1641	Structure and function of Rho-type molecular switches in plants. 2008 , 46, 380-93	75
1640	Using Bayesian multinomial classifier to predict whether a given protein sequence is intrinsically disordered. 2008 , 254, 799-803	8
1639	Subsequence-based feature map for protein function classification. 2008 , 32, 122-30	11
1638	Structural rationale for the coupled binding and unfolding of the c-Myc oncoprotein by small molecules. 2008 , 15, 1149-55	126
1637	Tryptophan fluorescence reveals induced folding of <i>Vibrio harveyi</i> acyl carrier protein upon interaction with partner enzymes. 2008 , 1784, 1835-43	7
1636	To be folded or to be unfolded?. 2004 , 13, 2871-7	63
1635	Identification of transient hub proteins and the possible structural basis for their multiple interactions. 2008 , 17, 72-8	55
1634	pH-induced folding of an apoptotic coiled coil. 2001 , 10, 2531-40	25
1633	Optimal region of average side-chain entropy for fast protein folding. 2000 , 9, 580-6	26
1632	Privileged scaffolds targeting reverse-turn and helix recognition. 2008 , 12, 101-14	29

1631	Protein folding intermediates of invasin protein IbeA from Escherichia coli. 2008 , 275, 458-69	7
1630	Abundance of intrinsic disorder in SV-IV, a multifunctional androgen-dependent protein secreted from rat seminal vesicle. 2008 , 275, 763-74	4
1629	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 Chlamydomonas reinhardtii. 2008 , 275, 1248-59	32
1628	Prediction of short loops in intrinsically disordered proteins. 2008 , 42, 949-959	3
1627	Malleable machines take shape in eukaryotic transcriptional regulation. 2008 , 4, 728-37	161
1626	Protein abundance profiling of the Escherichia coli cytosol. 2008 , 9, 102	353
1625	The unfoldomics decade: an update on intrinsically disordered proteins. 2008 , 9 Suppl 2, S1	408
1624	Short Linear Motifs recognized by SH2, SH3 and Ser/Thr Kinase domains are conserved in disordered protein regions. 2008 , 9 Suppl 2, S26	54
1623	Protein intrinsic disorder toolbox for comparative analysis of viral proteins. 2008 , 9 Suppl 2, S4	53
1622	A careful disorderliness in the proteome: sites for interaction and targets for future therapies. 2008 , 582, 1271-5	63
1621	Calcium-induced tripartite binding of intrinsically disordered calpastatin to its cognate enzyme, calpain. 2008 , 582, 2149-54	25
1620	Intrinsic disorder in scaffold proteins: getting more from less. 2008 , 98, 85-106	213
1619	Fuzzy complexes: polymorphism and structural disorder in protein-protein interactions. 2008 , 33, 2-8	788
1618	Protein folding and misfolding on surfaces. 2008 , 9, 2515-42	57
1617	Kinetics of folding and binding of an intrinsically disordered protein: the inhibitor of yeast aspartic proteinase YPrA. 2008 , 130, 11477-85	51
1616	Biophysical characterization of the unstructured cytoplasmic domain of the human neuronal adhesion protein neuroligin 3. 2008 , 95, 1928-44	34
1615	The twilight zone between protein order and disorder. 2008 , 95, 1612-26	27
1614	Potential implications of availability of short amino acid sequences in proteins: an old and new approach to protein decoding and design. 2008 , 14, 109-41	14

1613	Intrinsically disordered proteins in human diseases: introducing the D2 concept. 2008 , 37, 215-46		1018
1612	Conformational characteristics of unstructured peptides: alpha-synuclein. 2008 , 25, 505-15		35
1611	Intrinsic disorder in pathogenic and non-pathogenic microbes: discovering and analyzing the unfoldomes of early-branching eukaryotes. 2008 , 4, 328-40		101
1610	Biochemistry. Controlled chaos. 2008 , 322, 1340-1		59
1609	A comparative analysis of viral matrix proteins using disorder predictors. 2008 , 5, 126		51
1608	Regulation of cell division by intrinsically unstructured proteins: intrinsic flexibility, modularity, and signaling conduits. 2008 , 47, 7598-609		185
1607	Local structural preferences of calpastatin, the intrinsically unstructured protein inhibitor of calpain. 2008 , 47, 6936-45		44
1606	Protein Folding and Aggregation in in vitro Models of Parkinson's Disease. 2008 , 575-595		11
1605	Electrochemistry Investigation on Protein Protection by Alkanethiol Self-Assembled Monolayers against Urea Impact. 2008 , 112, 6013-6021		20
1604	The role of disorder in interaction networks: a structural analysis. 2008 , 4, 179		167
1603	Partially folded bovine pancreatic trypsin inhibitor analogues attain fully native structures when co-crystallized with S195A rat trypsin. <i>Journal of Molecular Biology</i> , 2008 , 375, 812-23	6.5	1
1602	Intrinsically disordered human C/EBP homologous protein regulates biological activity of colon cancer cells during calcium stress. <i>Journal of Molecular Biology</i> , 2008 , 380, 313-26	6.5	17
1601	Transfer of flexibility between ankyrin repeats in IkappaB* upon formation of the NF-kappaB complex. <i>Journal of Molecular Biology</i> , 2008 , 380, 917-31	6.5	56
1600	Denatured-state energy landscapes of a protein structural database reveal the energetic determinants of a framework model for folding. <i>Journal of Molecular Biology</i> , 2008 , 381, 1184-201	6.5	17
1599	Molecular titration and ultrasensitivity in regulatory networks. <i>Journal of Molecular Biology</i> , 2008 , 384, 1106-19	6.5	208
1598	Correlation of structural stability with functional remodeling of high-density lipoproteins: the importance of being disordered. 2008 , 47, 11393-7		33
1597	Role of backbone-solvent interactions in determining conformational equilibria of intrinsically disordered proteins. 2008 , 130, 7380-92		171
1596	How expression level influences the disorderness of proteins. 2008 , 371, 401-4		7

1595	DBD-Hunter: a knowledge-based method for the prediction of DNA-protein interactions. 2008 , 36, 3978-92	110
1594	Late Embryogenesis Abundant Proteins. 2008 , 211-255	86
1593	Protein Crystallography and Drug Discovery. 2008 , 605-634	1
1592	Tight regulation of unstructured proteins: from transcript synthesis to protein degradation. 2008 , 322, 1365-8	364
1591	Targeting the human cancer pathway protein interaction network by structural genomics. 2008 , 7, 2048-60	59
1590	Natively unfolded protein stability as a coil-to-globule transition in charge/hydrophobicity space. 2008 , 130, 9536-42	56
1589	Interconversion between two unrelated protein folds in the lysozyme native state. 2008 , 105, 5057-62	209
1588	Effect of methionine oxidation on the structural properties, conformational stability, and aggregation of immunoglobulin light chain LCN. 2008 , 47, 8665-77	30
1587	Membrane-induced folding of the cAMP-regulated phosphoprotein endosulfine- α . 2008 , 47, 12357-64	15
1586	Exploring the energy landscape of antibody-antigen complexes: protein dynamics, flexibility, and molecular recognition. 2008 , 47, 7237-47	59
1585	Protein disorder is positively correlated with gene expression in Escherichia coli. 2008 , 7, 2234-45	26
1584	The intrinsically disordered RNR inhibitor Sml1 is a dynamic dimer. 2008 , 47, 13428-37	45
1583	Identification of the copper(II) coordinating residues in the prion protein by metal-catalyzed oxidation mass spectrometry: evidence for multiple isomers at low copper(II) loadings. 2008 , 47, 9258-68	30
1582	The folding kinetics of the SDS-induced molten globule form of reduced cytochrome c. 2008 , 47, 5450-9	21
1581	Mass instability in isolated recombinant FixL heme domains of Bradyrhizobium japonicum. 2008 , 47, 1540-53	6
1580	Multidomain initiation factor 2 from Thermus thermophilus consists of the individual autonomous domains. 2008 , 47, 4992-5005	4
1579	The structure and interactions of the proline-rich domain of ASPP2. 2008 , 283, 18990-9	31
1578	Virulence factor of potato virus Y, genome-attached terminal protein VPg, is a highly disordered protein. 2008 , 283, 213-221	51

1577	Structural Perspectives on Protein Evolution. 2008 , 4, 3-21	6
1576	Prediction of disordered regions in proteins based on the meta approach. 2008 , 24, 1344-8	213
1575	Amyloidogenesis of natively unfolded proteins. 2008 , 5, 260-87	147
1574	Disordered flanks prevent peptide aggregation. 2008 , 4, e1000241	42
1573	Binding-induced folding of a natively unstructured transcription factor. 2008 , 4, e1000060	167
1572	Phosphoproteomic analysis of the mouse brain cytosol reveals a predominance of protein phosphorylation in regions of intrinsic sequence disorder. 2008 , 7, 1331-48	135
1571	Regulation of Escherichia coli SOS mutagenesis by dimeric intrinsically disordered umuD gene products. 2008 , 105, 1152-7	60
1570	Studying Protein Folding and Aggregation by Laser Light Scattering. 2008 , 673	1
1569	Conserved amphiphilic feature is essential for periplasmic chaperone HdeA to support acid resistance in enteric bacteria. 2008 , 412, 389-97	31
1568	The effects of conformational heterogeneity on the binding of the Notch intracellular domain to effector proteins: a case of biologically tuned disorder. 2008 , 36, 157-66	42
1567	Alpha-synuclein misfolding and neurodegenerative diseases. 2008 , 9, 507-40	163
1566	TOP-IDP-scale: a new amino acid scale measuring propensity for intrinsic disorder. 2008 , 15, 956-63	266
1565	Insilico investigations of disordered regions in hypothetical sequences from human proteome as drug targets. 2008 , 1, 187	
1564	Understanding eukaryotic linear motifs and their role in cell signaling and regulation. 2008 , 13, 6580-603	230
1563	Intrinsic disorder in proteins associated with neurodegenerative diseases. 2009 , 14, 5188-238	169
1562	Evidence for the concerted evolution between short linear protein motifs and their flanking regions. 2009 , 4, e6052	29
1561	Intrinsically Unstructured Proteins: Potential Targets for Drug Discovery. 2009 , 5, 126-134	5
1560	Real-time analysis of amyloid fibril formation of alpha-synuclein using a fibrillation-state-specific fluorescent probe of JC-1. 2009 , 418, 311-23	41

1559	Toward a quantitative theory of intrinsically disordered proteins and their function. 2009 , 106, 19819-23	88
1558	Interplay of alpha-synuclein binding and conformational switching probed by single-molecule fluorescence. 2009 , 106, 5645-50	327
1557	Molecular basis of coiled coil coactivator recruitment by the aryl hydrocarbon receptor nuclear translocator (ARNT). 2009 , 284, 15184-92	26
1556	CP12 from <i>Chlamydomonas reinhardtii</i> , a permanent specific "chaperone-like" protein of glyceraldehyde-3-phosphate dehydrogenase. 2009 , 284, 12735-44	33
1555	p57KIP2: "Kip"ing the cell under control. 2009 , 7, 1902-19	114
1554	Natively unfolded proteins: An overview. 2009 , 5, 53-58	15
1553	The C-terminal domain of the HIV-1 Vif protein is natively unfolded in its unbound state. 2009 , 22, 281-7	27
1552	Molecular Dynamics Simulations of Intrinsically Disordered Proteins in Human Diseases. 2009 , 5, 280-287	12
1551	Cross-seeding fibrillation of Q/N-rich proteins offers new pathomechanism of polyglutamine diseases. 2009 , 29, 5153-62	73
1550	The role of disordered ribosomal protein extensions in the early steps of eubacterial 50 S ribosomal subunit assembly. 2009 , 10, 817-34	35
1549	Intrinsic disorder in protein interactions: insights from a comprehensive structural analysis. 2009 , 5, e1000316	91
1548	Prediction of protein binding regions in disordered proteins. 2009 , 5, e1000376	419
1547	An overview of the importance of conformational flexibility in gene regulation by the transcription factors. 2009 , 2009, 210485	7
1546	Folding by numbers: primary sequence statistics and their use in studying protein folding. 2009 , 10, 1567-89	16
1545	Functional stabilization of an RNA recognition motif by a noncanonical N-terminal expansion. 2009 , 15, 1305-13	14
1544	Influence of sequence changes and environment on intrinsically disordered proteins. 2009 , 5, e1000497	37
1543	NMR and EPR studies of membrane transporters. 2009 , 390, 815-34	22
1542	Vaccine potentials of an intrinsically unstructured fragment derived from the blood stage-associated <i>Plasmodium falciparum</i> protein PFF0165c. 2009 , 77, 5701-9	41

1541	The GTOP database in 2009: updated content and novel features to expand and deepen insights into protein structures and functions. 2009 , 37, D333-7	27
1540	The rules of disorder or why disorder rules. 2009 , 99, 94-103	146
1539	Linking folding and binding. 2009 , 19, 31-8	813
1538	Fuzzy interactome: the limitations of models in molecular biology. 2009 , 34, 3	10
1537	Large-scale prediction of long disordered regions in proteins using random forests. 2009 , 10, 8	35
1536	Protein disorder in the human diseasome: unfoldomics of human genetic diseases. 2009 , 10 Suppl 1, S12	105
1535	Unfoldomics of human diseases: linking protein intrinsic disorder with diseases. 2009 , 10 Suppl 1, S7	199
1534	Functionalization of a nanopore: the nuclear pore complex paradigm. 2009 , 1793, 1533-9	18
1533	Janus chaperones: assistance of both RNA- and protein-folding by ribosomal proteins. 2009 , 583, 88-92	36
1532	Leucine-rich hydrophobic clusters promote folding of the N-terminus of the intrinsically disordered transactivation domain of p53. 2009 , 583, 556-60	25
1531	CDF it all: consensus prediction of intrinsically disordered proteins based on various cumulative distribution functions. 2009 , 583, 1469-74	99
1530	A strained DNA binding helix is conserved for site recognition, folding nucleation, and conformational modulation. 2009 , 91, 432-43	9
1529	Common key-signals in learning and neurodegeneration: focus on excito-amino acids, beta-amyloid peptides and alpha-synuclein. 2009 , 116, 953-74	7
1528	Probing the urea dependence of residual structure in denatured human alpha-lactalbumin. 2009 , 45, 121-31	8
1527	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
1526	Role of synucleins in Alzheimer's disease. 2009 , 16, 306-17	59
1525	Functional aspects of protein flexibility. 2009 , 66, 2231-47	161
1524	The protein meta-structure: a novel concept for chemical and molecular biology. 2009 , 66, 3625-39	41

1523	Order propensity of an intrinsically disordered protein, the cyclin-dependent-kinase inhibitor Sic1. 2009 , 76, 731-46	58
1522	Assessment of disorder predictions in CASP8. 2009 , 77 Suppl 9, 210-6	93
1521	Characterization of intrinsically disordered proteins with electrospray ionization mass spectrometry: conformational heterogeneity of alpha-synuclein. 2010 , 78, 714-22	73
1520	Relating protein conformational changes to packing efficiency and disorder. 2009 , 18, 1230-40	8
1519	Residual structure within the disordered C-terminal segment of p21(Waf1/Cip1/Sdi1) and its implications for molecular recognition. 2009 , 18, 337-47	27
1518	Development of an accurate classification system of proteins into structured and unstructured regions that uncovers novel structural domains: its application to human transcription factors. 2009 , 9, 26	32
1517	Theoretical framework for the histone modification network: modifications in the unstructured histone tails form a robust scale-free network. 2009 , 14, 789-806	12
1516	The nanny model for IDPs. 2009 , 5, 778-81	95
1515	Proteasome system of protein degradation and processing. 2009 , 74, 1411-42	95
1514	Solubility-dependent structural formation of a 25-residue, natively unfolded protein, induced by addition of a seven-residue peptide fragment. 2009 , 276, 2336-47	
1513	Intrinsic disorder and coiled-coil formation in prostate apoptosis response factor 4. 2009 , 276, 3710-28	22
1512	Calcium uptake by casein embedded in polyelectrolyte multilayer. 2009 , 343, 118-126	15
1511	Solution structure and dynamics of the chimeric SH3 domains, SHH- and SHA-"Bergeracs". 2009 , 1794, 1813-22	13
1510	Polyglutamine tract binding protein-1 is an intrinsically unstructured protein. 2009 , 1794, 936-43	19
1509	Conformational plasticity of DM43, a metalloproteinase inhibitor from Didelphis marsupialis: chemical and pressure-induced equilibrium (un)folding studies. 2009 , 1794, 1379-86	5
1508	The rod-shaped conformation of Starmaker. 2009 , 1794, 1616-24	15
1507	Electric charge balance mechanism of extended soluble proteins. 2005 , 14, 74-80	15
1506	Human full-length Securin is a natively unfolded protein. 2005 , 14, 1410-8	47

1505	Multiple diverse ligands binding at a single protein site: a matter of pre-existing populations. 2002 , 11, 184-97	321
1504	Aberrant mobility phenomena of the DNA repair protein XPA. 2001 , 10, 1353-62	61
1503	NMR detected hydrogen-deuterium exchange reveals differential dynamics of antibiotic- and nucleotide-bound aminoglycoside phosphotransferase 3'-IIIa. 2009 , 131, 8587-94	22
1502	Thermodynamic aspects of coupled binding and folding of an intrinsically disordered protein: a computational alanine scanning study. 2009 , 48, 11332-4	17
1501	Large-scale analysis of thermostable, mammalian proteins provides insights into the intrinsically disordered proteome. 2009 , 8, 211-26	61
1500	Intrinsic Disorder in Proteins Associated with Neurodegenerative Diseases. 2009 , 21-75	6
1499	Conformational changes specific for pseudophosphorylation at serine 262 selectively impair binding of tau to microtubules. 2009 , 48, 10047-55	102
1498	Mechanism of ligand-induced folding of a natively unfolded helixless variant of rabbit I-BABP. 2009 , 48, 7556-64	16
1497	The K-segment of maize DHN1 mediates binding to anionic phospholipid vesicles and concomitant structural changes. 2009 , 150, 1503-14	166
1496	Protein Folding and Misfolding: Neurodegenerative Diseases. 2009 ,	5
1495	Multiple independent binding sites for small-molecule inhibitors on the oncoprotein c-Myc. 2009 , 131, 7390-401	171
1494	Thermodynamic basis for the optimization of binding-induced biomolecular switches and structure-switching biosensors. 2009 , 106, 13802-7	121
1493	SECIS-binding protein 2, a key player in selenoprotein synthesis, is an intrinsically disordered protein. 2009 , 91, 1003-9	10
1492	Structural dynamics and folding of beta-lactoglobulin probed by heteronuclear NMR. 2009 , 1790, 527-37	86
1491	Reconciling binding mechanisms of intrinsically disordered proteins. 2009 , 382, 479-82	80
1490	Evaluation of two long synthetic merozoite surface protein 2 peptides as malaria vaccine candidates. 2009 , 27, 2653-61	20
1489	Role of intrinsically disordered protein regions/domains in transcriptional regulation. 2009 , 84, 189-93	54
1488	The desmoglein-specific cytoplasmic region is intrinsically disordered in solution and interacts with multiple desmosomal protein partners. <i>Journal of Molecular Biology</i> , 2009 , 386, 531-43	6.5 22

1487	A common interaction for the entry of colicin N and filamentous phage into Escherichia coli. <i>Journal of Molecular Biology</i> , 2009 , 388, 880-93	6.5	16
1486	At low concentrations, 3,4-dihydroxyphenylacetic acid (DOPAC) binds non-covalently to alpha-synuclein and prevents its fibrillation. <i>Journal of Molecular Biology</i> , 2009 , 388, 597-610	6.5	43
1485	Modular organization of rabies virus phosphoprotein. <i>Journal of Molecular Biology</i> , 2009 , 388, 978-96	6.5	93
1484	Structural interpretation of paramagnetic relaxation enhancement-derived distances for disordered protein states. <i>Journal of Molecular Biology</i> , 2009 , 390, 467-77	6.5	60
1483	Phosphorylation-induced activation of the response regulator VraR from Staphylococcus aureus: insights from hydrogen exchange mass spectrometry. <i>Journal of Molecular Biology</i> , 2009 , 391, 149-63	6.5	11
1482	Interaction between intrinsically disordered proteins frequently occurs in a human protein-protein interaction network. <i>Journal of Molecular Biology</i> , 2009 , 392, 1253-65	6.5	48
1481	Kinetic advantage of intrinsically disordered proteins in coupled folding-binding process: a critical assessment of the "fly-casting" mechanism. <i>Journal of Molecular Biology</i> , 2009 , 393, 1143-59	6.5	227
1480	Mapping the structure of an integral membrane protein under semi-denaturing conditions by laser-induced oxidative labeling and mass spectrometry. <i>Journal of Molecular Biology</i> , 2009 , 394, 968-81	6.5	44
1479	Rejuvenation of CcdB-poisoned gyrase by an intrinsically disordered protein domain. 2009 , 35, 154-63		118
1478	Two-site phosphorylation of EPRS coordinates multimodal regulation of noncanonical translational control activity. 2009 , 35, 164-80		89
1477	A single mutation at residue 25 populates the folding intermediate of E. coli RNase H and reveals a highly dynamic partially folded ensemble. <i>Journal of Molecular Biology</i> , 2009 , 391, 461-70	6.5	14
1476	Kinetics of contact formation and end-to-end distance distributions of swollen disordered peptides. 2009 , 96, 1515-28		40
1475	Binding-induced folding transitions in calpastatin subdomains A and C. 2003 , 12, 2327-36		28
1474	On the properties and sequence context of structurally ambivalent fragments in proteins. 2003 , 12, 2420-33		35
1473	Intrinsic disorder in Viral Proteins Genome-Linked: experimental and predictive analyses. 2009 , 6, 23		55
1472	The interaction between the measles virus nucleoprotein and the Interferon Regulator Factor 3 relies on a specific cellular environment. 2009 , 6, 59		20
1471	Protein intrinsic disorder and influenza virulence: the 1918 H1N1 and H5N1 viruses. 2009 , 6, 69		64
1470	From Protein Structure to Function with Bioinformatics. 2009 ,		19

1469	Optical signatures of molecular dissymmetry: combining theory with experiments to address stereochemical puzzles. 2009 , 42, 809-19	58
1468	Atomistic details of the disordered states of KID and pKID. Implications in coupled binding and folding. 2009 , 131, 5214-23	82
1467	Weak Links. 2009 ,	53
1466	Tandem and cryptic amino acid repeats accumulate in disordered regions of proteins. 2009 , 10, R59	87
1465	Insights into the regulation of intrinsically disordered proteins in the human proteome by analyzing sequence and gene expression data. 2009 , 10, R50	56
1464	Nucleocapsid structure and function. 2009 , 329, 103-28	53
1463	Characterization of inhibitory anti-insulin-like growth factor receptor antibodies with different epitope specificity and ligand-blocking properties: implications for mechanism of action in vivo. 2009 , 284, 10254-67	23
1462	Interaction of alphaS1-casein with curcumin and its biological implications. 2009 , 57, 10386-91	63
1461	Analysis of structured and intrinsically disordered regions of transmembrane proteins. 2009 , 5, 1688-1702	55
1460	Binding of small-molecule ligands to proteins: "what you see" is not always "what you get". 2009 , 17, 489-98	414
1459	Predicting intrinsic disorder in proteins: an overview. 2009 , 19, 929-49	328
1458	Studies of the biological function and structure of casein micelles, and future implications. 2009 , 147-169	1
1457	References. 2009 , 265-312	
1456	Linking new paradigms in protein chemistry to reversible membrane-protein interactions. 2009 , 10, 339-59	38
1455	Direct observation of structural heterogeneity in a beta-sheet. 2009 , 131, 5726-7	28
1454	The importance of being flexible: the case of basic region leucine zipper transcriptional regulators. 2009 , 10, 244-69	72
1453	Probing early events in ferrous cytochrome c folding with time-resolved natural and magnetic circular dichroism spectroscopies. 2009 , 10, 464-75	14
1452	Unfoldomics of human genetic diseases: illustrative examples of ordered and intrinsically disordered members of the human diseasome. 2009 , 16, 1533-47	52

1451	Protein Folding and Protein-Ligand Interactions Monitored by Electrospray Mass Spectrometry. 2009 , 5, 186-204	19
1450	Structural disorder in proteins of the rhabdoviridae replication complex. 2010 , 17, 979-87	23
1449	Membrane interactions of oligomeric alpha-synuclein: potential role in Parkinson's disease. 2010 , 11, 334-42	39
1448	Structural disorder in the HIV-1 Vif protein and interaction-dependent gain of structure. 2010 , 17, 988-98	17
1447	Protein Flexibility in In Silico Screening. 2010 , 867-887	
1446	Structural disorder within the measles virus nucleoprotein and phosphoprotein. 2010 , 17, 961-78	31
1445	POODLE-I: disordered region prediction by integrating POODLE series and structural information predictors based on a workflow approach. 2010 , 10, 185-91	20
1444	Probing the Structure and Function of Proteins by Mass Spectrometry. 2010 , 58, 185-194	
1443	Ability of a salivary intrinsically unstructured protein to bind different tannin targets revealed by mass spectrometry. 2010 , 398, 815-22	50
1442	Exploring tryptophan dynamics in acid-induced molten globule state of bovine alpha-lactalbumin: a wavelength-selective fluorescence approach. 2010 , 39, 1453-63	41
1441	Formation and stability of poly-L-lysine/casein multilayers. 2010 , 16, 241-248	9
1440	Stabilization of the spectrin-like domains of nesprin-1 by the evolutionarily conserved "adaptive" domain. 2010 , 3, 139-150	17
1439	A microscale protein NMR sample screening pipeline. 2010 , 46, 11-22	85
1438	On the lack of specificity of proteins and its consequences for a theory of biological organization. 2010 , 102, 45-52	19
1437	The protein kingdom extended: ordered and intrinsically disordered proteins, their folding, supramolecular complex formation, and aggregation. 2010 , 102, 73-84	157
1436	Structure-switching biosensors: inspired by Nature. 2010 , 20, 518-26	137
1435	Structural diversity in free and bound states of intrinsically disordered protein phosphatase 1 regulators. 2010 , 18, 1094-103	94
1434	Quantitative structural analysis of importin- β flexibility: paradigm for solenoid protein structures. 2010 , 18, 1171-83	72

