

# CITATION REPORT

List of articles citing

## Intrinsically unstructured proteins and their functions

DOI: 10.1038/nrm1589

Nature Reviews Molecular Cell Biology, 2005, 6, 197-208.

**Source:** <https://exaly.com/paper-pdf/38214911/citation-report.pdf>

**Version:** 2024-04-19

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
2337	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. <b>2005</b> , 14, 1975-92		125
2336	Determination of membrane protein structure and dynamics by magic-angle-spinning solid-state NMR spectroscopy. <b>2005</b> , 127, 12965-74		257
2335	The Cbf5-Nop10 complex is a molecular bracket that organizes box H/ACA RNPs. <b>2005</b> , 12, 1101-7		96
2334	Multistep and multimode cortical anchoring of tea1p at cell tips in fission yeast. <b>2005</b> , 24, 3690-9		80
2333	Flexible nets. The roles of intrinsic disorder in protein interaction networks. <b>2005</b> , 272, 5129-48		895
2332	RhoGDIs revisited: novel roles in Rho regulation. <b>2005</b> , 6, 957-66		96
2331	Raman optical activity: a tool for protein structure analysis. <b>2005</b> , 13, 1409-19		101
2330	Structural disorder throws new light on moonlighting. <b>2005</b> , 30, 484-9		381
2329	Protein-protein interactions in human disease. <b>2005</b> , 15, 441-6		234
2328	TonB-dependent outer membrane transport: going for Baroque?. <b>2005</b> , 15, 394-400		108
2327	Structuring the puzzle of prion propagation. <b>2005</b> , 15, 724-30		9
2326	Showing your ID: intrinsic disorder as an ID for recognition, regulation and cell signaling. <b>2005</b> , 18, 343-84		660
2325	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. <b>2005</b> , 6, 2242-6		13
2324	Implication of C-terminal deletion on the structure and stability of bovine beta-casein. <b>2005</b> , 24, 431-44		27
2323	The structure at 1.7 Å resolution of the protein product of the At2g17340 gene from <i>Arabidopsis thaliana</i> . <b>2005</b> , 61, 630-5		4
2322	Protein flexibility and rigidity predicted from sequence. <b>2005</b> , 61, 115-26		129
2321	Assessment of disorder predictions in CASP6. <b>2005</b> , 61 Suppl 7, 167-75		92

2320	Exploiting heterogeneous sequence properties improves prediction of protein disorder. <b>2005</b> , 61 Suppl 7, 176-82	423
2319	Assessing protein disorder and induced folding. <b>2006</b> , 62, 24-45	347
2318	PII structure in the model peptides for unfolded proteins: studies on ubiquitin fragments and several alanine-rich peptides containing QQQ, SSS, FFF, and VVV. <b>2006</b> , 63, 312-21	18
2317	Comparative genomics and disorder prediction identify biologically relevant SH3 protein interactions. <b>2005</b> , 1, e26	35
2316	Solution structure of the human immunodeficiency virus type 1 p6 protein. <b>2005</b> , 280, 42515-27	46
2315	Unstructured conformations are a substrate requirement for the Sir2 family of NAD-dependent protein deacetylases. <b>2005</b> , 280, 36073-8	39
2314	DNA-induced secondary structure of the carboxyl-terminal domain of histone H1. <b>2005</b> , 280, 32141-7	77
2313	Intrinsic Disorder and Prote in Modifications: Building an SVM Predictor for Methylation. <b>2005</b> ,	19
2312	Rational design of p53, an intrinsically unstructured protein, for the fabrication of novel molecular sensors. <b>2005</b> , 280, 35641-6	11
2311	FrankSum: new feature selection method for protein function prediction. <b>2005</b> , 15, 259-75	24
2310	Cell entry mechanism of enzymatic bacterial colicins: porin recruitment and the thermodynamics of receptor binding. <b>2005</b> , 102, 13849-54	81
2309	Fully metallated S134N Cu,Zn-superoxide dismutase displays abnormal mobility and intermolecular contacts in solution. <b>2005</b> , 280, 35815-21	51
2308	IUPred: web server for the prediction of intrinsically unstructured regions of proteins based on estimated energy content. <b>2005</b> , 21, 3433-4	1571
2307	MANY WAYS TO PICTURE A CELL. <b>2005</b> , 67, 363-368	3
2306	Periplasmic protein HdeA exhibits chaperone-like activity exclusively within stomach pH range by transforming into disordered conformation. <b>2005</b> , 280, 27029-34	111
2305	Mechanisms of protein degradation: an odyssey with ODC. <b>2005</b> , 4, 1461-4	40
2304	p53 proteasomal degradation: poly-ubiquitination is not the whole story. <b>2005</b> , 4, 1015-8	59
2303	Many Ways to Picture a Cell. <b>2005</b> , 67, 363-368	3

2302	Structure and function of steroid receptor AF1 transactivation domains: induction of active conformations. <b>2005</b> , 391, 449-64	156
2301	The active form of the <i>Saccharomyces cerevisiae</i> ribonucleotide reductase small subunit is a heterodimer in vitro and in vivo. <b>2005</b> , 44, 15366-77	28
2300	A structural model for unfolded proteins from residual dipolar couplings and small-angle x-ray scattering. <b>2005</b> , 102, 17002-7	357
2299	Monitoring the effects of antagonists on protein-protein interactions with NMR spectroscopy. <b>2005</b> , 127, 13220-6	65
2298	Use of urea and glycine betaine to quantify coupled folding and probe the burial of DNA phosphates in lac repressor-lac operator binding. <b>2005</b> , 44, 16896-911	46
2297	Assembly of tubulin by classic myelin basic protein isoforms and regulation by post-translational modification. <b>2005</b> , 44, 16672-83	43
2296	Distinct domains of small Tims involved in subunit interaction and substrate recognition. <b>2005</b> , 351, 839-49	38
2295	Bacterially produced human HIF-1alpha is competent for heterodimerization and specific DNA-binding. <b>2005</b> , 331, 464-70	18
2294	Gir2 is an intrinsically unstructured protein that is present in <i>Saccharomyces cerevisiae</i> as a group of heterogeneously electrophoretic migrating forms. <b>2005</b> , 332, 450-5	15
2293	Characterization of the PR domain of RIZ1 histone methyltransferase. <b>2005</b> , 333, 925-34	46
2292	The interplay between structure and function in intrinsically unstructured proteins. <b>2005</b> , 579, 3346-54	563
2291	Linear motifs: evolutionary interaction switches. <b>2005</b> , 579, 3342-5	246
2290	Uncovering the unfoldome: enriching cell extracts for unstructured proteins by acid treatment. <b>2005</b> , 4, 1610-8	59
2289	Coupled folding and binding with alpha-helix-forming molecular recognition elements. <b>2005</b> , 44, 12454-70	541
2288	Most nuclear systemic autoantigens are extremely disordered proteins: implications for the etiology of systemic autoimmunity. <b>2005</b> , 7, R1360-74	30
2287	What makes species unique? The contribution of proteins with obscure features. <b>2006</b> , 7, R57	54
2286	Disorder and sequence repeats in hub proteins and their implications for network evolution. <b>2006</b> , 5, 2985-95	273
2285	Abundance of intrinsic disorder in protein associated with cardiovascular disease. <b>2006</b> , 45, 10448-60	152

2284	The role of protein dynamics in increasing binding affinity for an engineered protein-protein interaction established by H/D exchange mass spectrometry. <b>2006</b> , 45, 8488-98	33
2283	Intrinsic disorder in transcription factors. <b>2006</b> , 45, 6873-88	518
2282	Coupling ligand recognition to protein folding in an engineered variant of rabbit ileal lipid binding protein. <b>2006</b> , 4623-5	14
2281	Free-energy distribution of binary protein-protein binding suggests cross-species interactome differences. <b>2006</b> , 103, 11527-32	12
2280	Characterizing residual structure in disordered protein States using nuclear magnetic resonance. <b>2007</b> , 350, 49-67	55
2279	Protonless NMR experiments for sequence-specific assignment of backbone nuclei in unfolded proteins. <b>2006</b> , 128, 3918-9	155
2278	Low resolution structure of the human alpha4 protein (IgBP1) and studies on the stability of alpha4 and of its yeast ortholog Tap42. <b>2006</b> , 1764, 724-34	15
2277	Configurational entropy change of netropsin and distamycin upon DNA minor-groove binding. <b>2006</b> , 91, 1460-70	42
2276	Protein-water and protein-buffer interactions in the aqueous solution of an intrinsically unstructured plant dehydrin: NMR intensity and DSC aspects. <b>2006</b> , 91, 2243-9	94
2275	The change of protein intradomain mobility on ligand binding: is it a commonly observed phenomenon?. <b>2006</b> , 91, 3002-13	30
2274	Quantitative relation between intermolecular and intramolecular binding of pro-rich peptides to SH3 domains. <b>2006</b> , 91, 3170-81	32
2273	Protein intrinsic disorder and human papillomaviruses: increased amount of disorder in E6 and E7 oncoproteins from high risk HPVs. <b>2006</b> , 5, 1829-42	117
2272	Proteomic studies of the intrinsically unstructured mammalian proteome. <b>2006</b> , 5, 2839-48	57
2271	Domain organization and quaternary structure of the <i>Saccharomyces cerevisiae</i> silent information regulator 3 protein, Sir3p. <b>2006</b> , 45, 15941-8	17
2270	Solute probes of conformational changes in open complex (RPo) formation by <i>Escherichia coli</i> RNA polymerase at the lambdaPR promoter: evidence for unmasking of the active site in the isomerization step and for large-scale coupled folding in the subsequent conversion to RPo. <b>2006</b> , 45, 2161-77	50
2269	Conservation of intrinsic disorder in protein domains and families: II. functions of conserved disorder. <b>2006</b> , 5, 888-98	107
2268	Identification of the <i>Aedes aegypti</i> peritrophic matrix protein AeIMUC1 as a heme-binding protein. <b>2006</b> , 45, 9540-9	75
2267	Configurational entropies of lipids in pure and mixed bilayers from atomic-level and coarse-grained molecular dynamics simulations. <b>2006</b> , 110, 15602-14	55

2266	Conformational properties of the SDS-bound state of alpha-synuclein probed by limited proteolysis: unexpected rigidity of the acidic C-terminal tail. <b>2006</b> , 45, 11523-31	49
2265	Prevalent structural disorder in E. coli and S. cerevisiae proteomes. <b>2006</b> , 5, 1996-2000	102
2264	Lipid-binding activity of intrinsically unstructured cytoplasmic domains of multichain immune recognition receptor signaling subunits. <b>2006</b> , 45, 15731-9	93
2263	Micelle-induced folding of spinach thylakoid soluble phosphoprotein of 9 kDa and its functional implications. <b>2006</b> , 45, 15633-43	14
2262	Interaction of the intrinsically unstructured phage lambda N Protein with Escherichia coli NusA. <b>2006</b> , 45, 4542-9	25
2261	Assessing induced folding of an intrinsically disordered protein by site-directed spin-labeling electron paramagnetic resonance spectroscopy. <b>2006</b> , 110, 20596-608	92
2260	B-myc: N-terminal recognition of myc binding proteins. <b>2006</b> , 45, 9857-65	12
2259	An isolated helix persists in a sparsely populated form of KIX under native conditions. <b>2006</b> , 45, 8885-93	27
2258	Conservation of intrinsic disorder in protein domains and families: I. A database of conserved predicted disordered regions. <b>2006</b> , 5, 879-87	99
2257	Intrinsically disordered structure of Bacillus pasteurii UreG as revealed by steady-state and time-resolved fluorescence spectroscopy. <b>2006</b> , 45, 8918-30	42
2256	The core of tau-paired helical filaments studied by scanning transmission electron microscopy and limited proteolysis. <b>2006</b> , 45, 6446-57	112
2255	Disordered domains and high surface charge confer hubs with the ability to interact with multiple proteins in interaction networks. <b>2006</b> , 580, 2041-5	217
2254	Chaperone-like activities of alpha-synuclein: alpha-synuclein assists enzyme activities of esterases. <b>2006</b> , 346, 1142-9	43
2253	Alternative splicing in human transcriptome: functional and structural influence on proteins. <b>2006</b> , 380, 63-71	51
2252	Intrinsically disordered loops inserted into the structural domains of human proteins. <b>2006</b> , 355, 845-57	29
2251	Multiple U2AF65 binding sites within SF3b155: thermodynamic and spectroscopic characterization of protein-protein interactions among pre-mRNA splicing factors. <b>2006</b> , 356, 664-83	55
2250	Folding transitions during assembly of the eukaryotic mRNA cap-binding complex. <b>2006</b> , 356, 982-92	30
2249	Human transcription factors contain a high fraction of intrinsically disordered regions essential for transcriptional regulation. <b>2006</b> , 359, 1137-49	206

2248	DNA recognition by the brinker repressor--an extreme case of coupling between binding and folding. <b>2006</b> , 361, 659-72	32
2247	Massive sequence perturbation of the Raf ras binding domain reveals relationships between sequence conservation, secondary structure propensity, hydrophobic core organization and stability. <b>2006</b> , 362, 151-71	7
2246	Analysis of molecular recognition features (MoRFs). <b>2006</b> , 362, 1043-59	579
2245	Heteronuclear NMR identifies a nascent helix in intrinsically disordered dynein intermediate chain: implications for folding and dimerization. <b>2006</b> , 362, 1082-93	47
2244	Binding-induced stabilization and assembly of the phage P22 tail accessory factor gp4. <b>2006</b> , 363, 558-76	41
2243	Delineation of protein structure classes from multivariate analysis of protein Raman optical activity data. <b>2006</b> , 363, 19-26	51
2242	Crystal structure of a Cbf5-Nop10-Gar1 complex and implications in RNA-guided pseudouridylation and dyskeratosis congenita. <b>2006</b> , 21, 249-60	138
2241	Model of formin-associated actin filament elongation. <b>2006</b> , 21, 455-66	144
2240	Comparative genomics of the sperm mitochondria-associated cysteine-rich protein gene. <b>2006</b> , 87, 382-91	24
2239	Biochemical properties of recombinant human and mouse N-acetylglutamate synthase. <b>2006</b> , 87, 226-32	31
2238	Gene synthesis, expression, purification, and characterization of human Jagged-1 intracellular region. <b>2006</b> , 47, 398-404	9
2237	The cell-specific activity of the estrogen receptor alpha may be fine-tuned by phosphorylation-induced structural gymnastics. <b>2006</b> , 4, e005	9
2236	Temperature-dependent loop formation kinetics in flexible peptides studied by time-resolved fluorescence spectroscopy. <b>2006</b> , 2006, 1-9	7
2235	Folding and unfolding for binding: large-scale protein dynamics in protein-protein interactions. <b>2006</b> , 34, 971-4	4
2234	Landscape of the hnRNP K protein-protein interactome. <b>2006</b> , 6, 2395-406	65
2233	Calmodulin signaling: analysis and prediction of a disorder-dependent molecular recognition. <b>2006</b> , 63, 398-410	86
2232	Conformational flexibility may explain multiple cellular roles of PEST motifs. <b>2006</b> , 63, 727-32	14
2231	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> . <b>2006</b> , 64, 486-501	55

2230	Criteria for downhill protein folding: calorimetry, chevron plot, kinetic relaxation, and single-molecule radius of gyration in chain models with subdued degrees of cooperativity. <b>2006</b> , 65, 373-91	63
2229	Characterization of the residual structure in the unfolded state of the Delta131Delta fragment of staphylococcal nuclease. <b>2006</b> , 65, 145-52	35
2228	Role of intrinsic disorder in transient interactions of hub proteins. <b>2007</b> , 66, 761-5	127
2227	Solution NMR structure of an immunodominant epitope of myelin basic protein. Conformational dependence on environment of an intrinsically unstructured protein. <b>2006</b> , 273, 601-14	34
2226	Mapping of the interaction site of CP12 with glyceraldehyde-3-phosphate dehydrogenase from <i>Chlamydomonas reinhardtii</i> . Functional consequences for glyceraldehyde-3-phosphate dehydrogenase. <b>2006</b> , 273, 3358-69	36
2225	Nuclear magnetic resonance studies of CXC chemokine receptor 4 allosteric peptide agonists in solution. <b>2006</b> , 66, 12-21	3
2224	Protein linguistics - a grammar for modular protein assembly?. <i>Nature Reviews Molecular Cell Biology</i> , <b>2006</b> , 7, 68-73	48.7 53
2223	Prediction of natively unfolded regions in protein chains. <b>2006</b> , 40, 298-304	18
2222	Solution structure of the partially folded high-risk human papilloma virus 45 oncoprotein E7. <b>2006</b> , 25, 5953-9	82
2221	Alzheimer's-disease-associated conformation of intrinsically disordered tau protein studied by intrinsically disordered protein liquid-phase competitive enzyme-linked immunosorbent assay. <b>2006</b> , 359, 230-7	14
2220	Casein kinases phosphorylate multiple residues spanning the entire hnRNP K length. <b>2006</b> , 1764, 299-306	12
2219	Unraveling the nature of the segmentation clock: Intrinsic disorder of clock proteins and their interaction map. <b>2006</b> , 30, 241-8	12
2218	According to current textbooks, a well-defined three-dimensional structure is a prerequisite for the function of a protein. Is this correct?. <b>2006</b> , 58, 107-9	18
2217	Role of unfolded state heterogeneity and en-route ruggedness in protein folding kinetics. <b>2006</b> , 15, 564-82	23
2216	NMR characterizations of an amyloidogenic conformational ensemble of the PI3K SH3 domain. <b>2006</b> , 15, 2552-7	14
2215	Sensitivity of secondary structure propensities to sequence differences between alpha- and gamma-synuclein: implications for fibrillation. <b>2006</b> , 15, 2795-804	547
2214	Thioredoxin-dependent regulation of photosynthetic glyceraldehyde-3-phosphate dehydrogenase: autonomous vs. CP12-dependent mechanisms. <b>2006</b> , 89, 263-75	72
2213	Characterization of TonB interactions with the FepA cork domain and FecA N-terminal signaling domain. <b>2006</b> , 19, 127-42	16



2212	Intrinsically disordered proteins in the neurodegenerative processes: formation of tau protein paired helical filaments and their analysis. <b>2006</b> , 26, 1085-97	48
2211	Comparative genomics reveals long, evolutionarily conserved, low-complexity islands in yeast proteins. <b>2006</b> , 63, 415-25	7
2210	Construction of a 3D model of CP12, a protein linker. <b>2006</b> , 25, 186-95	37
2209	Structural disorder within the replicative complex of measles virus: functional implications. <b>2006</b> , 344, 94-110	81
2208	Identification of the functional domains of the essential human cytomegalovirus UL34 proteins. <b>2006</b> , 353, 27-34	1
2207	An entropic mechanism to generate highly cooperative and specific binding from protein phosphorylations. <b>2006</b> , 16, 2150-5	33
2206	Structure and behaviour of biomolecules from Raman optical activity. <b>2006</b> , 16, 638-43	63
2205	Dual requirement for flexibility and specificity for binding of the coiled-coil tropomyosin to its target, actin. <b>2006</b> , 14, 43-50	64
2204	Crystal structure of the cytoplasmic domain of the chloride channel ClC-0. <b>2006</b> , 14, 299-307	92
2203	Protein-protein interaction through beta-strand addition. <b>2006</b> , 31, 436-44	150
2202	Rational drug design via intrinsically disordered protein. <b>2006</b> , 24, 435-42	199
2201	Post-translational signal peptide cleavage controls differential epitope recognition in the QP-rich domain of recombinant <i>Theileria parva</i> PIM. <b>2006</b> , 149, 144-54	6
2200	Abundance of intrinsically unstructured proteins in <i>P. falciparum</i> and other apicomplexan parasite proteomes. <b>2006</b> , 150, 256-67	91
2199	Length-dependent prediction of protein intrinsic disorder. <b>2006</b> , 7, 208	630
2198	Exhaustive assignment of compositional bias reveals universally prevalent biased regions: analysis of functional associations in human and <i>Drosophila</i> . <b>2006</b> , 7, 441	34
2197	Simple sequence proteins in prokaryotic proteomes. <b>2006</b> , 7, 141	8
2196	Raman optical activity of proteins, carbohydrates and glycoproteins. <b>2006</b> , 18, 103-15	71
2195	20S proteasomes and protein degradation "by default". <b>2006</b> , 28, 844-9	154

2194	Nanoimaging for protein misfolding and related diseases. <b>2006</b> , 99, 52-70	39
2193	Autophagy and related processes in trypanosomatids: insights from genomic and bioinformatic analyses. <b>2006</b> , 2, 107-18	62
2192	PROFBval: predict flexible and rigid residues in proteins. <b>2006</b> , 22, 891-3	117
2191	Serine/arginine-rich splicing factors belong to a class of intrinsically disordered proteins. <b>2006</b> , 34, 305-12	87
2190	Spritz: a server for the prediction of intrinsically disordered regions in protein sequences using kernel machines. <b>2006</b> , 34, W164-8	108
2189	Role of peripherin/rds in vertebrate photoreceptor architecture and inherited retinal degenerations. <b>2006</b> , 253, 131-75	61
2188	Control of intrinsically disordered stathmin by multisite phosphorylation. <b>2006</b> , 281, 16078-83	41
2187	Malaria: therapy, genes and vaccines. <b>2006</b> , 6, 309-26	14
2186	Exploring the molecular function of PIN1 by nuclear magnetic resonance. <b>2006</b> , 7, 179-94	20
2185	Intrinsic disorder is a common feature of hub proteins from four eukaryotic interactomes. <b>2006</b> , 2, e100	435
2184	Prediction of amyloidogenic and disordered regions in protein chains. <b>2006</b> , 2, e177	138
2183	Protein Folding Protocols. <b>2006</b> ,	
2182	Keap1 recruits Neh2 through binding to ETGE and DLG motifs: characterization of the two-site molecular recognition model. <b>2006</b> , 26, 2887-900	489
2181	Competitive recruitment of the periplasmic translocation portal TolB by a natively disordered domain of colicin E9. <b>2006</b> , 103, 12353-8	60
2180	Regions of IkappaBalpha that are critical for its inhibition of NF-kappaB.DNA interaction fold upon binding to NF-kappaB. <b>2006</b> , 103, 18951-6	80
2179	When viral oncoprotein meets tumor suppressor: a structural view. <b>2006</b> , 20, 2332-7	16
2178	Distinctive repertoire of contingency genes conferring mutation- based phase variation and combinatorial expression of surface lipoproteins in Mycoplasma capricolum subsp. capricolum of the Mycoplasma mycoides phylogenetic cluster. <b>2006</b> , 188, 4926-41	24
2177	The disordered amino-terminus of SIMPL interacts with members of the 70-kDa heat-shock protein family. <b>2006</b> , 25, 704-14	9

2176	Outer membrane active transport: structure of the BtuB:TonB complex. <b>2006</b> , 312, 1396-9	235
2175	Alternative splicing in concert with protein intrinsic disorder enables increased functional diversity in multicellular organisms. <b>2006</b> , 103, 8390-5	358
2174	Folding of the C-terminal bacterial binding domain in statherin upon adsorption onto hydroxyapatite crystals. <b>2006</b> , 103, 16083-8	84
2173	A hint for the function of human Sco1 from different structures. <b>2006</b> , 103, 8595-600	91
2172	Structural diversity in p160/CREB-binding protein coactivator complexes. <b>2006</b> , 281, 14787-95	61
2171	Intrinsic protein disorder, amino acid composition, and histone terminal domains. <b>2006</b> , 281, 1853-6	189
2170	Protein stability imposes limits on organism complexity and speed of molecular evolution. <b>2007</b> , 104, 16152-7	188
2169	Protein Misfolding, Aggregation, and Conformational Diseases. <b>2007</b> ,	13
2168	Expression and localization of RGS9-2/G 5/R7BP complex in vivo is set by dynamic control of its constitutive degradation by cellular cysteine proteases. <b>2007</b> , 27, 14117-27	56
2167	Intrinsic disorder and autonomous domain function in the multifunctional nuclear protein, MeCP2. <b>2007</b> , 282, 15057-64	97
2166	Intrinsic disorder in the C-terminal domain of the Shaker voltage-activated K <sup>+</sup> channel modulates its interaction with scaffold proteins. <b>2007</b> , 104, 13022-7	49
2165	Mechanical control of the directional stepping dynamics of the kinesin motor. <b>2007</b> , 104, 17382-7	106
2164	Multiple aromatic side chains within a disordered structure are critical for transcription and transforming activity of EWS family oncoproteins. <b>2007</b> , 104, 479-84	81
2163	POODLE-L: a two-level SVM prediction system for reliably predicting long disordered regions. <b>2007</b> , 23, 2046-53	120
2162	Predicting protein disorder and induced folding: from theoretical principles to practical applications. <b>2007</b> , 8, 135-49	67
2161	Inferring function using patterns of native disorder in proteins. <b>2007</b> , 3, e162	104
2160	Natively unstructured loops differ from other loops. <b>2007</b> , 3, e140	76
2159	PDZ domains: folding and binding. <b>2007</b> , 46, 8701-8	139

2158	Directed evolution of Tk-subtilisin from a hyperthermophilic archaeon: identification of a single amino acid substitution responsible for low-temperature adaptation. <b>2007</b> , 20, 143-53	23
2157	Prediction of protein disorder at the domain level. <b>2007</b> , 8, 161-71	65
2156	RNA chaperones, RNA annealers and RNA helicases. <b>2007</b> , 4, 118-30	247
2155	Conformational States and Protein Stability from a Proteomic Perspective. <b>2007</b> , 4, 44-52	3
2154	Towards proteomic approaches for the identification of structural disorder. <b>2007</b> , 8, 173-9	16
2153	A natively unfolded yeast prion monomer adopts an ensemble of collapsed and rapidly fluctuating structures. <b>2007</b> , 104, 2649-54	259
2152	A reversible form of lysine acetylation in the ER and Golgi lumen controls the molecular stabilization of BACE1. <b>2007</b> , 407, 383-95	94
2151	The human checkpoint sensor Rad9-Rad1-Hus1 interacts with and stimulates DNA repair enzyme TDG glycosylase. <b>2007</b> , 35, 6207-18	55
2150	A structural model of latent evolutionary potentials underlying neutral networks in proteins. <b>2007</b> , 1, 79-87	55
2149	RNA chaperone activity and RNA-binding properties of the E. coli protein StpA. <b>2007</b> , 35, 1257-69	57
2148	Expected packing density allows prediction of both amyloidogenic and disordered regions in protein chains. <b>2007</b> , 19, 285225	6
2147	Identification of a minimal myosin Va binding site within an intrinsically unstructured domain of melanophilin. <b>2007</b> , 282, 21518-28	29
2146	Substrate-dependent transmembrane signaling in TonB-dependent transporters is not conserved. <b>2007</b> , 104, 11975-80	32
2145	PrDOS: prediction of disordered protein regions from amino acid sequence. <b>2007</b> , 35, W460-4	537
2144	Local structural disorder imparts plasticity on linear motifs. <b>2007</b> , 23, 950-6	335
2143	Natively unstructured regions in proteins identified from contact predictions. <b>2007</b> , 23, 2376-84	102
2142	Structure and conformational changes in the C-terminal domain of the beta2-adrenoceptor: insights from fluorescence resonance energy transfer studies. <b>2007</b> , 282, 13895-905	133
2141	Polyelectrostatic interactions of disordered ligands suggest a physical basis for ultrasensitivity. <b>2007</b> , 104, 9650-5	186

2140	The mobile thylakoid phosphoprotein TSP9 interacts with the light-harvesting complex II and the peripheries of both photosystems. <b>2007</b> , 282, 16214-22	22
2139	Functional silencing of TATA-binding protein (TBP) by a covalent linkage of the N-terminal domain of TBP-associated factor 1. <b>2007</b> , 282, 22228-38	9
2138	Deletion and substitution analysis of the Escherichia coli TonB Q160 region. <b>2007</b> , 189, 4662-70	12
2137	His(20) provides the sole functionally significant side chain in the essential TonB transmembrane domain. <b>2007</b> , 189, 2825-33	34
2136	Mirl is highly upregulated and localized to nuclei during infectious hyphal growth in the rice blast fungus. <b>2007</b> , 20, 448-58	23
2135	Determination of protein regions responsible for interactions of amelogenin with CD63 and LAMP1. <b>2007</b> , 408, 347-54	37
2134	Structure and mechanism of cadherins and catenins in cell-cell contacts. <b>2007</b> , 23, 237-61	278
2133	Tropomyosin's periods are quasi-equivalent for actin binding but have specific regulatory functions. <b>2007</b> , 46, 14917-27	24
2132	Functional, structural, and immunological compartmentalisation of malaria invasive proteins. <b>2007</b> , 354, 363-71	21
2131	Nogo-B receptor possesses an intrinsically unstructured ectodomain and a partially folded cytoplasmic domain. <b>2007</b> , 360, 128-34	14
2130	Ultra-high field NMR studies of antibody binding and site-specific phosphorylation of alpha-synuclein. <b>2007</b> , 363, 795-9	36
2129	Fly-casting in protein-DNA binding: frustration between protein folding and electrostatics facilitates target recognition. <b>2007</b> , 129, 738-9	168
2128	Structural characterization of the intrinsically unfolded protein beta-synuclein, a natural negative regulator of alpha-synuclein aggregation. <b>2007</b> , 372, 708-22	96
2127	Structure and thermodynamics of the tubulin-stathmin interaction. <b>2007</b> , 158, 137-47	69
2126	Looking into live cells with in-cell NMR spectroscopy. <b>2007</b> , 158, 244-53	119
2125	Structural domains in the type III restriction endonuclease EcoP15I: characterization by limited proteolysis, mass spectrometry and insertional mutagenesis. <b>2007</b> , 366, 93-102	9
2124	Exploiting elements of transcriptional machinery to enhance protein stability. <b>2007</b> , 366, 103-16	11
2123	Functional characterization and conformational analysis of the Herpesvirus saimiri Tip-C484 protein. <b>2007</b> , 366, 1282-93	21

2122	Improved structural characterizations of the drkN SH3 domain unfolded state suggest a compact ensemble with native-like and non-native structure. <b>2007</b> , 367, 1494-510	99
2121	Intrinsically disordered regions of human plasma membrane proteins preferentially occur in the cytoplasmic segment. <b>2007</b> , 368, 902-13	80
2120	The structurally disordered KRAB repression domain is incorporated into a protease resistant core upon binding to KAP-1-RBCC domain. <b>2007</b> , 370, 269-89	20
2119	The cytoplasmic domain of the chloride channel CLC-0: structural and dynamic characterization of flexible regions. <b>2007</b> , 369, 1163-9	12
2118	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. <b>2007</b> , 371, 1365-77	18
2117	Molecular principles of the interactions of disordered proteins. <b>2007</b> , 372, 549-61	220
2116	The N terminus of <i>Saccharomyces cerevisiae</i> Msh6 is an unstructured tether to PCNA. <b>2007</b> , 26, 565-78	96
2115	X-ray structure of the PHF core C-terminus: insight into the folding of the intrinsically disordered protein tau in Alzheimer's disease. <b>2007</b> , 581, 5872-8	17
2114	Colicin biology. <b>2007</b> , 71, 158-229	753
2113	Protein Interactions. <b>2007</b> ,	5
2112	Structural characterization of flexible proteins using small-angle X-ray scattering. <b>2007</b> , 129, 5656-64	900
2111	Functional anthology of intrinsic disorder. 1. Biological processes and functions of proteins with long disordered regions. <b>2007</b> , 6, 1882-98	455
2110	The reticulons: a family of proteins with diverse functions. <b>2007</b> , 8, 234	135
2109	Distribution patterns of small-molecule ligands in the protein universe and implications for origin of life and drug discovery. <b>2007</b> , 8, R176	50
2108	Intrinsically Disordered Proteins: An Update. <b>2007</b> ,	
2107	The tetraspanin protein peripherin-2 forms a complex with melanoregulin, a putative membrane fusion regulator. <b>2007</b> , 46, 1256-72	33
2106	The carboxy-terminal domain of heat-shock factor 1 is largely unfolded but can be induced to collapse into a compact, partially structured state. <b>2007</b> , 46, 3405-15	17
2105	Unphosphorylated rhabdoviridae phosphoproteins form elongated dimers in solution. <b>2007</b> , 46, 10328-38	48

2104	Relevance of partially structured states in the non-classical secretion of acidic fibroblast growth factor. <b>2007</b> , 46, 9225-38	17
2103	Peripherin-2: an intracellular analogy to viral fusion proteins. <b>2007</b> , 46, 3605-13	16
2102	Mining alpha-helix-forming molecular recognition features with cross species sequence alignments. <b>2007</b> , 46, 13468-77	270
2101	Thermodynamic dissection of the Ezrin FERM/CERMAD interface. <b>2007</b> , 46, 12174-89	16
2100	The N-terminal subdomain of insulin-like growth factor (IGF) binding protein 6. Structure and interaction with IGFs. <b>2007</b> , 46, 3065-74	16
2099	Structural and thermodynamic characterization of the Escherichia coli RelBE toxin-antitoxin system: indication for a functional role of differential stability. <b>2007</b> , 46, 12152-63	28
2098	Phosphorylation of RNA helicase A by DNA-dependent protein kinase is indispensable for expression of the MDR1 gene product P-glycoprotein in multidrug-resistant human leukemia cells. <b>2007</b> , 46, 5766-75	13
2097	Alpha-synuclein tertiary contact dynamics. <b>2007</b> , 111, 2107-12	57
2096	Protein structure determination from NMR chemical shifts. <b>2007</b> , 104, 9615-20	440
2095	Structural basis for induced fit mechanisms in DNA recognition by the Pdx1 homeodomain. <b>2007</b> , 46, 2948-57	25
2094	Effects of zinc binding on the structure and dynamics of the intrinsically disordered protein prothymosin alpha: evidence for metalation as an entropic switch. <b>2007</b> , 46, 13120-30	47
2093	Functional anthology of intrinsic disorder. 2. Cellular components, domains, technical terms, developmental processes, and coding sequence diversities correlated with long disordered regions. <b>2007</b> , 6, 1899-916	215
2092	Sequence-specific resonance assignment of soluble nonglobular proteins by 7D APSY-NMR spectroscopy. <b>2007</b> , 129, 10823-8	65
2091	Intrinsic disorder and functional proteomics. <b>2007</b> , 92, 1439-56	571
2090	Binding of Ca <sup>2+</sup> to glutamic acid-rich polypeptides from the rod outer segment. <b>2007</b> , 92, 3207-14	19
2089	Macromolecular crowding induces a molten globule state in the C-terminal domain of histone H1. <b>2007</b> , 93, 2170-7	46
2088	Intrinsic dynamics of the partly unstructured PX domain from the Sendai virus RNA polymerase cofactor P. <b>2007</b> , 93, 2830-44	33
2087	Quantitative characterization of intrinsic disorder in polyglutamine: insights from analysis based on polymer theories. <b>2007</b> , 93, 1923-37	125