1433	Estimation and efficient computation of the true probability of recurrence of short linear protein sequence motifs in unrelated proteins. 2010 , 11, 14	18
1432	Predictors of natively unfolded proteins: unanimous consensus score to detect a twilight zone between order and disorder in generic datasets. 2010 , 11, 198	5
1431	Bayesian statistical modelling of human protein interaction network incorporating protein disorder information. 2010 , 11, 46	13
1430	Parameterization of disorder predictors for large-scale applications requiring high specificity by using an extended benchmark dataset. 2010 , 11 Suppl 1, S15	36
1429	Full length amelogenin binds to cell surface LAMP-1 on tooth root/periodontium associated cells. 2010 , 55, 417-25	29
1428	Generating artificial homologous proteins according to the representative family character in molecular mechanics properties--an attempt in validating an underlying rule of protein evolution. 2010 , 584, 1059-65	3
1427	Mapping the Binding Site of P53 on UBC9 by NMR Spectroscopy. 2010 , 20, 937-943	1
1426	Electrochemically Monitoring the Acid and Acidic Urea-Induced Unfolding of Hemoglobin and Its Electrocatalytic Ability. 2010 , 22, 2277-2283	10
1425	Structural Insights into Intrinsically Disordered Proteins by Small-Angle X-Ray Scattering. 2010 , 451-476	5
1424	Conformational Behavior of Intrinsically Disordered Proteins: Effects of Strong Denaturants, Temperature, PH, Counterions, and Macromolecular Crowding. 2010 , 545-568	
1423	The Structural Biology of IDPs inside Cells. 2010 , 37-58	
1422	Detecting Disordered Regions in Proteins by Limited Proteolysis. 2010 , 569-626	7
1421	Large-Scale Identification of Intrinsically Disordered Proteins. 2010 , 671-693	
1420	Nuclear Magnetic Resonance Spectroscopy Applied to (Intrinsically) Disordered Proteins. 2010 , 59-87	1
1419	Determining Structural Ensembles for Intrinsically Disordered Proteins. 2010 , 107-129	1
1418	PONDR-FIT: a meta-predictor of intrinsically disordered amino acids. 2010 , 1804, 996-1010	749
1417	Understanding protein non-folding. 2010 , 1804, 1231-64	875
1416	Aquifex aeolicus FlgM protein exhibits a temperature-dependent disordered nature. 2010 , 1804, 1457-66	7

1415	Polyglutamine tract-binding protein-1 binds to U5-15kD via a continuous 23-residue segment of the C-terminal domain. 2010 , 1804, 1500-7	11
1414	Isolation of short peptide fragments from alpha-synuclein fibril core identifies a residue important for fibril nucleation: a possible implication for diagnostic applications. 2010 , 1804, 2077-87	12
1413	Comparing interfacial dynamics in protein-protein complexes: an elastic network approach. 2010 , 10, 26	31
1412	Archaic chaos: intrinsically disordered proteins in Archaea. 2010 , 4 Suppl 1, S1	99
1411	Comparative characterization of random-sequence proteins consisting of 5, 12, and 20 kinds of amino acids. 2010 , 19, 786-95	24
1410	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
1409	¹⁹ F NMR studies of β -synuclein-membrane interactions. 2010 , 19, 1686-91	45
1408	Modularity of intrinsic disorder in the human proteome. 2010 , 78, 212-21	80
1407	Identification, analysis, and prediction of protein ubiquitination sites. 2010 , 78, 365-80	424
1406	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
1405	Fluctuations of backbone torsion angles obtained from NMR-determined structures and their prediction. 2010 , 78, 3353-62	25
1404	Prevalence of intrinsic disorder in the hepatitis C virus ARFP/Core+1/S protein. 2010 , 277, 774-89	13
1403	How disorder influences order and vice versa--mutual effects in fusion proteins containing an intrinsically disordered and a globular protein. 2010 , 277, 4438-51	15
1402	SPA: Short peptide analyzer of intrinsic disorder status of short peptides. 2010 , 15, 635-46	7
1401	Global analysis of functional relationships between histone point mutations and the effects of histone deacetylase inhibitors. 2010 , 15, 553-94	5
1400	The crystal structure of the TolB box of colicin A in complex with TolB reveals important differences in the recruitment of the common TolB translocation portal used by group A colicins. 2010 , 75, 623-36	21
1399	Multifunctionality of the linker histones: an emerging role for protein-protein interactions. 2010 , 20, 519-28	69
1398	Statistical analysis of unstructured amino acid residues in protein structures. 2010 , 75, 192-200	9

1397	Structural disorder within Henipavirus nucleoprotein and phosphoprotein: from predictions to experimental assessment. 2010 , 5, e11684	63
1396	Alterations in mGluR5 expression and signaling in Lewy body disease and in transgenic models of alpha-synucleinopathy--implications for excitotoxicity. 2010 , 5, e14020	54
1395	Critical lysine residues within the overlooked N-terminal domain of human APE1 regulate its biological functions. 2010 , 38, 8239-56	83
1394	Capillarity theory for the fly-casting mechanism. 2010 , 107, 2746-50	63
1393	Folding of Conjugated Proteins. 2010 , 6, 263-277	3
1392	Bioinformatical approaches to characterize intrinsically disordered/unstructured proteins. 2010 , 11, 225-43	99
1391	A single-amino-acid substitution in herpes simplex virus 1 envelope glycoprotein B at a site required for binding to the paired immunoglobulin-like type 2 receptor alpha (PILRalpha) abrogates PILRalpha-dependent viral entry and reduces pathogenesis. 2010 , 84, 10773-83	28
1390	Extended binding site on fibronectin for the functional upstream domain of protein F1 of <i>Streptococcus pyogenes</i> . 2010 , 285, 41087-99	48
1389	ComSin: database of protein structures in bound (complex) and unbound (single) states in relation to their intrinsic disorder. 2010 , 38, D283-7	24
1388	PB1-F2 influenza A virus protein adopts a beta-sheet conformation and forms amyloid fibers in membrane environments. 2010 , 285, 13233-43	50
1387	The subsequence composition of polypeptides. 2010 , 17, 1011-49	1
1386	Nanoelectronic detection of breast cancer biomarker. 2010 , 97, 233702	6
1385	Long synthetic peptides for the production of vaccines and drugs: a technological platform coming of age. 2010 , 2, 50rv3	15
1384	Proteomic analysis of potential keratan sulfate, chondroitin sulfate A, and hyaluronic acid molecular interactions. 2010 , 51, 4500-15	48
1383	The p53 core domain is a molten globule at low pH: functional implications of a partially unfolded structure. 2010 , 285, 2857-66	46
1382	Net charge per residue modulates conformational ensembles of intrinsically disordered proteins. 2010 , 107, 8183-8	376
1381	DNA search efficiency is modulated by charge composition and distribution in the intrinsically disordered tail. 2010 , 107, 21004-9	99
1380	The mysterious unfoldome: structureless, underappreciated, yet vital part of any given proteome. 2010 , 2010, 568068	173

1379	Influence of Conformational Entropy on the Protein Folding Rate. 2010 , 12, 961-982	7
1378	Computational prediction of O-linked glycosylation sites that preferentially map on intrinsically disordered regions of extracellular proteins. 2010 , 11, 4991-5008	50
1377	Hub promiscuity in protein-protein interaction networks. 2010 , 11, 1930-43	119
1376	Library of disordered patterns in 3D protein structures. 2010 , 6, e1000958	46
1375	Retro-MoRFs: identifying protein binding sites by normal and reverse alignment and intrinsic disorder prediction. 2010 , 11, 3725-47	35
1374	Intrinsically disordered proteins in a physics-based world. 2010 , 11, 5292-309	42
1373	Viral disorder or disordered viruses: do viral proteins possess unique features?. 2010 , 17, 932-51	96
1372	Comparing models of evolution for ordered and disordered proteins. 2010 , 27, 609-21	127
1371	Molecular insights into amyloid regulation by membrane cholesterol and sphingolipids: common mechanisms in neurodegenerative diseases. 2010 , 12, e27	127
1370	Structural disorder and dynamics of elastin. 2010 , 88, 239-50	120
1369	Biomolecular Structure and Modeling: Historical Perspective. 2010 , 1-40	
1368	Targeting intrinsically disordered proteins in neurodegenerative and protein dysfunction diseases: another illustration of the D(2) concept. 2010 , 7, 543-64	100
1367	Proline-rich salivary proteins have extended conformations. 2010 , 99, 656-65	70
1366	An unusual hydrophobic core confers extreme flexibility to HEAT repeat proteins. 2010 , 99, 1596-603	53
1365	Probing structural transitions in the intrinsically disordered C-terminal domain of the measles virus nucleoprotein by vibrational spectroscopy of cyanylated cysteines. 2010 , 99, 1676-83	43
1364	Universality in the timescales of internal loop formation in unfolded proteins and single-stranded oligonucleotides. 2010 , 99, 3959-68	17
1363	Interpretation of biomolecular NMR spin relaxation parameters. 2010 , 88, 131-42	17
1362	Radical redesign of a tandem array of four R67 dihydrofolate reductase genes yields a functional, folded protein possessing 45 substitutions. 2010 , 49, 7384-92	6

1361	Osmolyte-induced folding of an intrinsically disordered protein: folding mechanism in the absence of ligand. 2010 , 49, 5086-96		38
1360	Characterization of recombinant lysyl oxidase propeptide. 2010 , 49, 2962-72		30
1359	Prediction of tyrosine sulfation with mRMR feature selection and analysis. 2010 , 9, 6490-7		33
1358	Binding specificity of Escherichia coli single-stranded DNA binding protein for the chi subunit of DNA pol III holoenzyme and PriA helicase. 2010 , 49, 3555-66		55
1357	Single-molecule fluorescence studies of intrinsically disordered proteins. 2010 , 472, 179-204		94
1356	RNA polymerase II inhibitors dissociate antigenic peptide generation from normal viral protein synthesis: a role for nuclear translation in defective ribosomal product synthesis?. 2010 , 185, 6728-33		35
1355	Searching DNA via a "Monkey Bar" mechanism: the significance of disordered tails. <i>Journal of Molecular Biology</i> , 2010 , 396, 674-84	6.5	119
1354	A novel unstructured scaffold based on 4EBP1 enables the functional display of a wide range of bioactive peptides. <i>Journal of Molecular Biology</i> , 2010 , 404, 819-31	6.5	5
1353	Drugs for 'protein clouds': targeting intrinsically disordered transcription factors. 2010 , 10, 782-8		132
1352	The N-terminal part of Binder of Sperm 5 (BSP5), which promotes sperm capacitation in bovine species is intrinsically disordered. 2010 , 394, 1036-41		8
1351	Single-step affinity purification of recombinant proteins using the silica-binding Si-tag as a fusion partner. 2010 , 71, 91-5		38
1350	Molecular simulations of protein disorder. 2010 , 88, 269-90		65
1349	Tyr74 is essential for the formation, stability and function of Plasmodium falciparum triosephosphate isomerase dimer. 2010 , 494, 46-57		7
1348	Conformational selection in the molten globule state of the nuclear coactivator binding domain of CBP. 2010 , 107, 12535-40		135
1347	Intrinsic disorder in the core proteins of flaviviruses. 2010 , 17, 1019-25		26
1346	Protein Structure Analysis. 2010 , 63-105		2
1345	Computational resources for the prediction and analysis of native disorder in proteins. 2010 , 604, 369-93		11
1344	Quantifying the mechanisms of domain gain in animal proteins. 2010 , 11, R74		78

1343	Intrinsic disorder and protein multibinding in domain, terminal, and linker regions. 2010 , 6, 1821-8	19
1342	Malaria vaccine: why is it taking so long?. 2010 , 9, 111-4	3
1341	Membrane protein structural insights from chemical labeling and mass spectrometry. 2010 , 135, 1191-200	29
1340	Multicolor single-molecule FRET to explore protein folding and binding. 2010 , 6, 1540-7	61
1339	Conformational disorder of membrane peptides investigated from solid-state NMR line widths and line shapes. 2011 , 115, 10758-67	26
1338	Intrinsic Disorder in Putative Protein Sequences. 2011 ,	
1337	Studying disorder-to-order transitions from structural analysis. 2011 ,	
1336	The Ising model for prediction of disordered residues from protein sequence alone. 2011 , 8, 035004	51
1335	Direct observations of conformational distributions of intrinsically disordered p53 peptides using UV Raman and explicit solvent simulations. 2011 , 115, 9520-7	15
1334	Light-induced movement of the LOV2 domain in an Asp720Asn mutant LOV2-kinase fragment of Arabidopsis phototropin 2. 2011 , 50, 1174-83	22
1333	A free-energy landscape for coupled folding and binding of an intrinsically disordered protein in explicit solvent from detailed all-atom computations. 2011 , 133, 10448-58	89
1332	The expanding view of protein-protein interactions: complexes involving intrinsically disordered proteins. 2011 , 8, 035003	48
1331	Dual role of protein phosphorylation in DNA activator/coactivator binding. 2011 , 100, 469-77	13
1330	The calponin regulatory region is intrinsically unstructured: novel insight into actin-calponin and calmodulin-calponin interfaces using NMR spectroscopy. 2011 , 100, 1718-28	5
1329	The role of the LH subdomain in the function of the Cip/Kip cyclin-dependent kinase regulators. 2011 , 100, 2486-94	13
1328	Intrinsically Disordered Chaperones and Neurodegeneration. 2011 , 1-63	1
1327	Insights on the role of (dis)order from protein-protein interaction linear free-energy relationships. 2011 , 133, 9976-9	27
1326	Structure, interactions with host cell and functions of rhabdovirus phosphoprotein. 2011 , 6, 465-481	20

1325	Expanding the proteome: disordered and alternatively folded proteins. 2011 , 44, 467-518		132
1324	Mapping unstructured regions and synergistic folding in intrinsically disordered proteins with amide H/D exchange mass spectrometry. 2011 , 50, 8722-32		70
1323	Flexible nets of malleable guardians: intrinsically disordered chaperones in neurodegenerative diseases. 2011 , 111, 1134-66		59
1322	High Solubility of Random-Sequence Proteins Consisting of Five Kinds of Primitive Amino Acids. 2011 , 119-137		2
1321	The native ensemble and folding of a protein molten-globule: functional consequence of downhill folding. 2011 , 133, 12154-61		48
1320	Folding of a salivary intrinsically disordered protein upon binding to tannins. 2011 , 133, 7847-52		71
1319	Intrinsically disordered proteins from A to Z. 2011 , 43, 1090-103		322
1318	Promiscuity, stability and cold adaptation of a newly isolated acylaminoacyl peptidase. 2011 , 93, 1543-54		19
1317	Acute myeloid leukemia with mutated nucleophosmin (NPM1): any hope for a targeted therapy?. 2011 , 25, 247-54		64
1316	Molecular mechanisms of the anomalous thermal aggregation of green fluorescent protein. 2011 , 1814, 1930-9		14
1315	Targeting p27Kip1 protein: its relevance in the therapy of human cancer. 2011 , 15, 677-93		49
1314	Intrinsic disorder in S100 proteins. 2011 , 7, 2164-80		21
1313	Multispecific recognition: mechanism, evolution, and design. 2011 , 50, 602-11		42
1312	The cardiokine story unfolds: ischemic stress-induced protein secretion in the heart. 2011 , 17, 207-14		83
1311	Segmental conformational disorder and dynamics in the intrinsically disordered protein β synuclein and its chain length dependence. <i>Journal of Molecular Biology</i> , 2011 , 405, 1267-83	6.5	50
1310	Association of the disordered C-terminus of CDC34 with a catalytically bound ubiquitin. <i>Journal of Molecular Biology</i> , 2011 , 407, 425-38	6.5	18
1309	Solution structure of the mSin3A PAH2-PF1 SID1 complex: a Mad1/Mxd1-like interaction disrupted by MRG15 in the Rpd3S/Sin3S complex. <i>Journal of Molecular Biology</i> , 2011 , 408, 987-1000	6.5	20
1308	Time-resolved FRET detection of subtle temperature-induced conformational biases in ensembles of β synuclein molecules. <i>Journal of Molecular Biology</i> , 2011 , 411, 234-47	6.5	21

1307	Functional expression of milligram quantities of the synthetic human serotonin transporter gene in a tetracycline-inducible HEK293 cell line. 2011 , 76, 211-20	3
1306	Sequential melting of two hydrophobic clusters within the green fluorescent protein GFP-cycle3. 2011 , 50, 7735-44	13
1305	Conference of MSc students [Abstracts of the best contributions November 2010. 2011 , 55, 35	
1304	. 2011 ,	1
1303	. 2011 ,	9
1302	Complexity in Organismal Evolution. 2011 , 335-354	2
1301	Protein structural modularity and robustness are associated with evolvability. 2011 , 3, 456-75	27
1300	Alpha-Synuclein Interactions with Membranes. 2011 ,	
1299	Disordered patterns in clustered Protein Data Bank and in eukaryotic and bacterial proteomes. 2011 , 6, e27142	16
1298	Small cofactors may assist protein emergence from RNA world: clues from RNA-protein complexes. 2011 , 6, e22494	14
1297	Conformational plasticity of proNGF. 2011 , 6, e22615	11
1296	Mechanism of the interaction between the intrinsically disordered C-terminus of the pro-apoptotic ARTS protein and the Bir3 domain of XIAP. 2011 , 6, e24655	16
1295	Microsecond molecular dynamics simulations of intrinsically disordered proteins involved in the oxidative stress response. 2011 , 6, e27371	39
1294	Prediction of protein modification sites of pyrrolidone carboxylic acid using mRMR feature selection and analysis. 2011 , 6, e28221	9
1293	Do Viral Proteins Possess Unique Features?. 2011 , 1-34	4
1292	Intrinsic Disorder in Genome-Linked Viral Proteins VPgs of Potyviruses. 2011 , 277-312	
1291	Structural Disorder within the Nucleoprotein and Phosphoprotein from Measles, Nipah, and Hendra Viruses. 2011 , 47-94	5
1290	Structural Disorder within Sendai Virus Nucleoprotein and Phosphoprotein. 2011 , 95-114	

1289	Structural Disorder in Matrix Proteins of HIV-Related Viruses. 2011 , 143-167	
1288	Making Order in the Intrinsically Disordered Regions of HIV-1 Vif Protein. 2011 , 201-221	1
1287	Structural Disorder in Proteins of the Rhabdoviridae Replication Complex. 2011 , 115-141	
1286	Metallothioneins Based in part on the article Metallothioneins by Milan Vař & Jeremias H. R. Kři which appeared in the Encyclopedia of Inorganic Chemistry, First Edition.. 2011 ,	
1285	Nonequilibrium NMR Methods for Monitoring Protein and RNA Folding. 2011 , 225, 611-636	2
1284	Structural Disorder in Proteins from Influenza Virus. 2011 , 169-200	
1283	AMPA-receptor-mediated excitatory synaptic transmission is enhanced by iron-induced Eynuclein oligomers. 2011 , 117, 868-78	47
1282	Structure basis for the regulation of glyceraldehyde-3-phosphate dehydrogenase activity via the intrinsically disordered protein CP12. 2011 , 19, 1846-54	37
1281	Evolution and disorder. 2011 , 21, 441-6	198
1280	Uncoupled binding and folding of immune signaling-related intrinsically disordered proteins. 2011 , 106, 525-36	23
1279	Prediction of disorder with new computational tool: BVDEA. 2011 , 38, 14451-14459	9
1278	Denatured bactericidal proteins: active per se, or reservoirs of active peptides?. 2011 , 585, 2403-4	3
1277	Role of metal ions in aggregation of intrinsically disordered proteins in neurodegenerative diseases. 2011 , 3, 1163-80	88
1276	The intracellular distal tail of the Na ⁺ /H ⁺ exchanger NHE1 is intrinsically disordered: implications for NHE1 trafficking. 2011 , 50, 3469-80	50
1275	Multitude of binding modes attainable by intrinsically disordered proteins: a portrait gallery of disorder-based complexes. 2011 , 40, 1623-34	199
1274	Transient protein-protein interactions. 2011 , 24, 635-48	153
1273	Length-dependent aggregation of uninterrupted polyalanine peptides. 2011 , 50, 9200-11	39
1272	Structural biology: Breaking the protein rules. 2011 , 471, 151-3	133

1271	Case for an RNA-prion world: a hypothesis based on conformational diversity. 2011 , 37, 185-8	2
1270	Structure, function, and protein taxonomy. 2011 , 26, 533-545	6
1269	A functionally required unfoldome from the plant kingdom: intrinsically disordered N-terminal domains of GRAS proteins are involved in molecular recognition during plant development. 2011 , 77, 205-23	99
1268	PELPK1 (At5g09530) contains a unique pentapeptide repeat and is a positive regulator of germination in <i>Arabidopsis thaliana</i> . 2011 , 30, 1735-45	15
1267	Translating DRiPs: progress in understanding viral and cellular sources of MHC class I peptide ligands. 2011 , 68, 1481-9	55
1266	Why does the silica-binding protein "Si-tag" bind strongly to silica surfaces? Implications of conformational adaptation of the intrinsically disordered polypeptide to solid surfaces. 2011 , 86, 359-63	33
1265	Defining structural domains of an intrinsically disordered protein: Sic1, the cyclin-dependent kinase inhibitor of <i>Saccharomyces cerevisiae</i> . 2011 , 47, 34-42	10
1264	Binary classification of protein molecules into intrinsically disordered and ordered segments. 2011 , 11, 29	56
1263	Topology-based modeling of intrinsically disordered proteins: balancing intrinsic folding and intermolecular interactions. 2011 , 79, 1251-66	60
1262	Abundance and functional roles of intrinsic disorder in allergenic proteins and allergen representative peptides. 2011 , 79, 2595-606	5
1261	Evaluation of disorder predictions in CASP9. 2011 , 79 Suppl 10, 107-18	97
1260	Probing structural transitions in both structured and disordered proteins using site-directed spin-labeling EPR spectroscopy. 2011 , 17, 315-28	30
1259	Measuring rapid hydrogen exchange in the homodimeric 36 kDa HIV-1 integrase catalytic core domain. 2011 , 20, 500-12	26
1258	The N(0)-binding region of the vesicular stomatitis virus phosphoprotein is globally disordered but contains transient β helices. 2011 , 20, 542-56	46
1257	Context-dependent resistance to proteolysis of intrinsically disordered proteins. 2011 , 20, 1285-97	56
1256	The critical protein interactions and structures that elicit growth deregulation in cancer and viral replication. 2011 , 3, 48-73	12
1255	Theoretical study of the Raman optical activity spectra of 3(10)-helical polypeptides. 2011 , 12, 3291-306	17
1254	Intrinsically unstructured proteins and neurodegenerative diseases: conformational promiscuity at its best. 2011 , 63, 478-88	13

1253	High-resolution characterization of intrinsic disorder in proteins: expanding the suite of (13)C-detected NMR spectroscopy experiments to determine key observables. 2011 , 12, 2347-52	22
1252	Effect of hydrophilic polymer conjugation on heat-induced conformational changes in a protein. 2011 , 7, 1477-84	16
1251	Intrinsically disordered proteins may escape unwanted interactions via functional misfolding. 2011 , 1814, 693-712	52
1250	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
1249	Biophysical analysis of partially folded state of Hactalbumin in the presence of cationic and anionic surfactants. 2011 , 354, 234-47	19
1248	Structural Disorder within the Measles Virus Nucleoprotein and Phosphoprotein: Functional Implications for Transcription and Replication. 2011 , 95-125	6
1247	Natural tri- to hexapeptides self-assemble in water to amyloid beta-type fiber aggregates by unexpected alpha-helical intermediate structures. 2011 , 108, 1361-6	208
1246	Nuclear magnetic resonance analysis of protein-DNA interactions. 2011 , 8, 1065-78	24
1245	Proteins without 3D structure: definition, detection and beyond. 2011 , 27, 1449-54	28
1244	The diversity of physical forces and mechanisms in intermolecular interactions. 2011 , 8, 035002	30
1243	Characterization of the interactions between the nucleoprotein and the phosphoprotein of Henipavirus. 2011 , 286, 13583-602	51
1242	Overexpression of peroxisomal testis-specific 1 protein induces germ cell apoptosis and leads to infertility in male mice. 2011 , 22, 1766-79	17
1241	Actin capping protein and its inhibitor CARMIL: how intrinsically disordered regions function. 2011 , 8, 035005	11
1240	Elevated evolutionary rate in genes with homopolymeric amino acid repeats constituting nondisordered structure. 2011 , 28, 543-50	8
1239	Pleiotropic effects of the wheat dehydrin DHN-5 on stress responses in Arabidopsis. 2011 , 52, 676-88	53
1238	Proteins with RNA chaperone activity: a world of diverse proteins with a common task-impediment of RNA misfolding. 2011 , 2011, 532908	45
1237	ERBIN is a new SARA-interacting protein: competition between SARA and SMAD2 and SMAD3 for binding to ERBIN. 2011 , 124, 3209-22	20
1236	Covalent structural changes in unfolded GroES that lead to amyloid fibril formation detected by NMR: insight into intrinsically disordered proteins. 2011 , 286, 21796-805	8