2086	Intrinsic disorder in the Protein Data Bank. <b>2007</b> , 24, 325-42	116
2085	Oxygen as a paramagnetic probe of clustering and solvent exposure in folded and unfolded states of an SH3 domain. <b>2007</b> , 129, 1826-35	27
2084	The novel CXCL12gamma isoform encodes an unstructured cationic domain which regulates bioactivity and interaction with both glycosaminoglycans and CXCR4. <b>2007</b> , 2, e1110	80
2083	Botulinum neurotoxin heavy chain belt as an intramolecular chaperone for the light chain. <b>2007</b> , 3, 1191-4	74
2082	Natural disordered sequences in the amino terminal domain of nuclear receptors: lessons from the androgen and glucocorticoid receptors. <b>2007</b> , 5, e001	61
2081	Abundance of intrinsic disorder in SV-IV, a multifunctional androgen-dependent protein secreted from rat seminal vesicle. <b>2007</b> ,	
2080	A biological cosmos of parallel universes: does protein structural plasticity facilitate evolution?. <b>2007</b> , 29, 1095-104	31
2079	Conformational analyses of a partially-folded bioactive prodomain of human furin. <b>2007</b> , 86, 329-44	9
2078	The use of conformation-specific ligands and assays to dissect the molecular mechanisms of neurodegenerative diseases. <b>2007</b> , 85, 2285-97	16
2077	Large systematic errors compromise quantitation of intrinsically unstructured proteins. <b>2007</b> , 360, 321-3	19
2076	Identification of residues participating in the interaction between an intraluminal loop of inositol 1,4,5-trisphosphate receptor and a conserved N-terminal region of chromogranin B. <b>2007</b> , 1774, 502-9	9
2075	Structural disorder promotes assembly of protein complexes. <b>2007</b> , 7, 65	78
2074	Dynamic alpha-helices: conformations that do not conform. <b>2007</b> , 68, 109-22	15
2073	The N- and C-termini of the human Nogo molecules are intrinsically unstructured: bioinformatics, CD, NMR characterization, and functional implications. <b>2007</b> , 68, 100-8	35
2072	Mass spectrometry analysis of HIV-1 Vif reveals an increase in ordered structure upon oligomerization in regions necessary for viral infectivity. <b>2007</b> , 69, 270-84	41
2071	Intrinsic disorder in yeast transcriptional regulatory network. <b>2007</b> , 68, 602-5	55
2070	Operational definition of intrinsically unstructured protein sequences based on susceptibility to the 20S proteasome. <b>2008</b> , 70, 1357-66	80
2069	Assessment of disorder predictions in CASP7. <b>2007</b> , 69 Suppl 8, 129-36	87



2068	Critical assessment of methods of protein structure prediction-Round VII. <b>2007</b> , 69 Suppl 8, 3-9	189
2067	Huntingtin interacting protein HYPK is intrinsically unstructured. <b>2008</b> , 71, 1686-98	26
2066	Interaction with Keap1 does not lead to ubiquitination and degradation of prothymosin $\beta$ . <b>2007</b> , 41, 790-796	2
2065	Bim, Bad and Bmf: intrinsically unstructured BH3-only proteins that undergo a localized conformational change upon binding to prosurvival Bcl-2 targets. <b>2007</b> , 14, 128-36	179
2064	ERK1/2-dependent phosphorylation of BimEL promotes its rapid dissociation from Mcl-1 and Bcl-xL. <b>2007</b> , 26, 2856-67	143
2063	The redox-switch domain of Hsp33 functions as dual stress sensor. <b>2007</b> , 14, 556-63	143
2062	Structure and dynamics of a molten globular enzyme. <b>2007</b> , 14, 1202-6	92
2061	A pre-existing hydrophobic collapse in the unfolded state of an ultrafast folding protein. <b>2007</b> , 447, 106-9	134
2060	Mechanism of coupled folding and binding of an intrinsically disordered protein. <b>2007</b> , 447, 1021-5	852
2059	Crystal structure of the tetrameric inositol 1-phosphate phosphatase (TM1415) from the hyperthermophile, <i>Thermotoga maritima</i> . <b>2007</b> , 274, 2461-9	17
2058	The ammonium-inactivated cyanobacterial glutamine synthetase I is reactivated in vivo by a mechanism involving proteolytic removal of its inactivating factors. <b>2007</b> , 65, 166-79	22
2057	Neuropathology, biochemistry, and biophysics of alpha-synuclein aggregation. <b>2007</b> , 103, 17-37	373
2056	Predicting mostly disordered proteins by using structure-unknown protein data. <b>2007</b> , 8, 78	54
2055	Multiple domain insertions and losses in the evolution of the Rab prenylation complex. <b>2007</b> , 7, 140	17
2054	Protein structure: evolutionary bridges to new folds. <b>2007</b> , 17, R48-50	9
2053	Determination of conformationally heterogeneous states of proteins. <b>2007</b> , 17, 15-20	120
2052	Atomic-level characterization of disordered protein ensembles. <b>2007</b> , 17, 3-14	360
2051	Between order and disorder in protein structures: analysis of "dual personality" fragments in proteins. <b>2007</b> , 15, 1141-7	67

2050	Protein kinases and the proteasome join in the combinatorial control of transcription by nuclear retinoic acid receptors. <b>2007</b> , 17, 302-9	71
2049	How do ALS-associated mutations in superoxide dismutase 1 promote aggregation of the protein?. <b>2007</b> , 32, 78-85	203
2048	Thymosin beta4: actin regulation and more. <b>2007</b> , 1112, 76-85	20
2047	Molecular mimicry enables competitive recruitment by a natively disordered protein. <b>2007</b> , 129, 4800-7	89
2046	Small-angle X-ray scattering from RNA, proteins, and protein complexes. <b>2007</b> , 36, 307-27	253
2045	X-ray solution scattering (SAXS) combined with crystallography and computation: defining accurate macromolecular structures, conformations and assemblies in solution. <b>2007</b> , 40, 191-285	872
2044	The solution structure of ParD, the antidote of the ParDE toxin antitoxin module, provides the structural basis for DNA and toxin binding. <b>2007</b> , 16, 1676-88	57
2043	An experimental study of GFP-based FRET, with application to intrinsically unstructured proteins. <b>2007</b> , 16, 1429-38	115
2042	Protein reconstitution and three-dimensional domain swapping: benefits and constraints of covalency. <b>2007</b> , 16, 2317-33	48
2041	Dynamic behavior of an intrinsically unstructured linker domain is conserved in the face of negligible amino acid sequence conservation. <b>2007</b> , 65, 277-88	71
2040	Coverage of whole proteome by structural genomics observed through protein homology modeling database. <b>2006</b> , 7, 65-76	11
2039	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. <b>2007</b> , 38, 107-23	7
2038	Theoretical framework for NMR residual dipolar couplings in unfolded proteins. <b>2007</b> , 39, 1-16	28
2037	Energetics of OCP1-OCP2 complex formation. <b>2008</b> , 134, 64-71	12
2036	Peptide-mediated interactions in biological systems: new discoveries and applications. <b>2008</b> , 19, 344-50	185
2035	NMR structure note: alkaline proteinase inhibitor APRin from <i>Pseudomonas aeruginosa</i> . <b>2008</b> , 40, 213-7	3
2034	A simple method for amino acid selective isotope labeling of recombinant proteins in <i>E. coli</i> . <b>2008</b> , 42, 59-67	51
2033	Composition-driven surface domain structuring mediated by sphingolipids and membrane-active proteins. Above the nano- but under the micro-scale: mesoscopic biochemical/structural cross-talk in biomembranes. <b>2008</b> , 50, 79-109	31

2032	On the relevance of defining protein structures in cancer research. <b>2008</b> , 10, 204-12	
2031	Stochastic determinism underlying life: systematic theory for assisting the synthesis of artificial cells and new medicines. <b>2008</b> , 13, 10-17	11
2030	Inevitability of nTP: information & energy carriers. <b>2008</b> , 13, 81-83	6
2029	Structure and lability of archaeal dehydroquinase. <b>2008</b> , 64, 886-92	4
2028	Quantitative assessment of the structural bias in protein-protein interaction assays. <b>2008</b> , 8, 4657-67	21
2027	Structure-function analysis of Knr4/Smi1, a newly member of intrinsically disordered proteins family, indispensable in the absence of a functional PKC1-SLT2 pathway in <i>Saccharomyces cerevisiae</i> . <b>2008</b> , 25, 563-76	13
2026	Knitting and untying the protein network: modulation of protein ensembles as a therapeutic strategy. <b>2009</b> , 18, 481-93	18
2025	Residual structure in disordered peptides and unfolded proteins from multivariate analysis and ab initio simulation of Raman optical activity data. <b>2008</b> , 70, 823-33	63
2024	Modeling the accessible conformations of the intrinsically unstructured transactivation domain of p53. <b>2008</b> , 71, 587-98	38
2023	Sequence-similar, structure-dissimilar protein pairs in the PDB. <b>2008</b> , 71, 891-902	83
2022	Structural disorder serves as a weak signal for intracellular protein degradation. <b>2008</b> , 71, 903-9	84
2021	Unstructured intermediate states in single protein force experiments. <b>2008</b> , 71, 1145-55	1
2020	A robust approach for analyzing a heterogeneous structural ensemble. <b>2008</b> , 73, 918-28	8
2019	Mapping alpha-helical induced folding within the intrinsically disordered C-terminal domain of the measles virus nucleoprotein by site-directed spin-labeling EPR spectroscopy. <b>2008</b> , 73, 973-88	93
2018	Visualization of intrinsically disordered regions of proteins by high-speed atomic force microscopy. <b>2008</b> , 9, 1859-66	84
2017	Simulations of proteins with inhomogeneous degrees of freedom: The effect of thermostats. <b>2008</b> , 29, 1992-8	49
2016	Characterization of the structure and dynamics of mastoparan-X during folding in aqueous TFE by CD and NMR spectroscopy. <b>2008</b> , 89, 197-209	10
2015	Interaction with Al and Zn induces structure formation and aggregation in natively unfolded caseins. <b>2008</b> , 93, 36-43	16

2014	Preserving free thiols of intrinsically disordered tau protein without the use of a reducing agent. <b>2008</b> , 383, 343-5	4
2013	Structural rationale for the coupled binding and unfolding of the c-Myc oncoprotein by small molecules. <b>2008</b> , 15, 1149-55	126
2012	Identification of transient hub proteins and the possible structural basis for their multiple interactions. <b>2008</b> , 17, 72-8	55
2011	Protein design by directed evolution. <b>2008</b> , 37, 153-73	309
2010	Cell-type-specific function of BCL9 involves a transcriptional activation domain that synergizes with beta-catenin. <b>2008</b> , 28, 3526-37	43
2009	Privileged scaffolds targeting reverse-turn and helix recognition. <b>2008</b> , 12, 101-14	29
2008	Structure-function analysis of the filamentous actin binding domain of the neuronal scaffolding protein spinophilin. <b>2008</b> , 275, 59-68	8
2007	Abundance of intrinsic disorder in SV-IV, a multifunctional androgen-dependent protein secreted from rat seminal vesicle. <b>2008</b> , 275, 763-74	4
2006	Exploring CP12 binding proteins revealed aldolase as a new partner for the phosphoribulokinase/glyceraldehyde 3-phosphate dehydrogenase/CP12 complex--purification and kinetic characterization of this enzyme from <i>Chlamydomonas reinhardtii</i> . <b>2008</b> , 275, 1248-59	32
2005	Rwdd1, a thymus aging related molecule, is a new member of the intrinsically unstructured protein family. <b>2008</b> , 5, 333-9	8
2004	Implementing the LIM code: the structural basis for cell type-specific assembly of LIM-homeodomain complexes. <b>2008</b> , 27, 2018-29	61
2003	More complicated than it looks: assembly of Notch pathway transcription complexes. <b>2008</b> , 27, 5099-109	122
2002	Malleable machines take shape in eukaryotic transcriptional regulation. <b>2008</b> , 4, 728-37	161
2001	Potato virus A genome-linked protein VPg is an intrinsically disordered molten globule-like protein with a hydrophobic core. <b>2008</b> , 377, 280-8	59
2000	Selection against tandem splice sites affecting structured protein regions. <b>2008</b> , 8, 89	10
1999	The unfoldomics decade: an update on intrinsically disordered proteins. <b>2008</b> , 9 Suppl 2, S1	408
1998	Ubiquitin-independent degradation of proteins by the proteasome. <b>2008</b> , 1786, 153-77	106
1997	Structural plasticity in G-protein coupled receptors as demonstrated by the allosteric actions of homocysteine and computer-assisted analysis of disordered domains. <b>2008</b> , 58, 459-74	37

1996	A short Nur77-derived peptide converts Bcl-2 from a protector to a killer. <b>2008</b> , 14, 285-98	166
1995	Function and structure of inherently disordered proteins. <b>2008</b> , 18, 756-64	746
1994	Intrinsic disorder in scaffold proteins: getting more from less. <b>2008</b> , 98, 85-106	213
1993	Cell-cell signaling and the Agrobacterium tumefaciens Ti plasmid copy number fluctuations. <b>2008</b> , 60, 89-107	30
1992	Importin-beta: structural and dynamic determinants of a molecular spring. <b>2008</b> , 16, 906-15	44
1991	Protein metamorphosis: the two-state behavior of Mad2. <b>2008</b> , 16, 1616-25	114
1990	Fuzzy complexes: polymorphism and structural disorder in protein-protein interactions. <b>2008</b> , 33, 2-8	788
1989	Intriguing nucleic-acid-binding features of mammalian prion protein. <b>2008</b> , 33, 132-40	90
1988	Targeting metastable coiled-coil domains by computational design. <b>2008</b> , 130, 12038-44	20
1987	Conformational equilibria in monomeric alpha-synuclein at the single-molecule level. <b>2008</b> , 6, e6	159
1986	Prediction of protein disorder. <b>2008</b> , 426, 103-15	52
1985	Targeting synuclein-gamma to counteract drug resistance in cancer. <b>2008</b> , 12, 59-68	19
1984	First Steps of Protein Structure Prediction. <b>2008</b> , 39-62	
1983	Kinetics of folding and binding of an intrinsically disordered protein: the inhibitor of yeast aspartic proteinase YPrA. <b>2008</b> , 130, 11477-85	51
1982	Experimental parameterization of an energy function for the simulation of unfolded proteins. <b>2008</b> , 94, 182-92	50
1981	Biophysical characterization of the unstructured cytoplasmic domain of the human neuronal adhesion protein neuroligin 3. <b>2008</b> , 95, 1928-44	34
1980	The twilight zone between protein order and disorder. <b>2008</b> , 95, 1612-26	27
1979	Potential implications of availability of short amino acid sequences in proteins: an old and new approach to protein decoding and design. <b>2008</b> , 14, 109-41	14

1978	How much of protein sequence space has been explored by life on Earth?. <b>2008</b> , 5, 953-6	44
1977	Intrinsically disordered proteins in human diseases: introducing the D2 concept. <b>2008</b> , 37, 215-46	1018
1976	Intrinsic disorder in pathogenic and non-pathogenic microbes: discovering and analyzing the unfoldomes of early-branching eukaryotes. <b>2008</b> , 4, 328-40	101
1975	Biochemistry. Controlled chaos. <b>2008</b> , 322, 1340-1	59
1974	Protein Folding and Dynamics from Optical Single Molecule Spectroscopy. <b>2008</b> , 181-215	3
1973	Detailed structural characterization of unbound protein phosphatase 1 inhibitors. <b>2008</b> , 47, 12346-56	59
1972	A comparative analysis of viral matrix proteins using disorder predictors. <b>2008</b> , 5, 126	51
1971	Intimate molecular interactions of <i>P. falciparum</i> merozoite proteins involved in invasion of red blood cells and their implications for vaccine design. <b>2008</b> , 108, 3656-705	80
1970	Structural proteomics: high-throughput methods. Preface. <b>2008</b> , 426, v-vi	17
1969	Human regulatory protein Ki-1/57 has characteristics of an intrinsically unstructured protein. <b>2008</b> , 7, 4465-74	20
1968	Structure of KCNE1 and implications for how it modulates the KCNQ1 potassium channel. <b>2008</b> , 47, 7999-8006	164
1967	Single Molecules and Nanotechnology. <b>2008</b> ,	6
1966	Structural and dynamic characterization of intrinsically disordered human securin by NMR spectroscopy. <b>2008</b> , 130, 16873-9	63
1965	Regulation of cell division by intrinsically unstructured proteins: intrinsic flexibility, modularity, and signaling conduits. <b>2008</b> , 47, 7598-609	185
1964	Local structural preferences of calpastatin, the intrinsically unstructured protein inhibitor of calpain. <b>2008</b> , 47, 6936-45	44
1963	Protein Folding and Aggregation in in vitro Models of Parkinson's Disease. <b>2008</b> , 575-595	11
1962	Comprehensive mapping of the C-terminus of flap endonuclease-1 reveals distinct interaction sites for five proteins that represent different DNA replication and repair pathways. <b>2008</b> , 377, 679-90	27
1961	Partially folded bovine pancreatic trypsin inhibitor analogues attain fully native structures when co-crystallized with S195A rat trypsin. <b>2008</b> , 375, 812-23	1

1960	Novel enzymatic activity derived from the Semliki Forest virus capsid protein. <b>2008</b> , 376, 721-35	19
1959	Solution structure of the c-terminal dimerization domain of SARS coronavirus nucleocapsid protein solved by the SAIL-NMR method. <b>2008</b> , 380, 608-22	87
1958	Order-disorder-order transitions mediate the activation of cholera toxin. <b>2008</b> , 377, 748-60	38
1957	The fellowship of the RING: the RING-B-box linker region interacts with the RING in TRIM21/Ro52, contains a native autoantigenic epitope in Sjögren syndrome, and is an integral and conserved region in TRIM proteins. <b>2008</b> , 377, 431-49	22
1956	Small-angle X-ray scattering of reduced ribonuclease A: effects of solution conditions and comparisons with a computational model of unfolded proteins. <b>2008</b> , 377, 1576-92	36
1955	Pre-folding I $\kappa$ B $\alpha$ alters control of NF- $\kappa$ B signaling. <b>2008</b> , 380, 67-82	48
1954	Solution conformation, backbone dynamics and lipid interactions of the intrinsically unstructured malaria surface protein MSP2. <b>2008</b> , 379, 105-21	52
1953	Modulation by substrates of the interaction between the HasR outer membrane receptor and its specific TonB-like protein, HasB. <b>2008</b> , 378, 840-51	21
1952	Intrinsically disordered human C/EBP homologous protein regulates biological activity of colon cancer cells during calcium stress. <b>2008</b> , 380, 313-26	17
1951	Folding of the KIX domain: characterization of the equilibrium analog of a folding intermediate using <sup>15</sup> N/ <sup>13</sup> C relaxation dispersion and fast <sup>1</sup> H/ <sup>2</sup> H amide exchange NMR spectroscopy. <b>2008</b> , 380, 726-41	31
1950	Transfer of flexibility between ankyrin repeats in I $\kappa$ B $\alpha$ upon formation of the NF- $\kappa$ B complex. <b>2008</b> , 380, 917-31	56
1949	The SOCS box domain of SOCS3: structure and interaction with the elonginBC-cullin5 ubiquitin ligase. <b>2008</b> , 381, 928-40	83
1948	Subdomain competition, cooperativity, and topological frustration in the folding of CheY. <b>2008</b> , 382, 485-95	48
1947	Rate of loop formation in peptides: a simulation study. <b>2008</b> , 382, 556-65	19
1946	Kinetics and thermodynamics of ligand binding to a molten globular enzyme and its native counterpart. <b>2008</b> , 382, 971-7	60
1945	The affinity of Ets-1 for DNA is modulated by phosphorylation through transient interactions of an unstructured region. <b>2008</b> , 382, 1014-30	51
1944	Biochemical and structural characterization of an intramolecular interaction in FOXO3a and its binding with p53. <b>2008</b> , 384, 590-603	78
1943	Structure of a sigma28-regulated nonflagellar virulence protein from <i>Campylobacter jejuni</i> . <b>2008</b> , 384, 364-76	7

1942	Overexpression of post-translationally modified peptides in Escherichia coli by co-expression with modifying enzymes. <b>2008</b> , 57, 108-15	28
1941	Purification and reconstitution of the connexin43 carboxyl terminus attached to the 4th transmembrane domain in detergent micelles. <b>2008</b> , 59, 215-22	9
1940	Amino Acids, Peptides and Proteins. <b>2008</b> , 251-296	1
1939	Modelling. <b>2008</b> , 1-57	4
1938	Role of backbone-solvent interactions in determining conformational equilibria of intrinsically disordered proteins. <b>2008</b> , 130, 7380-92	171
1937	A novel nucleolar transcriptional activator ApLLP for long-term memory formation is intrinsically unstructured but functionally active. <b>2008</b> , 366, 585-91	16
1936	How expression level influences the disorderiness of proteins. <b>2008</b> , 371, 401-4	7
1935	Structural and mechanistic insights into STIM1-mediated initiation of store-operated calcium entry. <b>2008</b> , 135, 110-22	350
1934	Principles of protein-protein interactions: what are the preferred ways for proteins to interact?. <b>2008</b> , 108, 1225-44	463
1933	Intrinsic structural disorder of DF31, a Drosophila protein of chromatin decondensation and remodeling activities. <b>2008</b> , 7, 2291-9	16
1932	Quantitative conformational analysis of partially folded proteins from residual dipolar couplings: application to the molecular recognition element of Sendai virus nucleoprotein. <b>2008</b> , 130, 8055-61	120
1931	Binding of the proline-rich segment of myelin basic protein to SH3 domains: spectroscopic, microarray, and modeling studies of ligand conformation and effects of posttranslational modifications. <b>2008</b> , 47, 267-82	59
1930	Osmolyte-induced folding of an intrinsically disordered activation function subdomain of glucocorticoid receptor. <b>2008</b> , 28, 465-74	6
1929	TIC62 redox-regulated translocon composition and dynamics. <b>2008</b> , 283, 6656-67	63
1928	Variationally determined free energy profiles for structural models of proteins: characteristic temperatures for folding and trapping. <b>2008</b> , 112, 6074-82	7
1927	Phosphorylation of paxillin LD4 destabilizes helix formation and inhibits binding to focal adhesion kinase. <b>2008</b> , 47, 548-54	12
1926	The enigmatic LEA proteins and other hydrophilins. <b>2008</b> , 148, 6-24	558
1925	Interconversion between two unrelated protein folds in the lymphotactin native state. <b>2008</b> , 105, 5057-62	209



1924	Effect of methionine oxidation on the structural properties, conformational stability, and aggregation of immunoglobulin light chain LEN. <b>2008</b> , 47, 8665-77	30
1923	Extensive formation of off-pathway species during folding of an alpha-beta parallel protein is due to docking of (non)native structure elements in unfolded molecules. <b>2008</b> , 130, 16914-20	31
1922	NanoLC-MS/MS analysis provides new insights into the phosphorylation pattern of Cdc25B in vivo: full overlap with sites of phosphorylation by Chk1 and Cdk1/cycB kinases in vitro. <b>2008</b> , 7, 1264-73	10
1921	How the "melting" and "freezing" of protein molecules may be used in cell signaling. <b>2008</b> , 3, 89-91	6
1920	The intrinsically disordered RNR inhibitor Sml1 is a dynamic dimer. <b>2008</b> , 47, 13428-37	45
1919	Prevalence of intrinsic disorder in the intracellular region of human single-pass type I proteins: the case of the notch ligand Delta-4. <b>2008</b> , 7, 2496-506	35
1918	Structural and membrane binding properties of the prickle PET domain. <b>2008</b> , 47, 13524-36	19
1917	Starmaker exhibits properties of an intrinsically disordered protein. <b>2008</b> , 9, 2118-25	22
1916	Characterization of the prefusion and transition states of severe acute respiratory syndrome coronavirus S2-HR2. <b>2008</b> , 47, 6802-8	19
1915	Effect of side-chain length on the side-chain dynamics of alpha-helical poly(L-glutamic acid) as probed by a fluorescence blob model. <b>2008</b> , 112, 9209-18	23
1914	The low-pH unfolded state of the C-terminal domain of the ribosomal protein L9 contains significant secondary structure in the absence of denaturant but is no more compact than the low-pH urea unfolded state. <b>2008</b> , 47, 9565-73	20
1913	The intrinsically disordered cytoplasmic domain of the T cell receptor zeta chain binds to the nef protein of simian immunodeficiency virus without a disorder-to-order transition. <b>2008</b> , 47, 12942-4	45
1912	Structural characterization of the native NH2-terminal transactivation domain of the human androgen receptor: a collapsed disordered conformation underlies structural plasticity and protein-induced folding. <b>2008</b> , 47, 3360-9	78
1911	Colicins exploit native disorder to gain cell entry: a hitchhiker's guide to translocation. <b>2008</b> , 36, 1409-13	9
1910	Chaperone activity of ERD10 and ERD14, two disordered stress-related plant proteins. <b>2008</b> , 147, 381-90	308
1909	Solutes alter the conformation of the ligand binding loops in outer membrane transporters. <b>2008</b> , 47, 670-9	33
1908	The RPG gene of <i>Medicago truncatula</i> controls <i>Rhizobium</i> -directed polar growth during infection. <b>2008</b> , 105, 9817-22	88
1907	An unusual intrinsically disordered protein from the model legume <i>Lotus japonicus</i> stabilizes proteins in vitro. <b>2008</b> , 283, 31142-52	32

1906	To misfold or to lose structure?: Detection and degradation of oxidized proteins by the 20S proteasome. <b>2008</b> , 3, 386-8	20
1905	Disordered plant LEA proteins as molecular chaperones. <b>2008</b> , 3, 710-3	52
1904	Novel mechanistic concept of platelet inhibition. <b>2008</b> , 12, 677-92	18
1903	VRK1 phosphorylates CREB and mediates CCND1 expression. <b>2008</b> , 121, 3035-41	67
1902	Search for folding initiation sites from amino acid sequence. <b>2008</b> , 6, 681-91	6
1901	Phosphorylation of the carboxy-terminal domain of histone H1: effects on secondary structure and DNA condensation. <b>2008</b> , 36, 4719-26	66
1900	Evidence for a coiled-coil interaction mode of disordered proteins from bacterial type III secretion systems. <b>2008</b> , 283, 34062-8	35
1899	The structure and interactions of the proline-rich domain of ASPP2. <b>2008</b> , 283, 18990-9	31
1898	Intrinsically disordered gamma-subunit of cGMP phosphodiesterase encodes functionally relevant transient secondary and tertiary structure. <b>2008</b> , 105, 1505-10	82
1897	Structure-function relationships of pre-fibrillar protein assemblies in Alzheimer's disease and related disorders. <b>2008</b> , 5, 319-41	82
1896	Prediction of disordered regions in proteins based on the meta approach. <b>2008</b> , 24, 1344-8	213
1895	An integrative approach for predicting interactions of protein regions. <b>2008</b> , 24, i35-41	13
1894	Structural biology by NMR: structure, dynamics, and interactions. <b>2008</b> , 4, e1000168	94
1893	Expression analysis of the Arabidopsis CP12 gene family suggests novel roles for these proteins in roots and floral tissues. <b>2008</b> , 59, 3975-85	27
1892	Amyloidogenesis of natively unfolded proteins. <b>2008</b> , 5, 260-87	147
1891	P160/SRC/NCoA coactivators form complexes via specific interaction of their PAS-B domain with the CID/AD1 domain. <b>2008</b> , 36, 1847-60	12
1890	Binding-induced folding of a natively unstructured transcription factor. <b>2008</b> , 4, e1000060	167
1889	Intramolecular cohesion of coils mediated by phenylalanine-glycine motifs in the natively unfolded domain of a nucleoporin. <b>2008</b> , 4, e1000145	43

1888	Intrinsically disordered proteins display no preference for chaperone binding in vivo. <b>2008</b> , 4, e1000017	43
1887	Malleable machines in transcription regulation: the mediator complex. <b>2008</b> , 4, e1000243	91
1886	A filovirus-unique region of Ebola virus nucleoprotein confers aberrant migration and mediates its incorporation into virions. <b>2008</b> , 82, 6190-9	33
1885	Alg13p, the catalytic subunit of the endoplasmic reticulum UDP-GlcNAc glycosyltransferase, is a target for proteasomal degradation. <b>2008</b> , 19, 2169-78	14
1884	The IsdC protein from Staphylococcus aureus uses a flexible binding pocket to capture heme. <b>2008</b> , 283, 31591-600	55
1883	The animal in the genome: comparative genomics and evolution. <b>2008</b> , 363, 1453-61	18
1882	Dynamic equilibrium engagement of a polyvalent ligand with a single-site receptor. <b>2008</b> , 105, 17772-7	257
1881	Intrinsic structural disorder in adenovirus E1A: a viral molecular hub linking multiple diverse processes. <b>2008</b> , 82, 7252-63	113
1880	Phosphoproteomic analysis of the mouse brain cytosol reveals a predominance of protein phosphorylation in regions of intrinsic sequence disorder. <b>2008</b> , 7, 1331-48	135
1879	Spontaneous assembly of photosynthetic supramolecular complexes as mediated by the intrinsically unstructured protein CP12. <b>2008</b> , 283, 1831-8	58
1878	Biochemical and structural characterization of the Pak1-LC8 interaction. <b>2008</b> , 283, 27314-24	43
1877	Regulation of Escherichia coli SOS mutagenesis by dimeric intrinsically disordered umuD gene products. <b>2008</b> , 105, 1152-7	60
1876	Allovalency revisited: an analysis of multisite phosphorylation and substrate rebinding. <b>2008</b> , 128, 115106	9
1875	Eta(z)/kappa: a transverse relaxation optimized spectroscopy NMR experiment measuring longitudinal relaxation interference. <b>2008</b> , 128, 155103	3
1874	The therapeutical potential of alpha-synuclein antiaggregatory agents for dementia with Lewy bodies. <b>2008</b> , 15, 2748-59	19
1873	Chapter 1. Target selection in structural genomics projects to increase knowledge of protein structure and function space. <b>2008</b> , 75, 1-52	1
1872	Protein Structure Modeling. <b>2008</b> , 3-35	9
1871	New Frontiers in Characterizing Structure and Dynamics by NMR. <b>2008</b> , 655-679	1

1870	Conserved amphiphilic feature is essential for periplasmic chaperone HdeA to support acid resistance in enteric bacteria. <b>2008</b> , 412, 389-97	31
1869	The retinal cGMP phosphodiesterase gamma-subunit - a chameleon. <b>2008</b> , 9, 611-25	14
1868	Alpha-synuclein misfolding and neurodegenerative diseases. <b>2008</b> , 9, 507-40	163
1867	. <b>2008</b> ,	6
1866	Structural answers and persistent questions about how nicotinic receptors work. <b>2008</b> , 13, 5479-510	28
1865	Biomolecular Structures by Solution Nuclear Magnetic Resonance. <b>2009</b> , 963-987	
1864	Dynamic and combinatorial control of gene expression by nuclear retinoic acid receptors (RARs). <b>2009</b> , 7, e005	178
1863	Thioredoxins and Related Proteins. <b>2009</b> , 401-443	3
1862	Intrinsic disorder in proteins associated with neurodegenerative diseases. <b>2009</b> , 14, 5188-238	169
1861	Kaposi's sarcoma-associated herpesvirus ORF57 in viral RNA processing. <b>2009</b> , 14, 1516-28	34
1860	Evidence for the concerted evolution between short linear protein motifs and their flanking regions. <b>2009</b> , 4, e6052	29
1859	Human 90 kDa Heat Shock Protein Hsp90 as a Target for Cancer Therapeutics. <b>2009</b> , 3, 10-21	2
1858	Intrinsically Unstructured Proteins: Potential Targets for Drug Discovery. <b>2009</b> , 5, 126-134	5
1857	Substrate binding site flexibility of the small heat shock protein molecular chaperones. <b>2009</b> , 106, 15604-9	192
1856	The bioinformatics tools for the estimation of disordered regions in proteins. <b>2009</b> ,	1
1855	Conformational selection or induced fit: a flux description of reaction mechanism. <b>2009</b> , 106, 13737-41	417
1854	Secretory granule to the nucleus: role of a multiply phosphorylated intrinsically unstructured domain. <b>2009</b> , 284, 25723-34	34
1853	Formation of nuclear bodies of Arabidopsis CRY2 in response to blue light is associated with its blue light-dependent degradation. <b>2009</b> , 21, 118-30	108

1852	Trapping moving targets with small molecules. <b>2009</b> , 324, 213-5	133
1851	Toward a quantitative theory of intrinsically disordered proteins and their function. <b>2009</b> , 106, 19819-23	88
1850	Intrinsically disordered p53 extreme C-terminus binds to S100B(beta-beta) through "fly-casting". <b>2009</b> , 131, 2088-9	77
1849	At the crossroads of homeostasis and disease: roles of the PACS proteins in membrane traffic and apoptosis. <b>2009</b> , 421, 1-15	60
1848	Overlapping genes produce proteins with unusual sequence properties and offer insight into de novo protein creation. <b>2009</b> , 83, 10719-36	137
1847	Functional equivalence of HMGA- and histone H1-like domains in a bacterial transcriptional factor. <b>2009</b> , 106, 13546-51	14
1846	CP12 from <i>Chlamydomonas reinhardtii</i> , a permanent specific "chaperone-like" protein of glyceraldehyde-3-phosphate dehydrogenase. <b>2009</b> , 284, 12735-44	33
1845	Susceptibility of p53 unstructured N terminus to 20 S proteasomal degradation programs the stress response. <b>2009</b> , 284, 26234-42	45
1844	The PN2-3 domain of centrosomal P4.1-associated protein implements a novel mechanism for tubulin sequestration. <b>2009</b> , 284, 6909-17	39
1843	Protein ionizable groups: pK values and their contribution to protein stability and solubility. <b>2009</b> , 284, 13285-9	304
1842	Structure and interdomain dynamics of apoptosis-associated speck-like protein containing a CARD (ASC). <b>2009</b> , 284, 32932-41	98
1841	Natively unfolded proteins: An overview. <b>2009</b> , 5, 53-58	15
1840	The C-terminal domain of the HIV-1 Vif protein is natively unfolded in its unbound state. <b>2009</b> , 22, 281-7	27
1839	Membrane domains based on ankyrin and spectrin associated with cell-cell interactions. <b>2009</b> , 1, a003012	132
1838	Phosphorylated intrinsically disordered region of FACT masks its nucleosomal DNA binding elements. <b>2009</b> , 284, 24610-21	43
1837	Solution structure of human Pex5.Pex14.PTS1 protein complexes obtained by small angle X-ray scattering. <b>2009</b> , 284, 25334-42	34
1836	Determinants of histone H4 N-terminal domain function during nucleosomal array oligomerization: roles of amino acid sequence, domain length, and charge density. <b>2009</b> , 284, 16716-16722	27
1835	Interaction of Tim23 with Tim50 is essential for protein translocation by the mitochondrial TIM23 complex. <b>2009</b> , 284, 4865-72	50