1235	Importance of the proline-rich multimerization domain on the oligomerization and nucleic acid binding properties of HIV-1 Vif. 2011 , 39, 2404-15	28
1234	CSpritz: accurate prediction of protein disorder segments with annotation for homology, secondary structure and linear motifs. 2011 , 39, W190-6	66
1233	Assembly of a filamin four-domain fragment and the influence of splicing variant-1 on the structure. 2011 , 286, 26921-30	13
1232	Novel strategies for drug discovery based on Intrinsically Disordered Proteins (IDPs). 2011 , 12, 3205-19	42
1231	Coupled folding and specific binding: fishing for amphiphilicity. 2011 , 12, 1431-50	11
1230	Genome-wide survey of natural selection on functional, structural, and network properties of polymorphic sites in <i>Saccharomyces paradoxus</i> . 2011 , 28, 2615-27	18
1229	Anchoring intrinsically disordered proteins to multiple targets: lessons from N-terminus of the p53 protein. 2011 , 12, 1410-30	19
1228	Prediction of lysine ubiquitylation with ensemble classifier and feature selection. 2011 , 12, 8347-61	42
1227	Mutual synergistic protein folding in split intein. 2012 , 32, 433-42	15
1226	ESpritz: accurate and fast prediction of protein disorder. 2012 , 28, 503-9	317
1225	Conserved motifs in the Msn2-activating domain are important for Msn2-mediated yeast stress response. 2012 , 125, 3333-42	18
1224	A preformed binding interface in the unbound ensemble of an intrinsically disordered protein: evidence from molecular simulations. 2012 , 8, e1002605	98
1223	Using NMR chemical shifts to calculate the propensity for structural order and disorder in proteins. 2012 , 40, 1014-20	82
1222	Disease-associated mutations disrupt functionally important regions of intrinsic protein disorder. 2012 , 8, e1002709	95
1221	Analyzing a Potential Drug Target N-Myristoyltransferase of <i>Plasmodium falciparum</i> Through In Silico Approaches. 2012 , 4, 43-54	5
1220	Proteome-wide discovery of evolutionary conserved sequences in disordered regions. 2012 , 5, rs1	76
1219	Characterization and functional analysis of <i>atl</i> , a novel gene encoding autolysin in <i>Streptococcus suis</i> . 2012 , 194, 1464-73	38
1218	IDEAL: Intrinsically Disordered proteins with Extensive Annotations and Literature. 2012 , 40, D507-11	68

1217	Nanomechanics of Proteins, Both Folded and Disordered. 2012 , 1-47	
1216	HSF transcription factor family, heat shock response, and protein intrinsic disorder. 2012 , 13, 86-103	79
1215	Accurate prediction of protein structural classes using functional domains and predicted secondary structure sequences. 2012 , 29, 623-33	15
1214	The plant proteome folding project: structure and positive selection in plant protein families. 2012 , 4, 360-71	13
1213	Biophysical and computational fragment-based approaches to targeting protein-protein interactions: applications in structure-guided drug discovery. 2012 , 45, 383-426	74
1212	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
1211	Agonism/antagonism switching in allosteric ensembles. 2012 , 109, 4134-9	80
1210	Understanding Viral Transmission Behavior via Protein Intrinsic Disorder Prediction: Coronaviruses. 2012 , 2012, 738590	32
1209	Thermodynamic dissection of the intrinsically disordered N-terminal domain of human glucocorticoid receptor. 2012 , 287, 26777-87	37
1208	Plasticity in structural and functional interactions between the phosphoprotein and nucleoprotein of measles virus. 2012 , 287, 11951-67	30
1207	Curcumin-glucoside, a novel synthetic derivative of curcumin, inhibits β synuclein oligomer formation: relevance to Parkinson's disease. 2012 , 18, 76-84	37
1206	Local flexibility facilitates oxidization of buried methionine residues. 2012 , 19, 688-97	21
1205	Editorial: intrinsically disordered proteins: a focused look at fuzzy subjects. 2012 , 13, 2-5	1
1204	How random are intrinsically disordered proteins? A small angle scattering perspective. 2012 , 13, 55-75	225
1203	HIV-1 Tat Binding to PCAF Bromodomain: Structural Determinants from Computational Methods. 2012 , 1, 277-96	8
1202	Secondary Structure and Dynamics of a Family of Disordered Proteins. 2012 , 221-238	
1201	Intrinsically disordered proteins: a 10-year recap. 2012 , 37, 509-16	451
1200	Protein structure networks. 2012 , 11, 469-78	41

1199	Is a malleable protein necessarily highly dynamic? The hydrophobic core of the nuclear coactivator binding domain is well ordered. 2012 , 102, 1627-35	17
1198	Thermo-resistant intrinsically disordered proteins are efficient 20S proteasome substrates. 2012 , 8, 368-73	32
1197	Intrinsically disordered proteins in human mitochondria. 2012 , 17, 817-25	8
1196	Denaturant-induced conformational transitions in intrinsically disordered proteins. 2012 , 896, 197-213	3
1195	Intrinsically disordered proteins and novel strategies for drug discovery. 2012 , 7, 475-88	78
1194	Disordered Protein Diffusion under Crowded Conditions. 2012 , 3, 2703-2706	42
1193	Sequence repeats and protein structure. 2012 , 86, 050901	2
1192	Proteomic characterization of the human FTSJ3 preribosomal complexes. 2012 , 11, 3112-26	12
1191	Malaria vaccine development using synthetic peptides as a technical platform. 2012 , 114, 107-49	10
1190	A propensity scale for type II polyproline helices (PPII): aromatic amino acids in proline-rich sequences strongly disfavor PPII due to proline-aromatic interactions. 2012 , 51, 5041-51	65
1189	Exclusively heteronuclear (¹³ C)-detected amino-acid-selective NMR experiments for the study of intrinsically disordered proteins (IDPs). 2012 , 13, 2425-32	36
1188	Stochastic simulation of structural properties of natively unfolded and denatured proteins. 2012 , 18, 4503-16	2
1187	Speeding up sequence specific assignment of IDPs. 2012 , 53, 293-301	63
1186	High-throughput characterization of intrinsic disorder in proteins from the Protein Structure Initiative. 2012 , 180, 201-15	31
1185	Comparative nucleic acid chaperone properties of the nucleocapsid protein NCp7 and Tat protein of HIV-1. 2012 , 169, 349-60	23
1184	Direct Sequential Hit Strategy for Unambiguous and Accurate Backbone Assignment of ¹³ C/ ¹⁵ N Labeled Proteins. 2012 , 35, 389-399	5
1183	Thermodynamic and Kinetic Models for Aggregation of Intrinsically Disordered Proteins. 2012 , 413-440	1
1182	More than just tails: intrinsic disorder in histone proteins. 2012 , 8, 1886-901	87

1181	Occurrence of disordered patterns and homorepeats in eukaryotic and bacterial proteomes. 2012 , 8, 327-37		25
1180	Understanding the structural ensembles of a highly extended disordered protein. 2012 , 8, 308-19		31
1179	Correlation of disorder between <i>S. cerevisiae</i> interacting proteins. 2012 , 8, 417-25		
1178	Modulation of an IDP binding mechanism and rates by helix propensity and non-native interactions: association of HIF1 α with CBP. 2012 , 8, 256-67		78
1177	A comprehensive overview of computational protein disorder prediction methods. 2012 , 8, 114-21		79
1176	SPINE-D: accurate prediction of short and long disordered regions by a single neural-network based method. 2012 , 29, 799-813		126
1175	The roles of intrinsic disorder in orchestrating the Wnt-pathway. 2012 , 29, 843-61		37
1174	A functional loop spanning distant domains of glutaminyl-tRNA synthetase also stabilizes a molten globule state. 2012 , 51, 4429-37		10
1173	Wide-open flaps are key to urease activity. 2012 , 134, 9934-7		38
1172	The structural characteristics of human preprotein translocase of the inner mitochondrial membrane Tim23: implications for its physiological activities. 2012 , 82, 255-62		5
1171	Comparison of Secondary Structure Formation Using 10 Different Force Fields in Microsecond Molecular Dynamics Simulations. 2012 , 8, 2725-2740		150
1170	Influence of 63Ser phosphorylation and dephosphorylation on the structure of the stathmin helical nucleation sequence: a molecular dynamics study. 2012 , 51, 8455-63		7
1169	Towards the physical basis of how intrinsic disorder mediates protein function. 2012 , 524, 123-31		67
1168	Disordered competitive recruiter: fast and foldable. <i>Journal of Molecular Biology</i> , 2012 , 418, 267-8	6.5	20
1167	On the possible amyloid origin of protein folds. <i>Journal of Molecular Biology</i> , 2012 , 421, 417-26	6.5	89
1166	Electrostatically accelerated coupled binding and folding of intrinsically disordered proteins. <i>Journal of Molecular Biology</i> , 2012 , 422, 674-684	6.5	60
1165	Residual structure and dynamics in DMSO-d ₆ denatured dynein light chain protein. 2012 , 94, 231-41		6
1164	Role of the biomolecular energy gap in protein design, structure, and evolution. 2012 , 149, 262-73		83

1163	Interaction between the C-terminal domains of measles virus nucleoprotein and phosphoprotein: a tight complex implying one binding site. 2012 , 21, 1577-85	13
1162	Thermal unfolding of the N-terminal region of p53 monitored by circular dichroism spectroscopy. 2012 , 21, 1682-8	5
1161	MobiDB: a comprehensive database of intrinsic protein disorder annotations. 2012 , 28, 2080-1	112
1160	Predicting protein oxidation sites with feature selection and analysis approach. 2012 , 29, 650-8	21
1159	Chapter 5:NMR Studies of Disordered but Functional Proteins. 111-129	
1158	Fuzziness: linking regulation to protein dynamics. 2012 , 8, 168-77	128
1157	Intrinsically disordered regions have specific functions in mitochondrial and nuclear proteins. 2012 , 8, 247-55	9
1156	3.9 Intrinsically Disordered Proteins. 2012 , 170-211	0
1155	3.12 The Folding of Repeat Proteins. 2012 , 267-289	
1154	Why are we Interested in the Unfolded Peptides and Proteins?. 2012 , 1-54	4
1153	Regulation of protein phosphatase 1 by intrinsically disordered proteins. 2012 , 40, 969-74	32
1152	Using chemical shifts to assess transient secondary structure and generate ensemble structures of intrinsically disordered proteins. 2012 , 895, 139-52	11
1151	Circular dichroism techniques for the analysis of intrinsically disordered proteins and domains. 2012 , 895, 387-404	60
1150	Protein intrinsic disorder and induced pluripotent stem cells. 2012 , 8, 134-50	32
1149	The measles virus N(TAIL)-XD complex: an illustrative example of fuzziness. 2012 , 725, 126-41	19
1148	Fuzzy complexes: a more stochastic view of protein function. 2012 , 725, 1-14	162
1147	A folding-after-binding mechanism describes the recognition between the transactivation domain of c-Myb and the KIX domain of the CREB-binding protein. 2012 , 428, 205-9	65
1146	Quantifying protein modularity and evolvability: a comparison of different techniques. 2012 , 110, 22-33	8

1145	Solution model of the intrinsically disordered polyglutamine tract-binding protein-1. 2012 , 102, 1608-16		13
1144	Prediction of protein relative enthalpic stability from molecular dynamics simulations of the folded and unfolded states. 2012 , 103, 1762-73		3
1143	Homepeptide repeats: implications for protein structure, function and evolution. 2012 , 10, 217-25		6
1142	Structural features and cytotoxicity of amyloid oligomers: implications in Alzheimer's disease and other diseases with amyloid deposits. 2012 , 99, 226-45		138
1141	Probing the diverse landscape of protein flexibility and binding. 2012 , 22, 643-50		87
1140	The ubiquitin/proteasome system-dependent control of mitochondrial steps in apoptosis. 2012 , 23, 499-508		21
1139	Target binding to S100B reduces dynamic properties and increases Ca(2+)-binding affinity for wild type and EF-hand mutant proteins. <i>Journal of Molecular Biology</i> , 2012 , 423, 365-85	6.5	13
1138	Identification of intrinsically disordered proteins by a special 2D electrophoresis. 2012 , 896, 215-22		6
1137	Osmolyte-, binding-, and temperature-induced transitions of intrinsically disordered proteins. 2012 , 896, 257-66		1
1136	Protein Disorder and Human Genetic Disease. 2012 ,		2
1135	Multiparametric analysis of intrinsically disordered proteins: looking at intrinsic disorder through compound eyes. 2012 , 84, 2096-104		70
1134	Cell cycle regulation by the intrinsically disordered proteins p21 and p27. 2012 , 40, 981-8		149
1133	Bullied no more: when and how DNA shoves proteins around. 2012 , 45, 257-299		54
1132	Influence of serum proteins on conformation of prostate-specific antigen. 2012 , 29, 1051-64		16
1131	Intrinsically disordered regions as affinity tuners in protein-DNA interactions. 2012 , 8, 47-57		147
1130	Dynamic optimization of signal transduction via intrinsic disorder. 2012 , 8, 194-7		3
1129	Synergistic folding of two intrinsically disordered proteins: searching for conformational selection. 2012 , 8, 198-209		47
1128	Aromatic residues link binding and function of intrinsically disordered proteins. 2012 , 8, 237-46		24

1127	Intrinsic protein disorder in human pathways. 2012 , 8, 320-6	12
1126	Slow, reversible, coupled folding and binding of the spectrin tetramerization domain. 2012 , 103, 2203-14	35
1125	MOLECULAR BIOLOGY AT THE QUANTUM LEVEL: CAN MODERN DENSITY FUNCTIONAL THEORY FORGE THE PATH?. 2012 , 02, 1230006	7
1124	Glycation promotes the formation of genotoxic aggregates in glucose oxidase. 2012 , 43, 1311-22	29
1123	Bioinspiration. 2012 ,	15
1122	Order and disorder in viral proteins: new insights into an old paradigm. 2012 , 7, 1183-1191	7
1121	Intrinsically Disordered Protein Analysis. 2012 ,	8
1120	Inherent structural disorder and dimerisation of murine norovirus NS1-2 protein. 2012 , 7, e30534	24
1119	Analysis of conformational variation in macromolecular structural models. 2012 , 7, e39993	5
1118	VAPC, an human endogenous inhibitor for hepatitis C virus (HCV) infection, is intrinsically unstructured but forms a "fuzzy complex" with HCV NS5B. 2012 , 7, e40341	10
1117	Prediction of protein cleavage site with feature selection by random forest. 2012 , 7, e45854	32
1116	Covalent Synuclein dimers: chemico-physical and aggregation properties. 2012 , 7, e50027	30
1115	Applications of Bioinformatics and Experimental Methods to Intrinsic Disorder-Based Protein-Protein Interactions. 2012 ,	1
1114	Evolutionary Engineering of Artificial Proteins with Limited Sets of Primitive Amino Acids. 2012 ,	
1113	Folding of Intrinsically Disordered Protein Phosphatase 1 Regulatory Proteins. 2012 , 2, 107-114	9
1112	Prediction of protein domain with mRMR feature selection and analysis. 2012 , 7, e39308	74
1111	Protein Folding, Binding and Energy Landscape: A Synthesis. 2012 ,	10
1110	Ensemble modeling of protein disordered states: experimental restraint contributions and validation. 2012 , 80, 556-72	95

1109	Ordered and disordered proteins as nanomaterial building blocks. 2012 , 4, 204-18	18
1108	Coil-to-helix transitions in intrinsically disordered methyl CpG binding protein 2 and its isolated domains. 2012 , 21, 531-8	21
1107	Click strategies for single-molecule protein fluorescence. 2012 , 134, 5187-95	95
1106	Intrinsic protein flexibility in regulation of cell proliferation: advantages for signaling and opportunities for novel therapeutics. 2012 , 725, 27-49	25
1105	Interactions via intrinsically disordered regions: what kind of motifs?. 2012 , 64, 513-20	62
1104	Recent progress in NMR spectroscopy: toward the study of intrinsically disordered proteins of increasing size and complexity. 2012 , 64, 473-81	49
1103	Orderly order in protein intrinsic disorder distribution: disorder in 3500 proteomes from viruses and the three domains of life. 2012 , 30, 137-49	370
1102	Protein dynamics and the diversity of an antibody response. 2012 , 287, 27139-47	23
1101	Putting proteins in context: scientific illustrations bring together information from diverse sources to provide an integrative view of the molecular biology of cells. 2012 , 34, 718-20	3
1100	Intrinsically disordered proteins: from sequence and conformational properties toward drug discovery. 2012 , 13, 930-50	74
1099	Structural and energetic basis of allostery. 2012 , 41, 585-609	216
1098	Protein intrinsic disorder as a flexible armor and a weapon of HIV-1. 2012 , 69, 1211-59	82
1097	Characterization of molten globule PopB in absence and presence of its chaperone PcrH. 2012 , 31, 401-16	9
1096	Comparative genetics of the poly-Q tract of ataxin-1 and its binding protein PQBP-1. 2012 , 50, 309-17	3
1095	Nucleosome surface containing nucleosomal DNA entry/exit site regulates H3-K36me3 via association with RNA polymerase II and Set2. 2012 , 17, 65-81	9
1094	SASSIE: A program to study intrinsically disordered biological molecules and macromolecular ensembles using experimental scattering restraints. 2012 , 183, 382-389	93
1093	Role of β -synuclein penetration into the membrane in the mechanisms of oligomer pore formation. 2012 , 279, 1000-13	120
1092	Predict and analyze S-nitrosylation modification sites with the mRMR and IFS approaches. 2012 , 75, 1654-65	69

1091	Intrinsic disorder in cell signaling and gene transcription. 2012 , 348, 457-65	87
1090	Structural basis for molecular interactions involving MRG domains: implications in chromatin biology. 2012 , 20, 151-60	17
1089	Intrinsic disorder: signaling via highly specific but short-lived association. 2012 , 37, 43-8	109
1088	Disordered proteins studied by chemical shifts. 2012 , 60, 42-51	48
1087	Intrinsic disorder in putative protein sequences. 2012 , 10 Suppl 1, S19	20
1086	Search for identical octapeptides in unrelated proteins: Structural plasticity revisited. 2012 , 98, 11-26	16
1085	Enhanced and effective conformational sampling of protein molecular systems for their free energy landscapes. 2012 , 4, 27-44	48
1084	Structural basis for protein phosphatase 1 regulation and specificity. 2013 , 280, 596-611	144
1083	Folding and binding of an intrinsically disordered protein: fast, but not 'diffusion-limited'. 2013 , 135, 1415-22	96
1082	Comparative characteristics of the structure and function for animal syndecan-1 proteins. 2013 , 47, 446-452	5
1081	Ion mobility spectrometry focusing on speciation analysis of metals/metalloids bound to carbonic anhydrase. 2013 , 405, 7653-60	6
1080	Unusual biophysics of intrinsically disordered proteins. 2013 , 1834, 932-51	377
1079	Encyclopedia of Biophysics. 2013 , 2326-2327	
1078	Intrinsic disorder of the bacterial cell division protein ZipA: coil-to-brush conformational transition. 2013 , 27, 3363-75	18
1077	Time window expansion for HDX analysis of an intrinsically disordered protein. 2013 , 24, 1584-92	59
1076	The c-Abl/YAP/p73 Apoptotic Module and the HIPPO Pathway. 2013 , 173-195	1
1075	Modulation of the intrinsic helix propensity of an intrinsically disordered protein reveals long-range helix-helix interactions. 2013 , 135, 10155-63	39
1074	Cooperative unfolding of compact conformations of the intrinsically disordered protein osteopontin. 2013 , 52, 5167-75	61

1073	Single-molecule Studies of Proteins. 2013 ,	6
1072	IsUnstruct: prediction of the residue status to be ordered or disordered in the protein chain by a method based on the Ising model. 2013 , 31, 1034-43	35
1071	Analysis and consensus of currently available intrinsic protein disorder annotation sources in the MobiDB database. 2013 , 14 Suppl 7, S3	28
1070	An improved sequence based prediction protocol for DNA-binding proteins using SVM and comprehensive feature analysis. 2013 , 14, 90	56
1069	Protonation-dependent conformational variability of intrinsically disordered proteins. 2013 , 22, 1196-205	27
1068	Knockdown of prothymosin β leads to apoptosis and developmental defects in zebrafish embryos. 2013 , 91, 325-32	7
1067	Unfolded protein ensembles, folding trajectories, and refolding rate prediction. 2013 , 139, 121925	6
1066	Prediction of protein amidation sites by feature selection and analysis. 2013 , 288, 391-400	9
1065	Precision vs flexibility in GPCR signaling. 2013 , 135, 12305-12	41
1064	The heterogeneous structural behavior of E7 from HPV16 revealed by NMR spectroscopy. 2013 , 14, 1876-82	12
1063	Encyclopedia of Biophysics. 2013 , 2312-2315	
1062	Inherent relationships among different biophysical prediction methods for intrinsically disordered proteins. 2013 , 104, 488-95	11
1061	Under-folded proteins: Conformational ensembles and their roles in protein folding, function, and pathogenesis. 2013 , 99, 870-87	33
1060	The Hippo Signaling Pathway and Cancer. 2013 ,	5
1059	The tandem zipper: modular binding of tandem domains and linear motifs. 2013 , 587, 1164-71	18
1058	Recent Advances in Solution NMR Studies. 2013 , 80, 359-418	11
1057	Solvent interaction analysis of intrinsically disordered proteins in aqueous two-phase systems. 2013 , 9, 3068-79	14
1056	Structure prediction and analysis of DNA transposon and LINE retrotransposon proteins. 2013 , 288, 16127-38	10

1055	High-dimensionality ¹³ C direct-detected NMR experiments for the automatic assignment of intrinsically disordered proteins. 2013 , 57, 353-61	39
1054	NMR spectroscopic studies of intrinsically disordered proteins at near-physiological conditions. 2013 , 52, 11808-12	60
1053	Intrinsically disordered regions of p53 family are highly diversified in evolution. 2013 , 1834, 725-38	58
1052	Buried and accessible surface area control intrinsic protein flexibility. <i>Journal of Molecular Biology</i> , 2013 , 425, 3250-63	6.5 44
1051	Membrane association and destabilization by <i>Aggregatibacter actinomycetemcomitans</i> leukotoxin requires changes in secondary structures. 2013 , 28, 342-53	11
1050	Effects of Macromolecular Crowding on the Conformational Ensembles of Disordered Proteins. 2013 , 4,	44
1049	Frustration-induced protein intrinsic disorder. 2013 , 138, 105101	6
1048	Protein intrinsic disorder in the acetyome of intracellular and extracellular <i>Toxoplasma gondii</i> . 2013 , 9, 645-57	39
1047	Protein recognition and selection through conformational and mutually induced fit. 2013 , 110, 20545-50	41
1046	An assignment of intrinsically disordered regions of proteins based on NMR structures. 2013 , 181, 29-36	22
1045	Utilization of protein intrinsic disorder knowledge in structural proteomics. 2013 , 1834, 487-98	46
1044	On the functional and structural characterization of hubs in protein-protein interaction networks. 2013 , 31, 274-86	40
1043	Assembly of the SLIP1-SLBP complex on histone mRNA requires heterodimerization and sequential binding of SLBP followed by SLIP1. 2013 , 52, 520-36	12
1042	Energetic basis of uncoupling folding from binding for an intrinsically disordered protein. 2013 , 135, 1288-94	35
1041	Describing sequence-ensemble relationships for intrinsically disordered proteins. 2013 , 449, 307-18	80
1040	Prediction of active sites of enzymes by maximum relevance minimum redundancy (mRMR) feature selection. 2013 , 9, 61-9	26
1039	Exploring the binding diversity of intrinsically disordered proteins involved in one-to-many binding. 2013 , 22, 258-73	132
1038	A flash in the pan: dissecting dynamic amyloid intermediates using fluorescence. 2013 , 587, 1096-105	12

1037	Origin and evolution of the cystic fibrosis transmembrane regulator protein R domain. 2013 , 523, 137-46	18
1036	RAPID: fast and accurate sequence-based prediction of intrinsic disorder content on proteomic scale. 2013 , 1834, 1671-80	35
1035	Temperature and urea have opposing impacts on polyproline II conformational bias. 2013 , 52, 949-58	14
1034	Effects of confinement on the structure and dynamics of an intrinsically disordered peptide: a molecular-dynamics study. 2013 , 117, 3707-19	14
1033	Hydrogen-exchange mass spectrometry for the study of intrinsic disorder in proteins. 2013 , 1834, 1202-9	54
1032	Long indels are disordered: a study of disorder and indels in homologous eukaryotic proteins. 2013 , 1834, 890-7	25
1031	Prediction of Hydrodynamic and Other Solution Properties of Partially Disordered Proteins with a Simple, Coarse-Grained Model. 2013 , 9, 1678-85	17
1030	Diffusion-enhanced Förster resonance energy transfer and the effects of external quenchers and the donor quantum yield. 2013 , 117, 185-98	23
1029	Doing molecular biophysics: finding, naming, and picturing signal within complexity. 2013 , 42, 1-28	17
1028	Protein folding: a problem with multiple solutions. 2013 , 31, 351-62	24
1027	The contribution of intrinsic disorder prediction to the elucidation of protein function. 2013 , 23, 467-72	43
1026	Comparative analysis of 126 cyanobacterial genomes reveals evidence of functional diversity among homologs of the redox-regulated CP12 protein. 2013 , 161, 824-35	36
1025	A decade and a half of protein intrinsic disorder: biology still waits for physics. 2013 , 22, 693-724	341
1024	BEST-TROSY experiments for time-efficient sequential resonance assignment of large disordered proteins. 2013 , 55, 311-21	141
1023	Improving the chemical shift dispersion of multidimensional NMR spectra of intrinsically disordered proteins. 2013 , 55, 231-7	29
1022	Encyclopedia of Biophysics. 2013 , 2309-2309	
1021	Pathways of Amyloid Fibril Formation Using a Simplified Peptide Model. 2013 , 305-331	
1020	Potential conformational heterogeneity of p53 bound to S100B(β) <i>Journal of Molecular Biology</i> , 2013 , 425, 999-1010	6.5 22