1834	RTX calcium binding motifs are intrinsically disordered in the absence of calcium: implication for protein secretion. <b>2009</b> , 284, 1781-9	112
1833	Measles. <b>2009</b> ,	1
1832	Polycomb group protein Suppressor 2 of zeste is a functional homolog of Posterior Sex Combs. <b>2009</b> , 29, 515-25	39
1831	Molecular genetic analysis of Suppressor 2 of zeste identifies key functional domains. <b>2009</b> , 182, 999-1013	11
1830	An atypical CNG channel activated by a single cGMP molecule controls sperm chemotaxis. <b>2009</b> , 2, ra68	61
1829	Chapter 2 NMR Studies of Protein Folding. <b>2009</b> , 53-76	2
1828	Molecular Dynamics Simulations of Intrinsically Disordered Proteins in Human Diseases. <b>2009</b> , 5, 280-287	12
1827	Vpu matchmakers as a therapeutic strategy for HIV infection. <b>2009</b> , 5, e1000246	13
1826	The role of disordered ribosomal protein extensions in the early steps of eubacterial 50 S ribosomal subunit assembly. <b>2009</b> , 10, 817-34	35
1825	Intrinsic disorder in protein interactions: insights from a comprehensive structural analysis. <b>2009</b> , 5, e1000316	91
1824	Structural polymorphism of 441-residue tau at single residue resolution. <b>2009</b> , 7, e34	420
1823	Prediction of protein binding regions in disordered proteins. <b>2009</b> , 5, e1000376	419
1822	An overview of the importance of conformational flexibility in gene regulation by the transcription factors. <b>2009</b> , 2009, 210485	7
1821	Intrinsic structural disorder confers cellular viability on oncogenic fusion proteins. <b>2009</b> , 5, e1000552	63
1820	Influence of sequence changes and environment on intrinsically disordered proteins. <b>2009</b> , 5, e1000497	37
1819	NMR analysis of dynein light chain dimerization and interactions with diverse ligands. <b>2009</b> , 455, 237-58	10
1818	Is assembly of the SNARE complex enough to fuel membrane fusion?. <b>2009</b> , 284, 13143-52	57
1817	Structure of the disordered C terminus of Rab7 GTPase induced by binding to the Rab geranylgeranyl transferase catalytic complex reveals the mechanism of Rab prenylation. <b>2009</b> , 284, 13185-92	37

1816	Hepatitis C virus NS5A protein is a substrate for the peptidyl-prolyl cis/trans isomerase activity of cyclophilins A and B. <b>2009</b> , 284, 13589-13601	134
1815	Intrinsic conformational determinants signal protein misfolding to the Hrd1/Htm1 endoplasmic reticulum-associated degradation system. <b>2009</b> , 20, 3317-29	61
1814	Essential role of nuclear localization for yeast Ulp2 SUMO protease function. <b>2009</b> , 20, 2196-206	29
1813	Analysis of the varicella-zoster virus IE62 N-terminal acidic transactivating domain and its interaction with the human mediator complex. <b>2009</b> , 83, 6300-5	23
1812	Structure of bacteriophage SPP1 head-to-tail connection reveals mechanism for viral DNA gating. <b>2009</b> , 106, 8507-12	96
1811	Protein Structure Modeling and Docking at the Swiss Institute of Bioinformatics. <b>2009</b> , 219-246	
1810	Novel virus-associated proteins encoded by UL112-113 of human cytomegalovirus. <b>2009</b> , 90, 2840-2848	5
1809	Vaccine potentials of an intrinsically unstructured fragment derived from the blood stage-associated Plasmodium falciparum protein PFF0165c. <b>2009</b> , 77, 5701-9	41
1808	Physical requirements and functional consequences of complex formation between the cytomegalovirus IE1 protein and human STAT2. <b>2009</b> , 83, 12854-70	55
1807	Fibronectin binds to and induces conformational change in a disordered region of leptospiral immunoglobulin-like protein B. <b>2009</b> , 284, 23547-57	47
1806	A progesterone receptor co-activator (JDP2) mediates activity through interaction with residues in the carboxyl-terminal extension of the DNA binding domain. <b>2009</b> , 284, 24415-24	27
1805	Structural and functional analysis of SmeT, the repressor of the Stenotrophomonas maltophilia multidrug efflux pump SmeDEF. <b>2009</b> , 284, 14428-38	37
1804	Plasmodium falciparum merozoite surface protein 2 is unstructured and forms amyloid-like fibrils. <b>2009</b> , 166, 159-71	65
1803	The rules of disorder or why disorder rules. <b>2009</b> , 99, 94-103	146
1802	Linking folding and binding. <b>2009</b> , 19, 31-8	813
1801	Biophysical characterization of intrinsically disordered proteins. <b>2009</b> , 19, 23-30	270
1800	Computational studies of protein regulation by post-translational phosphorylation. <b>2009</b> , 19, 156-63	64
1799	The crystal structure of cobra venom factor, a cofactor for C3- and C5-convertase CVFBb. <b>2009</b> , 17, 611-9	26

1798	Do viral proteins possess unique biophysical features?. <b>2009</b> , 34, 53-9	182
1797	Cell regulation: determined to signal discrete cooperation. <b>2009</b> , 34, 471-82	132
1796	PreDisorder: ab initio sequence-based prediction of protein disordered regions. <b>2009</b> , 10, 436	76
1795	Large-scale prediction of long disordered regions in proteins using random forests. <b>2009</b> , 10, 8	35
1794	Protein disorder in the human diseasome: unfoldomics of human genetic diseases. <b>2009</b> , 10 Suppl 1, S12	105
1793	Unfoldomics of human diseases: linking protein intrinsic disorder with diseases. <b>2009</b> , 10 Suppl 1, S7	199
1792	Interaction of a potyviral VPg with anionic phospholipid vesicles. <b>2009</b> , 395, 114-20	12
1791	Cold stability of intrinsically disordered proteins. <b>2009</b> , 583, 465-9	37
1790	Leucine-rich hydrophobic clusters promote folding of the N-terminus of the intrinsically disordered transactivation domain of p53. <b>2009</b> , 583, 556-60	25
1789	Insight into "insoluble proteins" with pure water. <b>2009</b> , 583, 953-9	40
1788	CDF it all: consensus prediction of intrinsically disordered proteins based on various cumulative distribution functions. <b>2009</b> , 583, 1469-74	99
1787	Recent advances in understanding the structure of nicotinic acetylcholine receptors. <b>2009</b> , 61, 407-23	47
1786	Limitations of induced folding in molecular recognition by intrinsically disordered proteins. <b>2009</b> , 10, 1415-9	86
1785	Investigating the disorder-order transition of calmodulin binding domain upon binding calmodulin using molecular dynamics simulation. <b>2010</b> , 23, 360-8	8
1784	Intrinsic disorder explains diverse nuclear roles of chromatin remodeling proteins. <b>2009</b> , 22, 1-8	38
1783	Protein dynamics and conformational disorder in molecular recognition. <b>2010</b> , 23, 105-16	277
1782	Vertical and horizontal integration of bioinformatics education: A modular, interdisciplinary approach. <b>2009</b> , 37, 26-36	21
1781	Role of N-terminus of tyrosine hydroxylase in the biosynthesis of catecholamines. <b>2009</b> , 116, 1355-62	45



1780	H-start for exclusively heteronuclear NMR spectroscopy: the case of intrinsically disordered proteins. <b>2009</b> , 198, 275-81	71
1779	3D J-resolved NMR spectroscopy for unstructured polypeptides: fast measurement of 3J HNH alpha coupling constants with outstanding spectral resolution. <b>2009</b> , 44, 35-42	21
1778	Intrinsically disordered proteins and their environment: effects of strong denaturants, temperature, pH, counter ions, membranes, binding partners, osmolytes, and macromolecular crowding. <b>2009</b> , 28, 305-25	235
1777	Structural and biophysical properties of the integrin-associated cytoskeletal protein talin. <b>2009</b> , 1, 61-69	46
1776	Characterization, stoichiometry, and stability of salivary protein-tannin complexes by ESI-MS and ESI-MS/MS. <b>2009</b> , 395, 2535-45	44
1775	Functions of reticulons in plants: What we can learn from animals and yeasts. <b>2009</b> , 66, 584-95	33
1774	Functional aspects of protein flexibility. <b>2009</b> , 66, 2231-47	161
1773	The protein meta-structure: a novel concept for chemical and molecular biology. <b>2009</b> , 66, 3625-39	41
1772	Zn <sup>2+</sup> -linked dimerization of UreG from Helicobacter pylori, a chaperone involved in nickel trafficking and urease activation. <b>2009</b> , 74, 222-39	68
1771	Intrinsic structural disorder of mouse proNGF. <b>2009</b> , 75, 990-1009	47
1770	Isoform-specific variation in the intrinsic disorder of the ecdysteroid receptor N-terminal domain. <b>2009</b> , 76, 291-308	24
1769	On the relation between residue flexibility and local solvent accessibility in proteins. <b>2009</b> , 76, 617-36	67
1768	Order propensity of an intrinsically disordered protein, the cyclin-dependent-kinase inhibitor Sic1. <b>2009</b> , 76, 731-46	58
1767	Construct optimization for protein NMR structure analysis using amide hydrogen/deuterium exchange mass spectrometry. <b>2009</b> , 76, 882-94	33
1766	Characterization of intrinsically disordered proteins with electrospray ionization mass spectrometry: conformational heterogeneity of alpha-synuclein. <b>2010</b> , 78, 714-22	73
1765	Energetic determinants of protein binding specificity: insights into protein interaction networks. <b>2009</b> , 9, 1744-53	34
1764	Paramagnetic relaxation enhancements in unfolded proteins: theory and application to drkN SH3 domain. <b>2009</b> , 18, 1401-24	47
1763	Exploring functional roles of multibinding protein interfaces. <b>2009</b> , 18, 1674-83	24

1762	Structure of the Taz2 domain of p300: insights into ligand binding. <b>2009</b> , 65, 1301-8	9
1761	The acidic domains of the Toc159 chloroplast preprotein receptor family are intrinsically disordered protein domains. <b>2009</b> , 10, 35	31
1760	SoftWAXS: a computational tool for modeling wide-angle X-ray solution scattering from biomolecules. <b>2009</b> , 42, 932-943	53
1759	Development of an accurate classification system of proteins into structured and unstructured regions that uncovers novel structural domains: its application to human transcription factors. <b>2009</b> , 9, 26	32
1758	The apoptotic machinery as a biological complex system: analysis of its omics and evolution, identification of candidate genes for fourteen major types of cancer, and experimental validation in CML and neuroblastoma. <b>2009</b> , 2, 20	18
1757	An effective all-atom potential for proteins. <b>2009</b> , 2, 2	58
1756	Theoretical framework for the histone modification network: modifications in the unstructured histone tails form a robust scale-free network. <b>2009</b> , 14, 789-806	12
1755	Structural insight into recruitment of translesion DNA polymerase Dpo4 to sliding clamp PCNA. <b>2009</b> , 71, 678-91	66
1754	A non-synonymous mutation in a conserved site of the MTTP gene is strongly associated with protein activity and fatty acid profile in pigs. <b>2009</b> , 40, 813-20	24
1753	Unusual bipartite mode of interaction between the nonsense-mediated decay factors, UPF1 and UPF2. <b>2009</b> , 28, 2293-306	105
1752	Protein structure homology modeling using SWISS-MODEL workspace. <b>2009</b> , 4, 1-13	908
1751	Polyglutamine disruption of the huntingtin exon 1 N terminus triggers a complex aggregation mechanism. <b>2009</b> , 16, 380-9	336
1750	Multisite protein phosphorylation--from molecular mechanisms to kinetic models. <b>2009</b> , 276, 3177-98	187
1749	Intrinsic disorder and coiled-coil formation in prostate apoptosis response factor 4. <b>2009</b> , 276, 3710-28	22
1748	High levels of structural disorder in scaffold proteins as exemplified by a novel neuronal protein, CASK-interactive protein1. <b>2009</b> , 276, 3744-56	61
1747	New roles of flavoproteins in molecular cell biology: histone demethylase LSD1 and chromatin. <b>2009</b> , 276, 4304-12	61
1746	Structural disorder in amyloid fibrils: its implication in dynamic interactions of proteins. <b>2009</b> , 276, 5406-15	51
1745	Dynamic interactions of proteins in complex networks: a more structured view. <b>2009</b> , 276, 5390-405	81

1744	Coiled-coils in type III secretion systems: structural flexibility, disorder and biological implications. <b>2009</b> , 11, 719-29	36
1743	Characterization of protein secondary structure from NMR chemical shifts. <b>2009</b> , 54, 141-165	71
1742	Cross-saturation and transferred cross-saturation experiments. <b>2009</b> , 54, 123-140	39
1741	Incorporating <sup>1</sup> H chemical shift determination into <sup>13</sup> C-direct detected spectroscopy of intrinsically disordered proteins in solution. <b>2009</b> , 200, 354-8	33
1740	Solution structure and dynamics of the chimeric SH3 domains, SHH- and SHA-"Bergeracs". <b>2009</b> , 1794, 1813-22	13
1739	Small-molecule perturbation of competing interactions between c-Myc and Max. <b>2009</b> , 19, 807-10	44
1738	The rod-shaped conformation of Starmaker. <b>2009</b> , 1794, 1616-24	15
1737	A new function of GAPDH from <i>Chlamydomonas reinhardtii</i> : a thiol-disulfide exchange reaction with CP12. <b>2009</b> , 48, 6034-40	23
1736	Theory, practice, and applications of paramagnetic relaxation enhancement for the characterization of transient low-population states of biological macromolecules and their complexes. <b>2009</b> , 109, 4108-39	575
1735	Large-scale analysis of thermostable, mammalian proteins provides insights into the intrinsically disordered proteome. <b>2009</b> , 8, 211-26	61
1734	Intrinsic Disorder in Proteins Associated with Neurodegenerative Diseases. <b>2009</b> , 21-75	6
1733	The unfolded state of the C-terminal domain of the ribosomal protein L9 contains both native and non-native structure. <b>2009</b> , 48, 4707-19	27
1732	Dss1 regulates interaction of Brh2 with DNA. <b>2009</b> , 48, 11929-38	16
1731	Role of charge neutralization in the folding of the carboxy-terminal domain of histone H1. <b>2009</b> , 113, 12061-6	24
1730	Accurate random coil chemical shifts from an analysis of loop regions in native states of proteins. <b>2009</b> , 131, 16332-3	80
1729	Synchronous vs asynchronous chain motion in alpha-synuclein contact dynamics. <b>2009</b> , 113, 522-30	6
1728	The transcriptional repressor RYBP is a natively unfolded protein which folds upon binding to DNA. <b>2009</b> , 48, 1348-60	31
1727	Conformational changes specific for pseudophosphorylation at serine 262 selectively impair binding of tau to microtubules. <b>2009</b> , 48, 10047-55	102

1726	Comparison of the structure and dynamics of the antibiotic peptide polymyxin B and the inactive nonapeptide in aqueous trifluoroethanol by NMR spectroscopy. <b>2009</b> , 113, 544-51	26
1725	Mechanism of ligand-induced folding of a natively unfolded helixless variant of rabbit I-BABP. <b>2009</b> , 48, 7556-64	16
1724	The K-segment of maize DHN1 mediates binding to anionic phospholipid vesicles and concomitant structural changes. <b>2009</b> , 150, 1503-14	166
1723	Protein Folding and Misfolding: Neurodegenerative Diseases. <b>2009</b> ,	5
1722	Biological regulation via ankyrin repeat folding. <b>2009</b> , 4, 19-22	9
1721	Use of protonless NMR spectroscopy to alleviate the loss of information resulting from exchange-broadening. <b>2009</b> , 131, 7222-3	60
1720	Characterization of the Trypanosoma cruzi ortholog of the SBDS protein reveals an intrinsically disordered extended C-terminal region showing RNA-interacting activity. <b>2009</b> , 91, 475-83	3
1719	The spliceosome: design principles of a dynamic RNP machine. <b>2009</b> , 136, 701-18	1800
1718	Intrabody and Parkinson's disease. <b>2009</b> , 1792, 634-42	19
1717	DNA and heparin chaperone the refolding of purified recombinant replication protein A subunit 1 from Leishmania amazonensis. <b>2009</b> , 1790, 119-25	6
1716	Protein aggregation as a paradigm of aging. <b>2009</b> , 1790, 980-96	78
1715	Reconciling binding mechanisms of intrinsically disordered proteins. <b>2009</b> , 382, 479-82	80
1714	Membrane binding mode of intrinsically disordered cytoplasmic domains of T cell receptor signaling subunits depends on lipid composition. <b>2009</b> , 389, 388-93	34
1713	Exploring the evolutionary rate differences of party hub and date hub proteins in Saccharomyces cerevisiae protein-protein interaction network. <b>2009</b> , 429, 18-22	18
1712	Evolutionary constraints on hub and non-hub proteins in human protein interaction network: insight from protein connectivity and intrinsic disorder. <b>2009</b> , 434, 50-5	25
1711	Structural and functional relationships of the steroid hormone receptors' N-terminal transactivation domain. <b>2009</b> , 74, 877-83	37
1710	Translocation of botulinum neurotoxin light chain protease by the heavy chain protein-conducting channel. <b>2009</b> , 54, 565-9	41
1709	Role of RNA chaperones in virus replication. <b>2009</b> , 139, 253-66	45

1708	Role of intrinsically disordered protein regions/domains in transcriptional regulation. <b>2009</b> , 84, 189-93	54
1707	The desmoglein-specific cytoplasmic region is intrinsically disordered in solution and interacts with multiple desmosomal protein partners. <b>2009</b> , 386, 531-43	22
1706	Analysis of PKR structure by small-angle scattering. <b>2009</b> , 387, 910-20	36
1705	A common interaction for the entry of colicin N and filamentous phage into Escherichia coli. <b>2009</b> , 388, 880-93	16
1704	At low concentrations, 3,4-dihydroxyphenylacetic acid (DOPAC) binds non-covalently to alpha-synuclein and prevents its fibrillation. <b>2009</b> , 388, 597-610	43
1703	Conformational stability and DNA binding specificity of the cardiac T-box transcription factor Tbx20. <b>2009</b> , 389, 606-18	22
1702	Structural interpretation of paramagnetic relaxation enhancement-derived distances for disordered protein states. <b>2009</b> , 390, 467-77	60
1701	Structure and disorder in an unfolded state under nondenaturing conditions from ensemble models consistent with a large number of experimental restraints. <b>2009</b> , 391, 359-74	126
1700	Structural characterization of the natively unfolded N-terminal domain of human c-Src kinase: insights into the role of phosphorylation of the unique domain. <b>2009</b> , 391, 136-48	57
1699	Interaction between intrinsically disordered proteins frequently occurs in a human protein-protein interaction network. <b>2009</b> , 392, 1253-65	48
1698	All-atom Monte Carlo approach to protein-peptide binding. <b>2009</b> , 393, 1118-28	19
1697	Kinetic advantage of intrinsically disordered proteins in coupled folding-binding process: a critical assessment of the "fly-casting" mechanism. <b>2009</b> , 393, 1143-59	227
1696	Structural basis for the mutually exclusive anchoring of P body components EDC3 and Tral to the DEAD box protein DDX6/Me31B. <b>2009</b> , 33, 661-8	93
1695	A residue-level investigation of the equilibrium unfolding of the C2A domain of synaptotagmin 1. <b>2009</b> , 490, 158-62	2
1694	Insights from coarse-grained G $\beta$ models for protein folding and dynamics. <b>2009</b> , 10, 889-905	198
1693	Global signatures of protein and mRNA expression levels. <b>2009</b> , 5, 1512-26	614
1692	Interfacial water at protein surfaces: wide-line NMR and DSC characterization of hydration in ubiquitin solutions. <b>2009</b> , 96, 2789-98	36
1691	Novel anti-cancer compounds: structure-based discovery of chemical chaperons for p53. <b>2009</b> , 22, 739-44	2

1690	Determination of the free energy landscape of alpha-synuclein using spin label nuclear magnetic resonance measurements. <b>2009</b> , 131, 18314-26	156
1689	Animal Evolution. <b>2009</b> ,	3
1688	Intrinsic disorder in Viral Proteins Genome-Linked: experimental and predictive analyses. <b>2009</b> , 6, 23	55
1687	The interaction between the measles virus nucleoprotein and the Interferon Regulator Factor 3 relies on a specific cellular environment. <b>2009</b> , 6, 59	20
1686	Protein intrinsic disorder and influenza virulence: the 1918 H1N1 and H5N1 viruses. <b>2009</b> , 6, 69	64
1685	Hydration, cavities and volume in protein folding, aggregation and amyloid assembly. <b>2009</b> , 6, 015002	19
1684	Protein dynamism and evolvability. <b>2009</b> , 324, 203-7	637
1683	From Protein Structure to Function with Bioinformatics. <b>2009</b> ,	19
1682	Atomistic details of the disordered states of KID and pKID. Implications in coupled binding and folding. <b>2009</b> , 131, 5214-23	82
1681	Protein Folding, Misfolding, and Aggregation. <b>2009</b> , 345-367	
1680	Cellular Signaling in Health and Disease. <b>2009</b> ,	6
1679	Insights into the regulation of intrinsically disordered proteins in the human proteome by analyzing sequence and gene expression data. <b>2009</b> , 10, R50	56
1678	Regulating highly dynamic unstructured proteins and their coding mRNAs. <b>2009</b> , 10, 204	14
1677	Nucleocapsid structure and function. <b>2009</b> , 329, 103-28	53
1676	Diffusion coefficients of biomolecules using long-lived spin states. <b>2009</b> , 131, 7498-9	72
1675	High-resolution temperature-concentration diagram of alpha-synuclein conformation obtained from a single Föster resonance energy transfer image in a microfluidic device. <b>2009</b> , 81, 6929-35	27
1674	Structure and biochemistry of cadherins and catenins. <b>2009</b> , 1, a003053	307
1673	Length-dependent regulation of the Kv1.2 channel activation by its C-terminus. <b>2009</b> , 26, 186-93	3

1672	Quantitative approaches to defining normal and aberrant protein homeostasis. <b>2009</b> , 143, 277-91; discussion 359-72	8
1671	Analysis of structured and intrinsically disordered regions of transmembrane proteins. <b>2009</b> , 5, 1688-1702	55
1670	Structural basis for recruitment of CBP/p300 coactivators by STAT1 and STAT2 transactivation domains. <b>2009</b> , 28, 948-58	108
1669	Analysis of protein conformation and dynamics by hydrogen/deuterium exchange MS. <b>2009</b> , 81, 7870-5	285
1668	Prediction of the rotational tumbling time for proteins with disordered segments. <b>2009</b> , 131, 6814-21	39
1667	Biophysics of Parkinson's disease: structure and aggregation of alpha-synuclein. <b>2009</b> , 10, 483-99	250
1666	Studies of the biological function and structure of casein micelles, and future implications. <b>2009</b> , 147-169	1
1665	Protein Structure. 420-459	
1664	Mosaic, self-similarity logic, and biological attraction principles: three explanatory instruments in biology. <b>2009</b> , 2, 552-63	33
1663	References. <b>2009</b> , 265-312	
1662	Human 90 kDa Heat Shock Protein Hsp90 as a Target for Cancer Therapeutics. <b>2009</b> , 3, 330-341	11
1661	The importance of being flexible: the case of basic region leucine zipper transcriptional regulators. <b>2009</b> , 10, 244-69	72
1660	Membrane interactions of oligomeric alpha-synuclein: potential role in Parkinson's disease. <b>2010</b> , 11, 334-42	39
1659	Proteins: sequence to structure and function--current status. <b>2010</b> , 11, 498-514	47
1658	The Arabidopsis thaliana NAC transcription factor family: structure-function relationships and determinants of ANAC019 stress signalling. <b>2010</b> , 426, 183-96	274
1657	Structural disorder in the HIV-1 Vif protein and interaction-dependent gain of structure. <b>2010</b> , 17, 988-98	17
1656	Structural disorder within the measles virus nucleoprotein and phosphoprotein. <b>2010</b> , 17, 961-78	31
1655	Sequence signatures and mRNA concentration can explain two-thirds of protein abundance variation in a human cell line. <b>2010</b> , 6, 400	425

1654	Phosphorylation of Ser136 is critical for potent bone sialoprotein-mediated nucleation of hydroxyapatite crystals. <b>2010</b> , 428, 385-95	34
1653	The Wnt signaling pathway in cellular proliferation and differentiation: A tale of two coactivators. <b>2010</b> , 62, 1149-55	160
1652	Defining conformational ensembles of intrinsically disordered and partially folded proteins directly from chemical shifts. <b>2010</b> , 132, 1270-2	138
1651	cGMP-phosphodiesterase 6, transducin and Wnt5a/Frizzled-2-signaling control cGMP and Ca(2+) homeostasis in melanoma cells. <b>2010</b> , 67, 817-28	29
1650	Functions of disordered regions in mammalian early base excision repair proteins. <b>2010</b> , 67, 3573-87	52
1649	Ability of a salivary intrinsically unstructured protein to bind different tannin targets revealed by mass spectrometry. <b>2010</b> , 398, 815-22	50
1648	SDSL-ESR-based protein structure characterization. <b>2010</b> , 39, 499-511	11
1647	Exploring tryptophan dynamics in acid-induced molten globule state of bovine alpha-lactalbumin: a wavelength-selective fluorescence approach. <b>2010</b> , 39, 1453-63	41
1646	A diketoreductase exhibits unique renaturation profile from thermal-induced protein unfolding. <b>2010</b> , 39, 609-13	5
1645	HA-detected experiments for the backbone assignment of intrinsically disordered proteins. <b>2010</b> , 47, 171-81	47
1644	Strategy for complete NMR assignment of disordered proteins with highly repetitive sequences based on resolution-enhanced 5D experiments. <b>2010</b> , 48, 169-77	77
1643	FRIGIDA and related proteins have a conserved central domain and family specific N- and C-terminal regions that are functionally important. <b>2010</b> , 73, 493-505	27
1642	On the lack of specificity of proteins and its consequences for a theory of biological organization. <b>2010</b> , 102, 45-52	19
1641	The protein kingdom extended: ordered and intrinsically disordered proteins, their folding, supramolecular complex formation, and aggregation. <b>2010</b> , 102, 73-84	157
1640	How do new proteins arise?. <b>2010</b> , 20, 390-6	53
1639	Structure/function implications in a dynamic complex of the intrinsically disordered Sic1 with the Cdc4 subunit of an SCF ubiquitin ligase. <b>2010</b> , 18, 494-506	208
1638	The meandering of disordered proteins in conformational space. <b>2010</b> , 18, 416-9	13
1637	Systematic bioinformatics and experimental validation of yeast complexes reduces the rate of attrition during structural investigations. <b>2010</b> , 18, 1075-82	8



1636	Seven lessons from one IDP structural analysis. <b>2010</b> , 18, 1069-71	11
1635	The extended PP1 toolkit: designed to create specificity. <b>2010</b> , 35, 450-8	343
1634	Predictors of natively unfolded proteins: unanimous consensus score to detect a twilight zone between order and disorder in generic datasets. <b>2010</b> , 11, 198	5
1633	Bayesian statistical modelling of human protein interaction network incorporating protein disorder information. <b>2010</b> , 11, 46	13
1632	Intrinsically disordered domains deviate significantly from random sequences in mammalian proteins. <b>2010</b> , 11 Suppl 7, S7	8
1631	A versatile palindromic amphipathic repeat coding sequence horizontally distributed among diverse bacterial and eucaryotic microbes. <b>2010</b> , 11, 430	9
1630	Low-complexity regions within protein sequences have position-dependent roles. <b>2010</b> , 4, 43	143
1629	Leu628 of the KIX domain of CBP is a key residue for the interaction with the MLL transactivation domain. <b>2010</b> , 584, 4500-4	26
1628	C2C12 myoblasts release micro-vesicles containing mtDNA and proteins involved in signal transduction. <b>2010</b> , 316, 1977-84	186
1627	Glycosylation enhances peptide hydrophobic collapse by impairing solvation. <b>2010</b> , 11, 2367-74	16
1626	In silico functional profiling of human disease-associated and polymorphic amino acid substitutions. <b>2010</b> , 31, 335-46	55
1625	Naturally occurring organic osmolytes: from cell physiology to disease prevention. <b>2010</b> , 62, 891-5	92
1624	IDPs and Protein Degradation in the Cell. <b>2010</b> , 1-36	3
1623	Single-Molecule Spectroscopy of Unfolded Proteins. <b>2010</b> , 369-389	2
1622	Structural Insights into Intrinsically Disordered Proteins by Small-Angle X-Ray Scattering. <b>2010</b> , 451-476	5
1621	Detecting Disordered Regions in Proteins by Limited Proteolysis. <b>2010</b> , 569-626	7
1620	Large-Scale Identification of Intrinsically Disordered Proteins. <b>2010</b> , 671-693	
1619	Purification of Intrinsically Disordered Proteins. <b>2010</b> , 695-704	3

1618	Determining Structural Ensembles for Intrinsically Disordered Proteins. <b>2010</b> , 107-129	1
1617	Site-Directed Spin Labeling EPR Spectroscopy. <b>2010</b> , 131-169	3
1616	Protein Recognition. <b>2010</b> , 505-532	
1615	PONDR-FIT: a meta-predictor of intrinsically disordered amino acids. <b>2010</b> , 1804, 996-1010	749
1614	Understanding protein non-folding. <b>2010</b> , 1804, 1231-64	875
1613	Intrinsically disordered proteins are potential drug targets. <b>2010</b> , 14, 481-8	228
1612	Enzymatic activity in disordered states of proteins. <b>2010</b> , 14, 671-5	17
1611	NMR characterisation of the minimal interacting regions of centrosomal proteins 4.1R and NuMA1: effect of phosphorylation. <b>2010</b> , 11, 7	3
1610	Urea denatured state ensembles contain extensive secondary structure that is increased in hydrophobic proteins. <b>2010</b> , 19, 929-43	39
1609	Functional dissection of an intrinsically disordered protein: understanding the roles of different domains of Knr4 protein in protein-protein interactions. <b>2010</b> , 19, 1376-85	10
1608	Temperature-dependent structural changes in intrinsically disordered proteins: formation of alpha-helices or loss of polyproline II?. <b>2010</b> , 19, 1555-64	165
1607	Modularity of intrinsic disorder in the human proteome. <b>2010</b> , 78, 212-21	80
1606	Large-scale analysis of secondary structure changes in proteins suggests a role for disorder-to-order transitions in nucleotide binding proteins. <b>2010</b> , 78, 236-48	12
1605	Structural domain-domain interactions: assessment and comparison with protein-protein interaction data to improve the interactome. <b>2010</b> , 78, 109-17	19
1604	Sub-angstrom modeling of complexes between flexible peptides and globular proteins. <b>2010</b> , 78, 2029-40	273
1603	Can self-inhibitory peptides be derived from the interfaces of globular protein-protein interactions?. <b>2010</b> , 78, 3140-9	124
1602	Smoothing molecular interactions: the "kinetic buffer" effect of intrinsically disordered proteins. <b>2010</b> , 78, 3251-9	30
1601	On the mechanism of protein fold-switching by a molecular sensor. <b>2010</b> , 78, 3260-9	18

1600	Order within disorder: aggrecan chondroitin sulphate-attachment region provides new structural insights into protein sequences classified as disordered. <b>2010</b> , 78, 3317-27	9
1599	The regulatory action of the myxobacterial CarD/CarG complex: a bacterial enhanceosome?. <b>2010</b> , 34, 764-78	21
1598	Cytoskeleton-modulating effectors of enteropathogenic and enterohemorrhagic Escherichia coli: a case for EspB as an intrinsically less-ordered effector. <b>2010</b> , 277, 2409-15	16
1597	How disorder influences order and vice versa--mutual effects in fusion proteins containing an intrinsically disordered and a globular protein. <b>2010</b> , 277, 4438-51	15
1596	Functional classification of scaffold proteins and related molecules. <b>2010</b> , 277, 4348-55	59
1595	SPA: Short peptide analyzer of intrinsic disorder status of short peptides. <b>2010</b> , 15, 635-46	7
1594	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. <b>2010</b> , 75, 623-36	21
1593	Spinophilin directs protein phosphatase 1 specificity by blocking substrate binding sites. <b>2010</b> , 17, 459-64	142
1592	Structural basis for docking of peroxisomal membrane protein carrier Pex19p onto its receptor Pex3p. <b>2010</b> , 29, 4083-93	48
1591	Pupylation versus ubiquitylation: tagging for proteasome-dependent degradation. <b>2010</b> , 12, 424-31	31
1590	A comprehensive resource of interacting protein regions for refining human transcription factor networks. <b>2010</b> , 5, e9289	51
1589	Roles of electrostatics and conformation in protein-crystal interactions. <b>2010</b> , 5, e9330	61
1588	Dissection of structure and function of the N-terminal domain of mouse DNMT1 using regional frame-shift mutagenesis. <b>2010</b> , 5, e9831	4
1587	Distinct pathways mediate the sorting of tail-anchored proteins to the plastid outer envelope. <b>2010</b> , 5, e10098	53
1586	Structural disorder within Henipavirus nucleoprotein and phosphoprotein: from predictions to experimental assessment. <b>2010</b> , 5, e11684	63
1585	Reduction in structural disorder and functional complexity in the thermal adaptation of prokaryotes. <b>2010</b> , 5, e12069	56
1584	Aptamers to explore prion protein interactions with nucleic acids. <b>2010</b> , 15, 550-63	3
1583	Denatured states of low-complexity polypeptide sequences differ dramatically from those of foldable sequences. <b>2010</b> , 107, 11364-9	13

1582	Syncytial phenotype of C-terminally truncated herpes simplex virus type 1 gB is associated with diminished membrane interactions. <b>2010</b> , 84, 4923-35	33
1581	From the Cover: Charge interactions can dominate the dimensions of intrinsically disordered proteins. <b>2010</b> , 107, 14609-14	359
1580	Coronavirus nucleocapsid protein facilitates template switching and is required for efficient transcription. <b>2010</b> , 84, 2169-75	124
1579	Dual coding in alternative reading frames correlates with intrinsic protein disorder. <b>2010</b> , 107, 5429-34	60
1578	Capillarity theory for the fly-casting mechanism. <b>2010</b> , 107, 2746-50	63
1577	Bioinformatical approaches to characterize intrinsically disordered/unstructured proteins. <b>2010</b> , 11, 225-43	99
1576	Vinexin $\alpha$ an atypical "sensor" of retinoic acid receptor gamma signaling: union and sequestration, separation, and phosphorylation. <b>2010</b> , 24, 4523-34	26
1575	Structural characterisation of the natively unfolded enterocin EJ97. <b>2010</b> , 23, 507-18	7
1574	Improved sequence-based prediction of disordered regions with multilayer fusion of multiple information sources. <b>2010</b> , 26, i489-96	138
1573	c-Fos proteasomal degradation is activated by a default mechanism, and its regulation by NAD(P)H:quinone oxidoreductase 1 determines c-Fos serum response kinetics. <b>2010</b> , 30, 3767-78	35
1572	Genomic repertoires of DNA-binding transcription factors across the tree of life. <b>2010</b> , 38, 7364-77	102
1571	Recombinant protein vaccines against the asexual blood stages of Plasmodium falciparum. <b>2010</b> , 6, 39-53	48
1570	The dopamine D(4) receptor, the ultimate disordered protein. <b>2010</b> , 30, 331-6	18
1569	Fuzzy complexes of myelin basic protein: NMR spectroscopic investigations of a polymorphic organizational linker of the central nervous system. <b>2010</b> , 88, 143-55	30
1568	The Cryptochrome Blue Light Receptors. <b>2010</b> , 8, e0135	196
1567	A bimodal distribution of two distinct categories of intrinsically disordered structures with separate functions in FG nucleoporins. <b>2010</b> , 9, 2205-24	232
1566	Allosteric communication between cAMP binding sites in the RI subunit of protein kinase A revealed by NMR. <b>2010</b> , 285, 14062-70	12
1565	The 19-amino acid insertion in the tumor-associated splice isoform Rac1b confers specific binding to p120 catenin. <b>2010</b> , 285, 19153-61	30