1019	Encyclopedia of Biophysics. 2013 , 2324-2326		1
1018	Encyclopedia of Biophysics. 2013 , 2337-2339		
1017	Encyclopedia of Biophysics. 2013 , 2439-2447		2
1016	Regulation of protein-protein binding by coupling between phosphorylation and intrinsic disorder: analysis of human protein complexes. 2013 , 9, 1620-6		45
1015	Fuzzy complex formation between the intrinsically disordered prothymosin β and the Kelch domain of Keap1 involved in the oxidative stress response. <i>Journal of Molecular Biology</i> , 2013 , 425, 1011-27	6.5	34
1014	Rapid Conformational Fluctuations of Disordered HIV-1 Fusion Peptide in Solution. 2013 , 9, 2870-4		7
1013	Essential Tetraspanin Functions in the Vertebrate Retina. 2013 , 321-343		1
1012	Encyclopedia of Biophysics. 2013 , 2470-2475		1
1011	Structural biology: Signalling from disordered proteins. 2013 , 498, 308-10		17
1010	Virology: The virus whose family expanded. 2013 , 498, 310-1		21
1009	Analyses of the general rule on residue pair frequencies in local amino acid sequences of soluble, ordered proteins. 2013 , 22, 725-33		1
1008	Mass spectrometry methods for intrinsically disordered proteins. 2013 , 138, 32-42		67
1007	Dissecting partner recognition by an intrinsically disordered protein using descriptive random mutagenesis. <i>Journal of Molecular Biology</i> , 2013 , 425, 3495-509	6.5	21
1006	The most important thing is the tail: multitudinous functionalities of intrinsically disordered protein termini. 2013 , 587, 1891-901		95
1005	Encyclopedia of Biophysics. 2013 , 2531-2536		
1004	Revisiting ligand-induced conformational changes in proteins: essence, advancements, implications and future challenges. 2013 , 31, 630-48		35
1003	FlgM proteins from different bacteria exhibit different structural characteristics. 2013 , 1834, 808-16		6
1002	Analysis of Molecular Recognition Features (MoRFs) in membrane proteins. 2013 , 1834, 798-807		22

1001	Structural disorder and local order of hNopp140. 2013 , 1834, 342-50	22
1000	Native-based simulations of the binding interaction between RAP74 and the disordered FCP1 peptide. 2013 , 117, 3074-85	11
999	Aggregation of the salivary proline-rich protein IB5 in the presence of the tannin EgCG. 2013 , 29, 1926-37	82
998	Molecular dynamics simulations of amyloid fibrils: an in silico approach. 2013 , 45, 503-8	19
997	Prediction of protein phosphorylation sites by support vector machines. 2013 ,	
996	Bilberry anthocyanins neutralize the cytotoxicity of co-chaperonin GroES fibrillation intermediates. 2013 , 52, 9202-11	8
995	Distribution and cluster analysis of predicted intrinsically disordered protein Pfam domains. 2013 , 1, e25724	9
994	The alphabet of intrinsic disorder: II. Various roles of glutamic acid in ordered and intrinsically disordered proteins. 2013 , 1, e24684	54
993	Structural characterizations of phosphorylatable residues in transmembrane proteins from. 2013 , 1, e25713	5
992	Functional fragments of disorder in outer membrane barrel proteins. 2013 , 1, e24848	3
991	Digested disorder: Quarterly intrinsic disorder digest (April-May-June, 2013). 2013 , 1, e27454	6
990	Protein conformational disorder and enzyme catalysis. 2013 , 337, 41-67	42
989	What's in a name? Why these proteins are intrinsically disordered: Why these proteins are intrinsically disordered. 2013 , 1, e24157	171
988	A novel method of predicting protein disordered regions based on sequence features. 2013 , 2013, 414327	13
987	On the importance of polar interactions for complexes containing intrinsically disordered proteins. 2013 , 9, e1003192	46
986	Multifarious roles of intrinsic disorder in proteins illustrate its broad impact on plant biology. 2013 , 25, 38-55	103
985	A transient helical molecular recognition element in the disordered N-terminus of the Sgs1 helicase is critical for chromosome stability and binding of Top3/Rmi1. 2013 , 41, 10215-27	19
984	Population size dependence of fitness effect distribution and substitution rate probed by biophysical model of protein thermostability. 2013 , 5, 1584-93	28

983	Extracting structural information from charge-state distributions of intrinsically disordered proteins by non-denaturing electrospray-ionization mass spectrometry. 2013 , 1, e25068	22
982	mpMoRFsDB: a database of molecular recognition features in membrane proteins. 2013 , 29, 2517-8	7
981	The alphabet of intrinsic disorder: I. Act like a Pro: On the abundance and roles of proline residues in intrinsically disordered proteins. 2013 , 1, e24360	143
980	Structure of the transition state for the binding of c-Myb and KIX highlights an unexpected order for a disordered system. 2013 , 110, 14942-7	85
979	Development of a fluorescent monoclonal antibody-based assay to measure the allosteric effects of synthetic peptides on self-oligomerization of AGR2 protein. 2013 , 22, 1266-78	18
978	Structural divergence is more extensive than sequence divergence for a family of intrinsically disordered proteins. 2013 , 81, 1686-98	11
977	Tetraspanins. 2013 ,	10
976	Structural flexibility of intrinsically disordered proteins induces stepwise target recognition. 2013 , 139, 225103	13
975	Disorder in the lifetime of a protein. 2013 , 1, e26782	2
974	Quantifying the topography of the intrinsic energy landscape of flexible biomolecular recognition. 2013 , 110, E2342-51	49
973	Rapid evolutionary dynamics of structural disorder as a potential driving force for biological divergence in flaviviruses. 2013 , 5, 504-13	23
972	[Structural study of polyglutamine tract-binding protein 1]. 2013 , 133, 519-26	1
971	50 & 100 Years Ago. 2013 , 498, 310-310	13
970	NMR Spectroscopic Studies of Intrinsically Disordered Proteins at Near-Physiological Conditions. 2013 , 125, 12024-12028	12
969	Inter- and Intra-Chain Disulfide Bond Prediction Based on Optimal Feature Selection. 2013 , 20, 324-335	3
968	The switches.ELM resource: a compendium of conditional regulatory interaction interfaces. 2013 , 6, rs7	83
967	Multicanonical simulation of coupled folding and binding of intrinsically disordered protein using an Ising-like protein model. 2013 , 454, 012034	0
966	A coarse-grained protein model in a water-like solvent. 2013 , 3, 1841	10

965	Short Polypeptide with Metastable Structures. 2013 , 19, 29-34	0
964	The N-terminal intrinsically disordered domain of Mgm101p is localized to the mitochondrial nucleoid. 2013 , 8, e56465	8
963	Assigning quantitative function to post-translational modifications reveals multiple sites of phosphorylation that tune yeast pheromone signaling output. 2013 , 8, e56544	3
962	Electrostatic mis-interactions cause overexpression toxicity of proteins in E. coli. 2013 , 8, e64893	6
961	Conformational dissection of a viral intrinsically disordered domain involved in cellular transformation. 2013 , 8, e72760	14
960	Ordered disorder of the astrocytic dystrophin-associated protein complex in the norm and pathology. 2013 , 8, e73476	10
959	Intrinsic disorder-based protein interactions and their modulators. 2013 , 19, 4191-213	185
958	Sequence complexity of amyloidogenic regions in intrinsically disordered human proteins. 2014 , 9, e89781	15
957	The blast resistance gene Pi54of cloned from Oryza officinalis interacts with Avr-Pi54 through its novel non-LRR domains. 2014 , 9, e104840	59
956	iMethyl-PseAAC: identification of protein methylation sites via a pseudo amino acid composition approach. 2014 , 2014, 947416	126
955	How round is a protein? Exploring protein structures for globularity using conformal mapping. 2014 , 1, 26	7
954	Dynamic New World: Refining Our View of Protein Structure, Function and Evolution. 2014 , 2, 128-153	16
953	The triple power of D β protein intrinsic disorder in degenerative diseases. 2014 , 19, 181-258	62
952	. 2014 ,	3
951	Intrinsically Disordered Proteins: Methods for Structure and Dynamics Studies. 2014 , 181-190	3
950	The TFE-induced transient native-like structure of the intrinsically disordered H domain of Escherichia coli RNA polymerase. 2014 , 43, 581-94	7
949	Evolutionary and structural annotation of disease-associated mutations in human aminoacyl-tRNA synthetases. 2014 , 15, 1063	11
948	A six-dimensional alpha proton detection-based APSY experiment for backbone assignment of intrinsically disordered proteins. 2014 , 60, 231-40	17

947	Nanomechanics of Neurotoxic Proteins: Insights at the Start of the Neurodegeneration Cascade. 2014 , 57-68	
946	Kinetic modulation of a disordered protein domain by phosphorylation. 2014 , 5, 5272	53
945	The coronavirus nucleocapsid is a multifunctional protein. 2014 , 6, 2991-3018	517
944	What macromolecular crowding can do to a protein. 2014 , 15, 23090-140	318
943	Physicochemical mechanisms of protein regulation by phosphorylation. 2014 , 5, 270	94
942	Intrinsically Disordered Proteins: Where Computation Meets Experiment. 2014 , 6, 2684-2719	37
941	Synonymous constraint elements show a tendency to encode intrinsically disordered protein segments. 2014 , 10, e1003607	18
940	Specificity and affinity quantification of flexible recognition from underlying energy landscape topography. 2014 , 10, e1003782	21
939	Molecular Recognition of Intrinsically Disordered Proteins Studied by All-Atom Molecular Simulation. 2014 , 54, 096-099	
938	Actinous enigma or enigmatic actin: Folding, structure, and functions of the most abundant eukaryotic protein. 2014 , 2, e34500	10
937	"CON-CON" assignment strategy for highly flexible intrinsically disordered proteins. 2014 , 60, 209-18	28
936	Structural analysis of poly-SUMO chain recognition by the RNF4-SIMs domain. 2014 , 462, 53-65	22
935	Therapeutic strategies to inhibit MYC. 2014 , 4,	143
934	Microtubule-associated protein (MAP) 4 interacts with microtubules in an intrinsically disordered manner. 2014 , 78, 1864-70	2
933	Synthesis and structure-activity relationship studies of small molecule disruptors of EWS-FLI1 interactions in Ewing's sarcoma. 2014 , 57, 10290-303	14
932	Nucleolar stress induces ubiquitination-independent proteasomal degradation of PICT1 protein. 2014 , 289, 20802-12	10
931	Genome-scale prediction of proteins with long intrinsically disordered regions. 2014 , 82, 145-58	77
930	Identification of phosphatidylcholine transfer protein-like in the parasite <i>Entamoeba histolytica</i> . 2014 , 107 Pt B, 223-34	4

929	Accurate prediction of interfacial residues in two-domain proteins using evolutionary information: implications for three-dimensional modeling. 2014 , 82, 1219-34	6
928	New force field on modeling intrinsically disordered proteins. 2014 , 84, 253-69	84
927	An overview of the sequence features of N- and C-terminal segments of the human chemokine receptors. 2014 , 70, 141-50	11
926	Intrinsically disordered proteins (IDPs) in trypanosomatids. 2014 , 15, 1100	11
925	Plasmodium falciparum merozoite surface protein 2: epitope mapping and fine specificity of human antibody response against non-polymorphic domains. 2014 , 13, 510	15
924	Papillomavirus binding factor (PBF) is an intrinsically disordered protein with potential participation in osteosarcoma genesis, in silico evidence. 2014 , 11, 51	1
923	The DynaMine webserver: predicting protein dynamics from sequence. 2014 , 42, W264-70	89
922	Acquisition of a leucine zipper motif as a mechanism of antimorphy for an allele of the Drosophila Hox gene Sex combs reduced. 2014 , 4, 829-38	4
921	The eukaryotic linear motif resource ELM: 10 years and counting. 2014 , 42, D259-66	234
920	Free-energy landscape of intrinsically disordered proteins investigated by all-atom multicanonical molecular dynamics. 2014 , 805, 331-51	7
919	The staphylococcal elastin-binding protein regulates zinc-dependent growth/biofilm formation. 2014 , 156, 155-62	12
918	Assemblages: functional units formed by cellular phase separation. 2014 , 206, 579-88	187
917	In Silico Molecular Characterization of Cysteine Protease YopT from Yersinia pestis by Homology Modeling and Binding Site Identification. 2014 , 8, 1-9	15
916	Structural diversity of Alzheimer's disease amyloid- β dimers and their role in oligomerization and fibril formation. 2014 , 39, 583-600	21
915	IDEAL in 2014 illustrates interaction networks composed of intrinsically disordered proteins and their binding partners. 2014 , 42, D320-5	70
914	Mononuclear cells in dementia. 2014 , 431, 278-87	2
913	Homodimerization propensity of the intrinsically disordered N-terminal domain of Ultraspiracle from Aedes aegypti. 2014 , 1844, 1153-66	14
912	Bioinformatical Approaches to Unstructured/Disordered Proteins and Their Interactions. 2014 , 525-556	1

911	Coarse-Grained Modeling of Protein Dynamics. 2014 , 55-79	7
910	Insights into the Binding of Intrinsically Disordered Proteins from Molecular Dynamics Simulation. 2014 , 4, 182-198	50
909	Co-evolution of sphingomyelin and the ceramide transport protein CERT. 2014 , 1841, 704-19	34
908	Assessment of protein disorder region predictions in CASP10. 2014 , 82 Suppl 2, 127-37	123
907	Predicting DNA-binding sites of proteins based on sequential and 3D structural information. 2014 , 289, 489-99	14
906	Protein Conformational Dynamics. 2014 ,	9
905	Out-of-equilibrium biomolecular interactions monitored by picosecond fluorescence in microfluidic droplets. 2014 , 14, 1767-74	12
904	Physicochemical bases for protein folding, dynamics, and protein-ligand binding. 2014 , 57, 287-302	18
903	Thermal stability and folding kinetics analysis of disordered protein, securin. 2014 , 115, 2171-2178	4
902	A creature with a hundred waggly tails: intrinsically disordered proteins in the ribosome. 2014 , 71, 1477-504	98
901	Role of histidine for charge regulation of unstructured peptides at interfaces and in bulk. 2014 , 82, 657-67	29
900	Structure and assembly of filamentous bacteriophages. 2014 , 114, 80-122	74
899	Single-molecule studies of intrinsically disordered proteins. 2014 , 114, 3281-317	105
898	The ensemble nature of allostery. 2014 , 508, 331-9	785
897	Small-angle X-ray scattering- and nuclear magnetic resonance-derived conformational ensemble of the highly flexible antitoxin PaaA2. 2014 , 22, 854-65	44
896	Advantages of proteins being disordered. 2014 , 23, 539-50	118
895	Disordered proteinaceous machines. 2014 , 114, 6806-43	92
894	Pathological unfoldomics of uncontrolled chaos: intrinsically disordered proteins and human diseases. 2014 , 114, 6844-79	186

893	Structural disorder in viral proteins. 2014 , 114, 6880-911	133
892	Introducing protein intrinsic disorder. 2014 , 114, 6561-88	487
891	Contribution of proline to the pre-structuring tendency of transient helical secondary structure elements in intrinsically disordered proteins. 2014 , 1840, 993-1003	26
890	A mass-spectrometry-based framework to define the extent of disorder in proteins. 2014 , 86, 10979-91	71
889	Interplay between partner and ligand facilitates the folding and binding of an intrinsically disordered protein. 2014 , 111, 15420-5	112
888	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
887	Bioinspired single-chain polymer nanoparticles. 2014 , 63, 589-592	55
886	Accelerating the Conformational Sampling of Intrinsically Disordered Proteins. 2014 , 10, 5081-94	31
885	Evolutionarily conserved and conformationally constrained short peptides might serve as DNA recognition elements in intrinsically disordered regions. 2014 , 10, 1469-80	3
884	The intrinsic disorder status of the human hepatitis C virus proteome. 2014 , 10, 1345-63	52
883	Prepaying the entropic cost for allosteric regulation in KIX. 2014 , 111, 12067-72	50
882	Fundamentals of Protein Folding. 2014 , 1-61	
881	Proteome-wide analysis of human disease mutations in short linear motifs: neglected players in cancer?. 2014 , 10, 2626-42	62
880	Kinetics study on the HIV-1 ectodomain protein quaternary structure formation reveals coupling of chain folding and self-assembly in the refolding cascade. 2014 , 118, 12827-36	
879	Three-dimensional protein structure prediction: Methods and computational strategies. 2014 , 53PB, 251-276	107
878	Electrochemical detection of the oligomerization of PB1-F2 influenza A virus protein in infected cells. 2014 , 86, 9098-105	29
877	Effect of physical properties of nanogel particles on the kinetic constants of multipoint protein recognition process. 2014 , 15, 541-7	25
876	Toward a common aggregation mechanism for a β -barrel protein family: insights derived from a stable dimeric species. 2014 , 1844, 1599-607	7

875	Long-range effects of tag sequence on marginally stabilized structure in HIV-1 p24 capsid protein monitored using NMR. 2014 , 1844, 1638-47	
874	Introduction to intrinsically disordered proteins (IDPs). 2014 , 114, 6557-60	88
873	Disorder- and dynamics-based regulatory mechanisms in toxin-antitoxin modules. 2014 , 114, 6933-47	58
872	Macromolecular crowding effects on coupled folding and binding. 2014 , 118, 12621-9	17
871	Potential lactoferrin activity against pathogenic viruses. 2014 , 337, 581-95	58
870	VirtualSpectrum, a tool for simulating peak list for multi-dimensional NMR spectra. 2014 , 60, 51-66	4
869	Extended string binding mode of the phosphorylated transactivation domain of tumor suppressor p53. 2014 , 136, 14143-52	36
868	Classification of intrinsically disordered regions and proteins. 2014 , 114, 6589-631	1141
867	Comparison of structure determination methods for intrinsically disordered amyloid- β peptides. 2014 , 118, 6405-16	44
866	Rigidity, secondary structure, and the universality of the boson peak in proteins. 2014 , 106, 2667-74	50
865	Conditionally and transiently disordered proteins: awakening cryptic disorder to regulate protein function. 2014 , 114, 6779-805	136
864	Preventing β -synuclein aggregation: the role of the small heat-shock molecular chaperone proteins. 2014 , 1842, 1830-43	61
863	Physicochemical properties of cells and their effects on intrinsically disordered proteins (IDPs). 2014 , 114, 6661-714	301
862	Dancing retro: solution structure and micelle interactions of the retro-SH3-domain, retro-SHH-'Bergerac'. 2014 , 32, 257-72	7
861	Peptide Conformation Analysis Using an Integrated Bayesian Approach. 2014 , 10, 4152-4159	16
860	Presence and utility of intrinsically disordered regions in kinases. 2014 , 10, 2876-88	22
859	Recognition of the HIV capsid by the TRIM5 β restriction factor is mediated by a subset of pre-existing conformations of the TRIM5 β SPRY domain. 2014 , 53, 1466-76	18
858	Intrinsic disorder in proteins involved in the innate antiviral immunity: another flexible side of a molecular arms race. <i>Journal of Molecular Biology</i> , 2014 , 426, 1322-50	6.5 27

857	Generating NMR chemical shift assignments of intrinsically disordered proteins using carbon-detected NMR methods. 2014 , 449, 17-25	37
856	Dynamics and rigidity in an intrinsically disordered protein, Ecasein. 2014 , 118, 7317-26	39
855	Mechanism of Folding and Binding of an Intrinsically Disordered Protein As Revealed by ab Initio Simulations. 2014 , 10, 2224-31	29
854	Intrinsically disordered proteins and intrinsically disordered protein regions. 2014 , 83, 553-84	584
853	Short linear motifs: ubiquitous and functionally diverse protein interaction modules directing cell regulation. 2014 , 114, 6733-78	254
852	Retrospective on the all-in-one retroviral nucleocapsid protein. 2014 , 193, 2-15	26
851	Ubiquitin-independent proteasomal degradation. 2014 , 1843, 216-21	137
850	Protein dynamics and motions in relation to their functions: several case studies and the underlying mechanisms. 2014 , 32, 372-93	73
849	Wrecked regulation of intrinsically disordered proteins in diseases: pathogenicity of deregulated regulators. 2014 , 1, 6	68
848	ABSINTH Implicit Solvation Model and Force Field Paradigm for Use in Simulations of Intrinsically Disordered Proteins. 2014 , 208-231	
847	Intrinsically Disordered Protein: A Thermodynamic Perspective. 2014 , 232-259	
846	Long Molecular Dynamics Simulations of Intrinsically Disordered Proteins Reveal Preformed Structural Elements for Target Binding. 2014 , 260-283	
845	The RING Domain of the Scaffold Protein Ste5 Adopts a Molten Globular Character with High Thermal and Chemical Stability. 2014 , 126, 1344-1347	
844	The RING domain of the scaffold protein Ste5 adopts a molten globular character with high thermal and chemical stability. 2014 , 53, 1320-3	4
843	Improving protein order-disorder classification using charge-hydrophathy plots. 2014 , 15 Suppl 17, S4	38
842	Six- and seven-dimensional experiments by combination of sparse random sampling and projection spectroscopy dedicated for backbone resonance assignment of intrinsically disordered proteins. 2015 , 63, 283-90	14
841	Single-residue posttranslational modification sites at the N-terminus, C-terminus or in-between: To be or not to be exposed for enzyme access. 2015 , 15, 2525-46	20
840	Wheat Proteins. 2015 , 219-303	6

839	Evolutionarily Conserved Sequence Features Regulate the Formation of the FG Network at the Center of the Nuclear Pore Complex. 2015 , 5, 15795	19
838	Modeling Protein Folding Pathways. 2015 , 87-135	1
837	Caught in action: selecting peptide aptamers against intrinsically disordered proteins in live cells. 2015 , 5, 9402	17
836	Molecular-docking study of malaria drug target enzyme transketolase in Plasmodium falciparum 3D7 portends the novel approach to its treatment. 2015 , 10, 7	23
835	Unstructural biology of the Dengue virus proteins. 2015 , 282, 3368-94	43
834	Recent advances in potato genomics, transcriptomics, and transgenics under drought and heat stresses: a review. 2015 , 39, 920-940	16
833	Intrinsically disordered proteins: controlled chaos or random walk. 2015 , 6,	1
832	Earliest events in β -synuclein fibrillation probed with the fluorescence of intrinsic tyrosines. 2016 , 154, 16-23	13
831	Bayesian inference of protein ensembles from SAXS data. 2016 , 18, 5832-8	39
830	Prediction of Disordered Regions in Proteins Using Physicochemical Properties of Amino Acids. 2016 , 22, 31-36	1
829	Antimicrobial potentials and structural disorder of human and animal defensins. 2016 , 28, 95-111	45
828	Interpreting functional effects of coding variants: challenges in proteome-scale prediction, annotation and assessment. 2016 , 17, 841-62	13
827	Structural disorder: a tool for housekeeping proteins performing tissue-specific interactions. 2016 , 34, 1930-45	4
826	Abundance and functional roles of intrinsic disorder in the antimicrobial peptides of the NK-lysin family. 2017 , 35, 836-856	8
825	Structural Characterization of the Intrinsically Disordered Protein p53 Using Raman Spectroscopy. 2017 , 71, 823-832	20
824	Protein intrinsic disorder-based liquid-liquid phase transitions in biological systems: Complex coacervates and membrane-less organelles. 2017 , 239, 97-114	126
823	Molecular dynamics simulations show altered secondary structure of clawless in binary complex with DNA providing insights into aristaless-clawless-DNA ternary complex formation. 2017 , 35, 1153-1167	
822	Native State Volume Fluctuations in Proteins as a Mechanism for Dynamic Allostery. 2017 , 139, 3599-3602	30

821	Applications of Computational Methods to Simulations of Proteins Dynamics. 2017 , 1627-1669	1
820	Seeing the trees through the forest: sequence-based homo- and heteromeric protein-protein interaction sites prediction using random forest. 2017 , 33, 1479-1487	13
819	On the potential of using peculiarities of the protein intrinsic disorder distribution in mitochondrial cytochrome to identify the source of animal meats. 2017 , 5, e1264350	1
818	Dynein Binding of Competitive Regulators Dynactin and NudE Involves Novel Interplay between Phosphorylation Site and Disordered Spliced Linkers. 2017 , 25, 421-433	13
817	The thermodynamics of protein aggregation reactions may underpin the enhanced metabolic efficiency associated with heterosis, some balancing selection, and the evolution of ploidy levels. 2017 , 126, 1-21	2
816	Soft Cysteine Signaling Network: The Functional Significance of Cysteine in Protein Function and the Soft Acids/Bases Thiol Chemistry That Facilitates Cysteine Modification. 2017 , 30, 729-762	20
815	MARCKS phosphorylation is modulated by a peptide mimetic of MARCKS effector domain leading to increased radiation sensitivity in lung cancer cell lines. 2017 , 13, 1216-1222	9
814	Evidence for a Strong Correlation Between Transcription Factor Protein Disorder and Organismic Complexity. 2017 , 9, 1248-1265	33
813	Intrinsic protein disorder reduces small-scale gene duplicability. 2017 , 24, 435-444	3
812	On the role of residue phosphorylation in 14-3-3 partners: AANAT as a case study. 2017 , 7, 46114	7
811	Bioinformatics Approaches to the Structure and Function of Intrinsically Disordered Proteins. 2017 , 167-203	2
810	Molecular mechanism of multispecific recognition of Calmodulin through conformational changes. 2017 , 114, E3927-E3934	31
809	Insights into the conformations and dynamics of intrinsically disordered proteins using single-molecule fluorescence. 2017 , 1865, 1696-1706	27
808	Cross- β polymerization and hydrogel formation by low-complexity sequence proteins. 2017 , 126, 3-11	10
807	Biology, evolution, and medical importance of polyomaviruses: An update. 2017 , 54, 18-38	79
806	Enhancer of rudimentary homologue interacts with scaffold attachment factor B at the nuclear matrix to regulate SR protein phosphorylation. 2017 , 284, 2482-2500	9
805	Intrinsic disorder here, there, and everywhere, and nowhere to escape from it. 2017 , 74, 3065-3067	21
804	The underexplored question of β amyloid monomers. 2017 , 817, 71-75	17

803	Fcab-HER2 Interaction: a Mhage ^Trois. Lessons from X-Ray and Solution Studies. 2017 , 25, 878-889.e5	22
802	Intrinsically Disordered Proteins as Important Players during Desiccation Stress of Soybean Radicles. 2017 , 16, 2393-2409	10
801	Influence of Hyperglycemic Conditions on Self-Association of the Alzheimer's Amyloid [[A]] Peptide. 2017 , 2, 2134-2147	13
800	Probing the dynamics of disorder. 2017 , 128, 57-62	2
799	Proteus: a random forest classifier to predict disorder-to-order transitioning binding regions in intrinsically disordered proteins. 2017 , 31, 453-466	19
798	How order and disorder within paramyxoviral nucleoproteins and phosphoproteins orchestrate the molecular interplay of transcription and replication. 2017 , 74, 3091-3118	23
797	CtIP/Ctp1/Sae2, molecular form fit for function. 2017 , 56, 109-117	35
796	BDNF Propeptide: A Novel Modulator of Synaptic Plasticity. 2017 , 104, 19-28	21
795	Opposing Intermolecular Tuning of Ca Affinity for Calmodulin by Neurogranin and CaMKII Peptides. 2017 , 112, 1105-1119	8
794	The neglected functions of intrinsically disordered proteins and the origin of life. 2017 , 126, 31-46	11
793	From Fuzzy to Function: The New Frontier of Protein-Protein Interactions. 2017 , 50, 584-589	23
792	Automated Strong Cation-Exchange Cleanup To Remove Macromolecular Crowding Agents for Protein Hydrogen Exchange Mass Spectrometry. 2017 , 89, 1275-1282	5
791	Evolutionary studies of ligand binding sites in proteins. 2017 , 45, 85-90	17
790	Conformational heterogeneity in tails of DNA-binding proteins is augmented by proline containing repeats. 2017 , 13, 2531-2544	1
789	MFIB: a repository of protein complexes with mutual folding induced by binding. 2017 , 33, 3682-3684	41
788	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
787	Flexibility vs Preorganization: Direct Comparison of Binding Kinetics for a Disordered Peptide and Its Exact Preorganized Analogues. 2017 , 121, 10046-10054	16
786	Paradoxes and wonders of intrinsic disorder: Stability of instability. 2017 , 5, e1327757	16

785	Flexibility of the "rigid" classics or rugged bottom of the folding funnels of myoglobin, lysozyme, RNase A, chymotrypsin, cytochrome , and carboxypeptidase A1. 2017 , 5, e1355205	1
784	Affinity of IDPs to their targets is modulated by ion-specific changes in kinetics and residual structure. 2017 , 114, 9882-9887	38
783	Enhanced Sampling of Intrinsic Structural Heterogeneity of the BH3-Only Protein Binding Interface of Bcl-xL. 2017 , 121, 9160-9168	13
782	Structural and Kinetic Characterization of the Intrinsically Disordered Protein SeV N through Enhanced Sampling Simulations. 2017 , 121, 9572-9582	16
781	The Thermodynamic Basis of the Fuzzy Interaction of an Intrinsically Disordered Protein. 2017 , 129, 14686-14689	
780	The Thermodynamic Basis of the Fuzzy Interaction of an Intrinsically Disordered Protein. 2017 , 56, 14494-14497	20
779	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
778	Structure, Function and Evolution of the Hsp60 Chaperonins. 2017 , 3-20	3
777	Liquid-liquid phase separation of the microtubule-binding repeats of the Alzheimer-related protein Tau. 2017 , 8, 275	344
776	Two possible improvements for mass spectrometry analysis of intact biomolecules. 2017 , 23, 181-186	3
775	Native Hydrophobic Binding Interactions at the Transition State for Association between the TAZ1 Domain of CBP and the Disordered TAD-STAT2 Are Not a Requirement. 2017 , 56, 4145-4153	21
774	Effects of flexibility and electrostatic interactions on the coupled binding-folding mechanisms of Chz.core and H2A.z-H2B. 2017 , 13, 2152-2159	4
773	Structural and dynamic properties of the C-terminal region of the Escherichia coli RNA chaperone Hfq: integrative experimental and computational studies. 2017 , 19, 21152-21164	5
772	Functionality of intrinsic disorder in tumor necrosis factor- α and its receptors. 2017 , 284, 3589-3618	5
771	Exploring the dark foldable proteome by considering hydrophobic amino acids topology. 2017 , 7, 41425	16
770	Predictions of Backbone Dynamics in Intrinsically Disordered Proteins Using De Novo Fragment-Based Protein Structure Predictions. 2017 , 7, 6999	9
769	Intrinsic disorder is a common structural characteristic of RxLR effectors in oomycete pathogens. 2017 , 121, 911-919	10
768	Specific and intrinsic sequence patterns extracted by deep learning from intra-protein binding and non-binding peptide fragments. 2017 , 7, 14916	

767	The Mcm2-7-interacting domain of human mini-chromosome maintenance 10 (Mcm10) protein is important for stable chromatin association and origin firing. 2017 , 292, 13008-13021	15
766	Exploring Short Linear Motifs Using the ELM Database and Tools. 2017 , 58, 8.22.1-8.22.35	18
765	Structural disorder in plant proteins: where plasticity meets sessility. 2017 , 74, 3119-3147	22
764	Eukaryotic transcription factors: paradigms of protein intrinsic disorder. 2017 , 474, 2509-2532	75
763	Some additional remarks to the solution of the protein folding puzzle: Reply to comments on "There and back again: Two views on the protein folding puzzle". 2017 , 21, 77-79	2
762	A framework for the targeted selection of herbs with similar efficacy by exploiting drug repositioning technique and curated biomedical knowledge. 2017 , 208, 117-128	2
761	Supercharging SpyCatcher toward an intrinsically disordered protein with stimuli-responsive chemical reactivity. 2017 , 53, 8830-8833	21
760	Analyzing the Folding and Binding Steps of an Intrinsically Disordered Protein by Protein Engineering. 2017 , 56, 3780-3786	22
759	Intrinsically disordered proteins in overcrowded milieu: Membrane-less organelles, phase separation, and intrinsic disorder. 2017 , 44, 18-30	353
758	Intrinsic disorder in proteins involved in amyotrophic lateral sclerosis. 2017 , 74, 1297-1318	32
757	The Transactivation Domains of the p53 Protein. 2017 , 7,	63
756	Insights from the Shell Proteome: Biomineralization to Adaptation. 2017 , 34, 66-77	76
755	Prediction of Protein Secondary Structure. 2017 ,	2
754	How to Predict Disorder in a Protein of Interest. 2017 , 1484, 137-158	11
753	Intrinsic Disorder and Semi-disorder Prediction by SPINE-D. 2017 , 1484, 159-174	7
752	Erythropoietin and co.: intrinsic structure and functional disorder. 2016 , 13, 56-72	15
751	Effect of natural polymorphism on structure and function of the Yersinia pestis outer membrane porin F (OmpF protein): a computational study. 2017 , 35, 2588-2603	3
750	The Proline/Glycine-Rich Region of the Biofilm Adhesion Protein Aap Forms an Extended Stalk that Resists Compaction. <i>Journal of Molecular Biology</i> , 2017 , 429, 261-279	6.5 15

749	Structures and Short Linear Motif of Disordered Transcription Factor Regions Provide Clues to the Interactome of the Cellular Hub Protein Radical-induced Cell Death1. 2017 , 292, 512-527	36
748	Structural Characterization of Highly Flexible Proteins by Small-Angle Scattering. 2017 , 1009, 107-129	21
747	Interfacial Properties of N, an Intrinsically Disordered Protein. 2017 , 113, 2723-2735	5
746	Structural disorder and induced folding within two cereal, ABA stress and ripening (ASR) proteins. 2017 , 7, 15544	30
745	Perplexity of Amyloid β Protein Oligomer Formation: Relevance to Alzheimer's Disease. 2017 , 1-50	3
744	Pathogenic Mechanisms of the Prion Protein Gene Mutations: A Review and Speculative Hypotheses for Pathogenic Potential of the Pro39Leu Mutation in the Associated FTD-Like Phenotype. 2017 , 08,	3
743	A Comprehensive Survey of the Roles of Highly Disordered Proteins in Type 2 Diabetes. 2017 , 18,	23
742	Intrinsic Disorder in Proteins with Pathogenic Repeat Expansions. 2017 , 22,	33
741	On the Helix Propensity in Generalized Born Solvent Descriptions of Modeling the Dark Proteome. 2017 , 4, 3	5
740	Modular Organization of Residue-Level Contacts Shapes the Selection Pressure on Individual Amino Acid Sites of Ribosomal Proteins. 2017 , 9, 916-931	2
739	Hidden β helical propensity segments within disordered regions of the transcriptional activator CHOP. 2017 , 12, e0189171	6
738	Role of non-native electrostatic interactions in the coupled folding and binding of PUMA with Mcl-1. 2017 , 13, e1005468	28
737	Disentangling of Information About the Structure of Biomolecules Based on the Decomposition and Separation of Two-Dimensional Charge Distributions of Ions. 2017 , 72, 1300-1306	2
736	The Design of Repeat Proteins: Stability Conflicts with Functionality. 2017 , 03,	3
735	Biophysics: Past, Present, and Future. 2017 ,	
734	Functional Analysis of Human Hub Proteins and Their Interactors Involved in the Intrinsic Disorder-Enriched Interactions. 2017 , 18,	60
733	Disentangling polydispersity in the PCNA-p15PAF complex, a disordered, transient and multivalent macromolecular assembly. 2017 , 45, 1501-1515	28
732	Cancer/Testis Antigens: "Smart" Biomarkers for Diagnosis and Prognosis of Prostate and Other Cancers. 2017 , 18,	21

731	Fluorescent analysis of bioactive molecules in single cells based on microfluidic chips. 2018 , 18, 1151-1173	35
730	Fuzziness in Protein Interactions-A Historical Perspective. <i>Journal of Molecular Biology</i> , 2018 , 430, 2278-2287	85
729	Translational Control by Prion-like Proteins. 2018 , 28, 494-505	13
728	Amyloid growth and membrane damage: Current themes and emerging perspectives from theory and experiments on A β and hIAPP. 2018 , 1860, 1625-1638	62
727	Convergence of Artificial Protein Polymers and Intrinsically Disordered Proteins. 2018 , 57, 2405-2414	42
726	Exploration of nucleoprotein EMoRE and XD interactions of Nipah and Hendra viruses. 2018 , 24, 113	2
725	DNP-Enhanced MAS NMR: A Tool to Snapshot Conformational Ensembles of β Synuclein in Different States. 2018 , 114, 1614-1623	25
724	From a Highly Disordered to a Metastable State: Uncovering Insights of β Synuclein. 2018 , 9, 1051-1065	17
723	Arrestins: structural disorder creates rich functionality. 2018 , 9, 986-1003	16
722	Structures of human calpain-3 protease core with and without bound inhibitor reveal mechanisms of calpain activation. 2018 , 293, 4056-4070	20
721	Collapse Transitions of Proteins and the Interplay Among Backbone, Sidechain, and Solvent Interactions. 2018 , 47, 19-39	58
720	Phosphorylation of an intrinsically disordered region of Ets1 shifts a multi-modal interaction ensemble to an auto-inhibitory state. 2018 , 46, 2243-2251	22
719	MINAR1 is a Notch2-binding protein that inhibits angiogenesis and breast cancer growth. 2018 , 10, 195-204	10
718	Large-scale aggregation analysis of eukaryotic proteins reveals an involvement of intrinsically disordered regions in protein folding. 2018 , 8, 678	17
717	Unified understanding of folding and binding mechanisms of globular and intrinsically disordered proteins. 2018 , 10, 163-181	22
716	IDPs in macromolecular complexes: the roles of multivalent interactions in diverse assemblies. 2018 , 49, 36-43	54
715	Electrostatic Interactions in Protein Structure, Folding, Binding, and Condensation. 2018 , 118, 1691-1741	290
714	First Experimental Assessment of Protein Intrinsic Disorder Involvement in an RNA Virus Natural Adaptive Process. 2018 , 35, 38-49	22

713	Bioinformatic Analysis Reveals Conservation of Intrinsic Disorder in the Linker Sequences of Prokaryotic Dual-family Immunophilin Chaperones. 2018 , 16, 6-14		3
712	Exploring intrinsically disordered proteins in <i>Chlamydomonas reinhardtii</i> . 2018 , 8, 6805		16
711	Prosystemin, a prohormone that modulates plant defense barriers, is an intrinsically disordered protein. 2018 , 27, 620-632		7
710	An integrated computational hierarchy for identification of potent inhibitors against Shikimate Kinase enzyme from <i>Shigella sonnei</i> , a major cause of global dysentery. 2018 , 11, 283-293		1
709	How Robust Is the Mechanism of Folding-Upon-Binding for an Intrinsically Disordered Protein?. 2018 , 114, 1889-1894		27
708	Thermal denaturation of fibrinogen visualized by single-molecule atomic force microscopy. 2018 , 167, 370-376		12
707	Structural mechanisms of CFTR function and dysfunction. 2018 , 150, 539-570		53
706	On the Calculation of SAXS Profiles of Folded and Intrinsically Disordered Proteins from Computer Simulations. <i>Journal of Molecular Biology</i> , 2018 , 430, 2521-2539	6.5	41
705	Salt-bridge dynamics in intrinsically disordered proteins: A trade-off between electrostatic interactions and structural flexibility. 2018 , 1866, 624-641		14
704	An Extended Guinier Analysis for Intrinsically Disordered Proteins. <i>Journal of Molecular Biology</i> , 2018 , 430, 2540-2553	6.5	48
703	: A novel downregulated gene in laryngeal cancer. 2018 , 15, 4669-4675		2
702	High-Resolution 2D NMR of Disordered Proteins Enhanced by Hyperpolarized Water. 2018 , 90, 6169-6177		22
701	50+ Years of Protein Folding. 2018 , 83, S3-S18		16
700	The Molten Globule Concept: 45 Years Later. 2018 , 83, S33-S47		14
699	Exploring the sequence-structure-function relationship for the intrinsically disordered β -crystallin Hahellin. 2018 , 36, 1171-1181		4
698	Intrinsically Disordered Regions in Serum Albumin: What Are They For?. 2018 , 76, 39-57		12
697	Dissecting physical structure of calreticulin, an intrinsically disordered Ca-buffering chaperone from endoplasmic reticulum. 2018 , 36, 1617-1636		8
696	Intrinsic Disorder, Protein-Protein Interactions, and Disease. 2018 , 110, 85-121		66

695	Comparing NMR and X-ray protein structure: Lindemann-like parameters and NMR disorder. 2018 , 36, 2331-2341	7
694	Common molecular pathogenesis of disease-related intrinsically disordered proteins revealed by NMR analysis. 2018 , 163, 11-18	19
693	Prediction of protein disorder based on IUPred. 2018 , 27, 331-340	92
692	Intrinsically Disordered Proteome of Human Membrane-Less Organelles. 2018 , 18, e1700193	109
691	Potential functions of LEA proteins from the brine shrimp <i>Artemia franciscana</i> - anhydrobiosis meets bioinformatics. 2018 , 36, 3291-3309	17
690	Structural Dynamics of the GW182 Silencing Domain Including its RNA Recognition motif (RRM) Revealed by Hydrogen-Deuterium Exchange Mass Spectrometry. 2018 , 29, 158-173	4
689	In silico evaluation of the resistance of the T790M variant of epidermal growth factor receptor kinase to cancer drug Erlotinib. 2018 , 36, 4209-4219	10
688	Sequence fingerprints distinguish erroneous from correct predictions of intrinsically disordered protein regions. 2018 , 36, 4338-4351	9
687	NMR elucidation of monomer-dimer transition and conformational heterogeneity in histone-like DNA binding protein of <i>Helicobacter pylori</i> . 2018 , 56, 285-299	13
686	Parallel Tempering of Dark Matter from the Ebola Virus Proteome: Comparison of CHARMM36m and CHARMM22 Force Fields with Implicit Solvent. 2018 , 58, 111-118	2
685	Partner-Mediated Polymorphism of an Intrinsically Disordered Protein. <i>Journal of Molecular Biology</i> , 2018 , 430, 2493-2507	6.5 13
684	Molecular Recognition Features in Zika Virus Proteome. <i>Journal of Molecular Biology</i> , 2018 , 430, 2372-2388	46
683	Supramolecular Systems as Protein Ligands. 2018 , 1-20	
682	Evidence for allosteric effects on p53 oligomerization induced by phosphorylation. 2018 , 27, 523-530	6
681	. 2018 ,	7
680	Structural insights and characterization of human Npas4 protein. 2018 , 6, e4978	2
679	INTRINSICALLY DISORDERED PROTEINS (IDPS) IN HUMAN DISEASES: A REVIEW. 2018 , 9, 1-4	
678	pH-Induced Folding of the Caspase-Cleaved Par-4 Tumor Suppressor: Evidence of Structure Outside of the Coiled Coil Domain. 2018 , 8,	4

677	Where differences resemble: sequence-feature analysis in curated databases of intrinsically disordered proteins. 2018 , 2018,	6
676	Functions of short lifetime biological structures at large: the case of intrinsically disordered proteins. 2020 , 19, 60-68	11
675	Intrinsically Disordered Landscapes for Human CD4 Receptor Peptide. 2018 , 122, 11906-11921	7
674	An Intrinsically Disordered Peptide-Peptide Stapler for Highly Efficient Protein Ligation Both in Vivo and in Vitro. 2018 , 140, 17474-17483	22
673	Physical Background of the Disordered Nature of "Mutual Synergetic Folding" Proteins. 2018 , 19,	2
672	Diffusion-limited association of disordered protein by non-native electrostatic interactions. 2018 , 9, 4707	31
671	Using NMR Chemical Shifts to Determine Residue-Specific Secondary Structure Populations for Intrinsically Disordered Proteins. 2018 , 611, 101-136	7
670	Fluorescence Depolarization Kinetics to Study the Conformational Preference, Structural Plasticity, Binding, and Assembly of Intrinsically Disordered Proteins. 2018 , 611, 347-381	17
669	The Use of Mass Spectrometry to Examine IDPs: Unique Insights and Caveats. 2018 , 611, 459-502	4
668	Hybrid Methods for Modeling Protein Structures Using Molecular Dynamics Simulations and Small-Angle X-Ray Scattering Data. 2018 , 1105, 237-258	6
667	A comprehensive ensemble model for comparing the allosteric effect of ordered and disordered proteins. 2018 , 14, e1006393	12
666	Integrative Structural Biology with Hybrid Methods. 2018 ,	1
665	Analysis of NMR Spin-Relaxation Data Using an Inverse Gaussian Distribution Function. 2018 , 115, 2301-2309	7
664	Disorder in Proteins. 2018 ,	
663	Both Intrinsically Disordered Regions and Structural Domains Evolve Rapidly in Immune-Related Mammalian Proteins. 2018 , 19,	0
662	Structure-function studies of the asparaginyl-tRNA synthetase from understanding the role of catalytic and non-catalytic domains. 2018 , 475, 3377-3391	5
661	N transverse relaxation measurements for the characterization of μ s-ms dynamics are deteriorated by the deuterium isotope effect on N resulting from solvent exchange. 2018 , 72, 125-137	5
660	A Dimerization Function in the Intrinsically Disordered N-Terminal Region of Src. 2018 , 25, 449-463.e4	18

659	Expanded Interactome of the Intrinsically Disordered Protein Dss1. 2018 , 25, 862-870	8
658	Co-Evolution of Intrinsically Disordered Proteins with Folded Partners Witnessed by Evolutionary Couplings. 2018 , 19,	12
657	Effect of an Intrinsically Disordered Plant Stress Protein on the Properties of Water. 2018 , 115, 1696-1706	15
656	Computational Studies of Intrinsically Disordered Proteins. 2018 , 122, 10455-10469	17
655	Bringing Darkness to Light: Intrinsic Disorder as a Means to Dig into the Dark Proteome. 2018 , 18, e1800352	2
654	Formation of Heterotypic Amyloids: β Synuclein in Co-Aggregation. 2018 , 18, e1800059	5
653	The pursuit of precision in macromolecular science: Concepts, trends, and perspectives. 2018 , 155, 235-247	7
652	Folding and Binding Properties of Human Complement Receptor Type 1 Extracellular Domain. 2018 ,	
651	Flexibility of the Sec13/31 cage is influenced by the Sec31 C-terminal disordered domain. 2018 , 204, 250-260	6
650	Born This Way: Using Intrinsic Disorder to Map the Connections between SLITRKs, TSHR, and Male Sexual Orientation. 2018 , 18, e1800307	0
649	Cytokine Receptors. 2018 , 157-185	5
648	C-terminal intrinsically disordered region-dependent organization of the mycobacterial genome by a histone-like protein. 2018 , 8, 8197	5
647	Protein Regulation by Intrinsically Disordered Regions: A Role for Subdomains in the IDR of the HIV-1 Rev Protein. 2018 , 19, 1618-1624	5
646	Structural Diversity of Nucleosomes Characterized by Native Mass Spectrometry. 2018 , 90, 8217-8226	12
645	Sequence-to-Conformation Relationships of Disordered Regions Tethered to Folded Domains of Proteins. <i>Journal of Molecular Biology</i> , 2018 , 430, 2403-2421	6.5 36
644	A Low Computational Complexity Scheme for the Prediction of Intrinsically Disordered Protein Regions. 2018 , 2018, 1-7	7
643	IUPred2A: context-dependent prediction of protein disorder as a function of redox state and protein binding. 2018 , 46, W329-W337	548
642	Disordered peptide chains in an β C-based coarse-grained model. 2018 , 20, 19057-19070	16

641	Intrinsically disordered proteins in crowded milieu: when chaos prevails within the cellular gumbo. 2018 , 75, 3907-3929	48
640	Electrostatic control of calcineurin's intrinsically-disordered regulatory domain binding to calmodulin. 2018 , 1862, 2651-2659	4
639	A beacon at the dawn of the Universe. 2018 , 553, 410-411	
638	Intrinsic Disorder and Posttranslational Modifications: The Darker Side of the Biological Dark Matter. 2018 , 9, 158	111
637	IDPpi: Protein-Protein Interaction Analyses of Human Intrinsically Disordered Proteins. 2018 , 8, 10563	10
636	Tuning Mechanical Properties of Protein Hydrogels. 2018 , 295-309	
635	InSiDDe: A Server for Designing Artificial Disordered Proteins. 2017 , 19,	5
634	Understanding the Role of Intrinsic Disorder of Viral Proteins in the Oncogenicity of Different Types of HPV. 2018 , 19,	14
633	Discovery of Cryoprotective Activity in Human Genome-Derived Intrinsically Disordered Proteins. 2018 , 19,	9
632	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
631	Prediction of Disordered Regions and Their Roles in the Anti-Pathogenic and Immunomodulatory Functions of Butyrophilins. 2018 , 23,	4
630	A V-to-F substitution in SK2 channels causes Ca hypersensitivity and improves locomotion in a <i>C. elegans</i> ALS model. 2018 , 8, 10749	8
629	Efficient and simplified nanomechanical analysis of intrinsically disordered proteins. 2018 , 10, 16857-16867	5
628	Conformational response to charge clustering in synthetic intrinsically disordered proteins. 2018 , 1862, 2204-2214	8
627	Using H amide temperature coefficients to define intrinsically disordered regions: An alternative NMR method. 2018 , 27, 1821-1830	4
626	Discerning evolutionary trends in post-translational modification and the effect of intrinsic disorder: Analysis of methylation, acetylation and ubiquitination sites in human proteins. 2018 , 14, e1006349	16
625	<i>Caenorhabditis elegans</i> BRICHOS Domain-Containing Protein C09F5.1 Maintains Thermotolerance and Decreases Cytotoxicity of Aβ by Activating the UPR. 2018 , 9,	1
624	Interactions between the Intrinsically Disordered Proteins βSynuclein and βSynuclein. 2018 , 18, e1800109	5