1564	Directed epitope delivery across the Escherichia coli outer membrane through the porin OmpF. <b>2010</b> , 107, 21412-7	73
1563	Net charge per residue modulates conformational ensembles of intrinsically disordered proteins. <b>2010</b> , 107, 8183-8	376
1562	DNA search efficiency is modulated by charge composition and distribution in the intrinsically disordered tail. <b>2010</b> , 107, 21004-9	99
1561	Essential roles for imuA'- and imuB-encoded accessory factors in DnaE2-dependent mutagenesis in Mycobacterium tuberculosis. <b>2010</b> , 107, 13093-8	84
1560	Target gene context influences the transcriptional requirement for the KAT3 family of CBP and p300 histone acetyltransferases. <b>2010</b> , 5, 9-15	214
1559	The mysterious unfoldome: structureless, underappreciated, yet vital part of any given proteome. <b>2010</b> , 2010, 568068	173
1558	PLoS Computational Biology conference postcards from ISMB 2010. <b>2010</b> , 6, e1002000	0
1557	MOBI: a web server to define and visualize structural mobility in NMR protein ensembles. <b>2010</b> , 26, 2916-7	30
1556	Influence of Conformational Entropy on the Protein Folding Rate. <b>2010</b> , 12, 961-982	7
1555	Two distinct mechanisms for actin capping protein regulation--steric and allosteric inhibition. <b>2010</b> , 8, e1000416	58
1554	Hub promiscuity in protein-protein interaction networks. <b>2010</b> , 11, 1930-43	119
1553	Library of disordered patterns in 3D protein structures. <b>2010</b> , 6, e1000958	46
1552	Intrinsically disordered regions may lower the hydration free energy in proteins: a case study of nudix hydrolase in the bacterium Deinococcus radiodurans. <b>2010</b> , 6, e1000854	17
1551	Intrinsically disordered proteins in a physics-based world. <b>2010</b> , 11, 5292-309	42
1550	Characterization of structural variability sheds light on the specificity determinants of the interaction between effector domains and histone tails. <b>2010</b> , 5, 137-48	7
1549	From protein interaction profile to functional assignment: the human protein Ki-1/57 is associated with pre-mRNA splicing events. <b>2010</b> , 7, 268-71	4
1548	Viral disorder or disordered viruses: do viral proteins possess unique features?. <b>2010</b> , 17, 932-51	96
1547	Structural disorder within sendai virus nucleoprotein and phosphoprotein: insight into the structural basis of molecular recognition. <b>2010</b> , 17, 952-60	23

1546	The impact of gene expression regulation on evolution of extracellular signaling pathways. <b>2010</b> , 9, 2666-77	8
1545	Highly expressed and slowly evolving proteins share compositional properties with thermophilic proteins. <b>2010</b> , 27, 735-41	30
1544	Comparing models of evolution for ordered and disordered proteins. <b>2010</b> , 27, 609-21	127
1543	Head-to-tail intramolecular interaction of herpes simplex virus type 1 regulatory protein ICP27 is important for its interaction with cellular mRNA export receptor TAP/NXF1. <b>2010</b> , 1,	19
1542	The TonB dimeric crystal structures do not exist in vivo. <b>2010</b> , 1,	21
1541	Mechanisms of StpA-mediated RNA remodeling. <b>2010</b> , 7, 735-43	8
1540	Development and application of in vivo molecular traps reveals that dynein light chain occupancy differentially affects dynein-mediated processes. <b>2010</b> , 107, 3493-8	21
1539	The SCHOOL of nature: II. Protein order, disorder and oligomericity in transmembrane signaling. <b>2010</b> , 1, 89-102	14
1538	The SCHOOL of nature: III. From mechanistic understanding to novel therapies. <b>2010</b> , 1, 192-224	8
1537	Unusual biophysics of immune signaling-related intrinsically disordered proteins. <b>2010</b> , 1, 271-281	10
1536	Sequence-specific random coil chemical shifts of intrinsically disordered proteins. <b>2010</b> , 132, 18000-3	229
1535	Flexibility and mobility in mesophilic and thermophilic homologous proteins from molecular dynamics and FoldUnfold method. <b>2010</b> , 8, 377-94	10
1534	Targeting intrinsically disordered proteins in neurodegenerative and protein dysfunction diseases: another illustration of the D(2) concept. <b>2010</b> , 7, 543-64	100
1533	Novel enzymes through design and evolution. <b>2007</b> , 75, 241-94, xiii	14
1532	Modeling the relationship between the p53 C-terminal domain and its binding partners using molecular dynamics. <b>2010</b> , 114, 13201-13	17
1531	Cellular stress and protein misfolding during aging. <b>2010</b> , 648, 107-17	16
1530	Conformational analysis of the partially disordered measles virus N(TAIL)-XD complex by SDSL EPR spectroscopy. <b>2010</b> , 98, 1055-64	52
1529	Linking well-tempered metadynamics simulations with experiments. <b>2010</b> , 98, L44-6	50

1528	Proline-rich salivary proteins have extended conformations. <b>2010</b> , 99, 656-65	70
1527	Probing structural transitions in the intrinsically disordered C-terminal domain of the measles virus nucleoprotein by vibrational spectroscopy of cyanylated cysteines. <b>2010</b> , 99, 1676-83	43
1526	The O-glycosylated linker from the <i>Trichoderma reesei</i> Family 7 cellulase is a flexible, disordered protein. <b>2010</b> , 99, 3773-81	89
1525	The basic helix-loop-helix region of human neurogenin 1 is a monomeric natively unfolded protein which forms a "fuzzy" complex upon DNA binding. <b>2010</b> , 49, 1577-89	32
1524	Solution structure and membrane binding of the toxin fst of the par addiction module. <b>2010</b> , 49, 6567-75	25
1523	In situ misfolding of human islet amyloid polypeptide at interfaces probed by vibrational sum frequency generation. <b>2010</b> , 132, 5405-12	164
1522	Energy Matrix of Structurally Important Side-Chain/Side-Chain Interactions in Proteins. <b>2010</b> , 6, 2191-203	22
1521	Osmolyte-induced folding of an intrinsically disordered protein: folding mechanism in the absence of ligand. <b>2010</b> , 49, 5086-96	38
1520	The multifunctionality of dehydrins: an overview. <b>2010</b> , 5, 503-8	95
1519	The flexible polyelectrolyte hypothesis of protein-biomineral interaction. <b>2010</b> , 26, 18639-46	101
1518	Protein intrinsic disorder and oligomericity in cell signaling. <b>2010</b> , 6, 451-61	45
1517	Conformational dynamics of neurofilament side-arms. <b>2010</b> , 114, 8879-86	12
1516	Unfolded-state dynamics and structure of protein L characterized by simulation and experiment. <b>2010</b> , 132, 4702-9	80
1515	Automatic assignment of the intrinsically disordered protein Tau with 441-residues. <b>2010</b> , 132, 11906-7	100
1514	Biocrystallography: past, present, future. <b>2010</b> , 4, 109-21	16
1513	In vitro characterization of Arabidopsis CP12 isoforms reveals common biochemical and molecular properties. <b>2010</b> , 167, 939-50	31
1512	Oligomeric structure of brain abundant proteins GAP-43 and BASP1. <b>2010</b> , 170, 470-83	27
1511	Searching DNA via a "Monkey Bar" mechanism: the significance of disordered tails. <b>2010</b> , 396, 674-84	119

1510	Characterization of the regions involved in the calcium-induced folding of the intrinsically disordered RTX motifs from the bordetella pertussis adenylate cyclase toxin. <b>2010</b> , 397, 534-49	55
1509	Molecular basis for the structural stability of an enclosed $\beta$ -barrel loop. <b>2010</b> , 402, 475-89	11
1508	Power law distribution defines structural disorder as a structural element directly linked with function. <b>2010</b> , 403, 346-50	27
1507	Solution structure of the heterotrimeric complex between the interaction domains of RFX5 and RFXAP from the RFX gene regulatory complex. <b>2010</b> , 403, 40-51	4
1506	A structural hinge in eukaryotic MutY homologues mediates catalytic activity and Rad9-Rad1-Hus1 checkpoint complex interactions. <b>2010</b> , 403, 351-70	46
1505	Dynamic interactions between clathrin and locally structured elements in a disordered protein mediate clathrin lattice assembly. <b>2010</b> , 404, 274-90	40
1504	A novel unstructured scaffold based on 4EBP1 enables the functional display of a wide range of bioactive peptides. <b>2010</b> , 404, 819-31	5
1503	Reaching biological timescales with all-atom molecular dynamics simulations. <b>2010</b> , 10, 745-52	98
1502	HMGNS/NSBP1: a new member of the HMGN protein family that affects chromatin structure and function. <b>2010</b> , 1799, 86-92	56
1501	Interaction of two intrinsically disordered plant stress proteins (COR15A and COR15B) with lipid membranes in the dry state. <b>2010</b> , 1798, 1812-20	79
1500	NMR characterization of intramolecular interaction of osteopontin, an intrinsically disordered protein with cryptic integrin-binding motifs. <b>2010</b> , 393, 487-91	14
1499	Organization and dynamics of tryptophans in the molten globule state of bovine alpha-lactalbumin utilizing wavelength-selective fluorescence approach: comparisons with native and denatured states. <b>2010</b> , 394, 1082-6	26
1498	Solution structure of the N-terminal transactivation domain of ERM modified by SUMO-1. <b>2010</b> , 399, 104-10	14
1497	Hepatitis C virus nonstructural protein-5A activates sterol regulatory element-binding protein-1c through transcription factor Sp1. <b>2010</b> , 402, 549-53	25
1496	Overexpression and purification of PWL2D, a mutant of the effector protein PWL2 from <i>Magnaporthe grisea</i> . <b>2010</b> , 74, 24-31	11
1495	Molecular simulations of protein disorder. <b>2010</b> , 88, 269-90	65
1494	Influence of flanking sequences on signaling between the activation function AF1 and DNA-binding domain of the glucocorticoid receptor. <b>2010</b> , 496, 140-5	17
1493	Botulinum neurotoxin: a marvel of protein design. <b>2010</b> , 79, 591-617	325



1492	Strategies to optimize protein expression in <i>E. coli</i> . <b>2010</b> , Chapter 5, Unit 5.24.1-29	66
1491	Intrinsically disordered chaperones in plants and animals. <b>2010</b> , 88, 167-74	112
1490	Conformational selection in the molten globule state of the nuclear coactivator binding domain of CBP. <b>2010</b> , 107, 12535-40	135
1489	Evolutionary transients in the rice transcriptome. <b>2010</b> , 8, 211-28	8
1488	Harnessing disorder: onychophorans use highly unstructured proteins, not silks, for prey capture. <b>2010</b> , 277, 3255-63	29
1487	Probing conformational changes in Ape1 during the progression of base excision repair. <b>2010</b> , 49, 3786-96	22
1486	Taking charge of proteins from neurodegeneration to industrial biotechnology. <b>2010</b> , 79, 127-64	15
1485	Intrinsic disorder in the core proteins of flaviviruses. <b>2010</b> , 17, 1019-25	26
1484	Advances in Computational Biology. <b>2010</b> ,	2
1483	Single-biomolecule kinetics: the art of studying a single enzyme. <b>2010</b> , 3, 319-40	40
1482	Proteome Bioinformatics. <b>2010</b> ,	7
1481	Computational resources for the prediction and analysis of native disorder in proteins. <b>2010</b> , 604, 369-93	11
1480	How do proteins gain new domains?. <b>2010</b> , 11, 126	56
1479	A stoichiometry driven universal spatial organization of backbones of folded proteins: are there Chargaff's rules for protein folding?. <b>2010</b> , 28, 133-42	82
1478	Towards the role of metal ions in the structural variability of proteins: CdII speciation of a metal ion binding loop motif. <b>2011</b> , 3, 1331-9	16
1477	Rotational diffusion analysis of polyethylene glycol induced protein interactions. <b>2011</b> , 115, 11786-92	3
1476	Sensing coiled-coil proteins through conformational modulation of energy transfer processes □ selective detection of the oncogenic transcription factor c-Jun. <b>2011</b> , 2, 1984	13
1475	Partial high-resolution structure of phosphorylated and non-phosphorylated leucine-rich amelogenin protein adsorbed to hydroxyapatite. <b>2011</b> , 115, 13775-13785	39

1474	Direct observations of conformational distributions of intrinsically disordered p53 peptides using UV Raman and explicit solvent simulations. <b>2011</b> , 115, 9520-7	15
1473	Atomistic simulations reveal structural disorder in the RAP74-FCP1 complex. <b>2011</b> , 115, 13731-9	17
1472	Interactions between planar grafted neurofilament side-arms. <b>2011</b> , 115, 7541-9	16
1471	A free-energy landscape for coupled folding and binding of an intrinsically disordered protein in explicit solvent from detailed all-atom computations. <b>2011</b> , 133, 10448-58	89
1470	Structural characterization of partially disordered human Chibby: insights into its function in the Wnt-signaling pathway. <b>2011</b> , 50, 715-26	18
1469	The expanding view of protein-protein interactions: complexes involving intrinsically disordered proteins. <b>2011</b> , 8, 035003	48
1468	Transient enzyme-substrate recognition monitored by real-time NMR. <b>2011</b> , 133, 11154-62	17
1467	Dimerization-induced folding of MST1 SARAH and the influence of the intrinsically unstructured inhibitory domain: low thermodynamic stability of monomer. <b>2011</b> , 50, 10990-1000	21
1466	Assisted peptide folding by surface pattern recognition. <b>2011</b> , 100, 1306-15	18
1465	The calponin regulatory region is intrinsically unstructured: novel insight into actin-calponin and calmodulin-calponin interfaces using NMR spectroscopy. <b>2011</b> , 100, 1718-28	5
1464	The role of the LH subdomain in the function of the Cip/Kip cyclin-dependent kinase regulators. <b>2011</b> , 100, 2486-94	13
1463	Multiscale ensemble modeling of intrinsically disordered proteins: p53 N-terminal domain. <b>2011</b> , 101, 1450-8	72
1462	Chain collapse of an amyloidogenic intrinsically disordered protein. <b>2011</b> , 101, 1720-9	43
1461	A structural perspective on the dynamics of kinesin motors. <b>2011</b> , 101, 2749-59	24
1460	Atomistic ensemble modeling and small-angle neutron scattering of intrinsically disordered protein complexes: applied to minichromosome maintenance protein. <b>2011</b> , 101, 2999-3007	15
1459	Interactions of transcription factors with chromatin. <b>2011</b> , 52, 223-59	2
1458	Intrinsically Disordered Chaperones and Neurodegeneration. <b>2011</b> , 1-63	1
1457	Mutation-induced fold switching among lattice proteins. <b>2011</b> , 135, 195101	27

1456	Genomic and biochemical insights into the specificity of ETS transcription factors. <b>2011</b> , 80, 437-71	336
1455	Effective All-Atom Potentials for Proteins. <b>2011</b> , 111-126	
1454	Modeling disordered regions in proteins using Rosetta. <b>2011</b> , 6, e22060	21
1453	Insights on the role of (dis)order from protein-protein interaction linear free-energy relationships. <b>2011</b> , 133, 9976-9	27
1452	Classification of proteins: available structural space for molecular modeling. <b>2012</b> , 857, 1-31	6
1451	Effective techniques for protein structure mining. <b>2012</b> , 857, 33-54	1
1450	Automated projection spectroscopy and its applications. <b>2012</b> , 316, 21-47	17
1449	Protein disorder prevails under crowded conditions. <b>2011</b> , 50, 5834-44	69
1448	Expanding the proteome: disordered and alternatively folded proteins. <b>2011</b> , 44, 467-518	132
1447	Nuclear Magnetic Resonance of Amino Acids, Peptides, and Proteins. <b>2011</b> , 97-153	
1446	Mapping unstructured regions and synergistic folding in intrinsically disordered proteins with amide H/D exchange mass spectrometry. <b>2011</b> , 50, 8722-32	70
1445	DISC1: Structure, Function, and Therapeutic Potential for Major Mental Illness. <b>2011</b> , 2, 609-632	89
1444	Encyclopedia of Cancer. <b>2011</b> , 1803-1803	
1443	A Handbook of Transcription Factors. <b>2011</b> ,	11
1442	Flexible nets of malleable guardians: intrinsically disordered chaperones in neurodegenerative diseases. <b>2011</b> , 111, 1134-66	59
1441	The relationship between proteome size, structural disorder and organism complexity. <b>2011</b> , 12, R120	133
1440	Bringing order to protein disorder through comparative genomics and genetic interactions. <b>2011</b> , 12, R14	105
1439	Folding of a salivary intrinsically disordered protein upon binding to tannins. <b>2011</b> , 133, 7847-52	71

1438	Molecular chaperones and regulation of tau quality control: strategies for drug discovery in tauopathies. <b>2011</b> , 3, 1523-37	48
1437	Intrinsically disordered proteins from A to Z. <b>2011</b> , 43, 1090-103	322
1436	Promiscuity, stability and cold adaptation of a newly isolated acylaminoacyl peptidase. <b>2011</b> , 93, 1543-54	19
1435	Peripherin/rds co-distributes with putative binding partners in basal rod outer segment disks. <b>2011</b> , 92, 439-42	
1434	The intrinsically disordered late embryogenesis abundant protein LEA18 from Arabidopsis thaliana modulates membrane stability through binding and folding. <b>2011</b> , 1808, 446-53	41
1433	Structural transitions in the intrinsically disordered plant dehydration stress protein LEA7 upon drying are modulated by the presence of membranes. <b>2011</b> , 1808, 1879-87	51
1432	Molecular mechanisms of the anomalous thermal aggregation of green fluorescent protein. <b>2011</b> , 1814, 1930-9	14
1431	Senescence-associated barley NAC (NAM, ATAF1,2, CUC) transcription factor interacts with radical-induced cell death 1 through a disordered regulatory domain. <b>2011</b> , 286, 35418-35429	67
1430	Foldamer structuring by covalently bound macromolecules. <b>2011</b> , 133, 19650-2	18
1429	Intrinsic disorder in S100 proteins. <b>2011</b> , 7, 2164-80	21
1428	Structural instability tuning as a regulatory mechanism in protein-protein interactions. <b>2011</b> , 44, 734-44	28
1427	The acidic transcription activator Gcn4 binds the mediator subunit Gal11/Med15 using a simple protein interface forming a fuzzy complex. <b>2011</b> , 44, 942-53	120
1426	The cardiokine story unfolds: ischemic stress-induced protein secretion in the heart. <b>2011</b> , 17, 207-14	83
1425	Are structural proteins in insect cuticles dominated by intrinsically disordered regions?. <b>2011</b> , 41, 620-7	16
1424	Segmental conformational disorder and dynamics in the intrinsically disordered protein $\beta$ synuclein and its chain length dependence. <b>2011</b> , 405, 1267-83	50
1423	Solution structure of the mSin3A PAH2-Pf1 SID1 complex: a Mad1/Mxd1-like interaction disrupted by MRG15 in the Rpd3S/Sin3S complex. <b>2011</b> , 408, 987-1000	20
1422	Multi-scale sequence correlations increase proteome structural disorder and promiscuity. <b>2011</b> , 409, 439-49	11
1421	Backbone-driven collapse in unfolded protein chains. <b>2011</b> , 409, 250-62	89

1420	HTLV-1 HBZ protein deregulates interactions between cellular factors and the KIX domain of p300/CBP. <b>2011</b> , 409, 384-98	31
1419	Enzyme inhibition by allosteric capture of an inactive conformation. <b>2011</b> , 411, 999-1016	30
1418	Intrinsic disorder in ubiquitination substrates. <b>2011</b> , 412, 319-24	38
1417	The bacteriophage lambda gpNu3 scaffolding protein is an intrinsically disordered and biologically functional procapsid assembly catalyst. <b>2011</b> , 412, 723-36	10
1416	Production of protein complexes via co-expression. <b>2011</b> , 75, 1-14	44
1415	Functional expression of milligram quantities of the synthetic human serotonin transporter gene in a tetracycline-inducible HEK293 cell line. <b>2011</b> , 76, 211-20	3
1414	A general method of protein purification for recombinant unstructured non-acidic proteins. <b>2011</b> , 80, 47-51	10
1413	Genotype networks shed light on evolutionary constraints. <b>2011</b> , 26, 577-84	43
1412	Conserved, disordered C terminus of DnaK enhances cellular survival upon stress and DnaK in vitro chaperone activity. <b>2011</b> , 286, 31821-9	44
1411	Sequential melting of two hydrophobic clusters within the green fluorescent protein GFP-cycle3. <b>2011</b> , 50, 7735-44	13
1410	Soluble oligomerization provides a beneficial fitness effect on destabilizing mutations.. <b>2011</b> ,	
1409	Cell-context dependent TCF/LEF expression and function: alternative tales of repression, de-repression and activation potentials. <b>2011</b> , 21, 207-36	53
1408	. <b>2011</b> ,	1
1407	. <b>2011</b> ,	9
1406	Complexity in Organismal Evolution. <b>2011</b> , 335-354	2
1405	Organic matrix-related mineralization of sea urchin spicules, spines, test and teeth. <b>2011</b> , 16, 2540-60	16
1404	Disordered patterns in clustered Protein Data Bank and in eukaryotic and bacterial proteomes. <b>2011</b> , 6, e27142	16
1403	Elucidation of functional markers from <i>Aspergillus nidulans</i> developmental regulator FlbB and their phylogenetic distribution. <b>2011</b> , 6, e17505	6

1402	Crystal structure of the heteromolecular chaperone, AscE-AscG, from the type III secretion system in <i>Aeromonas hydrophila</i> . <b>2011</b> , 6, e19208	11
1401	Naturally occurring osmolyte, trehalose induces functional conformation in an intrinsically disordered activation domain of glucocorticoid receptor. <b>2011</b> , 6, e19689	16
1400	Markov models of amino acid substitution to study proteins with intrinsically disordered regions. <b>2011</b> , 6, e20488	31
1399	Small cofactors may assist protein emergence from RNA world: clues from RNA-protein complexes. <b>2011</b> , 6, e22494	14
1398	Microsecond molecular dynamics simulations of intrinsically disordered proteins involved in the oxidative stress response. <b>2011</b> , 6, e27371	39
1397	Do Viral Proteins Possess Unique Features?. <b>2011</b> , 1-34	4
1396	Intrinsic Disorder in Genome-Linked Viral Proteins VPgs of Potyviruses. <b>2011</b> , 277-312	
1395	Structural Disorder within the Nucleoprotein and Phosphoprotein from Measles, Nipah, and Hendra Viruses. <b>2011</b> , 47-94	5
1394	Structural Disorder within Sendai Virus Nucleoprotein and Phosphoprotein. <b>2011</b> , 95-114	
1393	Structural Disorder in Matrix Proteins of HIV-Related Viruses. <b>2011</b> , 143-167	
1392	Order from Disorder: Structure, Function, and Dynamics of the HIV-1 Transactivator of Transcription. <b>2011</b> , 223-256	
1391	Gene-specific transcription activation via long-range allosteric shape-shifting. <b>2011</b> , 439, 15-25	32
1390	Residues within a lipid-associated segment of the PECAM-1 cytoplasmic domain are susceptible to inducible, sequential phosphorylation. <b>2011</b> , 117, 6012-23	36
1389	Structural Disorder in Proteins of the Rhabdoviridae Replication Complex. <b>2011</b> , 115-141	
1388	The prion protein unstructured N-terminal region is a broad-spectrum molecular sensor with diverse and contrasting potential functions. <b>2012</b> , 120, 853-68	46
1387	Intrinsic disorder mediates the diverse regulatory functions of the Cdk inhibitor p21. <b>2011</b> , 7, 214-21	98
1386	Screening: Low-fat worms on drugs. <b>2011</b> , 7, 194-5	
1385	Protein dynamics: bridging the gap. <b>2011</b> , 7, 193-4	

1384	The evolutionary origin of orphan genes. <b>2011</b> , 12, 692-702	461
1383	CAMP (C13orf8, ZNF828) is a novel regulator of kinetochore-microtubule attachment. <b>2011</b> , 30, 130-44	33
1382	Biophysical characterization of recombinant human ameloblastin. <b>2011</b> , 119 Suppl 1, 261-9	17
1381	Structural characterization of the Boca/Mesd maturation factors for LDL-receptor-type $\beta$ propeller domains. <b>2011</b> , 19, 324-36	6
1380	Domain orientation in the N-Terminal PDZ tandem from PSD-95 is maintained in the full-length protein. <b>2011</b> , 19, 810-20	33
1379	Structure basis for the regulation of glyceraldehyde-3-phosphate dehydrogenase activity via the intrinsically disordered protein CP12. <b>2011</b> , 19, 1846-54	37
1378	How viruses hijack cell regulation. <b>2011</b> , 36, 159-69	260
1377	Dynamic protein-DNA recognition: beyond what can be seen. <b>2011</b> , 36, 415-23	116
1376	Intrinsically disordered proteins: regulation and disease. <b>2011</b> , 21, 432-40	422
1375	Unstructural biology coming of age. <b>2011</b> , 21, 419-25	251
1374	Protein disorder--a breakthrough invention of evolution?. <b>2011</b> , 21, 412-8	111
1373	Uncoupled binding and folding of immune signaling-related intrinsically disordered proteins. <b>2011</b> , 106, 525-36	23
1372	Functional analyses of mutants of the central core domain of an Avian Sarcoma/Leukemia Virus integrase. <b>2011</b> , 421, 42-50	2
1371	Structural analysis of heme proteins: implications for design and prediction. <b>2011</b> , 11, 13	88
1370	Selective and specific ion binding on proteins at physiologically-relevant concentrations. <b>2011</b> , 585, 3126-32	18
1369	Role of metal ions in aggregation of intrinsically disordered proteins in neurodegenerative diseases. <b>2011</b> , 3, 1163-80	88
1368	Multitude of binding modes attainable by intrinsically disordered proteins: a portrait gallery of disorder-based complexes. <b>2011</b> , 40, 1623-34	199
1367	Chemical and biological approaches for adapting proteostasis to ameliorate protein misfolding and aggregation diseases: progress and prognosis. <b>2011</b> , 3,	143

1366	Blm10 protein promotes proteasomal substrate turnover by an active gating mechanism. <b>2011</b> , 286, 42830-9	61
1365	Optimizing Protein-Solvent Force Fields to Reproduce Intrinsic Conformational Preferences of Model Peptides. <b>2011</b> , 7, 1220-30	127
1364	Extension of the HA-detection based approach: (HCA)CON(CA)H and (HCA)NCO(CA)H experiments for the main-chain assignment of intrinsically disordered proteins. <b>2011</b> , 49, 99-109	47
1363	Random coil chemical shift for intrinsically disordered proteins: effects of temperature and pH. <b>2011</b> , 49, 139-49	193
1362	Methods to determine slow diffusion coefficients of biomolecules: applications to Engrailed 2, a partially disordered protein. <b>2011</b> , 50, 209-18	17
1361	Annotation of novel transcripts putatively relevant for bovine fat metabolism. <b>2011</b> , 38, 2975-86	4
1360	MpAsr encodes an intrinsically unstructured protein and enhances osmotic tolerance in transgenic Arabidopsis. <b>2011</b> , 30, 1219-30	55
1359	Synphilin-1 inhibits alpha-synuclein degradation by the proteasome. <b>2011</b> , 68, 2643-54	26
1358	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. <b>2011</b> , 86, 359-63	33
1357	Defining structural domains of an intrinsically disordered protein: Sic1, the cyclin-dependent kinase inhibitor of <i>Saccharomyces cerevisiae</i> . <b>2011</b> , 47, 34-42	10
1356	Binary classification of protein molecules into intrinsically disordered and ordered segments. <b>2011</b> , 11, 29	56
1355	Messing up disorder: how do missense mutations in the tumor suppressor protein APC lead to cancer?. <b>2011</b> , 10, 101	114
1354	In-silico prediction of disorder content using hybrid sequence representation. <b>2011</b> , 12, 245	37
1353	Structure determination of a protein assembly by amino acid selective cross-saturation. <b>2011</b> , 79, 179-90	7
1352	Intrinsic disorder of <i>Drosophila melanogaster</i> hormone receptor 38 N-terminal domain. <b>2011</b> , 79, 376-92	13
1351	Topology-based modeling of intrinsically disordered proteins: balancing intrinsic folding and intermolecular interactions. <b>2011</b> , 79, 1251-66	60
1350	Analysis of protein function and its prediction from amino acid sequence. <b>2011</b> , 79, 2086-96	92
1349	Evaluation of disorder predictions in CASP9. <b>2011</b> , 79 Suppl 10, 107-18	97



1348	Probing structural transitions in both structured and disordered proteins using site-directed spin-labeling EPR spectroscopy. <b>2011</b> , 17, 315-28	30
1347	Characterization of the disordered-to-helical transition of IAI by SDSL-EPR spectroscopy. <b>2011</b> , 20, 150-9	28
1346	Measuring rapid hydrogen exchange in the homodimeric 36 kDa HIV-1 integrase catalytic core domain. <b>2011</b> , 20, 500-12	26
1345	The N(0)-binding region of the vesicular stomatitis virus phosphoprotein is globally disordered but contains transient helices. <b>2011</b> , 20, 542-56	46
1344	Context-dependent resistance to proteolysis of intrinsically disordered proteins. <b>2011</b> , 20, 1285-97	56
1343	The interplay between transient helix formation and side chain rotamer distributions in disordered proteins probed by methyl chemical shifts. <b>2011</b> , 20, 2023-34	11
1342	Fractal dimension of an intrinsically disordered protein: small-angle X-ray scattering and computational study of the bacteriophage IN protein. <b>2011</b> , 20, 1955-70	33
1341	Unraveling moonlighting functions with yeasts. <b>2011</b> , 63, 457-62	18
1340	Characterizing flexible and intrinsically unstructured biological macromolecules by SAS using the Porod-Debye law. <b>2011</b> , 95, 559-71	357
1339	Amino acids with hydrogen-bonding side chains have an intrinsic tendency to sample various turn conformations in aqueous solution. <b>2011</b> , 17, 6789-97	42
1338	Engineering protein switches: sensors, regulators, and spare parts for biology and biotechnology. <b>2011</b> , 12, 353-61	38
1337	Biomolecular electrostatics using a fast multipole BEM on up to 512 gpus and a billion unknowns. <b>2011</b> , 182, 1272-1283	60
1336	Intrinsically disordered proteins may escape unwanted interactions via functional misfolding. <b>2011</b> , 1814, 693-712	52
1335	Dynamics of protein folding: probing the kinetic network of folding-unfolding transitions with experiment and theory. <b>2011</b> , 1814, 1001-20	49
1334	Characterization of the single-stranded DNA binding protein pV(VGJ) of VGJ phage from <i>Vibrio cholerae</i> . <b>2011</b> , 1814, 1107-12	1
1333	Quantitative evaluation of protein conformation in pharmaceuticals using cross-linking reactions coupled with LC-MS/MS analysis. <b>2011</b> , 55, 574-82	3
1332	Intracellular and extracellular cytokine-like functions of prothymosin $\beta$ implications for the development of immunotherapies. <b>2011</b> , 3, 1199-208	29
1331	Protein stability in the presence of cosolutes. <b>2011</b> , 492, 61-125	23

1330	Structural Disorder within the Measles Virus Nucleoprotein and Phosphoprotein: Functional Implications for Transcription and Replication. <b>2011</b> , 95-125	6
1329	Crosstalk between phosphorylation and multi-site arginine/lysine methylation in C/EBPs. <b>2011</b> , 2, 3-8	20
1328	Effectiveness of Evalue analysis in the binding process of Arc repressor dimer. <b>2011</b> , 84, 011909	5
1327	SAHG, a comprehensive database of predicted structures of all human proteins. <b>2011</b> , 39, D487-93	11
1326	Evolution of nuclear retinoic acid receptor alpha (RAR $\alpha$ ) phosphorylation sites. Serine gain provides fine-tuned regulation. <b>2011</b> , 28, 2125-37	23
1325	The yeast kinase Yck2 has a tripartite palmitoylation signal. <b>2011</b> , 22, 2702-15	16
1324	Structural insights into the dynamics and function of the C-terminus of the E. coli RNA chaperone Hfq. <b>2011</b> , 39, 4900-15	65
1323	Outer membrane targeting of secretin PulD protein relies on disordered domain recognition by a dedicated chaperone. <b>2011</b> , 286, 38833-43	34
1322	Ebolavirus delta-peptide immunoadhesins inhibit marburgvirus and ebolavirus cell entry. <b>2011</b> , 85, 8502-13	38
1321	Characterization of the interactions between the nucleoprotein and the phosphoprotein of Henipavirus. <b>2011</b> , 286, 13583-602	51
1320	The balance of flexibility and rigidity in the active site residues of hen egg white lysozyme. <b>2011</b> , 20, 058701	3
1319	The many roles of the highly interactive HSV protein ICP27, a key regulator of infection. <b>2011</b> , 6, 1261-77	76
1318	Actin cytoskeleton remodeling by the alternatively spliced isoform of PDLIM4/RIL protein. <b>2011</b> , 286, 26849-59	12
1317	A biophysical protein folding model accounts for most mutational fitness effects in viruses. <b>2011</b> , 108, 9916-21	144
1316	A novel degradation signal derived from distal C-terminal frameshift mutations of KCNQ2 protein which cause neonatal epilepsy. <b>2011</b> , 286, 42949-58	7
1315	Structure of p300 bound to MEF2 on DNA reveals a mechanism of enhanceosome assembly. <b>2011</b> , 39, 4464-74	43
1314	Functional regulation of FEN1 nuclease and its link to cancer. <b>2011</b> , 39, 781-94	129
1313	The universally conserved prokaryotic GTPases. <b>2011</b> , 75, 507-42, second and third pages of table of content	127