623	Evolutionary Analysis of the Lysine-Rich N-terminal Cytoplasmic Domains of the Gastric H,K-ATPase and the Na,K-ATPase. 2018 , 251, 653-666		6
622	Structural metamorphism and polymorphism in proteins on the brink of thermodynamic stability. 2018 , 27, 1557-1567		25
621	Conformational Ensembles Exhibit Extensive Molecular Recognition Features. 2018 , 3, 9907-9920		3
620	Evolution of In Silico Strategies for Protein-Protein Interaction Drug Discovery. 2018 , 23,		50
619	Ageing-related receptors resolved. 2018 , 553, 409-410		11
618	Understanding the interactability of chikungunya virus proteins molecular recognition feature analysis.. 2018 , 8, 27293-27303		18
617	PAGE4 and Conformational Switching: Insights from Molecular Dynamics Simulations and Implications for Prostate Cancer. <i>Journal of Molecular Biology</i> , 2018 , 430, 2422-2438	6.5	24
616	The solvent side of proteinaceous membrane-less organelles in light of aqueous two-phase systems. 2018 , 117, 1224-1251		30
615	Comparative effect of cationic gemini surfactant and its monomeric counterpart on the conformational stability of phospholipase A2. 2019 , 1175, 49-55		19
614	Genome-wide identification, expression analysis and functional study of the GRAS gene family in Tartary buckwheat (<i>Fagopyrum tataricum</i>). 2019 , 19, 342		33
613	Proteasome Activation to Combat Proteotoxicity. 2019 , 24,		15
612	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
611	Information theoretic measures for quantifying sequence-ensemble relationships of intrinsically disordered proteins. 2019 , 32, 191-202		12
610	Intrinsically disordered proteins and structured proteins with intrinsically disordered regions have different functional roles in the cell. 2019 , 14, e0217889		44
609	Sequence-Specific DNA Binding by Noncovalent Peptide-Azocyclodextrin Dimer Complex as a Suitable Model for Conformational Fuzziness. 2019 , 24,		3
608	Using Small-Angle Scattering Data and Parametric Machine Learning to Optimize Force Field Parameters for Intrinsically Disordered Proteins. 2019 , 6, 64		11
607	Intrinsically disordered domains: Sequence ? disorder ? function relationships. 2019 , 28, 1652-1663		13
606	NMR characterization of solvent accessibility and transient structure in intrinsically disordered proteins. 2019 , 73, 305-317		19

605	Dynamics of the intrinsically disordered protein NUPR1 in isolation and in its fuzzy complexes with DNA and prothymosin β . 2019 , 1867, 140252	6
604	Molecular Dynamics Simulation Optimization Based on GROMACS on Sunway TaihuLight. 2019 , 112-123	
603	Microstructure and in-depth proteomic analysis of <i>Perna viridis</i> shell. 2019 , 14, e0219699	10
602	Immunogenicity of a recombinant fusion construct composed of intrinsically unstructured, low polymorphic segments derived from merozoite surface protein 2 and trophozoite exported protein 1. 2019 , 37, 5332-5340	
601	Introduction to intrinsically disordered proteins and regions. 2019 , 1-34	7
600	Single-molecule fluorescence studies of IDPs and IDRs. 2019 , 93-136	
599	Studies on Molecular Dynamics of Intrinsically Disordered Proteins and Their Fuzzy Complexes: A Mini-Review. 2019 , 17, 712-720	22
598	Characterization of protein extracts from different types of human teeth and insight in biomineralization. 2019 , 9, 9314	8
597	Predicting Protein-Protein Interfaces that Bind Intrinsically Disordered Protein Regions. <i>Journal of Molecular Biology</i> , 2019 , 431, 3157-3178	6.5 2
596	Perspective: the essential role of NMR in the discovery and characterization of intrinsically disordered proteins. 2019 , 73, 651-659	20
595	Working-age people with disability and labour force participation: Geographic variations in Australia. 2019 , 54, 323-340	1
594	Zika and Flavivirus Shell Disorder: Virulence and Fetal Morbidity. 2019 , 9,	17
593	Integrating disorder in globular multidomain proteins: Fuzzy sensors and the role of SH3 domains. 2019 , 677, 108161	6
592	Binding-induced folding under unfolding conditions: Switching between induced fit and conformational selection mechanisms. 2019 , 294, 16942-16952	13
591	DisProt: intrinsic protein disorder annotation in 2020. 2020 , 48, D269-D276	91
590	Intrinsic Disorder of the BAF Complex: Roles in Chromatin Remodeling and Disease Development. 2019 , 20,	7
589	Free-energy landscape of molecular interactions between endothelin 1 and human endothelin type B receptor: fly-casting mechanism. 2019 , 32, 297-308	7
588	Nanoparticle Mobility over a Surface as a Probe for Weak Transient Disordered Peptide-Peptide Interactions. 2019 , 19, 6524-6534	3

587	Identifying molecular recognition features in intrinsically disordered regions of proteins by transfer learning. 2020 , 36, 1107-1113	14
586	Sequential, Structural and Functional Properties of Protein Complexes Are Defined by How Folding and Binding Intertwine. <i>Journal of Molecular Biology</i> , 2019 , 431, 4408-4428	6.5 7
585	Diffusion coefficients of elastic macromolecules. 2019 , 878,	5
584	Investigation into Early Steps of Actin Recognition by the Intrinsically Disordered N-WASP Domain V. 2019 , 20,	2
583	Intrinsically Disordered Proteins and Their Mysterious (Meta)Physics. 2019 , 7,	188
582	Functions of intrinsic disorder in proteins involved in DNA demethylation during pre-implantation embryonic development. 2019 , 136, 962-979	1
581	Perspectives on drug discovery strategies based on IDPs. 2019 , 275-327	4
580	Residual Structures and Transient Long-Range Interactions of p53 Transactivation Domain: Assessment of Explicit Solvent Protein Force Fields. 2019 , 15, 4708-4720	17
579	Intrinsic Disorder-Based Emergence in Cellular Biology: Physiological and Pathological Liquid-Liquid Phase Transitions in Cells. 2019 , 11,	33
578	Ferroptosis - An iron- and disorder-dependent programmed cell death. 2019 , 135, 1052-1069	23
577	Tetramer formation by the caspase-activated fragment of the Par-4 tumor suppressor. 2019 , 286, 4060-4073	4
576	Interactions of Casein and Polypeptides in Multilayer Films Studied by FTIR and Molecular Dynamics. 2019 , 11,	11
575	Pharmacological targeting of Synuclein and TPPP/p25 in Parkinson's disease: challenges and opportunities in a Nutshell. 2019 , 593, 1641-1653	5
574	Review: Plant cell wall biochemical omics: The high-throughput biochemistry for polysaccharide biosynthesis. 2019 , 286, 49-56	3
573	Is the cell really a machine?. 2019 , 477, 108-126	60
572	Computational Protocol to Evaluate Side-Chain Vicinal Spin-Spin Coupling Constants and Karplus Equation in Amino Acids: Alanine Dipeptide Model. 2019 , 15, 4252-4263	1
571	Protein intrinsic disorder and structure-function continuum. 2019 , 166, 1-17	44
570	The dark proteome of cancer: Intrinsic disorder and functionality of HIF-1 along with its interacting proteins. 2019 , 166, 371-403	15

569	Revisiting the Concept of Host Range of Plant Pathogens. 2019 , 57, 63-90	28
568	HIV Vaccine Mystery and Viral Shell Disorder. 2019 , 9,	25
567	Computational Prediction of MoRFs, Short Disorder-to-order Transitioning Protein Binding Regions. 2019 , 17, 454-462	20
566	Stochasticity of Biological Soft Matter: Emerging Concepts in Intrinsically Disordered Proteins and Biological Phase Separation. 2019 , 44, 716-728	53
565	Structural dynamics and transient lipid binding of synaptobrevin-2 tune SNARE assembly and membrane fusion. 2019 , 116, 8699-8708	13
564	Gas-phase conformations of intrinsically disordered proteins and their complexes with ligands: Kinetically trapped states during transfer from solution to the gas phase. 2019 , 38, 483-500	5
563	Network mapping of the conformational heterogeneity of SOD1 by deploying statistical cluster analysis of FTIR spectra. 2019 , 76, 4145-4154	3
562	Structure of proteins: Evolution with unsolved mysteries. 2019 , 149, 160-172	8
561	The functional importance of structure in unstructured protein regions. 2019 , 56, 155-163	34
560	Modulation of Disordered Proteins with a Focus on Neurodegenerative Diseases and Other Pathologies. 2019 , 20,	20
559	Biomolecular NMR Spectroscopy?. 2019 , 20,	6
558	PRISMA: Protein Interaction Screen on Peptide Matrix Reveals Interaction Footprints and Modifications- Dependent Interactome of Intrinsically Disordered C/EBP β . 2019 , 13, 351-370	14
557	Dynamic Studies on Intrinsically Disordered Regions of Two Paralogous Transcription Factors Reveal Rigid Segments with Important Biological Functions. <i>Journal of Molecular Biology</i> , 2019 , 431, 1353-1369 ^{6.5} ¹³	13
556	Comparative analysis of mutational robustness of the intrinsically disordered viral protein VPg and of its interactor eIF4E. 2019 , 14, e0211725	11
555	The Prediction of Intrinsically Disordered Proteins Based on Feature Selection. 2019 , 12, 46	3
554	Extreme Fuzziness: Direct Interactions between Two IDPs. 2019 , 9,	11
553	Sequence Effects on Size, Shape, and Structural Heterogeneity in Intrinsically Disordered Proteins. 2019 , 123, 3462-3474	61
552	Structural Characterization of N-WASP Domain V Using MD Simulations with NMR and SAXS Data. 2019 , 116, 1216-1227	10

551	Troubleshooting Guide to Expressing Intrinsically Disordered Proteins for Use in NMR Experiments. 2018 , 5, 118	10
550	Side chain electrostatic interactions and pH-dependent expansion of the intrinsically disordered, highly acidic carboxyl-terminus of β -tubulin. 2019 , 28, 1095-1105	2
549	Intrinsic disorder associated with 14-3-3 proteins and their partners. 2019 , 166, 19-61	28
548	Temperature- and pH-dependent protein conformational changes investigated by terahertz dielectric spectroscopy. 2019 , 98, 260-265	8
547	Disordered domains in chromatin-binding proteins. 2019 , 63, 147-156	25
546	Position-, disorder-, and salt-dependent diffusion in binding-coupled-folding of intrinsically disordered proteins. 2019 , 21, 5634-5645	14
545	On the Need to Develop Guidelines for Characterizing and Reporting Intrinsic Disorder in Proteins. 2019 , 19, e1800415	3
544	Understanding Intramolecular Crosstalk in an Intrinsically Disordered Protein. 2019 , 14, 337-341	7
543	Misprediction of Structural Disorder in Halophiles. 2019 , 24,	4
542	A new technique for predicting intrinsically disordered regions based on average distance map constructed with inter-residue average distance statistics. 2019 , 19, 3	4
541	Ion Mobility Mass Spectrometry Uncovers the Impact of the Patterning of Oppositely Charged Residues on the Conformational Distributions of Intrinsically Disordered Proteins. 2019 , 141, 4908-4918	38
540	A dual role in regulation and toxicity for the disordered N-terminus of the toxin GraT. 2019 , 10, 972	19
539	SPOT-Disorder2: Improved Protein Intrinsic Disorder Prediction by Ensembled Deep Learning. 2019 , 17, 645-656	50
538	Towards a Processual Approach in Protein Studies. 2019 , 12, 469-480	1
537	Evolutionary conservation of the intrinsic disorder-based Radical-Induced Cell Death1 hub interactome. 2019 , 9, 18927	9
536	Characterization of an Extensive Interface on Vitronectin for Binding to Plasminogen Activator Inhibitor-1: Adoption of Structure in an Intrinsically Disordered Region. 2019 , 58, 5117-5134	3
535	Life in Phases: Intra- and Inter- Molecular Phase Transitions in Protein Solutions. 2019 , 9,	20
534	A Biosensor Study of Protein Interaction with the 20S Proteasome Core Particle. 2019 , 13, 324-328	

533	Binding of LcrV protein from <i>Yersinia pestis</i> to human T-cells induces apoptosis, which is completely blocked by specific antibodies. 2019 , 122, 1062-1070		5
532	Bioinformatical Approaches to Unstructured/Disordered Proteins and Their Complexes. 2019 , 561-596		
531	Protein Dynamics Simulations Using Coarse-Grained Models. 2019 , 61-87		1
530	Mutation and structure guided discovery of an antiviral small molecule that mimics an essential C-Terminal tripeptide of the vaccinia D4 processivity factor. 2019 , 162, 178-185		2
529	The Klotho proteins in health and disease. 2019 , 15, 27-44		213
528	Structural disorder in the proteome and interactome of Alkhurma virus (ALKV). 2019 , 76, 577-608		13
527	Molecular dynamics analysis of the effects of GTP, GDP and benzimidazole derivative on structural dynamics of a cell division protein FtsZ from. 2019 , 37, 4361-4373		8
526	Evolutionary Features in the Structure and Function of Bacterial Toxins. 2019 , 11,		11
525	Residual Structure Accelerates Binding of Intrinsically Disordered ACTR by Promoting Efficient Folding upon Encounter. <i>Journal of Molecular Biology</i> , 2019 , 431, 422-432	6.5	16
524	Identification and characterization of a carboxypeptidase N1 from red lip mullet (<i>Liza haematocheila</i>); revealing its immune relevance. 2019 , 84, 223-232		1
523	Targeting intrinsically disordered proteins at the edge of chaos. 2019 , 24, 217-227		60
522	A comprehensive review and comparison of existing computational methods for intrinsically disordered protein and region prediction. 2019 , 20, 330-346		73
521	Codon selection reduces GC content bias in nucleic acids encoding for intrinsically disordered proteins. 2020 , 77, 149-160		2
520	Disorder in milk proteins: adipophilin and TIP47, important constituents of the milk fat globule membrane. 2020 , 38, 1214-1229		1
519	Disorder-to-order transition in PE-PPE proteins of <i>Mycobacterium tuberculosis</i> augments the pro-pathogen immune response. 2020 , 10, 70-85		10
518	Sequence-dependent self-coacervation in high charge-density polyampholytes. 2020 , 5, 632-644		44
517	Getting to Know Your Neighbor: Protein Structure Prediction Comes of Age with Contextual Machine Learning. 2020 , 27, 796-814		12
516	Electrostatic interactions in molecular recognition of intrinsically disordered proteins. 2020 , 38, 4883-4894		8

515	Identification of a PAI-1-binding site within an intrinsically disordered region of vitronectin. 2020 , 29, 494-508	5
514	Stabilization of AIMP1/p43 and EMAP II recombinant proteins in the complexes with polysaccharide dextran-70. 2020 , 72, 238-245	2
513	Folding perspectives of an intrinsically disordered transactivation domain and its single mutation breaking the folding propensity. 2020 , 155, 1359-1372	6
512	Do sequence neighbours of intrinsically disordered regions promote structural flexibility in intrinsically disordered proteins?. 2020 , 209, 107428	2
511	Role of Intrinsically Disordered Regions in Acceleration of Protein-Protein Association. 2020 , 124, 20-27	4
510	Evolutionary Forces and Codon Bias in Different Flavors of Intrinsic Disorder in the Human Proteome. 2020 , 88, 164-178	18
509	Do Molecular Dynamics Force Fields Capture Conformational Dynamics of Alanine in Water?. 2020 , 16, 510-527	15
508	Proteins in Calcium Phosphates Biomineralization. 2020 ,	2
507	Ensemble-Based Thermodynamics of the Fuzzy Binding between Intrinsically Disordered Proteins and Small-Molecule Ligands. 2020 , 60, 4967-4974	3
506	Evolutionary Study of Disorder in Protein Sequences. 2020 , 10,	8
505	A Novel Strategy for the Development of Vaccines for SARS-CoV-2 (COVID-19) and Other Viruses Using AI and Viral Shell Disorder. 2020 , 19, 4355-4363	6
504	Cooperative unfolding of a single-layer β sheet protein, CPAP G-box. 2020 , 526, 105-109	1
503	Disorder driven allosteric control of protein activity. 2020 , 2, 191-203	13
502	Liquid-Liquid Phase Separation by Intrinsically Disordered Protein Regions of Viruses: Roles in Viral Life Cycle and Control of Virus-Host Interactions. 2020 , 21,	25
501	Structure-Function Insights of Jaburetox and Soyuretox: Novel Intrinsically Disordered Polypeptides Derived from Plant Ureases. 2020 , 25,	1
500	Characterization of partially ordered states in the intrinsically disordered N-terminal domain of p53 using millisecond molecular dynamics simulations. 2020 , 10, 12402	6
499	Diversity and genome mapping assessment of disordered and functional domains in trypanosomatids. 2020 , 227, 103919	2
498	Energetics and kinetics of substrate analog-coupled staphylococcal nuclease folding revealed by a statistical mechanical approach. 2020 , 117, 19953-19962	1

497	Exploring IDP-Ligand Interactions: tau K18 as A Test Case. 2020 , 21,	4
496	Shell Disorder Analysis Suggests That Pangolins Offered a Window for a Silent Spread of an Attenuated SARS-CoV-2 Precursor among Humans. 2020 , 19, 4543-4552	17
495	Performance of CHARMM36m with modified water model in simulating intrinsically disordered proteins: a case study. 2020 , 6, 80-87	3
494	Disorder and cysteines in proteins: A design for orchestration of conformational see-saw and modulatory functions. 2020 , 174, 331-373	4
493	The Dynamism of Intrinsically Disordered Proteins: Binding-Induced Folding, Amyloid Formation, and Phase Separation. 2020 , 124, 11541-11560	13
492	Drug Stability and Chemical Kinetics. 2020 ,	1
491	The exquisite structural biophysics of the Golgi Reassembly and Stacking Proteins. 2020 , 164, 3632-3644	2
490	Presence of intrinsically disordered proteins can inhibit the nucleation phase of amyloid fibril formation of A β (1-42) in amino acid sequence independent manner. 2020 , 10, 12334	3
489	Orchestration of signaling by structural disorder in class 1 cytokine receptors. 2020 , 18, 132	6
488	Analysis of Protein Disorder Predictions in the Light of a Protein Structural Alphabet. 2020 , 10,	5
487	Molecular Interaction Mechanism of a 14-3-3 Protein with a Phosphorylated Peptide Elucidated by Enhanced Conformational Sampling. 2020 , 60, 4867-4880	3
486	A disordered encounter complex is central to the yeast Abp1p SH3 domain binding pathway. 2020 , 16, e1007815	6
485	The Pathophysiological Significance of Fibulin-3. 2020 , 10,	5
484	Control of electron transfer by protein dynamics in photosynthetic reaction centers. 2020 , 55, 425-468	3
483	Exploring the molecular insights of intrinsically disordered mitochondrial intermembrane protein in its unbound and substrate-bound state. 2020 , 46, 1239-1247	
482	Zooming into the Dark Side of Human Annexin-S100 Complexes: Dynamic Alliance of Flexible Partners. 2020 , 21,	8
481	Intrinsic Disorder in Human Proteins Encoded by Core Duplicon Gene Families. 2020 , 124, 8050-8070	0
480	Relevance of Electrostatic Charges in Compactness, Aggregation, and Phase Separation of Intrinsically Disordered Proteins. 2020 , 21,	20

479	Moonlighting Proteins in the Fuzzy Logic of Cellular Metabolism. 2020 , 25,		9
478	Targeting Intrinsically Disordered Proteins through Dynamic Interactions. 2020 , 10,		16
477	Intrinsic Disorder in Tetratricopeptide Repeat Proteins. 2020 , 21,		2
476	Intrinsic disorder in protein sense-antisense recognition. 2020 , 33, e2868		3
475	Structural Description of the Nipah Virus Phosphoprotein and Its Interaction with STAT1. 2020 , 118, 2470-2488	14	
474	Hydrolysis of Peptide Bonds in Protein Micelles Promoted by a Zirconium(IV)-Substituted Polyoxometalate as an Artificial Protease. 2020 , 26, 11170-11179		4
473	FTIP: an accurate and efficient method for global protein surface comparison. 2020 , 36, 3056-3063		1
472	Specific Conformational Dynamics and Expansion Underpin a Multi-Step Mechanism for Specific Binding of p27 with Cdk2/Cyclin A. <i>Journal of Molecular Biology</i> , 2020 , 432, 2998-3017	6.5	10
471	Calcium ions modulate the structure of the intrinsically disordered Nucleobindin-2 protein. 2020 , 154, 1091-1104		4
470	Physical basis of the disorder-order transition. 2020 , 685, 108305		6
469	Investigations of the underlying mechanisms of HIF-1 α and CITED2 binding to TAZ1. 2020 , 117, 5595-5603		10
468	Epitope Mapping and Fine Specificity of Human T and B Cell Responses for Novel Candidate Blood-Stage Malaria Vaccine P27A. 2020 , 11, 412		
467	Shell disorder analysis predicts greater resilience of the SARS-CoV-2 (COVID-19) outside the body and in body fluids. 2020 , 144, 104177		46
466	Twenty years of research on the DFS70/LEDGF autoantibody-autoantigen system: many lessons learned but still many questions. 2020 , 11, 3		14
465	Probing Surfaces in Dynamic Protein Interactions. <i>Journal of Molecular Biology</i> , 2020 , 432, 2949-2972	6.5	8
464	Criticality in the conformational phase transition among self-similar groups in intrinsically disordered proteins: Probed by salt-bridge dynamics. 2020 , 1868, 140474		1
463	Experimentally Determined Long Intrinsically Disordered Protein Regions Are Now Abundant in the Protein Data Bank. 2020 , 21,		12
462	IDPs and their complexes in GPCR and nuclear receptor signaling. 2020 , 174, 105-155		3

461	Distinct residual and disordered structures of alpha-synuclein analyzed by amide-proton exchange and NMR signal intensity. 2020 , 1868, 140464	1
460	Untangling the Conformational Polymorphism of Disordered Proteins Associated With Neurodegeneration at the Single-Molecule Level. 2019 , 12, 309	6
459	Molecular basis of flexible peptide recognition by an antibody. 2020 , 167, 343-345	
458	Integrating All-Atom and Coarse-Grained Simulations-Toward Understanding of IDPs at Surfaces. 2020 , 16, 1843-1853	3
457	Order-disorder skewness in alpha-synuclein: a key mechanism to recognize membrane curvature. 2020 , 22, 5255-5263	7
456	Microsecond Simulation of the Proteoglycan-like Region of Carbonic Anhydrase IX and Design of Chemical Inhibitors Targeting pH Homeostasis in Cancer Cells. 2020 , 5, 4270-4281	7
455	Structure-Activity Relationships of Hydroxyapatite-Binding Peptides. 2020 , 36, 2729-2739	7
454	Comparative Analysis and Molecular Evolution of Class I PI3K Regulatory Subunit p85 Reveal the Structural Similarity Between nSH2 and cSH2 Domains. 2020 , 26, 2555-2569	
453	Flexible loop and helix 2 domains of TCTP are the functional domains of dimerized TCTP. 2020 , 10, 197	4
452	Sequence-Based Prediction of Fuzzy Protein Interactions. <i>Journal of Molecular Biology</i> , 2020 , 432, 2289-2303	46
451	Solution of Levinthal's Paradox and a Physical Theory of Protein Folding Times. 2020 , 10,	9
450	Macromolecular Interactions of Disordered Proteins. 2020 , 21,	0
449	A structural entropy index to analyse local conformations in intrinsically disordered proteins. 2020 , 210, 107464	7
448	Nipah shell disorder, modes of infection, and virulence. 2020 , 141, 103976	10
447	Deep learning methods in protein structure prediction. 2020 , 18, 1301-1310	80
446	100th Anniversary of Macromolecular Science Viewpoint: Opportunities in the Physics of Sequence-Defined Polymers. 2020 , 9, 216-225	51
445	Intrinsically Disordered Proteins. 2020 , 587-612	4
444	Distinct MCM10 Proteasomal Degradation Profiles by Primate Lentiviruses Vpr Proteins. 2020 , 12,	2

443	Supramolecular Protein Assembly Retains Its Structural Integrity at Liquid-Liquid Interface. 2020 , 7, 1901674	2
442	Controlling Structural Bias in Intrinsically Disordered Proteins Using Solution Space Scanning. 2020 , 16, 1794-1805	15
441	Analyzing Protein Disorder with IUPred2A. 2020 , 70, e99	83
440	Physical Chemistry of the Protein Backbone: Enabling the Mechanisms of Intrinsic Protein Disorder. 2020 , 124, 4379-4390	7
439	Secondary Mutation-Induced Alternative Splicing Suppresses RNA Splicing Defect of the Mutant. 2020 , 182, 2025-2034	
438	Intrinsically disordered proteins of viruses: Involvement in the mechanism of cell regulation and pathogenesis. 2020 , 174, 1-78	22
437	Hydropathy Patterning Complements Charge Patterning to Describe Conformational Preferences of Disordered Proteins. 2020 , 11, 3408-3415	34
436	A Coil-to-Helix Transition Serves as a Binding Motif for hSNF5 and BAF155 Interaction. 2020 , 21,	2
435	Charge Interactions Modulate the Encounter Complex Ensemble of Two Differently Charged Disordered Protein Partners of KIX. 2020 , 16, 3856-3868	8
434	Structural and Biophysical Insights into the Function of the Intrinsically Disordered Myc Oncoprotein. 2020 , 9,	23
433	Strategies for identifying dynamic regions in protein complexes: Flexibility changes accompany methylation in chemotaxis receptor signaling states. 2020 , 1862, 183312	2
432	Similar Yet Different-Structural and Functional Diversity among LEA_4 Proteins. 2020 , 21,	6
431	Optimizing the Specificity Window of Biomolecular Receptors Using Structure-Switching and Allostery. 2020 , 5, 1937-1942	6
430	Templated folding of intrinsically disordered proteins. 2020 , 295, 6586-6593	27
429	Dancing with Trojan horses: an interplay between the extracellular vesicles and viruses. 2021 , 39, 3034-3060	15
428	Unique and exclusive peptide signatures directly identify intrinsically disordered proteins from sequences without structural information. 2021 , 39, 2885-2893	3
427	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
426	Biom mineralization process in hard tissues: The interaction complexity within protein and inorganic counterparts. 2021 , 120, 20-37	24

425	Understanding COVID-19 via comparative analysis of dark proteomes of SARS-CoV-2, human SARS and bat SARS-like coronaviruses. 2021 , 78, 1655-1688	51
424	IDPology of the living cell: intrinsic disorder in the subcellular compartments of the human cell. 2021 , 78, 2371-2385	6
423	Unraveling protein's structural dynamics: from configurational dynamics to ensemble switching guides functional mesoscale assemblies. 2021 , 66, 129-138	9
422	Bioinformatics analysis of correlation between protein function and intrinsic disorder. 2021 , 167, 446-456	1
421	Accelerating atomistic simulations of proteins using multiscale enhanced sampling with independent tempering. 2021 , 42, 358-364	2
420	Hydrophobic residues advance the onset of simple coacervation in intrinsically disordered proteins at low densities: Insights from field theoretical simulations studies.	
419	Budding yeast Rad51: a paradigm for how phosphorylation and intrinsic structural disorder regulate homologous recombination and protein homeostasis. 2021 , 67, 389-396	1
418	Evolution-Structure Paradigm of Protein Complexes. 2021 , 153-196	
417	"Protein" no longer means what it used to. 2021 , 3, 146-152	0
416	Developing Inhibitors to the Amino-Terminus Domains of Steroid Hormone Receptors. 2021 , 613-642	
415	NMR reveals the interplay between SilE and SilB model peptides in the context of silver resistance. 2021 , 57, 8726-8729	
414	Shell disorder and the HIV vaccine mystery: lessons from the legendary Oswald Avery. 2021 , 1-10	2
413	Exploring Energy Landscapes of Intrinsically Disordered Proteins: Insights into Functional Mechanisms.	0
412	Using a sequence-specific coarse-grained model for studying protein liquid-liquid phase separation. 2021 , 646, 1-17	7
411	Tuning intrinsic disorder predictors for virus proteins. 2021 , 7, veaa106	1
410	The complexity of protein interactions unravelled from structural disorder. 2021 , 17, e1008546	3
409	Molecular Dynamic Simulation of Intrinsically Disordered Proteins and Relevant Forcefields. 2021 , 317-333	1
408	Using biochemistry and biophysics to extinguish androgen receptor signaling in prostate cancer. 2021 , 296, 100240	6

407	SARS-CoV-2 NSP1 C-terminal (residues 131-180) is an intrinsically disordered region in isolation. 2021 , 2, 100007	8
406	Assessing SIRAH's Capability to Simulate Intrinsically Disordered Proteins and Peptides. 2021 , 17, 599-604	5
405	Bioinformatics-based Identification of Proteins Expressed by Arthropod- borne Viruses Transmitted by Aedes Aegypti Mosquito. 2021 , 18, 81-94	1
404	Characterization of functional disordered regions within chromatin-associated proteins. 2021 , 24, 102070	6
403	The vaccinologist's "dirty little secret": a better understanding of structure-function relationships of viral immunogens might advance rational HIV vaccine design. 2021 , 166, 1297-1303	2
402	Intrinsic disorder in protein domains contributes to both organism complexity and clade-specific functions. 2021 , 11, 2985	10
401	In silico characterization and structural modeling of bacterial metalloprotease of family M4. 2021 , 19, 25	4
400	Recent Force Field Strategies for Intrinsically Disordered Proteins. 2021 , 61, 1037-1047	24
399	Fuzziness and Frustration in the Energy Landscape of Protein Folding, Function, and Assembly. 2021 , 54, 1251-1259	28
398	TIA1 potentiates tau phase separation and promotes generation of toxic oligomeric tau. 2021 , 118,	22
397	Proteomic Analysis of Src Family Kinase Phosphorylation States in Cancer Cells Suggests Deregulation of the Unique Domain. 2021 , 19, 957-967	0
396	Generalized-ensemble method study: A helix-mimetic compound inhibits protein-protein interaction by long-range and short-range intermolecular interactions. 2021 , 42, 956-969	1
395	Difference of binding modes among three ligands to a receptor mSin3B corresponding to their inhibitory activities. 2021 , 11, 6178	0
394	Adenosine triphosphate energy-independently controls protein homeostasis with unique structure and diverse mechanisms. 2021 , 30, 1277-1293	7
393	Exploring Energy Landscapes of Intrinsically Disordered Proteins: Insights into Functional Mechanisms. 2021 , 17, 3178-3187	5
392	Probing coupled conformational transitions of intrinsically disordered proteins in their interactions with target proteins. 2021 , 619, 114126	2
391	Comparative analysis of Pure Hubs and Pure Bottlenecks in Human Protein-protein Interaction Networks.	0
390	Intrinsically Disordered Proteins at the Nano-scale.	0

389	Effect of Disease Causing Missense Mutations on Intrinsically Disordered Regions in Proteins.		0
388	Sequence determinants of in cell condensate assembly morphology, dynamics, and oligomerization as measured by number and brightness analysis.		
387	Prevalence and functionality of intrinsic disorder in human FG-nucleoporins. 2021 , 175, 156-170		8
386	FLIPPER: Predicting and Characterizing Linear Interacting Peptides in the Protein Data Bank. <i>Journal of Molecular Biology</i> , 2021 , 433, 166900	6.5	3
385	14-3-3 Proteins: Novel Pharmacological Targets in Neurodegenerative Diseases. 2021 , 42, 226-238		9
384	diSBPred: A machine learning based approach for disulfide bond prediction. 2021 , 91, 107436		1
383	S100P Interacts with p53 while Pentamidine Inhibits This Interaction. 2021 , 11,		
382	Intrinsically Disordered Proteins as Regulators of Transient Biological Processes and as Untapped Drug Targets. 2021 , 26,		8
381	Conformational buffering underlies functional selection in intrinsically disordered protein regions.		1
380	Positive selection and intrinsic disorder are associated with multifunctional C4(AC4) proteins and geminivirus diversification. 2021 , 11, 11150		5
379	Recent Developments in the Field of Intrinsically Disordered Proteins: Intrinsic Disorder-Based Emergence in Cellular Biology in Light of the Physiological and Pathological Liquid-Liquid Phase Transitions. 2021 , 50, 135-156		23
378	AlphaFold and the amyloid landscape. <i>Journal of Molecular Biology</i> , 2021 , 433, 167059	6.5	10
377	Peptide array-based interactomics. 2021 , 413, 5561-5566		3
376	metapredict: a fast, accurate, and easy-to-use predictor of consensus disorder and structure.		3
375	Ubiquitin Interacting Motifs: Duality Between Structured and Disordered Motifs. 2021 , 8, 676235		1
374	Conserved allosteric ensembles in disordered proteins using TROSY/anti-TROSY R-filtered spectroscopy. 2021 , 120, 2498-2510		2
373	Prediction and Characterization of Disorder-Order Transition Regions in Proteins by Deep Learning.		
372	PRISMA and BioID disclose a motifs-based interactome of the intrinsically disordered transcription factor C/EBPβ 2021 , 24, 102686		2

371	Nonspecific Binding-Fundamental Concepts and Consequences for Biosensing Applications. 2021 , 121, 8095-8160		25
370	Sequence determinants of in cell condensate morphology, dynamics, and oligomerization as measured by number and brightness analysis. 2021 , 19, 65		4
369	Networks of Networks: An Essay on Multi-Level Biological Organization. 2021 , 12, 706260		7
368	Improving Docking Power for Short Peptides Using Random Forest. 2021 , 61, 3074-3090		3
367	What's in a name? From "fluctuation fit" to "conformational selection": rediscovery of a concept. 2021 , 43, 88		1
366	Illuminating Disorder Induced by Glu in a Stable Arg-Anchored Transmembrane Helix. 2021 , 6, 20611-20618		
365	Exploring Curated Conformational Ensembles of Intrinsically Disordered Proteins in the Protein Ensemble Database. 2021 , 1, e192		1
364	The disordered PCI-binding human proteins CSNAP and DSS1 have diverged in structure and function. 2021 , 30, 2069-2082		2
363	Uncovering the Conformational Distribution of a Small Protein with Nanoparticle-Aided Cryo-Electron Microscopy Sampling. 2021 , 12, 6565-6573		0
362	Revealing Intrinsic Disorder and Aggregation Properties of the DPF3a Zinc Finger Protein. 2021 , 6, 18793-18800		
361	Dynamics in Fip1 regulate eukaryotic mRNA 3'-end processing.		2
360	Cancer-Associated Mutations Perturb the Disordered Ensemble and Interactions of the Intrinsically Disordered p53 Transactivation Domain. <i>Journal of Molecular Biology</i> , 2021 , 433, 167048	6.5	5
359	Lattice protein design using Bayesian learning. 2021 , 104, 014404		0
358	Nrf2, the Major Regulator of the Cellular Oxidative Stress Response, is Partially Disordered. 2021 , 22,		3
357	On the roles of intrinsically disordered proteins and regions in cell communication and signaling. 2021 , 19, 88		15
356	What's in the BAGs? Intrinsic disorder angle of the multifunctionality of the members of a family of chaperone regulators. 2021 ,		1
355	Genome-wide analysis of HECT E3 ubiquitin ligase gene family in <i>Solanum lycopersicum</i> . 2021 , 11, 15891		2
354	Per aspera ad chaos: a personal journey to the wonderland of intrinsic disorder. 2021 , 478, 3015-3024		4

353	Enthalpy-Entropy Compensation in the Promiscuous Interaction of an Intrinsically Disordered Protein with Homologous Protein Partners. 2021 , 11,		2
352	Intrinsically disordered electronegative clusters improve stability and binding specificity of RNA-binding proteins. 2021 , 297, 100945		3
351	Unstructural Biology of TRP Ion Channels: The Role of Intrinsically Disordered Regions in Channel Function and Regulation. <i>Journal of Molecular Biology</i> , 2021 , 433, 166931	6.5	7
350	UV Resonance Raman explores protein structural modification upon fibrillation and ligand interaction. 2021 , 120, 4575-4589		1
349	AlphaFold and Implications for Intrinsically Disordered Proteins. <i>Journal of Molecular Biology</i> , 2021 , 433, 167208	6.5	48
348	The disordered regions of the methyltransferase SETD2 govern its function by regulating its proteolysis and phase separation. 2021 , 297, 101075		1
347	Dynamics in Fip1 regulate eukaryotic mRNA 3' end processing. 2021 , 35, 1510-1526		3
346	Nucleoporins' exclusive amino acid sequence features regulate their transient interaction with and selectivity of cargo complexes in the nuclear pore. 2021 , 32, ar31		3
345	Metapredict: a fast, accurate, and easy-to-use predictor of consensus disorder and structure. 2021 , 120, 4312-4319		17
344	Role of ORF4 in Hepatitis E virus regulation: analysis of intrinsically disordered regions. 1		2
343	Quantification of Conformational Entropy Unravels Effect of Disordered Flanking Region in Coupled Folding and Binding. 2021 , 143, 14540-14550		4
342	Integrating single-molecule spectroscopy and simulations for the study of intrinsically disordered proteins. 2021 , 193, 116-135		6
341	20S and 26S proteasome-binding proteins of the rabbit brain: A proteomic dataset. 2021 , 38, 107276		0
340	Intrinsically disordered protein regions at membrane contact sites. 2021 , 1866, 159020		1
339	Intrinsically disordered proteins: Chronology of a discovery. 2021 , 279, 106694		3
338	QUARTERplus: Accurate disorder predictions integrated with interpretable residue-level quality assessment scores. 2021 , 19, 2597-2606		3
337	Structural Aspects of Protein-Protein Interactions. 2021 , 61-112		
336	Folded domain charge properties influence the conformational behavior of disordered tails. 2021 , 3, 216-228		2

335	Static and Dynamic Disorder in IN VITRO Reconstituted Receptor-Adaptor Interaction. 195-215	2
334	Ensemble characterization of an intrinsically disordered FG-Nup peptide and its F>A mutant in DMSO-d. 2017 , 108, e23036	1
333	Immunotherapy Strategies for Lewy Body and Parkinson's Diseases. 2009 , 599-613	1
332	α-Synuclein Aggregation and Parkinson's Disease. 2007 , 61-110	2
331	Disordered RNA-Binding Region Prediction with DisoRDPbind. 2020 , 2106, 225-239	9
330	Quantitative Protein Disorder Assessment Using NMR Chemical Shifts. 2020 , 2141, 303-317	5
329	Predicting Conformational Properties of Intrinsically Disordered Proteins from Sequence. 2020 , 2141, 347-389	3
328	Analyzing IDPs in Interactomes. 2020 , 2141, 895-945	7
327	Analyzing the Sequences of Intrinsically Disordered Regions with CIDER and localCIDER. 2020 , 2141, 103-126	6
326	Bioinformatics Approaches to the Structure and Function of Intrinsically Disordered Proteins. 2009 , 113-140	1
325	Structural Disorder and Its Connection with Misfolding Diseases. 2009 , 1-19	4
324	"Fuzziness" in the cellular interactome: a historical perspective. 2012 , 725, 184-90	5
323	Biomineralization: Apatite Protein Interaction. 2012 , 135-159	1
322	POODLE: tools predicting intrinsically disordered regions of amino acid sequence. 2014 , 1137, 131-45	4
321	Prediction and analysis of intrinsically disordered proteins. 2015 , 1261, 35-59	6
320	Prediction of intrinsic disorder and its use in functional proteomics. 2007 , 408, 69-92	32
319	Cytokine Receptors. 2016 , 1-29	2
318	Evolutionary Perspectives on Protein Thermodynamics. 2004 , 718-727	2

317	Enhancing Protein Disorder Detection by Refined Secondary Structure Prediction. 2007 , 395-409	1
316	Computational Methods for Protein Structure Prediction and Fold Recognition. 2008 , 1-21	6
315	The Superfamily of Vertebrate-Secreted Ribonucleases. 2011 , 1-34	2
314	The Effect of Amino Acid Size on the Internal Dynamics and Conformational Freedom of Polypeptides. 2020 , 53, 9811-9822	4
313	When Darkness Becomes a Ray of Light in the Dark Times: Understanding the COVID-19 via the Comparative Analysis of the Dark Proteomes of SARS-CoV-2, Human SARS and Bat SARS-Like Coronaviruses.	12
312	Prediction of disordered regions in proteins with recurrent Neural Networks and protein dynamics.	6
311	SARS-CoV-2 NSP1 C-terminal region (residues 130-180) is an intrinsically disordered region.	4
310	Intrinsic disorder codes for leaps of protein expression.	1
309	A comprehensive motifs-based interactome of the C/EBP β transcription factor.	1
308	A 20S proteasome receptor for degradation of intrinsically disordered proteins.	2
307	Interplay between folding and binding modulates protein sequences, structures, functions and regulation.	1
306	Sequence effects on size, shape, and structural heterogeneity in Intrinsically Disordered Proteins.	2
305	New classification of intrinsic disorder in the Human proteome.	0
304	Damage response and dNTP regulation: the interaction between ribonucleotide reductase and its inhibitor, Sml1. 2000 , 65, 343-6	7
303	Networks of interbasin traffic in intrinsically disordered proteins. 2020 , 2,	4
302	Structural biology. Flipping a switch. 2001 , 291, 2329-30	11
301	Temperature-Dependent Molecular Adaptation Features in Proteins. 75-85	4
300	Computational Prediction of Protein Complexes from Protein Interaction Networks. 2017 ,	11

299	Constructing Reliable Protein-Protein Interaction (PPI) Networks. 2017 , 15	1
298	On the intrinsic disorder status of the major players in programmed cell death pathways. 2013 , 2, 190	18
297	New technologies to analyse protein function: an intrinsic disorder perspective. 2020 , 9,	9
296	Prediction of Intrinsic Disorder in MERS-CoV/HCoV-EMC Supports a High Oral-Fecal Transmission. 2013 , 5,	48
295	Residual structures, conformational fluctuations, and electrostatic interactions in the synergistic folding of two intrinsically disordered proteins. 2012 , 8, e1002353	73
294	Modeling disordered protein interactions from biophysical principles. 2017 , 13, e1005485	36
293	Nonnative interactions in coupled folding and binding processes of intrinsically disordered proteins. 2010 , 5, e15375	34
292	A model of a MAPK-substrate complex in an active conformation: a computational and experimental approach. 2011 , 6, e18594	17
291	Binding-folding induced regulation of AF1 transactivation domain of the glucocorticoid receptor by a cofactor that binds to its DNA binding domain. 2011 , 6, e25875	21
290	Intrinsically unstructured domain 3 of hepatitis C Virus NS5A forms a "fuzzy complex" with VAPB-MSP domain which carries ALS-causing mutations. 2012 , 7, e39261	34
289	Insight into role of selection in the evolution of polyglutamine tracts in humans. 2012 , 7, e41167	5
288	Prediction of protein-protein interaction sites by random forest algorithm with mRMR and IFS. 2012 , 7, e43927	69
287	Effects of molecular crowding on the dynamics of intrinsically disordered proteins. 2012 , 7, e49876	73
286	The intrinsically disordered regions of the Drosophila melanogaster Hox protein ultrabithorax select interacting proteins based on partner topology. 2014 , 9, e108217	12
285	Structural basis for inhibition of the MDM2:p53 interaction by an optimized MDM2-binding peptide selected with mRNA display. 2014 , 9, e109163	13
284	The Dimerization State of the Mammalian High Mobility Group Protein AT-Hook 2 (HMGA2). 2015 , 10, e0130478	16
283	Phosphorylation Regulates the Bound Structure of an Intrinsically Disordered Protein: The p53-TAZ2 Case. 2016 , 11, e0144284	11
282	Deciphering Mode of Action of Functionally Important Regions in the Intrinsically Disordered Paxillin (Residues 1-313) Using Its Interaction with FAT (Focal Adhesion Targeting Domain of Focal Adhesion Kinase). 2016 , 11, e0150153	6

281	Multiple-Localization and Hub Proteins. 2016 , 11, e0156455	20
280	Intrinsic Disorder in Transmembrane Proteins: Roles in Signaling and Topology Prediction. 2016 , 11, e0158594	35
279	Evolution of the Twist Subfamily Vertebrate Proteins: Discovery of a Signature Motif and Origin of the Twist1 Glycine-Rich Motifs in the Amino-Terminus Disordered Domain. 2016 , 11, e0161029	8
278	Transient helicity in intrinsically disordered Axin-1 studied by NMR spectroscopy and molecular dynamics simulations. 2017 , 12, e0174337	5
277	Mechanisms of Macromolecular Interactions Mediated by Protein Intrinsic Disorder. 2020 , 43, 899-908	6
276	H-Prune through GSK-3 β interaction sustains canonical WNT/ β -catenin signaling enhancing cancer progression in NSCLC. 2014 , 5, 5736-49	34
275	Single enantiomer of YK-4-279 demonstrates specificity in targeting the oncogene EWS-FLI1. 2012 , 3, 172-82	67
274	iPhos-PseEn: identifying phosphorylation sites in proteins by fusing different pseudo components into an ensemble classifier. 2016 , 7, 51270-51283	133
273	An Overview on Natively Unfolded Proteins. 2009 , 49, 004-010	1
272	Generation of a flexible loop structural ensemble and its application to induced-fit structural changes following ligand binding. 2006 , 2, 1-12	4
271	About TFE: Old and New Findings. 2019 , 20, 425-451	15
270	Coherent Behavior and the Bound State of Water and K(+) Imply Another Model of Bioenergetics: Negative Entropy Instead of High-energy Bonds. 2012 , 6, 139-59	6
269	Reporting on the future of integrative structural biology ORAU workshop. 2020 , 25, 43-68	1
268	Overexpression of the extracellular and cytoplasmic domains of the Drosophila adhesion protein, gliotactin. 2004 , 687-689	1
267	Intrinsic Disorder in Nuclear Receptor Amino Termini: From Investigational Challenge to Therapeutic Opportunity. 2019 , 6,	2
266	Structural Aspects and Prediction of Calmodulin-Binding Proteins. 2020 , 22,	7
265	Protein flexibility, not disorder, is intrinsic to molecular recognition. 2013 , 5, 2	54
264	Spin-label scanning reveals conformational sensitivity of the bound helical interfaces of IA3. 2018 , 5, 166-181	1

263	Multi-Agent Systems in Three-Dimensional Protein Structure Prediction. 2017 , 241-278	1
262	Complex interactomes and post-translational modifications of the regulatory proteins HABP4 and SERBP1 suggest pleiotropic cellular functions. 2019 , 10, 44-64	4
261	A widely employed germ cell marker is an ancient disordered protein with reproductive functions in diverse eukaryotes. 2016 , 5,	35
260	Probing protein flexibility reveals a mechanism for selective promiscuity. 2017 , 6,	14
259	Investigating the trade-off between folding and function in a multidomain Y-family DNA polymerase. 2020 , 9,	6
258	Intrinsically disordered caldesmon binds calmodulin via the "buttons on a string" mechanism. 2015 , 3, e1265	7
257	Malleable ribonucleoprotein machine: protein intrinsic disorder in the <i>Saccharomyces cerevisiae</i> spliceosome. 2013 , 1, e2	30
256	SubVis: an interactive R package for exploring the effects of multiple substitution matrices on pairwise sequence alignment. 2017 , 5, e3492	1
255	Association between intrinsic disorder and serine/threonine phosphorylation in <i>Mycobacterium tuberculosis</i> . 2015 , 3, e724	5
254	Functions of intrinsically disordered proteins through evolutionary lenses. 2021 , 183, 45-74	2
253	Intrinsic disorder in integral membrane proteins. 2021 , 183, 101-134	0
252	Target-binding behavior of IDPs via pre-structured motifs. 2021 , 183, 187-247	0
251	ECO: the Evidence and Conclusion Ontology, an update for 2022.. 2022 , 50, D1515-D1521	0
250	Protein intrinsic disorder on a dynamic nucleosomal landscape. 2021 , 183, 295-354	0
249	Improving the global dimensions of intrinsically disordered proteins in Martini 3.	1
248	When Order Meets Disorder: Modeling and Function of the Protein Interface in Fuzzy Complexes. 2021 , 11,	1
247	The potential of intrinsically disordered regions in vaccine development. 2021 , 1-3	1
246	AlphaDesign: A de novo protein design framework based on AlphaFold.	9

- 245 Role of "dual-personality" fragments in HEV adaptation-analysis of Y-domain region. **2021**, 19, 154 1
- 244 Protein β Sheet Partner Prediction by Neural Networks. **2000**, 3-9
- 243 On the problem of multidrug resistance: hypermutability as a mechanism to defense metabolic targets from toxic xenobiotics. **2004**, 20, 193-206
- 242 Analysis of unstructured regions of human cytoplasmic tyrosyl-tRNA synthetase by methods of bioinformatics. **2005**, 21, 446-453 2
- 241 Disordered Proteins. 1
- 240 Amyloid Fibril Formation of Natively Unfolded Proteins. 247
- 239 Computational Analysis of Modular Protein Architectures. 439
- 238 Functional Unfolded Proteins: How, When, Where, and Why?. **2009**, 124-136
- 237 Structural Properties of Fibril-forming Segments of β Synuclein. **2009**, 30, 623-629
- 236 Modes of p53 Interactions with DNA in the Chromatin Context. **2010**, 127-141
- 235 Recognition Mechanism of the Cell Polarity Protein Mammalian Inscuteable-LGN Complex. **2012**, 54, 206-212
- 234 References. 575-608
- 233 Neural Networks in Bioinformatics. **2013**, 505-525
- 232 Water Associated with Bio-Objects: Cells and Tissues. **2013**, 806-905
- 231 Protein Misfolding and Aggregation. **2015**, 95-127
- 230 Quantitative proteome-based guidelines for intrinsic disorder characterization.
- 229 Structure, Dynamics, and Function of Staphylococcal Nuclease. **2016**, 151-161 1
- 228 Applications of Computational Methods to Simulations of Protein Dynamics. **2016**, 1-43 0

- 227 Unfoldomes and Unfoldomics: Introducing Intrinsically Disordered Proteins. **2016**, 125-150 1
- 226 - Molecular Thermodynamic Modeling of Fluctuation Solution Theory Properties. **2016**, 252-283
- 225 Disordered Proteins. 1-11
- 224 Proteus: A Random Forest Classifier to Predict Disorder-to-Order Transitioning Binding Regions in Intrinsically Disordered Proteins.
- 223 The relationship between relative solvent accessible surface area (rASA) and irregular structures in protean segments (ProSs). **2016**, 12, 381-387
- 222 Cytokine Receptors. **2017**, 1-29 o
- 221 Evaluating Protein Complex Prediction Methods. **2017**, 91
- 220 Identifying Evolutionarily Conserved Protein Complexes. **2017**, 165
- 219 Identifying Dynamic Protein Complexes. **2017**, 145
- 218 Introduction to Protein Complex Prediction. **2017**, 1
- 217 Open Challenges in Protein Complex Prediction. **2017**, 107
- 216 Preface. **2017**, xi
- 215 References. **2017**, 233
- 214 Computational Methods for Protein Complex Prediction from PPI Networks. **2017**, 59
- 213 Protein Complex Prediction in the Era of Systems Biology. **2017**, 185
- 212 Conclusion. **2017**, 225
- 211 Handheld highly selective plasmonic chem/biosensor using engineered binding proteins for extreme conformational changes. **2017**,
- 210 Sequence fingerprints distinguish erroneous from correct predictions of Intrinsically Disordered Protein Regions.