1312	The C-terminus of ICLn is natively disordered but displays local structural preformation. <b>2011</b> , 28, 1203-10	9
1311	Bioinformatic approaches for predicting substrates of proteases. <b>2011</b> , 9, 149-78	24
1310	A novel family of dehydrin-like proteins is involved in stress response in the human fungal pathogen <i>Aspergillus fumigatus</i> . <b>2011</b> , 22, 1896-906	36
1309	New insights into the Lpt machinery for lipopolysaccharide transport to the cell surface: LptA-LptC interaction and LptA stability as sensors of a properly assembled transenvelope complex. <b>2011</b> , 193, 1042-53	69
1308	A discontinuous DNA glycosylase domain in a family of enzymes that excise 5-methylcytosine. <b>2011</b> , 39, 1473-84	20
1307	Molecular basis of the recognition of the ap65-1 gene transcription promoter elements by a Myb protein from the protozoan parasite <i>Trichomonas vaginalis</i> . <b>2011</b> , 39, 8992-9008	18
1306	The crystal structure of the TetR family transcriptional repressor SimR bound to DNA and the role of a flexible N-terminal extension in minor groove binding. <b>2011</b> , 39, 9433-47	49
1305	The dimeric SOS mutagenesis protein UmuD is active as a monomer. <b>2011</b> , 286, 3607-17	13
1304	Insights into the molecular activation mechanism of the RhoA-specific guanine nucleotide exchange factor, PDZRhoGEF. <b>2011</b> , 286, 35163-75	17
1303	ERBIN is a new SARA-interacting protein: competition between SARA and SMAD2 and SMAD3 for binding to ERBIN. <b>2011</b> , 124, 3209-22	20
1302	ARTS, the unusual septin: structural and functional aspects. <b>2011</b> , 392, 783-90	23
1301	Putting the pieces together: a crystal clear window into CLC anion channel regulation. <b>2011</b> , 5, 101-5	3
1300	Immediate early proto-oncoproteins and membranes: not just an innocent liaison. <b>2011</b> , 12, 685-90	3
1299	Late embryogenesis abundant proteins: versatile players in the plant adaptation to water limiting environments. <b>2011</b> , 6, 586-9	82
1298	New insights into the mechanism of odorant detection by the malaria-transmitting mosquito <i>Anopheles gambiae</i> . <b>2011</b> , 286, 34175-83	24
1297	DNA binding restricts the intrinsic conformational flexibility of methyl CpG binding protein 2 (MeCP2). <b>2011</b> , 286, 18938-48	25
1296	Structural and functional characterization of the <i>Streptococcus pneumoniae</i> RrgB pilus backbone D1 domain. <b>2011</b> , 286, 14588-97	17
1295	Transcriptional repression in the Notch pathway: thermodynamic characterization of CSL-MINT (Msx2-interacting nuclear target protein) complexes. <b>2011</b> , 286, 14892-902	35

1294	Disorder-to-order transition underlies the structural basis for the assembly of a transcriptionally active PGC-1 $\beta$ /ERR $\alpha$ complex. <b>2011</b> , 108, 18678-83	49
1293	Structural basis for hemoglobin capture by Staphylococcus aureus cell-surface protein, IsdH. <b>2011</b> , 286, 38439-38447	47
1292	RNase Y in Bacillus subtilis: a Natively disordered protein that is the functional equivalent of RNase E from Escherichia coli. <b>2011</b> , 193, 5431-41	80
1291	Calcium-induced folding of intrinsically disordered repeat-in-toxin (RTX) motifs via changes of protein charges and oligomerization states. <b>2011</b> , 286, 16997-7004	41
1290	Tapasin dependence of major histocompatibility complex class I molecules correlates with their conformational flexibility. <b>2011</b> , 25, 3989-98	54
1289	An intrinsically disordered C terminus allows the La protein to assist the biogenesis of diverse noncoding RNA precursors. <b>2011</b> , 108, 1308-13	35
1288	Mapping backbone and side-chain interactions in the transition state of a coupled protein folding and binding reaction. <b>2011</b> , 108, 3952-7	100
1287	Intrinsic disorder in measles virus nucleocapsids. <b>2011</b> , 108, 9839-44	151
1286	Tunable membrane binding of the intrinsically disordered dehydrin Lti30, a cold-induced plant stress protein. <b>2011</b> , 23, 2391-404	119
1285	CSpritz: accurate prediction of protein disorder segments with annotation for homology, secondary structure and linear motifs. <b>2011</b> , 39, W190-6	66
1284	Binding free energy landscape of domain-peptide interactions. <b>2011</b> , 7, e1002131	17
1283	Coupled folding and specific binding: fishing for amphiphilicity. <b>2011</b> , 12, 1431-50	11
1282	BIM(EL), an intrinsically disordered protein, is degraded by 20S proteasomes in the absence of poly-ubiquitylation. <b>2011</b> , 124, 969-77	59
1281	Multi-scaled explorations of binding-induced folding of intrinsically disordered protein inhibitor IA3 to its target enzyme. <b>2011</b> , 7, e1001118	64
1280	Proteins with complex architecture as potential targets for drug design: a case study of Mycobacterium tuberculosis. <b>2011</b> , 7, e1002118	17
1279	Bacteriophage assembly. <b>2011</b> , 3, 172-203	88
1278	Anchoring intrinsically disordered proteins to multiple targets: lessons from N-terminus of the p53 protein. <b>2011</b> , 12, 1410-30	19
1277	The dark sides of capillary morphogenesis gene 2. <b>2012</b> , 31, 3-13	58

1276	A flexible brace maintains the assembly of a hexameric replicative helicase during DNA unwinding. <b>2012</b> , 40, 2271-83	12
1275	Mutual synergistic protein folding in split intein. <b>2012</b> , 32, 433-42	15
1274	Order-disorder transitions govern kinetic cooperativity and allostery of monomeric human glucokinase. <b>2012</b> , 10, e1001452	43
1273	A preformed binding interface in the unbound ensemble of an intrinsically disordered protein: evidence from molecular simulations. <b>2012</b> , 8, e1002605	98
1272	A general G1/S-phase cell-cycle control module in the flowering plant <i>Arabidopsis thaliana</i> . <b>2012</b> , 8, e1002847	86
1271	Phosphorylation of intrinsically disordered regions in remorin proteins. <b>2012</b> , 3, 86	38
1270	Intramolecular interactions stabilizing compact conformations of the intrinsically disordered kinase-inhibitor domain of Sic1: a molecular dynamics investigation. <b>2012</b> , 3, 435	25
1269	Proteome-wide discovery of evolutionary conserved sequences in disordered regions. <b>2012</b> , 5, rs1	76
1268	Evolution of the hepatitis E virus polyproline region: order from disorder. <b>2012</b> , 86, 10186-93	22
1267	IDEAL: Intrinsically Disordered proteins with Extensive Annotations and Literature. <b>2012</b> , 40, D507-11	68
1266	Identification of a Skp1-like protein interacting with SFB, the pollen S determinant of the gametophytic self-incompatibility in <i>Prunus</i> . <b>2012</b> , 159, 1252-62	35
1265	Evolution of viral proteins originated de novo by overprinting. <b>2012</b> , 29, 3767-80	95
1264	Engineering and therapeutic application of single-chain bivalent TGF- $\beta$ family traps. <b>2012</b> , 11, 1477-87	14
1263	The Roles of MDM2 and MDMX Phosphorylation in Stress Signaling to p53. <b>2012</b> , 3, 274-82	19
1262	Oxidized base damage and single-strand break repair in mammalian genomes: role of disordered regions and posttranslational modifications in early enzymes. <b>2012</b> , 110, 123-53	55
1261	From A to B: a ride in the free energy surfaces of protein G domains suggests how new folds arise. <b>2012</b> , 136, 185101	8
1260	Structural biology. Versatility from protein disorder. <b>2012</b> , 337, 1460-1	163
1259	Differential transit peptide recognition during preprotein binding and translocation into flowering plant plastids. <b>2012</b> , 24, 3040-59	38

1258	The stability of the small nucleolar ribonucleoprotein (snoRNP) assembly protein Pih1 in <i>Saccharomyces cerevisiae</i> is modulated by its C terminus. <b>2012</b> , 287, 43205-14	19
1257	Syntenin-mediated regulation of Sox4 proteasomal degradation modulates transcriptional output. <b>2012</b> , 31, 2668-79	35
1256	The zinc regulated antivirulence pathway of <i>Salmonella</i> is a multiprotein immunoglobulin adhesion system. <b>2012</b> , 287, 32324-37	10
1255	The role of structural disorder in the rewiring of protein interactions through evolution. <b>2012</b> , 11, M111.014969	8
1254	DIP database of disordered protein predictions. <b>2013</b> , 41, D508-16	398
1253	Domain-domain interactions in full-length p53 and a specific DNA complex probed by methyl NMR spectroscopy. <b>2012</b> , 109, 15752-6	29
1252	NOT THAT RIGID MIDGETS AND NOT SO FLEXIBLE GIANTS: ON THE ABUNDANCE AND ROLES OF INTRINSIC DISORDER IN SHORT AND LONG PROTEINS. <b>2012</b> , 20, 471-511	16
1251	An intrinsically disordered protein, CP12: jack of all trades and master of the Calvin cycle. <b>2012</b> , 40, 995-9	50
1250	Dynamics and adaptive benefits of protein domain emergence and arrangements during plant genome evolution. <b>2012</b> , 4, 316-29	50
1249	Regulation of estrogen receptor N-terminus conformation and function by peptidyl prolyl isomerase Pin1. <b>2012</b> , 32, 445-57	58
1248	A vitellogenin polyserine cleavage site: highly disordered conformation protected from proteolysis by phosphorylation. <b>2012</b> , 215, 1837-46	14
1247	Determinants of exon-level evolutionary rates in <i>Arabidopsis</i> species. <b>2012</b> , 8, 389-415	3
1246	The N terminus and C terminus of herpes simplex virus 1 ICP4 cooperate to activate viral gene expression. <b>2012</b> , 86, 6862-74	13
1245	Structural disorder in eukaryotes. <b>2012</b> , 7, e34687	141
1244	Transcriptional activation by mitochondrial transcription factor A involves preferential distortion of promoter DNA. <b>2012</b> , 40, 614-24	51
1243	Functional transcriptional regulatory sequence (TRS) RNA binding and helix destabilizing determinants of murine hepatitis virus (MHV) nucleocapsid (N) protein. <b>2012</b> , 287, 7063-73	36
1242	Fast association and slow transitions in the interaction between two intrinsically disordered protein domains. <b>2012</b> , 287, 34316-24	72
1241	Transient structure and dynamics in the disordered c-Myc transactivation domain affect Bin1 binding. <b>2012</b> , 40, 6353-66	75

1240	The gateway to chloroplast: re-defining the function of chloroplast receptor proteins. <b>2012</b> , 393, 1263-77	12
1239	The lysine-rich motif of intrinsically disordered stress protein CDeT11-24 from <i>Craterostigma plantagineum</i> is responsible for phosphatidic acid binding and protection of enzymes from damaging effects caused by desiccation. <b>2012</b> , 63, 4919-29	39
1238	Thermodynamic dissection of the intrinsically disordered N-terminal domain of human glucocorticoid receptor. <b>2012</b> , 287, 26777-87	37
1237	Defining the functional footprint for recognition and repair of deaminated DNA. <b>2012</b> , 40, 11638-47	11
1236	Structural and functional analyses of the interaction of archaeal RNA polymerase with DNA. <b>2012</b> , 40, 9941-52	26
1235	Local flexibility facilitates oxidization of buried methionine residues. <b>2012</b> , 19, 688-97	21
1234	Editorial: intrinsically disordered proteins: a focused look at fuzzy subjects. <b>2012</b> , 13, 2-5	1
1233	How random are intrinsically disordered proteins? A small angle scattering perspective. <b>2012</b> , 13, 55-75	225
1232	Computational modelling of linear motif-mediated protein interactions. <b>2012</b> , 12, 1553-61	8
1231	The role of intrinsically disordered regions in the structure and functioning of small heat shock proteins. <b>2012</b> , 13, 76-85	62
1230	The complex of G protein regulator RGS9-2 and G $\alpha$ (5) controls sensitization and signaling kinetics of type 5 adenylyl cyclase in the striatum. <b>2012</b> , 5, ra63	38
1229	Comprehensive comparative assessment of in-silico predictors of disordered regions. <b>2012</b> , 13, 6-18	143
1228	Secondary Structure and Dynamics of a Family of Disordered Proteins. <b>2012</b> , 221-238	
1227	Structure and dynamic properties of membrane proteins using NMR. <b>2012</b> , 2, 1491-539	4
1226	Intrinsically disordered proteins: a 10-year recap. <b>2012</b> , 37, 509-16	451
1225	Small-molecule inhibition of c-MYC:MAX leucine zipper formation is revealed by ion mobility mass spectrometry. <b>2012</b> , 134, 19384-92	46
1224	Contribution of hydrophobic interactions to the folding and fibrillation of histone H1 and its carboxy-terminal domain. <b>2012</b> , 180, 101-9	9
1223	Intrinsically disordered proteins: lessons from colicins. <b>2012</b> , 40, 1534-8	7

1222	Crystallization and preliminary X-ray diffraction analysis of tau protein microtubule-binding motifs in complex with Tau5 and DC25 antibody Fab fragments. <b>2012</b> , 68, 1181-5	6
1221	Crystallization and preliminary X-ray diffraction analysis of two peptides from Alzheimer PHF in complex with the MN423 antibody Fab fragment. <b>2012</b> , 68, 1186-90	1
1220	NMR investigations of the dual targeting peptide of Thr-tRNA synthetase and its interaction with the mitochondrial Tom20 receptor in Arabidopsis thaliana. <b>2012</b> , 279, 3738-3748	4
1219	Is a malleable protein necessarily highly dynamic? The hydrophobic core of the nuclear coactivator binding domain is well ordered. <b>2012</b> , 102, 1627-35	17
1218	Role of the AAA protease Yme1 in folding of proteins in the intermembrane space of mitochondria. <b>2012</b> , 23, 4335-46	39
1217	The intrinsically disordered N-terminal region of AtREM1.3 remorin protein mediates protein-protein interactions. <b>2012</b> , 287, 39982-91	48
1216	Intrinsically disordered proteins and novel strategies for drug discovery. <b>2012</b> , 7, 475-88	78
1215	Intrinsically Disordered Proteins. <b>2012</b> , 136-152	5
1214	Further optimization of a hybrid united-atom and coarse-grained force field for folding simulations: Improved backbone hydration and interactions between charged side chains. <b>2012</b> , 8, 4413-4424	95
1213	Inhibition of human papillomavirus DNA replication by an E1-derived p80/UAF1-binding peptide. <b>2012</b> , 86, 3486-500	15
1212	The diacylglycerol lipases: structure, regulation and roles in and beyond endocannabinoid signalling. <b>2012</b> , 367, 3264-75	93
1211	A molecular analysis of desiccation tolerance mechanisms in the anhydrobiotic nematode Panagrolaimus superbus using expressed sequenced tags. <b>2012</b> , 5, 68	32
1210	Determination of secondary structure populations in disordered states of proteins using nuclear magnetic resonance chemical shifts. <b>2012</b> , 51, 2224-31	258
1209	Disorder-to-order transition of an intrinsically disordered region of sortase revealed by multiscale enhanced sampling. <b>2012</b> , 134, 7094-101	55
1208	Site-specific phosphorylation protects glycogen synthase kinase-3 $\beta$ from calpain-mediated truncation of its N and C termini. <b>2012</b> , 287, 22521-32	22
1207	Sekikaic Acid and Lobaric Acid Target a Dynamic Interface of the Coactivator CBP/p300. <b>2012</b> , 124, 11420-11424	43
1206	Sekikaic acid and lobaric acid target a dynamic interface of the coactivator CBP/p300. <b>2012</b> , 51, 11258-62	47
1205	When a domain is not a domain, and why it is important to properly filter proteins in databases: conflicting definitions and fold classification systems for structural domains make filtering of such databases imperative. <b>2012</b> , 34, 1060-9	5



1204	Detection of disordered regions in globular proteins using $^{13}\text{C}$ -detected NMR. <b>2012</b> , 21, 1954-60	8
1203	A comparative proteomic approach to analyse structure, function and evolution of rice chitinases: a step towards increasing plant fungal resistance. <b>2012</b> , 18, 4761-80	9
1202	Speeding up sequence specific assignment of IDPs. <b>2012</b> , 53, 293-301	63
1201	Deuterium isotope shifts for backbone $^1\text{H}$ , $^{15}\text{N}$ and $^{13}\text{C}$ nuclei in intrinsically disordered protein $\beta$ -synuclein. <b>2012</b> , 54, 181-91	33
1200	Modularity and functional plasticity of scaffold proteins as p(l)acemakers in cell signaling. <b>2012</b> , 24, 2143-65	60
1199	Novel insights through the integration of structural and functional genomics data with protein networks. <b>2012</b> , 179, 320-6	16
1198	High-throughput characterization of intrinsic disorder in proteins from the Protein Structure Initiative. <b>2012</b> , 180, 201-15	31
1197	Comparative nucleic acid chaperone properties of the nucleocapsid protein NCp7 and Tat protein of HIV-1. <b>2012</b> , 169, 349-60	23
1196	Thermodynamic and Kinetic Models for Aggregation of Intrinsically Disordered Proteins. <b>2012</b> , 413-440	1
1195	Occurrence of disordered patterns and homorepeats in eukaryotic and bacterial proteomes. <b>2012</b> , 8, 327-37	25
1194	Compaction and binding properties of the intrinsically disordered C-terminal domain of Henipavirus nucleoprotein as unveiled by deletion studies. <b>2012</b> , 8, 392-410	38
1193	Understanding the structural ensembles of a highly extended disordered protein. <b>2012</b> , 8, 308-19	31
1192	Intrinsic disorder in the androgen receptor: identification, characterisation and drugability. <b>2012</b> , 8, 82-90	54
1191	Correlation of disorder between <i>S. cerevisiae</i> interacting proteins. <b>2012</b> , 8, 417-25	
1190	Assigning kinetic 3D-signatures to glycocodes. <b>2012</b> , 14, 5843-8	16
1189	A comprehensive overview of computational protein disorder prediction methods. <b>2012</b> , 8, 114-21	79
1188	SLIMPrints: conservation-based discovery of functional motif fingerprints in intrinsically disordered protein regions. <b>2012</b> , 40, 10628-41	57
1187	Attributes of short linear motifs. <b>2012</b> , 8, 268-81	362

1186	Uncertainty analysis in protein disorder prediction. <b>2012</b> , 8, 381-91	14
1185	The roles of intrinsic disorder in orchestrating the Wnt-pathway. <b>2012</b> , 29, 843-61	37
1184	Reduced dimensionality (4,3)D-HN(C)NH for rapid assignment of 1H(N)-15N HSQC peaks in proteins: an analytical tool for protein folding, proteomics, and drug discovery programs. <b>2012</b> , 84, 10404-10	6
1183	The neuroendocrine protein 7B2 is intrinsically disordered. <b>2012</b> , 51, 7456-64	7
1182	Investigation of the Polymeric Properties of $\beta$ -Synuclein and Comparison with NMR Experiments: A Replica Exchange Molecular Dynamics Study. <b>2012</b> , 8, 3929-3942	28
1181	Mapping the potential energy landscape of intrinsically disordered proteins at amino acid resolution. <b>2012</b> , 134, 15138-48	91
1180	Hydrophobic moments, shape, and packing in disordered proteins. <b>2012</b> , 116, 6326-35	13
1179	Intrinsically disordered N-terminus of calponin homology-associated smooth muscle protein (CHASM) interacts with the calponin homology domain to enable tropomyosin binding. <b>2012</b> , 51, 2694-705	8
1178	Mutation of Ser-50 and Cys-66 in Snapin modulates protein structure and stability. <b>2012</b> , 51, 3470-84	6
1177	Side-chain interactions form late and cooperatively in the binding reaction between disordered peptides and PDZ domains. <b>2012</b> , 134, 599-605	35
1176	Self-assembly of flexible $\beta$ -strands into immobile amyloid-like $\beta$ -sheets in membranes as revealed by solid-state 19F NMR. <b>2012</b> , 134, 6512-5	70
1175	Mechanism of cell cycle entry mediated by the intrinsically disordered protein p27(Kip1). <b>2012</b> , 7, 678-82	26
1174	End effects influence short model peptide conformation. <b>2012</b> , 134, 1571-6	30
1173	Small terminase couples viral DNA binding to genome-packaging ATPase activity. <b>2012</b> , 20, 1403-13	43
1172	Evaluation of thymosin $\beta$ 4 in the regulation of epithelial-mesenchymal transformation in urothelial carcinoma. <b>2012</b> , 30, 167-76	18
1171	Profiling the dynamic interfaces of fluorinated transcription complexes for ligand discovery and characterization. <b>2012</b> , 7, 1345-50	49
1170	Nuclear transport receptor binding avidity triggers a self-healing collapse transition in FG-nucleoporin molecular brushes. <b>2012</b> , 109, 16911-6	78
1169	Tertiary structure-function analysis reveals the pathogenic signaling potentiation mechanism of <i>Helicobacter pylori</i> oncogenic effector CagA. <b>2012</b> , 12, 20-33	112

1168	Cell signaling, post-translational protein modifications and NMR spectroscopy. <b>2012</b> , 54, 217-36	129
1167	Influence of 63Ser phosphorylation and dephosphorylation on the structure of the stathmin helical nucleation sequence: a molecular dynamics study. <b>2012</b> , 51, 8455-63	7
1166	Homotropic allosteric regulation in monomeric mammalian glucokinase. <b>2012</b> , 519, 103-11	33
1165	Towards the physical basis of how intrinsic disorder mediates protein function. <b>2012</b> , 524, 123-31	67
1164	Prediction of short linear protein binding regions. <b>2012</b> , 415, 193-204	57
1163	N-terminal segments modulate the helical propensities of the intrinsically disordered basic regions of bZIP proteins. <b>2012</b> , 416, 287-99	48
1162	The transthyretin amyloidoses: from delineating the molecular mechanism of aggregation linked to pathology to a regulatory-agency-approved drug. <b>2012</b> , 421, 185-203	227
1161	Kinetic basis for the competitive recruitment of TolB by the intrinsically disordered translocation domain of colicin E9. <b>2012</b> , 418, 269-80	21
1160	The transition state of coupled folding and binding for a flexible $\beta$ -finger. <b>2012</b> , 417, 253-61	34
1159	Disordered competitive recruiter: fast and foldable. <b>2012</b> , 418, 267-8	20
1158	Electrostatically accelerated coupled binding and folding of intrinsically disordered proteins. <b>2012</b> , 422, 674-684	60
1157	Tissue-specific splicing of disordered segments that embed binding motifs rewires protein interaction networks. <b>2012</b> , 46, 871-83	272
1156	A mutually inhibitory feedback loop between the 20S proteasome and its regulator, NQO1. <b>2012</b> , 47, 76-86	81
1155	C-Terminal acidic domain of ubiquitin-conjugating enzymes: a multi-functional conserved intrinsically disordered domain in family 3 of E2 enzymes. <b>2012</b> , 178, 245-59	16
1154	$\beta$ -Synuclein misfolding and Parkinson's disease. <b>2012</b> , 1822, 261-85	406
1153	Ascending the nucleosome face: recognition and function of structured domains in the histone H2A-H2B dimer. <b>2012</b> , 1819, 892-901	19
1152	Biophysical studies with AICD-47 reveal unique binding behavior characteristic of an unfolded domain. <b>2012</b> , 425, 201-6	2
1151	Structural disorder in proteins brings order to crystal growth in biomineralization. <b>2012</b> , 51, 528-34	91

1150	Role of the biomolecular energy gap in protein design, structure, and evolution. <b>2012</b> , 149, 262-73	83
1149	Insights into RNA biology from an atlas of mammalian mRNA-binding proteins. <b>2012</b> , 149, 1393-406	1328
1148	A dynamic C-terminal segment in the Mycobacterium tuberculosis Mn/Fe R2lox protein can adopt a helical structure with possible functional consequences. <b>2012</b> , 9, 1981-8	2
1147	Loops and repeats in proteins as footprints of molecular evolution. <b>2012</b> , 77, 1487-99	5
1146	Protein disorder in plants: a view from the chloroplast. <b>2012</b> , 12, 165	23
1145	Lipid Metabolism in Neurodegenerative Diseases. <b>2012</b> , 269-296	1
1144	Introduction to genome biology: features, processes, and structures. <b>2012</b> , 855, 3-49	1
1143	Mutual effects of disorder and order in fusion proteins between intrinsically disordered domains and fluorescent proteins. <b>2012</b> , 8, 105-13	3
1142	Competitive binding between dynamic p53 transactivation subdomains to human MDM2 protein: implications for regulating the p53/MDM2/MDMX interaction. <b>2012</b> , 287, 30376-84	19
1141	Fuzziness: linking regulation to protein dynamics. <b>2012</b> , 8, 168-77	128
1140	Searching for the Holy Grail; protein-protein interaction analysis and modulation. <b>2012</b> , 13, 877-9	17
1139	3.5 Characterization of the Denatured State. <b>2012</b> , 72-114	4
1138	3.9 Intrinsically Disordered Proteins. <b>2012</b> , 170-211	0
1137	Why are we Interested in the Unfolded Peptides and Proteins?. <b>2012</b> , 1-54	4
1136	On the supertertiary structure of proteins. <b>2012</b> , 8, 597-600	53
1135	Regulation of protein phosphatase 1 by intrinsically disordered proteins. <b>2012</b> , 40, 969-74	32
1134	Measurement and analysis of NMR residual dipolar couplings for the study of intrinsically disordered proteins. <b>2012</b> , 895, 115-25	9
1133	Using chemical shifts to assess transient secondary structure and generate ensemble structures of intrinsically disordered proteins. <b>2012</b> , 895, 139-52	11

1132	The measles virus N(TAIL)-XD complex: an illustrative example of fuzziness. <b>2012</b> , 725, 126-41	19
1131	Trifluoromethyl-Substituted $\beta$ -Amino Acids as Solid-State $^{19}\text{F}$ NMR Labels for Structural Studies of Membrane-Bound Peptides. <b>2012</b> , 91-138	20
1130	Structural characterization of intrinsically disordered proteins by the combined use of NMR and SAXS. <b>2012</b> , 40, 955-62	65
1129	The N-terminal ectodomain of Ninjurin1 liberated by MMP9 has chemotactic activity. <b>2012</b> , 428, 438-44	11
1128	Coupled folding-binding in a hydrophobic/polar protein model: impact of synergistic folding and disordered flanks. <b>2012</b> , 102, 569-78	29
1127	A delicate interplay of structure, dynamics, and thermodynamics for function: a high pressure NMR study of outer surface protein A. <b>2012</b> , 102, 916-26	33
1126	Low folding cooperativity of HP35 revealed by single-molecule force spectroscopy and molecular dynamics simulation. <b>2012</b> , 102, 1944-51	14
1125	Structural role of RKS motifs in chromatin interactions: a molecular dynamics study of HP1 bound to a variably modified histone tail. <b>2012</b> , 102, 1926-33	34
1124	Analysis of the relationships between evolvability, thermodynamics, and the functions of intrinsically disordered proteins/regions. <b>2012</b> , 41, 51-7	13
1123	Bromodomains: a new target class for small molecule drug discovery. <b>2012</b> , 9, e111-e120	25
1122	Enterohaemorrhagic Escherichia coli exploits a tryptophan switch to hijack host f-actin assembly. <b>2012</b> , 20, 1692-703	26
1121	Order by disorder in plant signaling. <b>2012</b> , 17, 625-32	51
1120	High-pressure macromolecular crystallography and NMR: status, achievements and prospects. <b>2012</b> , 22, 636-42	51
1119	Ensemble structure of the modular and flexible full-length vesicular stomatitis virus phosphoprotein. <b>2012</b> , 423, 182-97	33
1118	Small molecule bromodomain inhibitors: extending the druggable genome. <b>2012</b> , 51, 1-55	35
1117	Single-molecule force spectroscopy of chimeric polyprotein constructs containing intrinsically disordered domains. <b>2012</b> , 896, 47-56	4
1116	Characterization of oligomerization-aggregation products of neurodegenerative target proteins by ion mobility mass spectrometry. <b>2012</b> , 896, 399-412	10
1115	Selective isotope labeling of recombinant proteins in Escherichia coli. <b>2012</b> , 896, 439-48	4

1114	HAMLET: functional properties and therapeutic potential. <b>2012</b> , 8, 1301-13	21
1113	Cell cycle regulation by the intrinsically disordered proteins p21 and p27. <b>2012</b> , 40, 981-8	149
1112	Tooth-Inspired Nanocomposites. <b>2012</b> ,	
1111	Molecular dynamics simulation in virus research. <b>2012</b> , 3, 258	36
1110	Influence of serum proteins on conformation of prostate-specific antigen. <b>2012</b> , 29, 1051-64	16
1109	Disease mutations in disordered regions--exception to the rule?. <b>2012</b> , 8, 27-32	64
1108	Intrinsically disordered regions as affinity tuners in protein-DNA interactions. <b>2012</b> , 8, 47-57	147
1107	Roles of intrinsic disorder in protein-nucleic acid interactions. <b>2012</b> , 8, 97-104	60
1106	Synergistic folding of two intrinsically disordered proteins: searching for conformational selection. <b>2012</b> , 8, 198-209	47
1105	Aromatic residues link binding and function of intrinsically disordered proteins. <b>2012</b> , 8, 237-46	24
1104	Is there a biological cost of protein disorder? Analysis of cancer-associated mutations. <b>2012</b> , 8, 296-307	40
1103	Intrinsic protein disorder in human pathways. <b>2012</b> , 8, 320-6	12
1102	Structural modelling pipelines in next generation sequencing projects. <b>2012</b> , 89, 117-67	15
1101	Expedient chemical synthesis of 75mer DNA binding domain of MafA: an insight on its binding to insulin enhancer. <b>2012</b> , 43, 1995-2003	26
1100	An omics perspective of protein disorder. <b>2012</b> , 8, 185-93	10
1099	In silico strategies toward enzyme function and dynamics. <b>2012</b> , 87, 249-92	2
1098	Novel Sampling Approaches in Higher Dimensional NMR. <b>2012</b> ,	13
1097	Intrinsically Disordered Protein Analysis. <b>2012</b> ,	8

1096	TANGLE: two-level support vector regression approach for protein backbone torsion angle prediction from primary sequences. <b>2012</b> , 7, e30361	30
1095	Inherent structural disorder and dimerisation of murine norovirus NS1-2 protein. <b>2012</b> , 7, e30534	24
1094	Free cysteine modulates the conformation of human C/EBP homologous protein. <b>2012</b> , 7, e34680	3
1093	The hepatitis E virus polyproline region is involved in viral adaptation. <b>2012</b> , 7, e35974	59
1092	VAPC, an human endogenous inhibitor for hepatitis C virus (HCV) infection, is intrinsically unstructured but forms a "fuzzy complex" with HCV NS5B. <b>2012</b> , 7, e40341	10
1091	The impact of small molecule binding on the energy landscape of the intrinsically disordered protein C-myc. <b>2012</b> , 7, e41070	51
1090	GAGE cancer-germline antigens are recruited to the nuclear envelope by germ cell-less (GCL). <b>2012</b> , 7, e45819	13
1089	Disordered binding regions and linear motifs—bridging the gap between two models of molecular recognition. <b>2012</b> , 7, e46829	49
1088	Computational prediction of protein-protein interactions in Leishmania predicted proteomes. <b>2012</b> , 7, e51304	26
1087	Structure and pathology of tau protein in Alzheimer disease. <b>2012</b> , 2012, 731526	200
1086	Applications of Bioinformatics and Experimental Methods to Intrinsic Disorder-Based Protein-Protein Interactions. <b>2012</b> ,	1
1085	NEURODEGENERATIVE DISEASES AND TAU: PATHOLOGICAL EVENTS AND MOLECULAR TARGETS. <b>2012</b> ,	
1084	Folding of Intrinsically Disordered Protein Phosphatase 1 Regulatory Proteins. <b>2012</b> , 2, 107-114	9
1083	Surf the post-translational modification network of p53 regulation. <b>2012</b> , 8, 672-84	159
1082	Prediction of protein-protein binding free energies. <b>2012</b> , 21, 396-404	58
1081	Representing and comparing protein folds and fold families using three-dimensional shape-density representations. <b>2012</b> , 80, 530-45	6
1080	The N-terminal domains of SOCS proteins: a conserved region in the disordered N-termini of SOCS4 and 5. <b>2012</b> , 80, 946-57	32
1079	In vivo protein complex topologies: sights through a cross-linking lens. <b>2012</b> , 12, 1565-75	62

1078	Coil-to-helix transitions in intrinsically disordered methyl CpG binding protein 2 and its isolated domains. <b>2012</b> , 21, 531-8	21
1077	Kinesin tail domains are intrinsically disordered. <b>2012</b> , 80, 2437-46	14
1076	Carbon-Detected (15)N NMR Spin Relaxation of an Intrinsically Disordered Protein: FCP1 Dynamics Unbound and in Complex with RAP74. <b>2012</b> , 3, 1409-13	23
1075	Linked Landscapes and Conformational Conversions: How Proteins Fold and Misfold. <b>2012</b> , 1-16	
1074	Spatial and temporal organization of multi-protein assemblies: achieving sensitive control in information-rich cell-regulatory systems. <b>2012</b> , 370, 3023-39	22
1073	High-speed atomic force microscopy coming of age. <b>2012</b> , 23, 062001	252
1072	Unmasking functional motifs within disordered regions of proteins. <b>2012</b> , 5, pe17	19
1071	How a single residue in individual $\beta$ -thymosin/WH2 domains controls their functions in actin assembly. <b>2012</b> , 31, 1000-13	45
1070	Intrinsic protein flexibility in regulation of cell proliferation: advantages for signaling and opportunities for novel therapeutics. <b>2012</b> , 725, 27-49	25
1069	Coexistence of phases in a protein heterodimer. <b>2012</b> , 137, 035101	19
1068	Meta-structure correlation in protein space unveils different selection rules for folded and intrinsically disordered proteins. <b>2012</b> , 8, 411-6	11
1067	High-yield Escherichia coli-based cell-free expression of human proteins. <b>2012</b> , 53, 43-51	23
1066	How do dynamic cellular signals travel long distances?. <b>2012</b> , 8, 22-6	28
1065	Orderly order in protein intrinsic disorder distribution: disorder in 3500 proteomes from viruses and the three domains of life. <b>2012</b> , 30, 137-49	370
1064	Intrinsically disordered proteins: from sequence and conformational properties toward drug discovery. <b>2012</b> , 13, 930-50	74
1063	Flexible-meccano: a tool for the generation of explicit ensemble descriptions of intrinsically disordered proteins and their associated experimental observables. <b>2012</b> , 28, 1463-70	236
1062	Towards a robust description of intrinsic protein disorder using nuclear magnetic resonance spectroscopy. <b>2012</b> , 8, 58-68	84
1061	Conformational selection and folding-upon-binding of intrinsically disordered protein CP12 regulate photosynthetic enzymes assembly. <b>2012</b> , 287, 21372-83	48



1060	The imprinted NPAP1/C15orf2 gene in the Prader-Willi syndrome region encodes a nuclear pore complex associated protein. <b>2012</b> , 21, 4038-48	21
1059	High dimensional and high resolution pulse sequences for backbone resonance assignment of intrinsically disordered proteins. <b>2012</b> , 52, 329-37	48
1058	4D non-uniformly sampled HCBCACON and $\square$ (NC)-selective HCBCANCO experiments for the sequential assignment and chemical shift analysis of intrinsically disordered proteins. <b>2012</b> , 53, 139-48	36
1057	Evolution of immunity: no development without risk. <b>2012</b> , 52, 176-81	5
1056	Protein Folding in the 2D Hydrophobic $\square$ Hydrophilic (HP) Square Lattice Model is Chaotic. <b>2012</b> , 4, 98-114	6
1055	The short form of the recombinant CAL-A-type lipase UM03410 from the smut fungus Ustilago maydis exhibits an inherent trans-fatty acid selectivity. <b>2012</b> , 94, 141-50	18
1054	A comparison of Frost expression among species and life stages of Drosophila. <b>2012</b> , 21, 31-9	16
1053	Computational approaches to the interpretation of NMR data for studying protein dynamics. <b>2012</b> , 396, 124-134	8
1052	Polyethylene glycol-based protein nanocapsules for functional delivery of a differentiation transcription factor. <b>2012</b> , 33, 5459-67	17
1051	Motif switches: decision-making in cell regulation. <b>2012</b> , 22, 378-85	107
1050	Suppression of sampling artefacts in high-resolution four-dimensional NMR spectra using signal separation algorithm. <b>2012</b> , 214, 91-102	43
1049	Intrinsic disorder in cell signaling and gene transcription. <b>2012</b> , 348, 457-65	87
1048	Structural and functional analysis of domains of the progesterone receptor. <b>2012</b> , 348, 418-29	62
1047	A protein export pathway involving Escherichia coli porins. <b>2012</b> , 20, 1154-66	37
1046	Intrinsic disorder: signaling via highly specific but short-lived association. <b>2012</b> , 37, 43-8	109
1045	Disordered proteins studied by chemical shifts. <b>2012</b> , 60, 42-51	48
1044	BQP35 is a novel member of the intrinsically unstructured protein (IUP) family which is a potential antigen for the sero-diagnosis of Babesia sp. BQ1 (Lintan) infection. <b>2012</b> , 187, 421-30	7
1043	Specific domains of FoxD4/5 activate and repress neural transcription factor genes to control the progression of immature neural ectoderm to differentiating neural plate. <b>2012</b> , 365, 363-75	23

1042	Fused in sarcoma (FUS) interacts with the cytolinker protein plectin: implications for FUS subcellular localization and function. <b>2012</b> , 318, 653-61	9
1041	The secondary structure of peptides derived from the third intracellular loop of the serpentine-type receptors and its interrelation with their biological activity. <b>2012</b> , 6, 197-210	1
1040	Linker histone H1 stimulates DNA strand exchange between short oligonucleotides retaining high sensitivity to heterology. <b>2012</b> , 97, 229-39	4
1039	Drug design for ever, from hype to hope. <b>2012</b> , 26, 137-50	29
1038	Efficient sequential assignments in proteins with reduced dimensionality 3D HN(CA)NH. <b>2012</b> , 52, 115-26	13
1037	Temperature and solvent dependence of the dynamical landscape of tau protein conformations. <b>2012</b> , 38, 169-79	8
1036	Unraveling the Helicobacter pylori UreG zinc binding site using X-ray absorption spectroscopy (XAS) and structural modeling. <b>2012</b> , 17, 353-61	31
1035	Structural basis for protein phosphatase 1 regulation and specificity. <b>2013</b> , 280, 596-611	144
1034	NMR determines transient structure and dynamics in the disordered C-terminal domain of WASp interacting protein. <b>2013</b> , 105, 481-93	21
1033	Thermodynamics of binding by calmodulin correlates with target peptide $\alpha$ helical propensity. <b>2013</b> , 81, 607-12	18
1032	Transcriptional/epigenetic regulator CBP/p300 in tumorigenesis: structural and functional versatility in target recognition. <b>2013</b> , 70, 3989-4008	198
1031	Nucleolar scaffold protein, WDR46, determines the granular compartmental localization of nucleolin and DDX21. <b>2013</b> , 18, 780-97	12
1030	Encyclopedia of Biophysics. <b>2013</b> , 316-317	
1029	Probing local backbone geometries in intrinsically disordered proteins by cross-correlated NMR relaxation. <b>2013</b> , 52, 4604-6	13
1028	The RNA-binding protein repertoire of embryonic stem cells. <b>2013</b> , 20, 1122-30	320
1027	Intrinsic disorder of the bacterial cell division protein ZipA: coil-to-brush conformational transition. <b>2013</b> , 27, 3363-75	18
1026	Modulation of the intrinsic helix propensity of an intrinsically disordered protein reveals long-range helix-helix interactions. <b>2013</b> , 135, 10155-63	39
1025	When "IUPs" were "BAPs": How to study the nonconformation of intrinsically unfolded polyaminoacid chains. <b>2013</b> , 100, 592-600	6

1024	Role of osteopontin in modulation of hydroxyapatite formation. <b>2013</b> , 93, 348-54	93
1023	IsUnstruct: prediction of the residue status to be ordered or disordered in the protein chain by a method based on the Ising model. <b>2013</b> , 31, 1034-43	35
1022	Phylogenetic patterns of emergence of new genes support a model of frequent de novo evolution. <b>2013</b> , 14, 117	158
1021	Repeat-encoded poly-Q tracts show statistical commonalities across species. <b>2013</b> , 14, 76	6
1020	Chemical shift prediction for denatured proteins. <b>2013</b> , 55, 201-9	16
1019	Membrane Proteins. <b>2013</b> ,	3
1018	Unfolded protein ensembles, folding trajectories, and refolding rate prediction. <b>2013</b> , 139, 121925	6
1017	A conserved N-terminal motif is required for complex formation between FUS, EWSR1, TAF15 and their oncogenic fusion proteins. <b>2013</b> , 27, 4965-74	22
1016	Prediction and design of outer membrane protein-protein interactions. <b>2013</b> , 1063, 183-96	3
1015	Intrinsic Disorder in the Kinesin Superfamily. <b>2013</b> , 5, 233	14
1014	Analyzing the Solution State of Protein Structure, Interactions, and Ligands by Spectroscopic Methods. <b>2013</b> , 73-98	3
1013	Conformational entropy of intrinsically disordered protein. <b>2013</b> , 117, 5503-9	25
1012	Bacterial EPIYA effectors--where do they come from? What are they? Where are they going?. <b>2013</b> , 15, 377-85	39
1011	Structural landscape of the proline-rich domain of Sos1 nucleotide exchange factor. <b>2013</b> , 175-176, 54-62	6
1010	Biochemical characterization of the Caenorhabditis elegans FBF.CPB-1 translational regulation complex identifies conserved protein interaction hotspots. <b>2013</b> , 425, 725-37	11
1009	Exploring the accessible conformations of N-terminal acetylated $\beta$ -synuclein. <b>2013</b> , 587, 1128-38	27
1008	Promiscuity as a functional trait: intrinsically disordered regions as central players of interactomes. <b>2013</b> , 454, 361-9	123
1007	Reduction and expansion in microsporidian genome evolution: new insights from comparative genomics. <b>2013</b> , 5, 2285-303	74

1006	An intrinsically disordered domain has a dual function coupled to compartment-dependent redox control. <b>2013</b> , 425, 594-608	16
1005	Under-folded proteins: Conformational ensembles and their roles in protein folding, function, and pathogenesis. <b>2013</b> , 99, 870-87	33
1004	The conformational ensemble of the disordered and aggregation-protective 182-291 region of ataxin-3. <b>2013</b> , 1830, 5236-47	13
1003	Polyproline-II helix in proteins: structure and function. <b>2013</b> , 425, 2100-32	330
1002	Evolutionary Origin of Orphan Genes. <b>2013</b> ,	5
1001	Arginine and disordered amyloid- $\beta$ peptide structures: molecular level insights into the toxicity in Alzheimer's disease. <b>2013</b> , 4, 1549-58	22
1000	From sequence and forces to structure, function, and evolution of intrinsically disordered proteins. <b>2013</b> , 21, 1492-9	144
999	The conformational landscape of an intrinsically disordered DNA-binding domain of a transcription regulator. <b>2013</b> , 117, 13842-50	19
998	Structural and thermodynamic dissection of linear motif recognition by the E. coli sliding clamp. <b>2013</b> , 56, 8665-73	18
997	Electron microscopy structure of human APC/C(CDH1)-EMI1 reveals multimodal mechanism of E3 ligase shutdown. <b>2013</b> , 20, 827-35	73
996	Vitamin A and retinoid signaling: genomic and nongenomic effects. <b>2013</b> , 54, 1761-75	236
995	Partially disordered proteins studied by ion mobility-mass spectrometry: implications for the preservation of solution phase structure in the gas phase. <b>2013</b> , 85, 10471-8	44
994	Spectrin- and ankyrin-based membrane domains and the evolution of vertebrates. <b>2013</b> , 72, 1-37	99
993	Peptide docking and structure-based characterization of peptide binding: from knowledge to know-how. <b>2013</b> , 23, 894-902	72
992	Inactivation of the bacterial RNA polymerase due to acquisition of secondary structure by the $\beta$ subunit. <b>2013</b> , 288, 25076-25087	17
991	Recent Advances in Solution NMR Studies. <b>2013</b> , 80, 359-418	11
990	Solvent interaction analysis of intrinsically disordered proteins in aqueous two-phase systems. <b>2013</b> , 9, 3068-79	14
989	Conformational Dynamics of the Partially Disordered Yeast Transcription Factor GCN4. <b>2013</b> , 9,	29

988	Structure prediction and analysis of DNA transposon and LINE retrotransposon proteins. <b>2013</b> , 288, 16127-38	10
987	Describing intrinsically disordered proteins at atomic resolution by NMR. <b>2013</b> , 23, 426-35	161
986	HN(CA)N and HN(COCA)N experiments for assignment of large disordered proteins. <b>2013</b> , 57, 83-9	9
985	High-dimensionality <sup>13</sup> C direct-detected NMR experiments for the automatic assignment of intrinsically disordered proteins. <b>2013</b> , 57, 353-61	39
984	Genetic recombination is associated with intrinsic disorder in plant proteomes. <b>2013</b> , 14, 772	15
983	Intrinsically disordered regions of p53 family are highly diversified in evolution. <b>2013</b> , 1834, 725-38	58
982	Molecular crowding stabilizes both the intrinsically disordered calcium-free state and the folded calcium-bound state of a repeat in toxin (RTX) protein. <b>2013</b> , 135, 11929-34	33
981	RNA polymerase II C-terminal domain: Tethering transcription to transcript and template. <b>2013</b> , 113, 8423-55	118
980	Highly sensitive SERS quantification of the oncogenic protein c-Jun in cellular extracts. <b>2013</b> , 135, 10314-7	95
979	Perspective: Reaches of chemical physics in biology. <b>2013</b> , 139, 121701	19
978	Effects of Macromolecular Crowding on the Conformational Ensembles of Disordered Proteins. <b>2013</b> , 4,	44
977	In-depth analysis of hyaline fibromatosis syndrome frameshift mutations at the same site reveal the necessity of personalized therapy. <b>2013</b> , 34, 1005-17	13
976	Protein intrinsic disorder in the acetylome of intracellular and extracellular <i>Toxoplasma gondii</i> . <b>2013</b> , 9, 645-57	39
975	An assignment of intrinsically disordered regions of proteins based on NMR structures. <b>2013</b> , 181, 29-36	22
974	FOXOs: signalling integrators for homeostasis maintenance. <i>Nature Reviews Molecular Cell Biology</i> , <b>2013</b> , 14, 83-97	48.7 664
973	New insights into desiccation-associated gene regulation by <i>Lilium longiflorum</i> ASR during pollen maturation and in transgenic <i>Arabidopsis</i> . <b>2013</b> , 301, 37-94	11
972	Utilization of protein intrinsic disorder knowledge in structural proteomics. <b>2013</b> , 1834, 487-98	46
971	On the functional and structural characterization of hubs in protein-protein interaction networks. <b>2013</b> , 31, 274-86	40

970	Structural ensemble of an intrinsically disordered polypeptide. <b>2013</b> , 117, 118-24	64
969	Characterization of disordered proteins with ENSEMBLE. <b>2013</b> , 29, 398-9	115
968	Energetic basis of uncoupling folding from binding for an intrinsically disordered protein. <b>2013</b> , 135, 1288-94	35
967	Describing sequence-ensemble relationships for intrinsically disordered proteins. <b>2013</b> , 449, 307-18	80
966	Photocrosslinking approaches to interactome mapping. <b>2013</b> , 17, 90-101	93
965	Solution NMR studies of cell-penetrating peptides in model membrane systems. <b>2013</b> , 65, 1002-11	26
964	The quiet renaissance of protein nuclear magnetic resonance. <b>2013</b> , 52, 1303-20	39
963	Exploring the binding diversity of intrinsically disordered proteins involved in one-to-many binding. <b>2013</b> , 22, 258-73	132
962	Direct Prediction of NMR Residual Dipolar Couplings from the Primary Sequence of Unfolded Proteins. <b>2013</b> , 125, 715-718	4
961	Direct prediction of NMR residual dipolar couplings from the primary sequence of unfolded proteins. <b>2013</b> , 52, 687-90	18
960	How is functional specificity achieved through disordered regions of proteins?. <b>2013</b> , 35, 17-22	12
959	Protein dynamics: Complex by itself. <b>2013</b> , 18, 48-56	13
958	NMR investigations of structural and dynamics features of natively unstructured drug peptide - salmon calcitonin: implication to rational design of potent sCT analogs. <b>2013</b> , 19, 33-45	9
957	A flash in the pan: dissecting dynamic amyloid intermediates using fluorescence. <b>2013</b> , 587, 1096-105	12
956	Interaction of the eukaryotic initiation factor 4E with 4E-BP2 at a dynamic bipartite interface. <b>2013</b> , 21, 2186-96	64
955	Essential roles of Leu/Ile/Phe-rich domain of JC virus agnoprotein in dimer/oligomer formation, protein stability and splicing of viral transcripts. <b>2013</b> , 443, 161-76	22
954	An abundant LEA protein in the anhydrobiotic midge, PvLEA4, acts as a molecular shield by limiting growth of aggregating protein particles. <b>2013</b> , 43, 1055-67	51
953	The UBE2E proteins as conjugating dispersers: extending function with extended extensions. <b>2013</b> , 425, 4067-70	3

952	The stability of 2-state, 3-state and more-state proteins from simple spectroscopic techniques... plus the structure of the equilibrium intermediates at the same time. <b>2013</b> , 531, 4-13	43
951	The role of semidisorder in temperature adaptation of bacterial FlgM proteins. <b>2013</b> , 105, 2598-605	4
950	Conserved RNA helicase FRH acts nonenzymatically to support the intrinsically disordered neurospora clock protein FRQ. <b>2013</b> , 52, 832-43	52
949	NMR binding and crystal structure reveal that intrinsically-unstructured regulatory domain auto-inhibits PAK4 by a mechanism different from that of PAK1. <b>2013</b> , 438, 169-74	18
948	FhCaBP3: a Fasciola hepatica calcium binding protein with EF-hand and dynein light chain domains. <b>2013</b> , 95, 751-8	19
947	The disordered C-terminal domain of human DNA glycosylase NEIL1 contributes to its stability via intramolecular interactions. <b>2013</b> , 425, 2359-71	33
946	Recommendations of the wwPDB NMR Validation Task Force. <b>2013</b> , 21, 1563-70	117
945	Experimental and bioinformatic investigation of the proteolytic degradation of the C-terminal domain of a fungal tyrosinase. <b>2013</b> , 121, 37-45	18
944	Metalloproteins and Metallopeptides [Natural Metallofoldamers. <b>2013</b> , 1-50	
943	Searching for protein signatures using a multilevel alphabet. <b>2013</b> , 81, 1058-68	1
942	A decade and a half of protein intrinsic disorder: biology still waits for physics. <b>2013</b> , 22, 693-724	341
941	Improving the chemical shift dispersion of multidimensional NMR spectra of intrinsically disordered proteins. <b>2013</b> , 55, 231-7	29
940	Encyclopedia of Biophysics. <b>2013</b> , 327-327	
939	mTOR inhibits autophagy by controlling ULK1 ubiquitylation, self-association and function through AMBRA1 and TRAF6. <b>2013</b> , 15, 406-16	522
938	The Amyloid Phenomenon and Its Significance. <b>2013</b> , 1-19	2
937	Identification of genes differentially expressed during the growth of Bambusa oldhamii. <b>2013</b> , 63, 217-26	5
936	Encyclopedia of Biophysics. <b>2013</b> , 423-426	
935	Protein truncation as a common denominator of human neurodegenerative foldopathies. <b>2013</b> , 48, 516-32	12

934	Fuzzy complex formation between the intrinsically disordered prothymosin $\beta$ and the Kelch domain of Keap1 involved in the oxidative stress response. <b>2013</b> , 425, 1011-27	34
933	Single-molecule spectroscopy of protein folding dynamics--expanding scope and timescales. <b>2013</b> , 23, 36-47	215
932	Phosphorylation-coupled intramolecular dynamics of unstructured regions in chromatin remodeler FACT. <b>2013</b> , 104, 2222-34	16
931	Structure, function and networks of transcription factors involved in abiotic stress responses. <b>2013</b> , 14, 5842-78	204
930	Alternative splicing of intrinsically disordered regions and rewiring of protein interactions. <b>2013</b> , 23, 443-50	134
929	Essential Tetraspanin Functions in the Vertebrate Retina. <b>2013</b> , 321-343	1
928	The Effects of Mutations on Protein Function: A Comparative Study of Three Databases of Mutations in Humans. <b>2013</b> , 53, 217-226	2
927	The intrinsic conformational features of amino acids from a protein coil library and their applications in force field development. <b>2013</b> , 15, 3413-28	49
926	Coupled solid phase extraction and microparticle-based stability and purity-indicating immunosensor for the determination of recombinant human myelin basic protein in transgenic milk. <b>2013</b> , 109, 7-12	8
925	Mechanistic insights into the nongenomic regulation of phospholipid synthesizing enzymes. <b>2013</b> , 65, 584-92	12
924	Modulation of allostery by protein intrinsic disorder. <b>2013</b> , 498, 390-4	255
923	Conformational propensities of intrinsically disordered proteins from NMR chemical shifts. <b>2013</b> , 14, 3034-45	57
922	RNA-binding proteins in Mendelian disease. <b>2013</b> , 29, 318-27	171
921	mSYD1A, a mammalian synapse-defective-1 protein, regulates synaptogenic signaling and vesicle docking. <b>2013</b> , 78, 1012-23	39
920	The intrinsically disordered C-terminal region of Arabidopsis thaliana TCP8 transcription factor acts both as a transactivation and self-assembly domain. <b>2013</b> , 9, 2282-95	25
919	Mass spectrometry methods for intrinsically disordered proteins. <b>2013</b> , 138, 32-42	67
918	Dissecting partner recognition by an intrinsically disordered protein using descriptive random mutagenesis. <b>2013</b> , 425, 3495-509	21
917	Assessing induced folding within the intrinsically disordered C-terminal domain of the Henipavirus nucleoproteins by site-directed spin labeling EPR spectroscopy. <b>2013</b> , 31, 453-71	30



916	The most important thing is the tail: multitudinous functionalities of intrinsically disordered protein termini. <b>2013</b> , 587, 1891-901	95
915	Encyclopedia of Biophysics. <b>2013</b> , 414-415	
914	FlgM proteins from different bacteria exhibit different structural characteristics. <b>2013</b> , 1834, 808-16	6
913	Analysis of Molecular Recognition Features (MoRFs) in membrane proteins. <b>2013</b> , 1834, 798-807	22
912	Native-based simulations of the binding interaction between RAP74 and the disordered FCP1 peptide. <b>2013</b> , 117, 3074-85	11
911	Quantifying Changes in Intrinsic Molecular Motion Using Support Vector Machines. <b>2013</b> , 9, 868-75	7
910	Non-interacting molecules as innate structural probes in surface plasmon resonance. <b>2013</b> , 29, 4068-76	24
909	Allosteric communication in the KIX domain proceeds through dynamic repacking of the hydrophobic core. <b>2013</b> , 8, 1600-10	50
908	Families of Sequence-Specific DNA-Binding Domains in Transcription Factors across the Tree of Life. <b>2013</b> , 383-420	
907	Specialized Dynamical Properties of Promiscuous Residues Revealed by Simulated Conformational Ensembles. <b>2013</b> , 9, 5127-5147	30
906	Structure and assembly of the NOT module of the human CCR4-NOT complex. <b>2013</b> , 20, 1289-97	74
905	The denatured state ensemble contains significant local and long-range structure under native conditions: analysis of the N-terminal domain of ribosomal protein L9. <b>2013</b> , 52, 2662-71	23
904	A folded excited state of ligand-free nuclear coactivator binding domain (NCBD) underlies plasticity in ligand recognition. <b>2013</b> , 52, 1686-93	34
903	Ordering a dynamic protein via a small-molecule stabilizer. <b>2013</b> , 135, 3363-6	61
902	Hydrogen exchange mass spectrometry of functional membrane-bound chemotaxis receptor complexes. <b>2013</b> , 52, 8833-42	10
901	Effects of phosphorylation on the structure and backbone dynamics of the intrinsically disordered connexin43 C-terminal domain. <b>2013</b> , 288, 24857-70	44
900	Spliceosome. <b>2013</b> ,	23
899	MALDI/post ionization-ion mobility mass spectrometry of noncovalent complexes of dopamine receptors' epitopes. <b>2013</b> , 12, 1668-77	8

898	Efficient protocol for backbone and side-chain assignments of large, intrinsically disordered proteins: transient secondary structure analysis of 49.2 kDa microtubule associated protein 2c. <b>2013</b> , 56, 291-301	33
897	Reduced dimensionality (4,3)D-hnCOCANH experiment: an efficient backbone assignment tool for NMR studies of proteins. <b>2013</b> , 14, 109-18	4
896	Distribution and cluster analysis of predicted intrinsically disordered protein Pfam domains. <b>2013</b> , 1, e25724	9
895	The alphabet of intrinsic disorder: II. Various roles of glutamic acid in ordered and intrinsically disordered proteins. <b>2013</b> , 1, e24684	54
894	Multiple fuzzy interactions in the moonlighting function of thymosin- $\beta$ 4. <b>2013</b> , 1, e26204	8
893	Transient disorder: Calcineurin as an example. <b>2013</b> , 1, e26412	14
892	Do intrinsically disordered proteins possess high specificity in protein-protein interactions?. <b>2013</b> , 19, 4462-7	31
891	Phosphorylation at intrinsically disordered regions of PAM2 motif-containing proteins modulates their interactions with PABPC1 and influences mRNA fate. <b>2013</b> , 19, 295-305	31
890	Digested disorder: Quarterly intrinsic disorder digest (April-May-June, 2013). <b>2013</b> , 1, e27454	6
889	Electrostatically accelerated encounter and folding for facile recognition of intrinsically disordered proteins. <b>2013</b> , 9, e1003363	67
888	CENP-T provides a structural platform for outer kinetochore assembly. <b>2013</b> , 32, 424-36	147
887	Ligand clouds around protein clouds: a scenario of ligand binding with intrinsically disordered proteins. <b>2013</b> , 9, e1003249	60
886	Polycation- $\pi$ interactions are a driving force for molecular recognition by an intrinsically disordered oncoprotein family. <b>2013</b> , 9, e1003239	50
885	Comprehensive repertoire of foldable regions within whole genomes. <b>2013</b> , 9, e1003280	28
884	Protein intrinsic disorder in plants. <b>2013</b> , 4, 363	43
883	What's in a name? Why these proteins are intrinsically disordered: Why these proteins are intrinsically disordered. <b>2013</b> , 1, e24157	171
882	A novel method of predicting protein disordered regions based on sequence features. <b>2013</b> , 2013, 414327	13
881	On the importance of polar interactions for complexes containing intrinsically disordered proteins. <b>2013</b> , 9, e1003192	46

880	Exploring Protein-Peptide Binding Specificity through Computational Peptide Screening. <b>2013</b> , 9, e1003277	28
879	Systematic analysis of compositional order of proteins reveals new characteristics of biological functions and a universal correlate of macroevolution. <b>2013</b> , 9, e1003346	5
878	Atomic resolution description of the interaction between the nucleoprotein and phosphoprotein of Hendra virus. <b>2013</b> , 9, e1003631	56
877	Structure prediction of partial-length protein sequences. <b>2013</b> , 14, 14892-907	5
876	Distinct types of disorder in the human proteome: functional implications for alternative splicing. <b>2013</b> , 9, e1003030	48
875	Protein kinase A regulates MYC protein through transcriptional and post-translational mechanisms in a catalytic subunit isoform-specific manner. <b>2013</b> , 288, 14158-14169	26
874	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. <b>2013</b> , 41, 10215-27	19
873	Extracting structural information from charge-state distributions of intrinsically disordered proteins by non-denaturing electrospray-ionization mass spectrometry. <b>2013</b> , 1, e25068	22
872	Regulation of the structurally dynamic N-terminal domain of progesterone receptor by protein-induced folding. <b>2013</b> , 288, 30285-30299	34
871	The alphabet of intrinsic disorder: I. Act like a Pro: On the abundance and roles of proline residues in intrinsically disordered proteins. <b>2013</b> , 1, e24360	143
870	Intrinsic disorder in pathogen effectors: protein flexibility as an evolutionary hallmark in a molecular arms race. <b>2013</b> , 25, 3153-7	48
869	Pin1 regulates the dynamics of c-Myc DNA binding to facilitate target gene regulation and oncogenesis. <b>2013</b> , 33, 2930-49	80
868	Conformations of intrinsically disordered proteins are influenced by linear sequence distributions of oppositely charged residues. <b>2013</b> , 110, 13392-7	493
867	The Helical structure of prodomains promotes translocation of intrinsically disordered neuropeptide hormones into the endoplasmic reticulum. <b>2013</b> , 288, 13961-13973	13
866	Intrinsically disordered enamel matrix protein ameloblastin forms ribbon-like supramolecular structures via an N-terminal segment encoded by exon 5. <b>2013</b> , 288, 22333-45	29
865	Isolating contributions from intersegmental transfer to DNA searching by alkyladenine DNA glycosylase. <b>2013</b> , 288, 24550-9	24
864	The allosteric mechanism induced by protein kinase A (PKA) phosphorylation of dematin (band 4.9). <b>2013</b> , 288, 8313-8320	12
863	Development of QSAR-Improved Statistical Potential for the Structure-Based Analysis of Protein?Peptide Binding Affinities. <b>2013</b> , 32, 783-92	24

862	Intrinsically unstructured proteins by design-electrostatic interactions can control binding, folding, and function of a helix-loop-helix heterodimer. <b>2013</b> , 19, 461-9	4
861	Structural transitions in tau k18 on micelle binding suggest a hierarchy in the efficacy of individual microtubule-binding repeats in filament nucleation. <b>2013</b> , 22, 1037-48	38
860	Structural features and interfacial properties of WH2, $\beta$ -thymosin domains and other intrinsically disordered domains in the regulation of actin cytoskeleton dynamics. <b>2013</b> , 70, 686-705	23
859	Modelling and computer simulation of food structures. <b>2013</b> , 336-385	4
858	Structural divergence is more extensive than sequence divergence for a family of intrinsically disordered proteins. <b>2013</b> , 81, 1686-98	11
857	A quantitative measure for protein conformational heterogeneity. <b>2013</b> , 139, 121907	51
856	Impact of the K24N mutation on the transactivation domain of p53 and its binding to murine double-minute clone 2. <b>2013</b> , 81, 1738-47	14
855	Tetraspanins. <b>2013</b> ,	10
854	Probing Macromolecular and Supramolecular Structure, Dynamics, and Function by Magnetic Resonance. <b>2013</b> , 295-320	2
853	Single-molecule spectroscopy of the unexpected collapse of an unfolded protein at low pH. <b>2013</b> , 139, 121930	20
852	Intrinsically disordered protein threads through the bacterial outer-membrane porin OmpF. <b>2013</b> , 340, 1570-4	96
851	Multiscaled exploration of coupled folding and binding of an intrinsically disordered molecular recognition element in measles virus nucleoprotein. <b>2013</b> , 110, E3743-52	86
850	Structural flexibility of intrinsically disordered proteins induces stepwise target recognition. <b>2013</b> , 139, 225103	13
849	Disorder in the lifetime of a protein. <b>2013</b> , 1, e26782	2
848	Quantifying the topography of the intrinsic energy landscape of flexible biomolecular recognition. <b>2013</b> , 110, E2342-51	49
847	Charge-dependent secretion of an intrinsically disordered protein via the autotransporter pathway. <b>2013</b> , 110, E4246-55	33
846	Unstructured to structured transition of an intrinsically disordered protein peptide in coupling $\text{Ca}^{2+}$ -sensing and SK channel activation. <b>2013</b> , 110, 4828-33	50
845	Tumor suppressor protein Pdcd4 interacts with Daxx and modulates the stability of Daxx and the Hipk2-dependent phosphorylation of p53 at serine 46. <b>2013</b> , 2, e37	23

844	Amino acid composition of proteins reduces deleterious impact of mutations. <b>2013</b> , 3, 2919	34
843	HIV-1 Tat recruits transcription elongation factors dispersed along a flexible AFF4 scaffold. <b>2013</b> , 110, E123-31	60
842	Dynamic structure of the translocon SecYEG in membrane: direct single molecule observations. <b>2013</b> , 288, 16848-16854	26
841	Exon-phase symmetry and intrinsic structural disorder promote modular evolution in the human genome. <b>2013</b> , 41, 4409-22	11
840	Rapid evolutionary dynamics of structural disorder as a potential driving force for biological divergence in flaviviruses. <b>2013</b> , 5, 504-13	23
839	New insights into the determination of HDL structure by apolipoproteins: Thematic review series: high density lipoprotein structure, function, and metabolism. <b>2013</b> , 54, 2034-2048	112
838	A disorder-to-order structural transition in the COOH-tail of Fz4 determines misfolding of the L501fsX533-Fz4 mutant. <b>2013</b> , 3, 2659	16
837	Identifying molecular recognition features in intrinsically disordered regions of proteins by transfer learning. <b>2020</b> , 36, 1107-1113	14
836	Covalent Cross-Linking as an Enabler for Structural Mass Spectrometry. <b>2019</b> , 91, 12808-12818	1
835	Quantum Chemical Calculations of NMR Chemical Shifts in Phosphorylated Intrinsically Disordered Proteins. <b>2019</b> , 15, 5642-5658	2
834	Probing the Basis of $\beta$ -Synuclein Aggregation by Comparing Simulations to Single-Molecule Experiments. <b>2019</b> , 117, 1125-1135	9
833	Sequential, Structural and Functional Properties of Protein Complexes Are Defined by How Folding and Binding Intertwine. <b>2019</b> , 431, 4408-4428	7
832	Targeting transcription factors in cancer - from undruggable to reality. <b>2019</b> , 19, 611-624	208
831	Diffusion coefficients of elastic macromolecules. <b>2019</b> , 878,	5
830	Role of physical nucleation theory in understanding conformational conversion between pathogenic and nonpathogenic aggregates of low-complexity amyloid peptides. <b>2019</b> , 45, 5357-5373	2
829	Minireview - Microtubules and Tubulin Oligomers: Shape Transitions and Assembly by Intrinsically Disordered Protein Tau and Cationic Biomolecules. <b>2019</b> , 35, 15970-15978	2
828	Structural Plasticity of Intrinsically Disordered LEA Proteins from Provides Protection and. <b>2019</b> , 10, 1272	10
827	Role of protein conformation and weak interactions on $\beta$ -gliadin liquid-liquid phase separation. <b>2019</b> , 9, 13391	14

826	Protein Abundance Biases the Amino Acid Composition of Disordered Regions to Minimize Non-functional Interactions. <b>2019</b> , 431, 4978-4992	11
825	Extensive tests and evaluation of the CHARMM36IDPSFF force field for intrinsically disordered proteins and folded proteins. <b>2019</b> , 21, 21918-21931	25
824	Enhanced stability of an intrinsically disordered protein against proteolytic cleavage through interactions with silver nanoparticles.. <b>2019</b> , 9, 28746-28753	2
823	Investigation into Early Steps of Actin Recognition by the Intrinsically Disordered N-WASP Domain V. <b>2019</b> , 20,	2
822	Quantitative Conformational Analysis of Functionally Important Electrostatic Interactions in the Intrinsically Disordered Region of Delta Subunit of Bacterial RNA Polymerase. <b>2019</b> , 141, 16817-16828	7
821	The non-glycosylated N-terminal domain of human thrombopoietin is a molten globule under native conditions. <b>2019</b> , 286, 1717-1733	
820	Intrinsically Disordered Proteins and Their Mysterious[(Meta)Physics. <b>2019</b> , 7,	188
819	Structural mass spectrometry approaches to study the 20S proteasome. <b>2019</b> , 619, 179-223	7
818	Domain insertion permissibility-guided engineering of allostery in ion channels. <b>2019</b> , 10, 290	11
817	Interference with Amyloid- $\beta$ Nucleation by Transient Ligand Interaction. <b>2019</b> , 24,	7
816	Unfolded states under folding conditions accommodate sequence-specific conformational preferences with random coil-like dimensions. <b>2019</b> , 116, 12301-12310	28
815	Functions of intrinsic disorder in proteins involved in DNA demethylation during pre-implantation embryonic development. <b>2019</b> , 136, 962-979	1
814	New pathologic mechanisms in nucleotide repeat expansion disorders. <b>2019</b> , 130, 104515	35
813	Perspectives on drug discovery strategies based on IDPs. <b>2019</b> , 275-327	4
812	Residual Structures and Transient Long-Range Interactions of p53 Transactivation Domain: Assessment of Explicit Solvent Protein Force Fields. <b>2019</b> , 15, 4708-4720	17
811	The molecular basis of interaction domains of full-length PrP with lipid membranes. <b>2019</b> , 11, 12087-12091	1
810	Intrinsic Disorder-Based Emergence in Cellular Biology: Physiological and Pathological Liquid-Liquid Phase Transitions in Cells. <b>2019</b> , 11,	33
809	Using Dimensionality Reduction to Analyze Protein Trajectories. <b>2019</b> , 6, 46	22

808	Molecular Mechanisms of Membrane Curvature Sensing by a Disordered Protein. <b>2019</b> , 141, 10361-10371	30
807	The Structural and Functional Diversity of Intrinsically Disordered Regions in Transmembrane Proteins. <b>2019</b> , 252, 273-292	8
806	Similarity of Coomassie Dye Spectral Absorbance Dynamic of Sequentially Distant Polymeric N-Terminal Segments of Glycine and GABA Transporters. <b>2019</b> , 4, 6304-6308	2
805	Mechanistic Insights from Replica Exchange Molecular Dynamics Simulations into Mutation Induced Disordered-to-Ordered Transition in Hahellin, a $\beta$ -Crystallin. <b>2019</b> , 123, 5086-5098	5
804	The Impact of Protein Architecture on Adaptive Evolution. <b>2019</b> , 36, 2013-2028	13
803	P311, a novel intrinsically disordered protein, regulates adipocyte development. <b>2019</b> , 515, 234-240	1
802	Efficient and robust preparation of tyrosine phosphorylated intrinsically disordered proteins. <b>2019</b> , 67, 16-22	2
801	Self-assembly in elastin-like recombinamers: a mechanism to mimic natural complexity. <b>2019</b> , 2, 100007	14
800	Protein intrinsic disorder and structure-function continuum. <b>2019</b> , 166, 1-17	44
799	The dark proteome of cancer: Intrinsic disorder and functionality of HIF-1 $\alpha$ along with its interacting proteins. <b>2019</b> , 166, 371-403	15
798	Bacterial functional amyloids: Order from disorder. <b>2019</b> , 1867, 954-960	21
797	Integrin $\beta$ 4 Recognition of a Linear Motif of Bullous Pemphigoid Antigen BP230 Controls Its Recruitment to Hemidesmosomes. <b>2019</b> , 27, 952-964.e6	7
796	Computational Prediction of MoRFs, Short Disorder-to-order Transitioning Protein Binding Regions. <b>2019</b> , 17, 454-462	20
795	Overlapping Clusters and Support Vector Machines Based Interval Type-2 Fuzzy System for the Prediction of Peptide Binding Affinity. <b>2019</b> , 7, 49756-49764	4
794	The disordered boundary of the cell: emerging properties of membrane-bound intrinsically disordered proteins. <b>2019</b> , 10, 25-36	3
793	The functional importance of structure in unstructured protein regions. <b>2019</b> , 56, 155-163	34
792	Lipid Metabolism in Neurons: A Brief Story of a Novel c-Fos-Dependent Mechanism for the Regulation of Their Synthesis. <b>2019</b> , 13, 198	9
791	Structural Analysis of the 42 kDa Parvulin of. <b>2019</b> , 9,	