- 209 Protein structures as shapes: Analysing protein structure variation using geometric morphometrics.
- 208 Salt-bridge Dynamics in Intrinsically Disordered Proteins: A trade-off between electrostatic interactions and structural flexibility.
- 207 Protein Interaction Screen on Peptide Matrix (PRISMA) reveals interaction footprints and the PTM-dependent interactome of intrinsically disordered C/EBP β
- 206 PAGE4 and Conformational Switching: Insights from Molecular Dynamics Simulations and Implications for Prostate Cancer. 1
- 205 Dual roles of electrostatic-steering and conformational dynamics in the binding of calcineurin β intrinsically-disordered recognition domain to calmodulin.
- 204 A comprehensive ensemble model for comparing the allosteric effect of ordered and disordered proteins. 2
- 203 Intrinsically Disordered Regions in PE/PPE Protein Family of Mycobacterium tuberculosis: Moonlighting Function. **2019**, 151-170 0
- 202 Multi-Agent Systems in Three-Dimensional Protein Structure Prediction. **2019**, 1031-1068
- 201 Novel Interaction Mechanism between the Intrinsically Disordered Proteins. **2019**, 59, 202-204
- 200 Intrinsically disordered proteins and structured proteins with intrinsically disordered regions have different functional roles in the cell. 1
- 199 Role of Pre-molten Globule Structure in Protein Amyloid Fibril Formation. **2019**, 7, 35-42
- 198 Controlling Structural Bias in Intrinsically Disordered Proteins Using Solution Space Scanning.
- 197 Investigations of the Underlying Mechanisms of HIF-1 β and CITED2 Binding to TAZ1.
- 196 Disorder and interfaces in proteins are two sides of the same coin.
- 195 Production of glycosylphosphatidylinositol-anchored proteins for vaccines and directed binding of immunoliposomes to specific cell types. **2020**, 26, e20200032 1
- 194 Enhanced Molecular Dynamics Simulations of Intrinsically Disordered Proteins. **2020**, 2141, 391-411 1
- 193 Letter to the Editor: A still unresolved mystery in the interaction between intrinsically disordered proteins: How do they recognize multiple target proteins? A commentary on "No folding upon binding of intrinsically disordered proteins: Still interesting but not unique and novel. by Sigalov, A. B., Biophysics and Physicobiology 17, 156-158 (2020). DOI: 10.2142/biophysico.BSJ-2020025". **2020**, 17, 159-160 1
- 192 A disordered encounter complex is central to the yeast Abp1p SH3 domain binding pathway.

191	Strategies for identifying dynamic regions in protein complexes: flexibility changes accompany methylation in chemotaxis receptor signaling states.	
190	Molecular interaction mechanism of a 14-3-3 protein with a phosphorylated peptide elucidated by enhanced conformational sampling.	2
189	Transient disorder along pathways to amyloid. 2021 , 281, 106711	11
188	Rapid Identification of Secondary Structure and Binding Site Residues in an Intrinsically Disordered Protein Segment. 2021 , 12, 755292	2
187	Computational Prediction of Intrinsic Disorder in Protein Sequences with the disCoP Meta-predictor. 2020 , 2141, 21-35	3
186	Stability Studies of Proteinous Compounds. 2020 , 187-236	
185	Intrinsic Disorder in Plant Transcription Factor Systems: Functional Implications. 2020 , 21,	2
184	Cancer-Associated Mutations Perturb the Structure and Interactions of the Intrinsically Disordered p53 Transactivation Domain.	
183	A novel mode of interaction between intrinsically disordered proteins. 2020 , 17, 86-93	5
182	Hydropathy patterning complements charge patterning to describe conformational preferences of disordered proteins.	2
181	NeProc predicts binding segments in intrinsically disordered regions without learning binding region sequences. 2020 , 17, 147-154	1
180	Disorder for Dummies: Functional Mutagenesis of Transient Helical Segments in Disordered Proteins. 2020 , 2141, 3-20	0
179	Obtaining Hydrodynamic Radii of Intrinsically Disordered Protein Ensembles by Pulsed Field Gradient NMR Measurements. 2020 , 2141, 285-302	1
178	Experimentally determined long intrinsically disordered protein regions are now abundant in the Protein Data Bank.	1
177	Criticality in the conformational phase transition among self-similar groups in intrinsically disordered proteins: probed by salt-bridge dynamics.	
176	The protein disorder cycle.. 2021 , 13, 1155-1162	3
175	AlphaFold Models Illuminate Half of Dark Human Proteins.	0
174	Local Structure Prediction of Proteins. 2007 , 207-254	1

173	Bibliography. 277-298	
172	Methods for improving protein disorder prediction.	3
171	Tuning intrinsic disorder predictors for virus proteins.	
170	Network of inter-basin traffic in intrinsically disordered PUMA protein. 2020 , 132, 28002	
169	Functionality and the evolution of marginal stability in proteins: inferences from lattice simulations. 2007 , 2, 91-101	14
168	Physicochemical biology: conquered boundaries and new horizons. 2012 , 4, 36-43	1
167	Modulation of p53 Transactivation Domain Conformations by Ligand Binding and Cancer-Associated Mutations. 2020 , 25, 195-206	4
166	Prediction of secondary structure population and intrinsic disorder of proteins using multitask deep learning. 2020 , 2020, 1325-1334	
165	Microsecond simulations and CD spectroscopy reveals the intrinsically disordered nature of SARS-CoV-2 spike-C-terminal cytoplasmic tail (residues 1242-1273) in isolation. 2021 , 566, 42-55	3
164	Missense Mutations Modify the Conformational Ensemble of the -Synuclein Monomer Which Exhibits a Two-Phase Characteristic.. 2021 , 8, 786123	1
163	Protein conformational dynamics and phenotypic switching.. 2021 , 13, 1127-1138	0
162	Cross-Linking Mass Spectrometry for Investigating Protein Conformations and Protein-Protein Interactions-A Method for All Seasons. 2021 ,	11
161	Molecular Simulations of Intrinsically Disordered Proteins and Their Binding Mechanisms. 2022 , 2376, 343-362	
160	Effect of Disease Causing Missense Mutations on Intrinsically Disordered Regions in Proteins. 2021 ,	0
159	Engineering of a protein probe with multiple inputs and multiple outputs for evaluation of alpha synuclein aggregation states.. 2022 , 178,	1
158	Probing functional conformation-state fluctuation dynamics in recognition binding between calmodulin and target peptide.. 2022 , 156, 055102	0
157	Enzymatic Approach in Calcium Phosphate Biomineralization: A Contribution to Reconcile the Physicochemical with the Physiological View. 2021 , 22,	1
156	Protein folding, misfolding, and un/non-folding: overview of the SP16 Session at the 20 IUPAB congress, 45 Annual Meeting of SBBf, and 50 Annual Meeting of SBBq.. 2021 , 13, 879-882	0

155	Low-Complexity Regions in Plasmodium falciparum Proteins. 2001 , 11, 218-229	9
154	Unveiling induced folding of intrinsically disordered proteins - Protein engineering, frustration and emerging themes.. 2021 , 72, 153-160	1
153	Macromolecular Crowding Induces a Binding Competent Transient Structure in Intrinsically Disordered Gab1.. <i>Journal of Molecular Biology</i> , 2021 , 434, 167407	6.5 1
152	Co-opting disorder into order: Intrinsically disordered proteins and the early evolution of complex multicellularity.. 2022 , 201, 29-36	1
151	Binding affinity of curcumin to bovine serum albumin enhanced by pulsed electric field pretreatment.. 2021 , 377, 131945	2
150	Cryoprotective activities of FK20, a human genome-derived intrinsically disordered peptide against cryosensitive enzymes without a stereospecific molecular interaction. 3, e20	
149	Intrinsically Disordered Proteins (IDP): Purification Under Denaturing Conditions.. 2022 , 2406, 359-370	1
148	The Inherent Coupling of Intrinsically Disordered Regions in the Multidomain Receptor Tyrosine Kinase KIT.. 2022 , 23,	2
147	Seeking Solvation: Exploring the Role of Protein Hydration in Silk Gelation.. 2022 , 27,	1
146	Molecular simulations to study IDP-IDP interactions and their complexes. 2022 , 565-574	
145	Rational design of a helical peptide inhibitor targeting c-Myb-KIX interaction.. 2022 , 12, 816	2
144	Probing Small-Angle Molecular Motions with EPR Spectroscopy: Dynamical Transition and Molecular Packing in Disordered Solids. 2022 , 8, 19	0
143	Experimental Evidence of Intrinsic Disorder and Amyloid Formation by the W Proteins.. 2022 , 23,	1
142	Experimental methods to study intrinsically disordered proteins. 2022 , 505-533	2
141	Grape ASR-Silencing Sways Nuclear Proteome, Histone Marks and Interplay of Intrinsically Disordered Proteins.. 2022 , 23,	1
140	Conformational and Solvation Dynamics of an Amyloidogenic Intrinsically Disordered Domain of a Melanosomal Protein.. 2022 ,	0
139	Multisite Phosphorylation and Binding Alter Conformational Dynamics of the 4E-BP2 Protein.	
138	How sticky are our proteins? Quantifying hydrophobicity of the human proteome.	1

137	Intrinsically disordered proteins/regions and insight into their biomolecular interactions.. 2022 , 283, 106769	5
136	An MP2/Molecular Dynamics study of the solvent effects on the conformational equilibrium of the glycine dipeptide. 2022 , 351, 118557	
135	The group 3 LEA protein of <i>Artemia franciscana</i> for cryopreservation.. 2022 ,	
134	A FRET-Based Biosensor for the Src N-Terminal Regulatory Element.. 2022 , 12,	
133	Sequence- and chemical specificity define the functional landscape of intrinsically disordered regions.	0
132	Computational, Experimental, and Clinical Evidence of a Specific but Peculiar Evolutionary Nature of (COVID-19) SARS-CoV-2.. 2022 ,	3
131	Protein Symmetry, Function and Stability. 2022 ,	
130	Computational Models for the Study of Protein Aggregation.. 2022 , 2340, 51-78	
129	Intrinsically Disordered Proteins: Perspective on COVID-19 Infection and Drug Discovery.. 2022 ,	4
128	Changes in colostrum ingredients of Hu sheep, as well as the missense mutation genes associated with colostrum yield.. 2022 , 1-13	0
127	MafB, WDR77, and Ectenin interact with each other and have similar genome association profiles.	
126	Protein Dynamics to Define and Refine Disordered Protein Ensembles.. 2022 ,	1
125	Salt Induced Transitions in the Conformational Ensembles of Intrinsically Disordered Proteins.	0
124	The dark proteome of rodent hepatitis E virus: Analysis of intrinsically disordered regions. 2022 , 8, 005-011	0
123	Intrinsically disordered proteins play diverse roles in cell signaling.. 2022 , 20, 20	8
122	Examples of Extreme Survival: Tardigrade Genomics and Molecular Anhydrobiology.. 2022 , 10, 17-37	2
121	Intrinsic disorder in proteins associated with oxidative stress-induced JNK signaling.. 2022 , 79, 202	2
120	The C-terminal end of mycobacterial HadBC regulates AcpM interaction during the FAS-II pathway: a structural perspective.. 2022 ,	1

119	Characterization of intrinsically disordered regions in proteins informed by human genetic diversity.. 2022 , 18, e1009911	0
118	Stereochemistry of transient protein-protein interactions in a signaling hub: exploring G3BP1-mediated regulation of CFTR deubiquitination.	
117	BMI1 Silencing Induces Mitochondrial Dysfunction in Lung Epithelial Cells Exposed to Hyperoxia.. 2022 , 13, 814510	
116	The PentUnFOLD algorithm as a tool to distinguish the dark and the light sides of the structural instability of proteins.. 2022 , 1	0
115	In Silico Three-Dimensional (3D) Modeling of the SecY Protein of <i>Candidatus Phytoplasma Solani</i> Strains Associated with Grapevine Bois Noir and Its Possible Relationship with Strain Virulence. 2022 , 13, 15-30	0
114	Proteomic analysis of heat-stable proteins revealed an increased proportion of proteins with compositionally biased regions.. 2022 , 12, 4347	0
113	Intrinsically disordered proteins: Ensembles at the limits of Anfinsen's dogma. 2022 , 3, 011306	1
112	Effects of Nanometer Confinement on the Self-Assembly and Dynamics of Poly(L-benzyl-L-glutamate) and Its Copolymer with Poly(isobutylene).	
111	Improving Martini 3 for Disordered and Multidomain Proteins.. 2022 ,	5
110	Characterization of the High-Affinity Fuzzy Complex between the Disordered Domain of the E7 Oncoprotein from High-Risk HPV and the TAZ2 Domain of CBP.. 2021 , 60, 3887-3898	0
109	Examining the Ensembles of Amyloid- β Monomer Variants and Their Propensities to Form Fibers Using an Energy Landscape Visualization Method.. 2021 ,	4
108	Impact of monomeric and aggregated wild-type and A30P/A53T double-mutant β synuclein on antioxidant mechanism and glutamate metabolic profile of cultured astrocytes.. 2021 ,	0
107	Intrinsically Disordered Proteins (IDPs). 2022 , 201-225	
106	Liquid-liquid phase separation as an organizing principle of intracellular space: overview of the evolution of the cell compartmentalization concept.. 2022 , 79, 251	9
105	idpr: A package for profiling and analyzing Intrinsically Disordered Proteins in R.. 2022 , 17, e0266929	0
104	AlphaFold illuminates half of the dark human proteins.. 2022 , 74, 102372	6
103	Chapter 12. Molecular Modelling and Simulations Applied to Challenging Drug Discovery Targets. 317-348	
102	Image_1.tif. 2020 ,	

101	Image_2.TIF. 2020 ,		
100	Image_3.TIF. 2020 ,		
99	Data_Sheet_1.PDF. 2019 ,		
98	Insights into Membrane Curvature Sensing and Membrane Remodeling by Intrinsically Disordered Proteins and Protein Regions.. 2022 , 1		2
97	Prediction of disordered regions in proteins with recurrent Neural Networks and protein dynamics.. <i>Journal of Molecular Biology</i> , 2022 , 167579	6.5	1
96	AlphaFold2: A Role for Disordered Protein/Region Prediction?. 2022 , 23,		3
95	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
94	First report on molecular characterization and in silico analysis of caprine TCIM gene. 2022 , 106723		0
93	Design and discovery of metamorphic proteins.. 2022 , 74, 102380		0
92	MafB, WDR77, and Ectenin interact with each other and have similar genome association profiles.. 2022 , 17, e0264799		
91	Exploring Nearest Neighbor Interactions and Their Influence on the Gibbs Energy Landscape of Unfolded Proteins and Peptides. 2022 , 23, 5643		1
90	Intrinsically Disordered Proteins. 2022 , 1-7		
89	ADOPT: intrinsic protein disorder prediction through deep bidirectional transformers.		1
88	Intrinsic disorder, extraterrestrial peptides, and prebiotic life on the earth. 1-5		0
87	Dynamical Behavior of Disordered Regions in Disease-Related Proteins Revealed by Quasielastic Neutron Scattering. 2022 , 58, 795		0
86	Electronic Polarization at the Interface between the p53 Transactivation Domain and Two Binding Partners.		
85	More is simpler: Decomposition of ligand-binding affinity for proteins being disordered. 2022 , 31,		0
84	Multi-task learning to leverage partially annotated data for PPI interface prediction. 2022 , 12,		0

83	Wild-Type β -Synuclein and Variants Occur in Different Disordered Dimers and Pre-Fibrillar Conformations in Early Stage of Aggregation. 9,	2
82	SETH predicts nuances of residue disorder from protein embeddings.	0
81	Activation of p53: How phosphorylated Ser15 triggers sequential phosphorylation of p53 at Thr18 by CK1 α	0
80	The Wako-Saito-Eaton Model for Predicting Protein Folding and Dynamics. 2022 , 27, 4460	
79	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
78	Multisite Phosphorylation and Binding Alter Conformational Dynamics of the 4E-BP2 Protein. 2022 ,	0
77	Editorial: Intrinsically Disordered Proteins and Regions: The Challenge to the Structure-Function Relationship. 9,	0
76	Comparative study of structures and functional motifs in lectins from the commercially important photosynthetic microorganisms. 2022 , 201, 63-74	0
75	Hepatitis C Virus Infection and Intrinsic Disorder in the Signaling Pathways Induced by Toll-Like Receptors. 2022 , 11, 1091	0
74	Lighting up Nobel Prize-winning studies with protein intrinsic disorder. 2022 , 79,	0
73	A Trajectory of Discovery: Metabolic Regulation by the Conditionally Disordered Chloroplast Protein, CP12. 2022 , 12, 1047	0
72	Conformational buffering underlies functional selection in intrinsically disordered protein regions. 2022 , 29, 781-790	3
71	Tau liquid-liquid phase separation: At the crossroads of tau physiology and tauopathy.	2
70	Impact of aromatic residues on the intrinsic disorder and transitional behaviour of model IDPs. 2022 , 100400	
69	Inhibition of Melittin Activity Using a Small Molecule with an Indole Ring. 2022 , 126, 5793-5802	0
68	Global genetic diversity and evolutionary patterns among Potato leafroll virus populations. 13,	0
67	The LEF-1 high-mobility group box adopts residual structure in its DNA-free form. 2022 , 12-13, 100074	0
66	Enhanced sampling for lipid-protein interactions during membrane dynamics. 2023 , 47, 1-14	0

65	Anchor Residues Govern Binding and Folding of an Intrinsically Disordered Domain.	0
64	Tryptophan mutations in G3BP1 tune the stability of a cellular signaling hub by weakening transient interactions with Caprin1 and USP10. 2022 , 102552	0
63	Silica adsorption tag derived from the silica polycondensation protein glassin for the immobilization of soluble proteins. 2022 ,	0
62	Solvent paramagnetic relaxation enhancement as a versatile method for studying structure and dynamics of biomolecular systems. 2022 ,	1
61	Functional benefit of structural disorder for the replication of measles, Nipah and Hendra viruses.	2
60	Toward Accurate Coarse-Grained Simulations of Disordered Proteins and Their Dynamic Interactions. 2022 , 62, 4523-4536	1
59	Integration of Nanometer-Range Label-to-Label Distances and Their Distributions into Modelling Approaches. 2022 , 12, 1369	0
58	Protein Function Analysis through Machine Learning. 2022 , 12, 1246	0
57	A Study on the Nature of SARS-CoV-2 Using the Shell Disorder Models: Reproducibility, Evolution, Spread, and Attenuation. 2022 , 12, 1353	1
56	Lineage-specific protein repeat expansions and contractions reveal malleable regions of immune genes.	0
55	Trehalose and tardigrade CAHS proteins work synergistically to promote desiccation tolerance. 2022 , 5,	0
54	Intrinsic protein disorder uncouples affinity from binding specificity. 2022 , 31,	2
53	Protein folding problem: enigma, paradox, solution.	0
52	SETH predicts nuances of residue disorder from protein embeddings. 2,	0
51	Ferritin self-assembly, structure, function, and biotechnological applications. 2022 ,	0
50	Perspectives on evolutionary and functional importance of intrinsically disordered proteins. 2022 ,	0
49	Looking at the Pathogenesis of the Rabies Lyssavirus Strain Pasteur Vaccins through a Prism of the Disorder-Based Bioinformatics. 2022 , 12, 1436	0
48	DMFpred: Predicting protein disorder molecular functions based on protein cubic language model. 2022 , 18, e1010668	0

47	Molecular determinants of fibrillation in a viral amyloidogenic domain from combined biochemical and biophysical studies.	2
46	Self-Assembly of Tunable Intrinsically Disordered Peptide Amphiphiles.	0
45	Structure-function relationships in eukaryotic transcription factors: The role of intrinsically disordered regions in gene regulation. 2022 , 82, 3970-3984	0
44	Antibodies as specific chaperones. 2004 , 69, 1233-1238	0
43	Droplets of life: role of phase separation in virus replication and compartmentalization. 2023 , 567-615	0
42	Biochemical and structural biology aspects of liquid-liquid phase separation: protein side of liquid-liquid phase separation, membrane-less organelles, and biomolecular condensates. 2023 , 101-132	0
41	Liquid-liquid phase separation, membrane-less organelles, and biomolecular condensates in cardiovascular disease. 2023 , 663-679	0
40	Rapid Prediction and Analysis of Protein Intrinsic Disorder.	2
39	Enrichment of charge-absent regions in phase separated proteins.	0
38	Intrinsically Disordered Proteins: An Overview. 2022 , 23, 14050	2
37	Temperature Dependence of Non-uniformity in Energy of Systems with Holonomic Constraints. 2023 , 190,	0
36	Biological soft matter: intrinsically disordered proteins in liquid-liquid phase separation and biomolecular condensates.	3
35	Molecular and environmental determinants of biomolecular condensate formation.	0
34	Enrichment patterns of intrinsic disorder in proteins.	0
33	Intrinsic disorder and posttranslational modification: an evolutionary perspective. 2023 , 377-396	0
32	Thermodynamic perspective of protein disorder and phase separation: model systems. 2023 , 97-126	0
31	Structure and disorder: protein functions depend on this new binary transforming lock-and-key into structure-function continuum. 2023 , 127-148	0
30	How binding to surfaces affects disorder?. 2023 , 455-489	0

- 29 Prediction of protein structure and intrinsic disorder in the era of deep learning. **2023**, 199-224 0
- 28 Role of plasticity and disorder in protein moonlighting: blurring of lines between biocatalysts and other biologically active proteins. **2023**, 279-301 0
- 27 Structural ensembles of disordered proteins from hierarchical chain growth and simulation. **2023**, 78, 102501 0
- 26 Computer simulation of molecular recognition in biomolecular system: from in silico screening to generalized ensembles. 1
- 25 Dissection of hubs and bottlenecks in a Protein-protein Interaction Network. **2022**, 107802 0
- 24 EGFR TKI resistance in lung cancer cells using RNA sequencing and analytical bioinformatics tools. 1-20 0
- 23 The biophysics of disordered proteins from the point of view of single-molecule fluorescence spectroscopy. **2022**, 66, 875-890 1
- 22 Evolution of SLiM-mediated hijack functions in intrinsically disordered viral proteins. **2022**, 66, 945-958 1
- 21 Dynamic Interactomics by Cross-Linking Mass Spectrometry: Mapping the Daily Cell Life in Postgenomic Era. **2022**, 26, 633-649 0
- 20 NMR insights into dynamic, multivalent interactions of intrinsically disordered regions: from discrete complexes to condensates. **2022**, 66, 863-873 2
- 19 Self-Assembly of Tunable Intrinsically Disordered Peptide Amphiphiles. 0
- 18 Initial Investigations of Intrinsically Disordered Regions in Inherited Retinal Diseases. **2023**, 24, 1060 0
- 17 The Residual Structure of Unfolded Proteins Was Elucidated From The Standard Deviation Of NMR Intensity Differences. **2023**, 30, 0
- 16 Illuminating Intrinsically Disordered Proteins with Integrative Structural Biology. **2023**, 13, 124 0
- 15 Molecular Determinants of Fibrillation in a Viral Amyloidogenic Domain from Combined Biochemical and Biophysical Studies. **2023**, 24, 399 0
- 14 Evolutionary fine-tuning of residual helix structure in disordered proteins manifests in complex structure and lifetime. **2023**, 6, 0
- 13 Structural preferences shape the entropic force of disordered protein ensembles. 0
- 12 NMR Studies of Disordered but Functional Proteins. **2012**, 111-129 0

- 11 Molecular Mechanisms of Functional Modulation of Transcriptional Coactivator PC4 via Phosphorylation on Its Intrinsically Disordered Region. ○
- 10 Structural intrinsic disorder in a functionalized potyviral coat protein as a main viability determinant of its assembled nanoparticles. **2023**, 236, 123958 ○
- 9 Disordered proteins mitigate the temperature dependence of site-specific binding free energies. **2023**, 299, 102984 ○
- 8 Coupled binding and folding of disordered SPIN N-terminal region in myeloperoxidase inhibition. 10, ○
- 7 Computational Prediction of Protein Intrinsically Disordered Region Related Interactions and Functions. **2023**, 14, 432 ○
- 6 Computational prediction of disordered binding regions. **2023**, 21, 1487-1497 1
- 5 Site-Specific Phosphorylation of RTK KIT Kinase Insert Domain: Interactome Landscape Perspectives. **2023**, 1, 39-71 ○
- 4 SOURSOP: A Python package for the analysis of simulations of intrinsically disordered proteins. ○
- 3 DR-BERT: A Protein Language Model to Annotate Disordered Regions. ○
- 2 Computational Methods to Predict Intrinsically Disordered Regions and Functional Regions in Them. **2023**, 231-245 ○
- 1 Assessing structure and disorder prediction tools for de novo emerged proteins in the age of machine learning. 12, 347 ○