790	Med15: Glutamine-Rich Mediator Subunit with Potential for Plasticity. <b>2019</b> , 44, 737-751	10
789	Modulation of Disordered Proteins with a Focus on Neurodegenerative Diseases and Other Pathologies. <b>2019</b> , 20,	20
788	Biomolecular NMR Spectroscopy?. <b>2019</b> , 20,	6
787	The combined force field-sampling problem in simulations of disordered amyloid- $\beta$ peptides. <b>2019</b> , 150, 104108	25
786	Enhanced stability, structural characterization and simulated gastrointestinal digestion of coenzyme Q10 loaded ternary nanoparticles. <b>2019</b> , 94, 333-344	40
785	Memory effects in a random walk description of protein structure ensembles. <b>2019</b> , 150, 064911	
784	Structural and Dynamical Order of a Disordered Protein: Molecular Insights into Conformational Switching of PAGE4 at the Systems Level. <b>2019</b> , 9,	11
783	Characterization of structural conformers of $\beta$ -casein utilizing fluorescence spectroscopy. <b>2019</b> , 131, 89-96	9
782	Extreme Fuzziness: Direct Interactions between Two IDPs. <b>2019</b> , 9,	11
781	Phase separation of ligand-activated enhancers licenses cooperative chromosomal enhancer assembly. <b>2019</b> , 26, 193-203	141
780	Quality and bias of protein disorder predictors. <b>2019</b> , 9, 5137	52
779	Protein complexes associated with $\beta$ -catenin differentially influence the differentiation profile of neonatal and adult CD8 T cells. <b>2019</b> , 234, 18639-18652	1
778	Minimal Reconstitution of Membranous Web Induced by a Vesicle-Peptide Sol-Gel Transition. <b>2019</b> , 20, 1709-1718	3
777	Structural Characterization of N-WASP Domain V Using MD Simulations with NMR and SAXS Data. <b>2019</b> , 116, 1216-1227	10
776	Functional Segments on Intrinsically Disordered Regions in Disease-Related Proteins. <b>2019</b> , 9,	8
775	Role of Phosphorylation in the Modulation of the Glucocorticoid Receptor's Intrinsically Disordered Domain. <b>2019</b> , 9,	13
774	Complete Phase Diagram for Liquid-Liquid Phase Separation of Intrinsically Disordered Proteins. <b>2019</b> , 10, 1644-1652	128
773	The free energy landscape of the oncogene protein E7 of human papillomavirus type 16 reveals a complex interplay between ordered and disordered regions. <b>2019</b> , 9, 5822	6



772	Side chain electrostatic interactions and pH-dependent expansion of the intrinsically disordered, highly acidic carboxyl-terminus of $\beta$ -tubulin. <b>2019</b> , 28, 1095-1105	2
771	On the Need to Develop Guidelines for Characterizing and Reporting Intrinsic Disorder in Proteins. <b>2019</b> , 19, e1800415	3
770	All-atom structure ensembles of islet amyloid polypeptides determined by enhanced sampling and experiment data restraints. <b>2019</b> , 87, 541-550	8
769	Self-binding peptides: Binding-upon-folding versus folding-upon-binding. <b>2019</b> , 469, 25-34	55
768	Manipulating Active Structure and Function of Cationic Antimicrobial Peptide CM15 with the Polysulfonated Drug Suramin: A Step Closer to in Vivo Complexity. <b>2019</b> , 20, 1578-1590	11
767	Understanding Intramolecular Crosstalk in an Intrinsically Disordered Protein. <b>2019</b> , 14, 337-341	7
766	Conformational Stabilization and Rapid Labeling of a 29-Residue Peptide by a Small Molecule Reaction Partner. <b>2019</b> , 58, 1343-1353	7
765	Specific and Fuzzy Interactions Cooperate in Modulating Protein Half-Life. <b>2019</b> , 431, 1700-1707	1
764	Discovering MoRFs by trisecting intrinsically disordered protein sequence into terminals and middle regions. <b>2019</b> , 19, 378	7
763	Small heat shock proteins: multifaceted proteins with important implications for life. <b>2019</b> , 24, 295-308	32
762	Mechanism of the light-driven proton pump of bacteriorhodopsin based on the consistency principle. <b>2019</b> , 16, 274-279	4
761	SPOT-Disorder2: Improved Protein Intrinsic Disorder Prediction by Ensembled Deep Learning. <b>2019</b> , 17, 645-656	50
760	Peroxisomes: Biogenesis, Function, and Role in Human Disease. <b>2019</b> ,	1
759	In Silico Study of Rett Syndrome Treatment-Related Genes, , , and , by Evolutionary Classification and Disordered Region Assessment. <b>2019</b> , 20,	9
758	Unraveling the Role of Silent Mutation in the $\beta$ Subunit of RNA Polymerase: Structure Transition Inhibits Transcription. <b>2019</b> , 4, 17714-17725	5
757	Sequence-Derived Markers of Drug Targets and Potentially Druggable Human Proteins. <b>2019</b> , 10, 1075	7
756	Structured and intrinsically disordered domains within Amphiphysin1 work together to sense and drive membrane curvature. <b>2019</b> , 15, 8706-8717	10
755	Rational discovery of antimetastatic agents targeting the intrinsically disordered region of MBD2. <b>2019</b> , 5, eaav9810	12

754	The intrinsically disordered C terminus of troponin T binds to troponin C to modulate myocardial force generation. <b>2019</b> , 294, 20054-20069	13
753	Novel Small Molecules Targeting the Intrinsically Disordered Structural Ensemble of $\beta$ Synuclein Protect Against Diverse $\beta$ Synuclein Mediated Dysfunctions. <b>2019</b> , 9, 16947	14
752	Sequence and Structure Properties Uncover the Natural Classification of Protein Complexes Formed by Intrinsically Disordered Proteins via Mutual Synergistic Folding. <b>2019</b> , 20,	0
751	A Novel Mechanism for Zika Virus Host-Cell Binding. <b>2019</b> , 11,	2
750	Towards a Processual Approach in Protein Studies. <b>2019</b> , 12, 469-480	1
749	Critical phenomena in the temperature-pressure-crowding phase diagram of a protein. <b>2019</b> , 9,	11
748	Characterization of an Extensive Interface on Vitronectin for Binding to Plasminogen Activator Inhibitor-1: Adoption of Structure in an Intrinsically Disordered Region. <b>2019</b> , 58, 5117-5134	3
747	Evolutionary Analyses of Sequence and Structure Space Unravel the Structural Facets of SOD1. <b>2019</b> , 9,	3
746	NBS1 interacts with HP1 to ensure genome integrity. <b>2019</b> , 10, 951	8
745	Life in Phases: Intra- and Inter- Molecular Phase Transitions in Protein Solutions. <b>2019</b> , 9,	20
744	Binding of LcrV protein from <i>Yersinia pestis</i> to human T-cells induces apoptosis, which is completely blocked by specific antibodies. <b>2019</b> , 122, 1062-1070	5
743	Bioinformatical Approaches to Unstructured/Disordered Proteins and Their Complexes. <b>2019</b> , 561-596	
742	FBP21's C-Terminal Domain Remains Dynamic When Wrapped around the c-Sec63 Unit of Brr2 Helicase. <b>2019</b> , 116, 406-418	2
741	Does Intrinsic Disorder in Proteins Favor Their Interaction with Lipids?. <b>2019</b> , 19, e1800098	11
740	The relevance of buffer system ionic strength in immunoassay development. <b>2019</b> , 465, 27-30	
739	Single-Molecule Förster Resonance Energy Transfer Measurement Reveals the Dynamic Partially Ordered Structure of the Epidermal Growth Factor Receptor C-Tail Domain. <b>2019</b> , 123, 571-581	6
738	The Ciona myogenic regulatory factor functions as a typical MRF but possesses a novel N-terminus that is essential for activity. <b>2019</b> , 448, 210-225	3
737	The Klotho proteins in health and disease. <b>2019</b> , 15, 27-44	213

736	Structural disorder in the proteome and interactome of Alkhurma virus (ALKV). <b>2019</b> , 76, 577-608	13
735	Physical and functional interaction between nucleoid-associated proteins HU and Lsr2 of Mycobacterium tuberculosis: altered DNA binding and gene regulation. <b>2019</b> , 111, 981-994	13
734	The nature of the biological material and the irreproducibility problem in biomedical research. <b>2019</b> , 38,	1
733	Residual Structure Accelerates Binding of Intrinsically Disordered ACTR by Promoting Efficient Folding upon Encounter. <b>2019</b> , 431, 422-432	16
732	Improving Coarse-Grained Protein Force Fields with Small-Angle X-ray Scattering Data. <b>2019</b> , 123, 1026-1034	16
731	Modulation of $\beta$ -Synuclein Aggregation by Cytochrome c Binding and Hetero-dityrosine Adduct Formation. <b>2019</b> , 10, 1300-1310	9
730	Expression of novel proteins by polyomaviruses and recent advances in the structural and functional features of agnoprotein of JC virus, BK virus, and simian virus 40. <b>2019</b> , 234, 8295-8315	17
729	Price of disorder in the lac repressor hinge helix. <b>2019</b> , 110, e23239	1
728	Targeting intrinsically disordered proteins at the edge of chaos. <b>2019</b> , 24, 217-227	60
727	Insight into a Transcriptional Adaptor Zinc Finger Encoded by a Putative Protein in the White Spot Syndrome Virus Genome. <b>2019</b> , 11, 145-151	3
726	Codon selection reduces GC content bias in nucleic acids encoding for intrinsically disordered proteins. <b>2020</b> , 77, 149-160	2
725	The Amyloid Phenomenon and Its Significance in Biology and Medicine. <b>2020</b> , 12,	65
724	Disorder in milk proteins: adipophilin and TIP47, important constituents of the milk fat globule membrane. <b>2020</b> , 38, 1214-1229	1
723	Ligand interactions and the protein order-disorder energetic continuum. <b>2020</b> , 99, 78-85	4
722	A comprehensive proteomics analysis of JC virus Agnoprotein-interacting proteins: Agnoprotein primarily targets the host proteins with coiled-coil motifs. <b>2020</b> , 540, 104-118	6
721	Getting to Know Your Neighbor: Protein Structure Prediction Comes of Age with Contextual Machine Learning. <b>2020</b> , 27, 796-814	12
720	Biomolecular condensation of the microtubule-associated protein tau. <b>2020</b> , 99, 202-214	16
719	A Catalogue of 59,732 Human-Specific Regulatory Sequences Reveals Unique-to-Human Regulatory Patterns Associated with Virus-Interacting Proteins, Pluripotency, and Brain Development. <b>2020</b> , 39, 126-143	5

7 <sup>18</sup>	Identification of a PAI-1-binding site within an intrinsically disordered region of vitronectin. <b>2020</b> , 29, 494-508	5
7 <sup>17</sup>	Rapid Biophysical Characterization and NMR Spectroscopy Structural Analysis of Small Proteins from Bacteria and Archaea. <b>2020</b> , 21, 1178-1187	14
7 <sup>16</sup>	Changes in hydrophobicity mainly promotes the aggregation tendency of ALS associated SOD1 mutants. <b>2020</b> , 145, 904-913	4
7 <sup>15</sup>	Accuracy of protein-level disorder predictions. <b>2020</b> , 21, 1509-1522	24
7 <sup>14</sup>	Interplay between intrinsically disordered proteins inside membraneless protein liquid droplets. <b>2019</b> , 11, 1269-1275	10
7 <sup>13</sup>	Potential and limits of a colloid approach to protein solutions. <b>2020</b> , 16, 307-323	29
7 <sup>12</sup>	Regulation of the 20S Proteasome by a Novel Family of Inhibitory Proteins. <b>2020</b> , 32, 636-655	11
7 <sup>11</sup>	Protein aggregate formation permits millennium-old brain preservation. <b>2020</b> , 17, 20190775	4
7 <sup>10</sup>	Stabilization of AIMP1/p43 and EMAP II recombinant proteins in the complexes with polysaccharide dextran-70. <b>2020</b> , 72, 238-245	2
7 <sup>09</sup>	The regulation mechanism of phosphorylation and mutations in intrinsically disordered protein 4E-BP2. <b>2020</b> , 22, 2938-2948	2
7 <sup>08</sup>	DEPICTER: Intrinsic Disorder and Disorder Function Prediction Server. <b>2020</b> , 432, 3379-3387	22
7 <sup>07</sup>	Ordered structure-forming properties of the intrinsically disordered AB region of hRXR $\alpha$ and its ability to promote liquid-liquid phase separation. <b>2020</b> , 198, 105571	6
7 <sup>06</sup>	HRP2: Transforming Malaria Diagnosis, but with Caveats. <b>2020</b> , 36, 112-126	35
7 <sup>05</sup>	Prediction of the initial folding sites and the entire folding processes for Ig-like beta-sandwich proteins. <b>2020</b> , 88, 740-758	
7 <sup>04</sup>	Gain-of-Function MN1 Truncation Variants Cause a Recognizable Syndrome with Craniofacial and Brain Abnormalities. <b>2020</b> , 106, 13-25	11
7 <sup>03</sup>	Do Molecular Dynamics Force Fields Capture Conformational Dynamics of Alanine in Water?. <b>2020</b> , 16, 510-527	15
7 <sup>02</sup>	Dynamic multivalent interactions of intrinsically disordered proteins. <b>2020</b> , 62, 9-13	23
7 <sup>01</sup>	The Ambivalent Role of Proline Residues in an Intrinsically Disordered Protein: From Disorder Promoters to Compaction Facilitators. <b>2020</b> , 432, 3093-3111	35

700	Genome-wide investigation of proline transporter (ProT) gene family in tomato: Bioinformatics and expression analyses in response to drought stress. <b>2020</b> , 157, 13-22	5
699	Cancer and SOX proteins: New insight into their role in ovarian cancer progression/inhibition. <b>2020</b> , 161, 105159	9
698	Computational methods-guided design of modulators targeting protein-protein interactions (PPIs). <b>2020</b> , 207, 112764	9
697	Osteopontin regulates biomimetic calcium phosphate crystallization from disordered mineral layers covering apatite crystallites. <b>2020</b> , 10, 15722	11
696	The construction of resveratrol-loaded protein-polysaccharide-tea saponin complex nanoparticles for controlling physicochemical stability and digestion. <b>2020</b> , 11, 9973-9983	15
695	Protein droplets in systems of disordered homopeptides and the amyloid glass phase. <b>2020</b> , 22, 15592-15599	10
694	Fast energy minimization of the CCDC drug-subset structures by molecule-in-cluster computations allows independent structure validation and model completion. <b>2020</b> , 22, 7420-7431	4
693	Influence of electrostatic forces on the association kinetics and conformational ensemble of an intrinsically disordered protein. <b>2020</b> , 88, 1607-1619	2
692	COVID-19 during Pregnancy and Postpartum. <b>2020</b> , 1-28	8
691	Client proximity enhancement inside cellular membrane-less compartments governed by client-compartment interactions. <b>2020</b> , 11, 5642	8
690	Phosphorylation-Dependent Conformations of the Disordered Carboxyl-Terminus Domain in the Epidermal Growth Factor Receptor. <b>2020</b> , 11, 10037-10044	7
689	Liquid-Liquid Phase Separation by Intrinsically Disordered Protein Regions of Viruses: Roles in Viral Life Cycle and Control of Virus-Host Interactions. <b>2020</b> , 21,	25
688	Adenoviral E1A Exploits Flexibility and Disorder to Target Cellular Proteins. <b>2020</b> , 10,	3
687	Lipid membrane templated misfolding and self-assembly of intrinsically disordered tau protein. <b>2020</b> , 10, 13324	11
686	Characterization of partially ordered states in the intrinsically disordered N-terminal domain of p53 using millisecond molecular dynamics simulations. <b>2020</b> , 10, 12402	6
685	Diversity and genome mapping assessment of disordered and functional domains in trypanosomatids. <b>2020</b> , 227, 103919	2
684	Bifurcated Hydrogen Bonds and the Fold Switching of Lymphotactin. <b>2020</b> , 124, 6555-6564	4
683	NFAT5, which protects against hypertonicity, is activated by that stress via structuring of its intrinsically disordered domain. <b>2020</b> , 117, 20292-20297	5

682	Genus-specific pattern of intrinsically disordered central regions in the nucleocapsid protein of coronaviruses. <b>2020</b> , 18, 1884-1890	11
681	Performance of CHARMM36m with modified water model in simulating intrinsically disordered proteins: a case study. <b>2020</b> , 6, 80-87	3
680	Impact of microfluidization and thermal treatment on the structure, stability and in vitro digestion of curcumin loaded zein-propylene glycol alginate complex nanoparticles. <b>2020</b> , 138, 109817	16
679	The Dynamism of Intrinsically Disordered Proteins: Binding-Induced Folding, Amyloid Formation, and Phase Separation. <b>2020</b> , 124, 11541-11560	13
678	Unravelling Structural Dynamics within a Photoswitchable Single Peptide: A Step Towards Multimodal Bioinspired Nanodevices. <b>2020</b> , 132, 22743-22751	2
677	Conformational diversity facilitates antibody mutation trajectories and discrimination between foreign and self-antigens. <b>2020</b> , 117, 22341-22350	4
676	Unravelling Structural Dynamics within a Photoswitchable Single Peptide: A Step Towards Multimodal Bioinspired Nanodevices. <b>2020</b> , 59, 22554-22562	9
675	A code within the genetic code: codon usage regulates co-translational protein folding. <b>2020</b> , 18, 145	26
674	Evidence that immunization with TP0751, a bipartite <i>Treponema pallidum</i> lipoprotein with an intrinsically disordered region and lipocalin fold, fails to protect in the rabbit model of experimental syphilis. <b>2020</b> , 16, e1008871	3
673	Zooming into the Dark Side of Human Annexin-S100 Complexes: Dynamic Alliance of Flexible Partners. <b>2020</b> , 21,	8
672	Intrinsic Disorder in Human Proteins Encoded by Core Duplicon Gene Families. <b>2020</b> , 124, 8050-8070	0
671	ODiNPred: comprehensive prediction of protein order and disorder. <b>2020</b> , 10, 14780	25
670	Mechanism of ribosome rescue by alternative ribosome-rescue factor B. <b>2020</b> , 11, 4106	14
669	The Role of Protein Disorder in Nuclear Transport and in Its Subversion by Viruses. <b>2020</b> , 9,	7
668	Much More Than a Cytoskeletal Protein: Physiological and Pathological Functions of the Non-microtubule Binding Region of Tau. <b>2020</b> , 11, 590059	12
667	Open gaps in the evolution of the eukaryotic nucleotide excision repair. <b>2020</b> , 95, 102955	2
666	Intrinsically disordered regions are abundant in simplexvirus proteomes and display signatures of positive selection. <b>2020</b> , 6, veaa028	6
665	Evidence for mutations in SARS-CoV-2 Italian isolates potentially affecting virus transmission. <b>2020</b> , 92, 2232-2237	21

664	Immunostimulatory efficacy and protective potential of putative TgERK7 protein in mice experimentally infected by <i>Toxoplasma gondii</i> . <b>2020</b> , 310, 151432	2
663	Targeting Intrinsically Disordered Proteins through Dynamic Interactions. <b>2020</b> , 10,	16
662	The proteasome as a druggable target with multiple therapeutic potentialities: Cutting and non-cutting edges. <b>2020</b> , 213, 107579	32
661	Intrinsic Disorder in Tetratricopeptide Repeat Proteins. <b>2020</b> , 21,	2
660	Impact of the Hereditary P301L Mutation on the Correlated Conformational Dynamics of Human Tau Protein Revealed by the Paramagnetic Relaxation Enhancement NMR Experiments. <b>2020</b> , 21,	6
659	Ultrasensitive Change in Nucleosome Binding by Multiple Phosphorylations to the Intrinsically Disordered Region of the Histone Chaperone FACT. <b>2020</b> , 432, 4637-4657	2
658	Physicochemical and structural properties of lunasin revealed by spectroscopic, chromatographic and molecular dynamics approaches. <b>2020</b> , 1868, 140440	2
657	Phosphorylation of multiple proteins involved in ciliogenesis by Tau Tubulin kinase 2. <b>2020</b> , 31, 1032-1046	12
656	Targeting an Interaction Between Two Disordered Domains by Using a Designed Peptide. <b>2020</b> , 26, 10240-10249	9
655	Specific Conformational Dynamics and Expansion Underpin a Multi-Step Mechanism for Specific Binding of p27 with Cdk2/Cyclin A. <b>2020</b> , 432, 2998-3017	10
654	Physical basis of the disorder-order transition. <b>2020</b> , 685, 108305	6
653	Myelin basic protein dynamics from out-of-equilibrium functional state to degraded state in myelin. <b>2020</b> , 1862, 183256	2
652	Molecular Dynamics Ensemble Refinement of Intrinsically Disordered Peptides According to Deconvoluted Spectra from Circular Dichroism. <b>2020</b> , 118, 1665-1678	10
651	The structure of the TOM core complex in the mitochondrial outer membrane. <b>2020</b> , 401, 687-697	6
650	Investigations of the underlying mechanisms of HIF-1 $\alpha$ and CITED2 binding to TAZ1. <b>2020</b> , 117, 5595-5603	10
649	Protein folding: how, why, and beyond. <b>2020</b> , 3-22	22
648	Kinetic Selection and Relaxation of the Intrinsically Disordered Region of a Protein upon Binding. <b>2020</b> , 16, 2835-2845	9
647	The AVR2 Effector Escapes R2 Recognition Through Effector Disordering. <b>2020</b> , 33, 921-931	7

646	Multidomain protein structure prediction using information about residues interacting on multimeric protein interfaces. <b>2020</b> , 17, 2-13	1
645	Probing Surfaces in Dynamic Protein Interactions. <b>2020</b> , 432, 2949-2972	8
644	Disordered protein-graphene oxide co-assembly and supramolecular biofabrication of functional fluidic devices. <b>2020</b> , 11, 1182	32
643	Criticality in the conformational phase transition among self-similar groups in intrinsically disordered proteins: Probed by salt-bridge dynamics. <b>2020</b> , 1868, 140474	1
642	Effect of Structure on Polypeptide Blobs: A Model Study Using Poly(l-lysine). <b>2020</b> , 36, 7980-7990	6
641	Transient knots in intrinsically disordered proteins and neurodegeneration. <b>2020</b> , 174, 79-103	2
640	IDPs and their complexes in GPCR and nuclear receptor signaling. <b>2020</b> , 174, 105-155	3
639	A partially disordered region connects gene repression and activation functions of EZH2. <b>2020</b> , 117, 16992-17002	3
638	Designing heterotropically activated allosteric conformational switches using supercharging. <b>2020</b> , 117, 5291-5297	6
637	Single-Molecule FRET of Intrinsically Disordered Proteins. <b>2020</b> , 71, 391-414	23
636	Structural insights into TAZ2 domain-mediated CBP/p300 recruitment by transactivation domain 1 of the lymphopoietic transcription factor E2A. <b>2020</b> , 295, 4303-4315	2
635	Taurine Induces an Ordered but Functionally Inactive Conformation in Intrinsically Disordered Casein Proteins. <b>2020</b> , 10, 3503	4
634	Transcription Factor Inhibition: Lessons Learned and Emerging Targets. <b>2020</b> , 26, 508-518	32
633	Integrating All-Atom and Coarse-Grained Simulations-Toward Understanding of IDPs at Surfaces. <b>2020</b> , 16, 1843-1853	3
632	Microsecond Simulation of the Proteoglycan-like Region of Carbonic Anhydrase IX and Design of Chemical Inhibitors Targeting pH Homeostasis in Cancer Cells. <b>2020</b> , 5, 4270-4281	7
631	Molecular Basis of Plant Oil Biosynthesis: Insights Gained From Studying the WRINKLED1 Transcription Factor. <b>2020</b> , 11, 24	19
630	Structure-Activity Relationships of Hydroxyapatite-Binding Peptides. <b>2020</b> , 36, 2729-2739	7
629	Fabrication, characterization and in vitro digestion of food grade complex nanoparticles for co-delivery of resveratrol and coenzyme Q10. <b>2020</b> , 105, 105791	40



628	The E3 ubiquitin ligase TRIP12 participates in cell cycle progression and chromosome stability. <b>2020</b> , 10, 789	9
627	Structural analysis of the intrinsically disordered splicing factor Spp2 and its binding to the DEAH-box ATPase Prp2. <b>2020</b> , 117, 2948-2956	12
626	Hyper-phosphorylation of nsp2-related proteins of porcine reproductive and respiratory syndrome virus. <b>2020</b> , 543, 63-75	1
625	Free Energy Profile and Kinetics of Coupled Folding and Binding of the Intrinsically Disordered Protein p53 with MDM2. <b>2020</b> , 60, 1551-1558	9
624	Intrinsically disordered protein domains in flavivirus infection. <b>2020</b> , 683, 108298	3
623	Intrinsically disordered regions regulate the activities of ATP binding cassette transporters. <b>2020</b> , 1862, 183202	4
622	Biotin proximity tagging favours unfolded proteins and enables the study of intrinsically disordered regions. <b>2020</b> , 3, 38	14
621	Supercharged Proteins and Polypeptides. <b>2020</b> , 32, e1905309	28
620	Electrostatic Forces Control the Negative Allosteric Regulation in a Disordered Protein Switch. <b>2020</b> , 11, 864-868	8
619	The lac repressor hinge helix in context: The effect of the DNA binding domain and symmetry. <b>2020</b> , 1864, 129538	2
618	Intrinsically Disordered Proteins. <b>2020</b> , 587-612	4
617	GTP Binding is Necessary for the Activation of a Toxic Mutant Isoform of the Essential GTPase ObgE. <b>2019</b> , 21,	2
616	Controlling Structural Bias in Intrinsically Disordered Proteins Using Solution Space Scanning. <b>2020</b> , 16, 1794-1805	15
615	Physical Chemistry of the Protein Backbone: Enabling the Mechanisms of Intrinsic Protein Disorder. <b>2020</b> , 124, 4379-4390	7
614	Influence of calcium ions on the stability, microstructure and in vitro digestion fate of zein-propylene glycol alginate-tea saponin ternary complex particles for the delivery of resveratrol. <b>2020</b> , 106, 105886	36
613	Intrinsically disordered proteins of viruses: Involvement in the mechanism of cell regulation and pathogenesis. <b>2020</b> , 174, 1-78	22
612	FASPR: an open-source tool for fast and accurate protein side-chain packing. <b>2020</b> , 36, 3758-3765	16
611	Charge Interactions Modulate the Encounter Complex Ensemble of Two Differently Charged Disordered Protein Partners of KIX. <b>2020</b> , 16, 3856-3868	8

610	A Placenta Derived C-Terminal Fragment of $\beta$ -Hemoglobin With Combined Antibacterial and Antiviral Activity. <b>2020</b> , 11, 508	17
609	Structural and Biophysical Insights into the Function of the Intrinsically Disordered Myc Oncoprotein. <b>2020</b> , 9,	23
608	A secreted fungal histidine- and alanine-rich protein regulates metal ion homeostasis and oxidative stress. <b>2020</b> , 227, 1174-1188	16
607	Strategies for identifying dynamic regions in protein complexes: Flexibility changes accompany methylation in chemotaxis receptor signaling states. <b>2020</b> , 1862, 183312	2
606	Similar Yet Different-Structural and Functional Diversity among LEA_4 Proteins. <b>2020</b> , 21,	6
605	Mechanism of Coupled Folding-upon-Binding of an Intrinsically Disordered Protein. <b>2020</b> , 142, 11092-11101	26
604	Ratiometric Single-Molecule FRET Measurements to Probe Conformational Subpopulations of Intrinsically Disordered Proteins. <b>2020</b> , 12, e80	1
603	Membranes as the third genetic code. <b>2020</b> , 47, 4093-4097	1
602	Entropy Hotspots for the Binding of Intrinsically Disordered Ligands to a Receptor Domain. <b>2020</b> , 118, 2502-2512	3
601	Unique and exclusive peptide signatures directly identify intrinsically disordered proteins from sequences without structural information. <b>2021</b> , 39, 2885-2893	3
600	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. <b>2021</b> , 39, 2490-2501	6
599	RFPR-IDP: reduce the false positive rates for intrinsically disordered protein and region prediction by incorporating both fully ordered proteins and disordered proteins. <b>2021</b> , 22, 2000-2011	9
598	IDP-Seq2Seq: identification of intrinsically disordered regions based on sequence to sequence learning. <b>2021</b> , 36, 5177-5186	46
597	IDPology of the living cell: intrinsic disorder in the subcellular compartments of the human cell. <b>2021</b> , 78, 2371-2385	6
596	Intrinsically disordered features of carbonic anhydrase IX proteoglycan-like domain. <b>2021</b> , 78, 2059-2067	2
595	Binding and folding in transcriptional complexes. <b>2021</b> , 66, 156-162	1
594	The MemMoRF database for recognizing disordered protein regions interacting with cellular membranes. <b>2021</b> , 49, D355-D360	0
593	COVID-19 outbreak: history, mechanism, transmission, structural studies and therapeutics. <b>2021</b> , 49, 199-213	46

592	Drugs, host proteins and viral proteins: how their promiscuities shape antiviral design. <b>2021</b> , 96, 205-222	4
591	The Methods and Tools for Intrinsic Disorder Prediction and their Application to Systems Medicine. <b>2021</b> , 159-169	1
590	Dynamics of aqueous peptide solutions in folded and disordered states examined by dynamic light scattering and dielectric spectroscopy. <b>2021</b> , 23, 15020-15029	3
589	Hydrophobic residues advance the onset of simple coacervation in intrinsically disordered proteins at low densities: Insights from field theoretical simulations studies.	
588	Developing Inhibitors to the Amino-Terminus Domains of Steroid Hormone Receptors. <b>2021</b> , 613-642	
587	Testing the length limit of loop grafting in a helical repeat protein. <b>2021</b> , 3, 30-40	2
586	Consistent Force Field Captures Homolog Resolved HP1 Phase Separation.	2
585	Recent advances in atomic molecular dynamics simulation of intrinsically disordered proteins. <b>2021</b> , 23, 777-784	14
584	Exploring Energy Landscapes of Intrinsically Disordered Proteins: Insights into Functional Mechanisms.	0
583	New genotypes of Helicobacter Pylori VacA d-region identified from global strains. <b>2021</b> , 22, 4	2
582	Applications of three phase partitioning and macro-(affinity ligand) facilitated three phase partitioning in protein refolding. <b>2021</b> , 197-222	
581	Effects of microfluidization and thermal treatment on the characterization and digestion of curcumin loaded protein-polysaccharide-tea saponin complex nanoparticles. <b>2021</b> , 12, 1192-1206	15
580	A Universal Peptide Matrix Interactomics Approach to Disclose Motif-Dependent Protein Binding. <b>2021</b> , 20, 100135	3
579	The complexity of protein interactions unravelled from structural disorder. <b>2021</b> , 17, e1008546	3
578	The N-terminal region of Jaw1 has a role to inhibit the formation of organized smooth endoplasmic reticulum as an intrinsically disordered region. <b>2021</b> , 11, 753	1
577	Human neurotropic polyomavirus, JC virus, agnoprotein targets mitochondrion and modulates its functions. <b>2021</b> , 553, 135-153	2
576	Structure-based peptide design targeting intrinsically disordered proteins: Novel histone H4 and H2A peptidic inhibitors. <b>2021</b> , 19, 934-948	8
575	Systematic Differences between Current Molecular Dynamics Force Fields To Represent Local Properties of Intrinsically Disordered Proteins. <b>2021</b> , 125, 798-804	6

574	Structure and Dynamics of Ribonuclease A during Thermal Unfolding: The Failure of the Zimm Model. <b>2021</b> , 125, 780-788	0
573	Using biochemistry and biophysics to extinguish androgen receptor signaling in prostate cancer. <b>2021</b> , 296, 100240	6
572	Ultrasensitive Nucleosome Binding Regulation Mediated by Intrinsically Disordered Regions. <b>2021</b> , 61, 312-315	
571	Assessing SIRAH's Capability to Simulate Intrinsically Disordered Proteins and Peptides. <b>2021</b> , 17, 599-604	5
570	Protein Folding   Protein Folding and Assembly. <b>2021</b> , 105-115	
569	Interesting Biochemistries in the Structure and Function of Bacterial Effectors. <b>2021</b> , 11, 608860	2
568	Fundamental Challenges and Outlook in Simulating Liquid-Liquid Phase Separation of Intrinsically Disordered Proteins. <b>2021</b> , 12, 1644-1656	5
567	Fluorescence-based techniques for the detection of the oligomeric status of proteins: implication in amyloidogenic diseases. <b>2021</b> , 50, 671-685	1
566	Intrinsic disorder in protein domains contributes to both organism complexity and clade-specific functions. <b>2021</b> , 11, 2985	10
565	High resolution ensemble description of metamorphic and intrinsically disordered proteins using an efficient hybrid parallel tempering scheme. <b>2021</b> , 12, 958	17
564	Inference of Joint Conformational Distributions from Separately Acquired Experimental Measurements. <b>2021</b> , 12, 1606-1611	2
563	Exploring the conformational dynamics and flexibility of intrinsically disordered HIV-1 Nef protein using molecular dynamic network approaches. <b>2021</b> , 11, 156	
562	Prediction of protein-peptide-binding amino acid residues regions using machine learning algorithms. <b>2021</b> ,	
561	Generalized-ensemble method study: A helix-mimetic compound inhibits protein-protein interaction by long-range and short-range intermolecular interactions. <b>2021</b> , 42, 956-969	1
560	Difference of binding modes among three ligands to a receptor mSin3B corresponding to their inhibitory activities. <b>2021</b> , 11, 6178	0
559	Structural Analysis of the cl-Par-4 Tumor Suppressor as a Function of Ionic Environment. <b>2021</b> , 11,	1
558	The Conservation of Low Complexity Regions in Bacterial Proteins Depends on the Pathogenicity of the Strain and Subcellular Location of the Protein. <b>2021</b> , 12,	1
557	Mutations of Intrinsically Disordered Protein Regions Can Drive Cancer but Lack Therapeutic Strategies. <b>2021</b> , 11,	7

556	Conformational Dynamics of $\beta$ -Synuclein during the Interaction with Phospholipid Nanodiscs by Millisecond Hydrogen-Deuterium Exchange Mass Spectrometry. <b>2021</b> , 32, 1169-1179	2
555	Estrogen Receptor Modulators. 1-74	
554	Exploring Energy Landscapes of Intrinsically Disordered Proteins: Insights into Functional Mechanisms. <b>2021</b> , 17, 3178-3187	5
553	PhosIDP: a web tool to visualize the location of phosphorylation sites in disordered regions.	
552	Sequence effects on internal structure of droplets of associative polymers. <b>2021</b> , 120, 1210-1218	0
551	Consistent Force Field Captures Homologue-Resolved HP1 Phase Separation. <b>2021</b> , 17, 3134-3144	9
550	Isolation and Characterization of Human Colon Adenocarcinoma Stem-Like Cells Based on the Endogenous Expression of the Stem Markers. <b>2021</b> , 22,	0
549	Effects of pH on an IDP conformational ensemble explored by molecular dynamics simulation. <b>2021</b> , 271, 106552	6
548	Changes in Amino Acid Profiles and Bioactive Compounds of Thai Silk Cocoons as Affected by Water Extraction. <b>2021</b> , 26,	0
547	Insights into the evolutionary forces that shape the codon usage in the viral genome segments encoding intrinsically disordered protein regions. <b>2021</b> , 22,	3
546	DNAzyme walker induced DNAzyme working cascade signal amplification strategy for sensitive detection of protein. <b>2021</b> , 333, 129551	10
545	Abundance Imparts Evolutionary Constraints of Similar Magnitude on the Buried, Surface, and Disordered Regions of Proteins. <b>2021</b> , 8, 626729	0
544	Oncogenic Potential of the Dual-Function Protein MEX3A. <b>2021</b> , 10,	2
543	PhosIDP: a web tool to visualize the location of phosphorylation sites in disordered regions. <b>2021</b> , 11, 9930	1
542	IUPred3: prediction of protein disorder enhanced with unambiguous experimental annotation and visualization of evolutionary conservation. <b>2021</b> , 49, W297-W303	43
541	Intrachain interaction topology can identify functionally similar intrinsically disordered proteins. <b>2021</b> , 120, 1860-1868	4
540	Conformations and diffusion of flexibly linked colloidal chains. <b>2021</b> , 4, 035002	1
539	Sequence of Events during Peptide Unbinding from RNase S: A Complete Experimental Description. <b>2021</b> , 12, 5201-5207	4

538	Binding mechanism underlying FIH-1 suppression caused by the N-terminal disordered region of Mint3.	
537	Kn1 participates in spindle assembly checkpoint signaling in maize. <b>2021</b> , 118,	4
536	Molecular and Ionic Diffusion in Ion Exchange Membranes and Biological Systems (Cells and Proteins) Studied by NMR. <b>2021</b> , 11,	4
535	ADAM10 Site-Dependent Biology: Keeping Control of a Pervasive Protease. <b>2021</b> , 22,	1
534	Peptide array-based interactomics. <b>2021</b> , 413, 5561-5566	3
533	"Janus-Faced" $\beta$ Synuclein: Role in Parkinson's Disease. <b>2021</b> , 9, 673395	3
532	Applications of isothermal titration calorimetry in pure and applied research from 2016 to 2020. <b>2021</b> , 34, e2901	8
531	Prediction and Characterization of Disorder-Order Transition Regions in Proteins by Deep Learning.	
530	Reversible protein aggregation as cytoprotective mechanism against heat stress. <b>2021</b> , 67, 849-855	2
529	A community-driven roadmap to advance research on translated open reading frames detected by Ribo-seq.	4
528	An essential role of the autophagy activating kinase ULK1 in snRNP biogenesis. <b>2021</b> , 49, 6437-6455	2
527	Functional and Predictive Structural Characterization of WRINKLED2, A Unique Oil Biosynthesis Regulator in Avocado. <b>2021</b> , 12, 648494	1
526	Identification of a protein unique to the genus Plasmodium that contains a WD40 repeat domain and extensive low-complexity sequence. <b>2021</b> , 120, 2617-2629	
525	p53/p73 Protein Network in Colorectal Cancer and Other Human Malignancies. <b>2021</b> , 13,	4
524	PRISMA and BioID disclose a motifs-based interactome of the intrinsically disordered transcription factor C/EBP $\beta$ . <b>2021</b> , 24, 102686	2
523	Progressive Phosphorylation Modulates the Self-Association of a Variably Modified Histone H3 Peptide. <b>2021</b> , 8, 698182	2
522	Molecular Details of a Coupled Binding and Folding Reaction between the Amyloid Precursor Protein and a Folded Domain. <b>2021</b> , 16, 1191-1200	1
521	Molecular Mechanisms Regulating the DNA Repair Protein APE1: A Focus on Its Flexible N-Terminal Tail Domain. <b>2021</b> , 22,	4

520	Nonspecific Binding-Fundamental Concepts and Consequences for Biosensing Applications. <b>2021</b> , 121, 8095-8160	25
519	Application of Thermoresponsive Intrinsically Disordered Protein Polymers in Nanostructured and Microstructured Materials. <b>2021</b> , 21, e2100129	2
518	Beyond Microsatellite Instability: Intrinsic Disorder as a Potential Link Between Protein Short Tandem Repeats and Cancer. <b>2021</b> , 1,	0
517	Analysis of the dark proteome of Chandipura virus reveals maximum propensity for intrinsic disorder in phosphoprotein. <b>2021</b> , 11, 13253	3
516	Interfacial Liquid-Liquid Phase Separation-Driven Polymerization-Induced Electrostatic Self-Assembly. <b>2021</b> , 54, 5577-5585	1
515	Networks of Networks: An Essay on Multi-Level Biological Organization. <b>2021</b> , 12, 706260	7
514	A Tale of Loops and Tails: The Role of Intrinsically Disordered Protein Regions in R-Loop Recognition and Phase Separation. <b>2021</b> , 8, 691694	6
513	Roles of Phase Separation for Cellular Redox Maintenance. <b>2021</b> , 12, 691946	3
512	Multiple regulatory intrinsically disordered motifs control FOXO4 transcription factor binding and function. <b>2021</b> , 36, 109446	4
511	Uncovering the Conformational Distribution of a Small Protein with Nanoparticle-Aided Cryo-Electron Microscopy Sampling. <b>2021</b> , 12, 6565-6573	0
510	Identification and functional characterization of transcriptional activators in human cells.	
509	Dynamics in Fip1 regulate eukaryotic mRNA 3'-end processing.	2
508	The C-terminal tail extension of myosin 16 acts as a molten globule, including intrinsically disordered regions, and interacts with the N-terminal ankyrin. <b>2021</b> , 297, 100716	1
507	Cancer-Associated Mutations Perturb the Disordered Ensemble and Interactions of the Intrinsically Disordered p53 Transactivation Domain. <b>2021</b> , 433, 167048	5
506	Subsecond Time-Resolved Mass Spectrometry in Dynamic Structural Biology. <b>2021</b> ,	3
505	Prion-Like Proteins in Phase Separation and Their Link to Disease. <b>2021</b> , 11,	3
504	What's in the BAGs? Intrinsic disorder angle of the multifunctionality of the members of a family of chaperone regulators. <b>2021</b> ,	1
503	Enthalpy-Entropy Compensation in the Promiscuous Interaction of an Intrinsically Disordered Protein with Homologous Protein Partners. <b>2021</b> , 11,	2

502	Multiple in vivo roles for the C-terminal domain of the RNA chaperone Hfq.	
501	The disordered regions of the methyltransferase SETD2 govern its function by regulating its proteolysis and phase separation. <b>2021</b> , 297, 101075	1
500	Exploration of the Role of the C-Terminal Domain of Human DNA Topoisomerase II $\beta$ in Catalytic Activity. <b>2021</b> , 6, 25892-25903	1
499	Dynamics in Fip1 regulate eukaryotic mRNA 3' end processing. <b>2021</b> , 35, 1510-1526	3
498	The sequence-ensemble relationship in fuzzy protein complexes. <b>2021</b> , 118,	0
497	Two stripe rust effectors impair wheat resistance by suppressing import of host Fe-S protein into chloroplasts. <b>2021</b> , 187, 2530-2543	2
496	The Intrinsically Disordered Region in the Human STN1 OB-Fold Domain Is Important for Protecting Genome Stability. <b>2021</b> , 10,	
495	Contiguously-hydrophobic sequences are functionally significant throughout the human exome.	0
494	Liquid condensation of reprogramming factor KLF4 with DNA provides a mechanism for chromatin organization. <b>2021</b> , 12, 5579	7
493	Barcoded Bulk QTL mapping reveals highly polygenic and epistatic architecture of complex traits in yeast.	1
492	Mammalian acetate-dependent acetyl CoA synthetase 2 contains multiple protein destabilization and masking elements. <b>2021</b> , 297, 101037	0
491	DisoLipPred: Accurate prediction of disordered lipid binding residues in protein sequences with deep recurrent networks and transfer learning. <b>2021</b> ,	9
490	The N-terminal intrinsically disordered region mediates intracellular localization and self-oligomerization of ALS2. <b>2021</b> , 569, 106-111	1
489	Splicing modulators elicit global translational repression by condensate-prone proteins translated from introns. <b>2021</b> ,	0
488	Role of ORF4 in Hepatitis E virus regulation: analysis of intrinsically disordered regions. 1	2
487	Quantification of Conformational Entropy Unravels Effect of Disordered Flanking Region in Coupled Folding and Binding. <b>2021</b> , 143, 14540-14550	4
486	Integrating single-molecule spectroscopy and simulations for the study of intrinsically disordered proteins. <b>2021</b> , 193, 116-135	6
485	Advanced Sampling Methods for Multiscale Simulation of Disordered Proteins and Dynamic Interactions. <b>2021</b> , 11,	3



484	Plasticity of the lettuce infectious yellows virus minor coat protein (CPm) in mediating the foregut retention and transmission of a chimeric CPm mutant by whitefly vectors. <b>2021</b> , 102,	0
483	Expression, solubility monitoring, and purification of the co-folded LUBAC LTM domain by structure-guided tandem folding in autoinducing cultures. <b>2021</b> , 187, 105953	1
482	High concentrations of casein proteins exacerbate radical chain reactions and increase the extent of oxidative damage. <b>2021</b> , 121, 107060	4
481	Unifying coarse-grained force fields for folded and disordered proteins. <b>2021</b> , 72, 63-70	4
480	Molecular basis of small-molecule binding to $\beta$ -synuclein.	0
479	The diversity of molecular interactions involving intrinsically disordered proteins: A molecular modeling perspective. <b>2021</b> , 19, 3817-3828	0
478	Structural Aspects of Protein-Protein Interactions. <b>2021</b> , 61-112	
477	Suppression of aggregate and amyloid formation by a novel intrinsically disordered region in metazoan Hsp110 chaperones. <b>2021</b> , 296, 100567	4
476	Suppression of aggregate and amyloid formation by a novel intrinsically disordered region in metazoan Hsp110 chaperones.	
475	Computational investigations on the dynamic binding effect of molecular tweezer CLR01 toward intrinsically disordered HIV-1 Nef. <b>2021</b> , 68, 513-530	1
474	SCHOOL model and new targeting strategies. <b>2008</b> , 640, 268-311	13
473	Application of Isothermal Titration Calorimetry in Exploring the Extended Interface. <b>2007</b> , 231-254	4
472	$\beta$ -Synuclein Aggregation and Parkinson's Disease. <b>2007</b> , 61-110	2
471	Disordered RNA-Binding Region Prediction with DisoRDPbind. <b>2020</b> , 2106, 225-239	9
470	Quantitative Protein Disorder Assessment Using NMR Chemical Shifts. <b>2020</b> , 2141, 303-317	5
469	Computational Prediction of Disordered Protein Motifs Using SLiMSuite. <b>2020</b> , 2141, 37-72	4
468	Analyzing IDPs in Interactomes. <b>2020</b> , 2141, 895-945	7
467	Analyzing the Sequences of Intrinsically Disordered Regions with CIDER and localCIDER. <b>2020</b> , 2141, 103-126	6

466	Bioinformatics Approaches to the Structure and Function of Intrinsically Disordered Proteins. <b>2009</b> , 113-140	1
465	Structural Disorder and Its Connection with Misfolding Diseases. <b>2009</b> , 1-19	4
464	Enhanced prediction of conformational flexibility and phosphorylation in proteins. <b>2010</b> , 680, 307-19	8
463	Interplay between protein order, disorder and oligomericity in receptor signaling. <b>2012</b> , 725, 50-73	6
462	Insoluble protein characterization by circular dichroism (CD) spectroscopy and nuclear magnetic resonance (NMR). <b>2015</b> , 1258, 371-85	2
461	Prediction and analysis of intrinsically disordered proteins. <b>2015</b> , 1261, 35-59	6
460	In silico protein motif discovery and structural analysis. <b>2011</b> , 760, 341-53	1
459	Fusion Oncogenes of Sarcomas. <b>2015</b> , 321-331	1
458	Cytokine Receptors. <b>2016</b> , 1-29	2
457	No Molecule Is an Island: Molecular Evolution and the Study of Sequence Space. <b>2009</b> , 675-704	1
456	Extracting Structural Information from Residual Chemical Shift Anisotropy: Analytic Solutions for Peptide Plane Orientations and Applications to Determine Protein Structure. <b>2013</b> , 271-284	2
455	Overview of Fibrillar and Oligomeric Assemblies of Amyloidogenic Proteins. <b>2012</b> , 1-36	2
454	Conformational Motions of Disordered Proteins. <b>2018</b> , 381-399	1
453	Allosteric Modulation of Intrinsically Disordered Proteins. <b>2019</b> , 1163, 335-357	4
452	Overview of Autophagy. <b>2016</b> , 3-73	1
451	How to learn from inconsistencies: Integrating molecular simulations with experimental data. <b>2020</b> , 170, 123-176	35
450	Recent advances in measuring the kinetics of biomolecules by NMR relaxation dispersion spectroscopy. <b>2017</b> , 628, 81-91	19
449	miRNA mediated regulation of NAC transcription factors in plant development and environment stress response. <b>2017</b> , 11, 190-198	27

448	Making the Case for Disordered Proteins and Biomolecular Condensates in Bacteria. <b>2020</b> , 45, 668-680	30
447	The Effects of Chain Length on the Structural Properties of Intrinsically Disordered Proteins in Concentrated Solutions. <b>2020</b> , 124, 11843-11853	9
446	The Effect of Amino Acid Size on the Internal Dynamics and Conformational Freedom of Polypeptides. <b>2020</b> , 53, 9811-9822	4
445	Intrinsically disordered proteins and membranes: a marriage of convenience for cell signalling?. <b>2020</b> , 48, 2669-2689	14
444	Intrinsically disordered protein regions and phase separation: sequence determinants of assembly or lack thereof. <b>2020</b> , 4, 307-329	42
443	Mapping the transition state for a binding reaction between ancient intrinsically disordered proteins. <b>2020</b> , 295, 17698-17712	7
442	Genomic, phylogenetic, and cell biological insights into metazoan origins. <b>2009</b> , 24-32	12
441	The mouth, the anus, and the blastopore—open questions about questionable openings. <b>2009</b> , 33-40	18
440	Origins of metazoan body plans: the larval revolution. <b>2009</b> , 43-51	2
439	Assembling the spiralian tree of life. <b>2009</b> , 52-64	26
438	The origins and evolution of the Ecdysozoa. <b>2009</b> , 71-79	2
437	Deciphering deuterostome phylogeny: molecular, morphological, and palaeontological perspectives. <b>2009</b> , 80-92	5
436	Invertebrate Problematica: kinds, causes, and solutions. <b>2009</b> , 107-126	2
435	Improvement of molecular phylogenetic inference and the phylogeny of Bilateria. <b>2009</b> , 127-138	1
434	Beyond linear sequence comparisons: the use of genome-level characters for phylogenetic reconstruction. <b>2009</b> , 139-147	1
433	The animal in the genome: comparative genomics and evolution. <b>2009</b> , 148-156	1
432	MicroRNAs and metazoan phylogeny: big trees from little genes. <b>2009</b> , 157-170	26
431	Reassembling animal evolution: a four-dimensional puzzle. <b>2009</b> , 191-196	2

430	Connecting the dots: from nanodomains to physiological functions of REMORINs. <b>2021</b> , 185, 632-649	8
429	Characterization of the banana streak virus capsid protein and mapping of the immunodominant continuous B-cell epitopes to the surface-exposed N terminus. <b>2016</b> , 97, 3446-3457	6
428	Human cytomegalovirus phosphoproteins are hypophosphorylated and intrinsically disordered. <b>2017</b> , 98, 471-485	6
427	The mechanism of coupled folding-upon-binding of an intrinsically disordered protein.	0
426	How mutations of intrinsically disordered protein regions can drive cancer.	4
425	Kinome-wide RNAi screen uncovers role of Ballchen in maintenance of gene activation by trithorax group in Drosophila.	0
424	A comprehensive motifs-based interactome of the C/EBP $\beta$ transcription factor.	1
423	Environmental Dependence of the Structure of the C-terminal Domain of the SARS-CoV-2 Envelope Protein.	1
422	A 20S proteasome receptor for degradation of intrinsically disordered proteins.	2
421	Interplay between folding and binding modulates protein sequences, structures, functions and regulation.	1
420	Cellular labelling favours unfolded proteins.	4
419	The impact of protein architecture on adaptive evolution.	0
418	Regulation of the 20S proteasome by a novel family of inhibitory proteins.	1
417	Interplay of disordered and ordered regions of a human small heat shock protein yields an ensemble of "quasi-ordered" states.	1
416	Networks of interbasin traffic in intrinsically disordered proteins. <b>2020</b> , 2,	4
415	What macromolecular crystallogensis tells us - what is needed in the future. <b>2017</b> , 4, 340-349	9
414	Crystal structures of human Fabs targeting the Bexsero meningococcal vaccine antigen NHBA. <b>2017</b> , 73, 305-314	4
413	The atypical thiol-disulfide exchange protein DsbA2 from Wolbachia pipientis is a homotrimeric disulfide isomerase. <b>2019</b> , 75, 283-295	3

412	Temperature-Dependent Molecular Adaptation Features in Proteins. 75-85	4
411	Computational Prediction of Protein Complexes from Protein Interaction Networks. <b>2017</b> ,	11
410	Constructing Reliable Protein-Protein Interaction (PPI) Networks. <b>2017</b> , 15	1
409	On the intrinsic disorder status of the major players in programmed cell death pathways. <b>2013</b> , 2, 190	18
408	Why do proteins aggregate? "Intrinsically insoluble proteins" and "dark mediators" revealed by studies on "insoluble proteins" solubilized in pure water. <b>2013</b> , 2, 94	29
407	An intrinsically disordered proteins community for ELIXIR. <b>2019</b> , 8,	7
406	New technologies to analyse protein function: an intrinsic disorder perspective. <b>2020</b> , 9,	9
405	Prediction of Intrinsic Disorder in MERS-CoV/HCoV-EMC Supports a High Oral-Fecal Transmission. <b>2013</b> , 5,	48
404	Residual structures, conformational fluctuations, and electrostatic interactions in the synergistic folding of two intrinsically disordered proteins. <b>2012</b> , 8, e1002353	73
403	Molecular Dynamics of "Fuzzy" Transcriptional Activator-Coactivator Interactions. <b>2016</b> , 12, e1004935	9
402	Recognition of HIV-1 peptides by host CTL is related to HIV-1 similarity to human proteins. <b>2007</b> , 2, e823	23
401	Identification of a novel modulator of thyroid hormone receptor-mediated action. <b>2007</b> , 2, e1183	37
400	Improved disorder prediction by combination of orthogonal approaches. <b>2009</b> , 4, e4433	157
399	A peek into tropomyosin binding and unfolding on the actin filament. <b>2009</b> , 4, e6336	24
398	Human sirt-1: molecular modeling and structure-function relationships of an unordered protein. <b>2008</b> , 4, e7350	49
397	Sequencing of DISC1 pathway genes reveals increased burden of rare missense variants in schizophrenia patients from a northern Swedish population. <b>2011</b> , 6, e23450	41
396	Binding-folding induced regulation of AF1 transactivation domain of the glucocorticoid receptor by a cofactor that binds to its DNA binding domain. <b>2011</b> , 6, e25875	21
395	High affinity antibodies to Plasmodium falciparum merozoite antigens are associated with protection from malaria. <b>2012</b> , 7, e32242	44

394	Biochemical characterization and evaluation of a <i>Brugia malayi</i> small heat shock protein as a vaccine against lymphatic filariasis. <b>2012</b> , 7, e34077	39
393	MSMEG_2731, an uncharacterized nucleic acid binding protein from <i>Mycobacterium smegmatis</i> , physically interacts with RPS1. <b>2012</b> , 7, e36666	2
392	Intrinsically unstructured domain 3 of hepatitis C Virus NS5A forms a "fuzzy complex" with VAPB-MSP domain which carries ALS-causing mutations. <b>2012</b> , 7, e39261	34
391	Molecular phylogeny of OVOL genes illustrates a conserved C2H2 zinc finger domain coupled by hypervariable unstructured regions. <b>2012</b> , 7, e39399	19
390	Protein disorder and short conserved motifs in disordered regions are enriched near the cytoplasmic side of single-pass transmembrane proteins. <b>2012</b> , 7, e44389	14
389	PROSPER: an integrated feature-based tool for predicting protease substrate cleavage sites. <b>2012</b> , 7, e50300	186
388	The <i>Arabidopsis thaliana</i> SERK1 kinase domain spontaneously refolds to an active state in vitro. <b>2012</b> , 7, e50907	5
387	Interaction of the transactivation domain of B-Myb with the TAZ2 domain of the coactivator p300: molecular features and properties of the complex. <b>2012</b> , 7, e52906	6
386	Genome-wide analysis of protein disorder in <i>Arabidopsis thaliana</i> : implications for plant environmental adaptation. <b>2013</b> , 8, e55524	44
385	Marked variability in the extent of protein disorder within and between viral families. <b>2013</b> , 8, e60724	40
384	Highly efficient NMR assignment of intrinsically disordered proteins: application to B- and T cell receptor domains. <b>2013</b> , 8, e62947	39
383	The transcriptional repressor domain of Gli3 is intrinsically disordered. <b>2013</b> , 8, e76972	5
382	On the encoding of proteins for disordered regions prediction. <b>2013</b> , 8, e82252	8
381	The intrinsically disordered regions of the <i>Drosophila melanogaster</i> Hox protein ultrabithorax select interacting proteins based on partner topology. <b>2014</b> , 9, e108217	12
380	A disordered region in the EvpP protein from the type VI secretion system of <i>Edwardsiella tarda</i> is essential for EvpC binding. <b>2014</b> , 9, e110810	5
379	The lifestyle switch protein Bd0108 of <i>Bdellovibrio bacteriovorus</i> is an intrinsically disordered protein. <b>2014</b> , 9, e115390	5
378	An ensemble method with hybrid features to identify extracellular matrix proteins. <b>2015</b> , 10, e0117804	18
377	Systematically constructing kinetic transition network in polypeptide from top to down: trajectory mapping. <b>2015</b> , 10, e0125932	9

376	Evolutionarily conserved network properties of intrinsically disordered proteins. <b>2015</b> , 10, e0126729	12
375	Continuous Distributed Representation of Biological Sequences for Deep Proteomics and Genomics. <b>2015</b> , 10, e0141287	329
374	Mutation of the CH1 Domain in the Histone Acetyltransferase CREBBP Results in Autism-Relevant Behaviors in Mice. <b>2016</b> , 11, e0146366	13
373	Transient helicity in intrinsically disordered Axin-1 studied by NMR spectroscopy and molecular dynamics simulations. <b>2017</b> , 12, e0174337	5
372	The crystal structure of the Leishmania infantum Silent Information Regulator 2 related protein 1: Implications to protein function and drug design. <b>2018</b> , 13, e0193602	11
371	Mechanisms of Macromolecular Interactions Mediated by Protein Intrinsic Disorder. <b>2020</b> , 43, 899-908	6
370	Regularization of Environment-Induced Transitions in Nanoscopic Systems. <b>2016</b> , 61, 627-647	3
369	Snf1 cooperates with the CWI MAPK pathway to mediate the degradation of Med13 following oxidative stress. <b>2018</b> , 5, 357-370	13
368	Is histone acetylation the most important physiological function for CBP and p300?. <b>2012</b> , 4, 247-55	78
367	Role of p27 as a transcriptional regulator. <b>2018</b> , 9, 26259-26278	18
366	Intra molecular interactions in the regulation of p53 pathway. <b>2016</b> , 5, 639-649	3
365	An Overview on Natively Unfolded Proteins. <b>2009</b> , 49, 004-010	1
364	Generation of a flexible loop structural ensemble and its application to induced-fit structural changes following ligand binding. <b>2006</b> , 2, 1-12	4
363	Disrupting self-assembly and toxicity of amyloidogenic protein oligomers by "molecular tweezers" - from the test tube to animal models. <b>2014</b> , 20, 2469-83	36
362	The Ubiquitin-Proteasome Pathway and Resistance Mechanisms Developed Against the Proteasomal Inhibitors in Cancer Cells. <b>2020</b> , 21, 1313-1325	3
361	Recent Studies on Design and Development of Drugs Against Alzheimer's Disease (AD) Based on Inhibition of BACE-1 and Other AD-causative Agents. <b>2020</b> , 20, 1195-1213	4
360	Ion Mobility Spectrometry-Mass Spectrometry of Intrinsically Unfolded Proteins: Trying to Put Order into Disorder. <b>2013</b> , 9, 181-191	19
359	A structural model of latent evolutionary potentials underlying neutral networks in proteins. <b>2007</b> , 1, 79-87	33

358	Molecular Dynamics Simulations in Drug Discovery and Pharmaceutical Development. <b>2021</b> , 9, 71	34
357	Protein flexibility, not disorder, is intrinsic to molecular recognition. <b>2013</b> , 5, 2	54
356	Spin-label scanning reveals conformational sensitivity of the bound helical interfaces of IA3. <b>2018</b> , 5, 166-181	1
355	Molecular signaling involving intrinsically disordered proteins in prostate cancer. <b>2016</b> , 18, 673-81	5
354	Nonalgorithmicity and algorithmicity of protein science. <b>2011</b> , 02, 340-346	1
353	Complex interactomes and post-translational modifications of the regulatory proteins HABP4 and SERBP1 suggest pleiotropic cellular functions. <b>2019</b> , 10, 44-64	4
352	Arabidopsis thaliana Remorins Interact with SnRK1 and Play a Role in Susceptibility to Beet Curly Top Virus and Beet Severe Curly Top Virus. <b>2014</b> , 30, 269-78	30
351	Multiple hTAF(II)31-binding motifs in the intrinsically unfolded transcriptional activation domain of VP16. <b>2009</b> , 42, 411-7	16
350	Intrinsic disorder within an AKAP-protein kinase A complex guides local substrate phosphorylation. <b>2013</b> , 2, e01319	79
349	A physical model describing the interaction of nuclear transport receptors with FG nucleoporin domain assemblies. <b>2016</b> , 5,	46
348	Origin of a folded repeat protein from an intrinsically disordered ancestor. <b>2016</b> , 5,	23
347	Dual interaction of scaffold protein Tim44 of mitochondrial import motor with channel-forming translocase subunit Tim23. <b>2017</b> , 6,	30
346	Development of Bag-1L as a therapeutic target in androgen receptor-dependent prostate cancer. <b>2017</b> , 6,	23
345	Cryo-EM structure of the SAGA and NuA4 coactivator subunit Tra1 at 3.7 angstrom resolution. <b>2017</b> , 6,	28
344	Autoinhibition of ankyrin-B/G membrane target bindings by intrinsically disordered segments from the tail regions. <b>2017</b> , 6,	14
343	Interplay of disordered and ordered regions of a human small heat shock protein yields an ensemble of 'quasi-ordered' states. <b>2019</b> , 8,	23
342	Intrinsically disordered caldesmon binds calmodulin via the "buttons on a string" mechanism. <b>2015</b> , 3, e1265	7
341	Bioinformatics analysis identifies several intrinsically disordered human E3 ubiquitin-protein ligases. <b>2016</b> , 4, e1725	19



340	Malleable ribonucleoprotein machine: protein intrinsic disorder in the <i>Saccharomyces cerevisiae</i> spliceosome. <b>2013</b> , 1, e2	30
339	Charge neutralization as the major factor for the assembly of nucleocapsid-like particles from C-terminal truncated hepatitis C virus core protein. <b>2016</b> , 4, e2670	4
338	SubVis: an interactive R package for exploring the effects of multiple substitution matrices on pairwise sequence alignment. <b>2017</b> , 5, e3492	1
337	Association between intrinsic disorder and serine/threonine phosphorylation in <i>Mycobacterium tuberculosis</i> . <b>2015</b> , 3, e724	5
336	Functions of intrinsically disordered proteins through evolutionary lenses. <b>2021</b> , 183, 45-74	2
335	Flexible spandrels of the global plant virome: Proteomic-wide evolutionary patterns of structural intrinsic protein disorder elucidate modulation at the functional virus-host interplay. <b>2021</b> , 183, 355-409	
334	Intrinsic disorder in integral membrane proteins. <b>2021</b> , 183, 101-134	0
333	ECO: the Evidence and Conclusion Ontology, an update for 2022.. <b>2022</b> , 50, D1515-D1521	0
332	Intrinsically disordered proteins: modes of binding with emphasis on disordered domains. <b>2021</b> , 11, 210222	6
331	Flanking Disorder of the Folded Hub Domain from Radical Induced Cell Death1 Affects Transcription Factor Binding by Ensemble Redistribution. <b>2021</b> , 433, 167320	6
330	Structural and thermodynamical insights into the binding and inhibition of FIH-1 by the N-terminal disordered region of Mint3. <b>2021</b> , 297, 101304	4
329	Elucidation of Conformational Dynamics of MDM2 and Alterations Induced Upon Inhibitor Binding Using Elastic Network Simulations and Molecular Docking. <b>2021</b> , 20, 751-763	1
328	Integrative structural dynamics probing of the conformational heterogeneity in synaptosomal-associated protein 25. <b>2021</b> , 2, 100616-100616	2
327	Conservation and coevolution determine evolvability of different classes of disordered residues in human intrinsically disordered proteins. <b>2021</b> ,	1
326	Disorder-to-order transition of the amyloid- $\beta$ peptide upon lipid binding. <b>2022</b> , 280, 106700	16
325	Role of "dual-personality" fragments in HEV adaptation-analysis of Y-domain region. <b>2021</b> , 19, 154	1
324	Analysis of unstructured regions of human cytoplasmic tyrosyl-tRNA synthetase by methods of bioinformatics. <b>2005</b> , 21, 446-453	2
323	Secondary Structure Breaker in Soluble Protein. <b>2007</b> , 47, 049-053	

322 Disordered Proteins.

1

321 Research Using Energy Landscape. **2007**, 51, 487-498

320 Functional Unfolded Proteins: How, When, Where, and Why?. **2009**, 124-136

319 Mapping Protein Folding Landscapes by NMR Relaxation. **2009**, 1-11

318 Conserved developmental processes and the evolution of novel traits: wounds, embryos, veins, and butterfly eyespots. **2009**, 183-190

317 The Ediacaran emergence of bilaterians: congruence between the genetic and the geological fossil records. **2009**, 15-23

316 The evolution of nervous system centralization. **2009**, 65-70

315 The evolution of developmental gene networks: lessons from comparative studies on holometabolous insects. **2009**, 171-182

314 The earliest fossil record of the animals and its significance. **2009**, 3-14

313 Molecular genetic insights into deuterostome evolution from the direct-developing hemichordate *Saccoglossus kowalevskii*. **2009**, 93-104

312 Novel Perspectives on Protein Structure Prediction. **2010**, 179-207

311 Encyclopedia of Cancer. **2011**, 1901-1904

310 Intrinsically Disordered Proteins.

309 Spatial and Temporal Organisation of Multiprotein Systems of Cell Regulation and Signalling: What Can We Learn from NHEJ System of Double-Strand Break Repair?. **2012**, 1-31

308 A Rational Basis for System Biology in the Aging-Associated Diseases: Are Genes or Protein Modifications the Upstream Cause?. **2012**, 1, 3

307 Encyclopedia of Cancer. **2012**, 1-4

306 References. 575-608

305 Constructing Structure Ensembles of Intrinsically Disordered Proteins from Chemical Shift Data. **2015**, 108-121

0

- 304 Quantitative proteome-based guidelines for intrinsic disorder characterization.
- 303 Stability of human recombinant AIMP1/P43 protein in complex with tRNA. **2016**, 21, 49-52
- 302 Stability of human recombinant AIMP1/-43 protein in nanocomposite complex with beta-cyclodextrin. **2016**, 20, 15-18
- 301 Structure, Dynamics, and Function of Staphylococcal Nuclease. **2016**, 151-161 1
- 300 Application of linker technique to trap transiently interacting protein complexes for structural studies. **2016**, 3, e34
- 299 Antitumor Complexes Formed by Oleic Acid and Molten Globule Intermediates of Proteins. **2016**, 245-270
- 298 Unfoldomes and Unfoldomics: Introducing Intrinsically Disordered Proteins. **2016**, 125-150 1
- 297 Evolution of eIF4E-Interacting Proteins. **2016**, 207-234 1
- 296 - Molecular Thermodynamic Modeling of Fluctuation Solution Theory Properties. **2016**, 252-283
- 295 Disordered Proteins. 1-11
- 294 The relationship between relative solvent accessible surface area (rASA) and irregular structures in protean segments (ProSs). **2016**, 12, 381-387
- 293 Cytokine Receptors. **2017**, 1-29 0
- 292 Application of the ATTRACT Coarse-Grained Docking and Atomistic Refinement for Predicting Peptide-Protein Interactions. **2017**, 1561, 49-68
- 291 Intrinsically Unstructured Proteins. **2017**, 2337-2339
- 290 Evaluating Protein Complex Prediction Methods. **2017**, 91
- 289 Identifying Evolutionarily Conserved Protein Complexes. **2017**, 165
- 288 Structural propensity database of proteins.
- 287 Identifying Dynamic Protein Complexes. **2017**, 145

286 Introduction to Protein Complex Prediction. **2017**, 1

285 Open Challenges in Protein Complex Prediction. **2017**, 107

284 Preface. **2017**, xi

283 References. **2017**, 233

282 Computational Methods for Protein Complex Prediction from PPI Networks. **2017**, 59

281 Protein Complex Prediction in the Era of Systems Biology. **2017**, 185

280 Conclusion. **2017**, 225

279 Handheld highly selective plasmonic chem/biosensor using engineered binding proteins for extreme conformational changes. **2017**,

278 Sequence fingerprints distinguish erroneous from correct predictions of Intrinsically Disordered Protein Regions.

277 Successful aggregation of Tau protein labelled on its native cysteines.

276 Reconstitution of Helical Soluble  $\alpha$ -Synuclein through Transient Interaction with Lipid Interfaces.

275 Transcription activator-coactivator specificity is mediated by a large and dynamic fuzzy protein-protein complex.

274 Multi-Funnel Landscape of the Fold-Switching Protein RfaH-CTD.

273 Conformation of disordered peptides modulated by distributions of charged residues: Case study of random peptides composed of arginines and aspartic acids. **2018**, 67, 058701 1

272 Dual roles of electrostatic-steering and conformational dynamics in the binding of calcineurin $\beta$  intrinsically-disordered recognition domain to calmodulin.

271 ROLE OF THE NOTCH1 GENE IN FORMATION OF AORTIC ANEURYSM. **2018**, 53-59 0

270 Integrin  $\alpha$ 4 recognition of a linear motif of bullous pemphigoid antigen BP230 controls its recruitment to hemidesmosomes. 1

269 Analysis of genomic loci harboring 59,732 human-specific regulatory sequences reveals unique to human regulatory patterns associated with brain development.

- 268 Mechanistic insights from replica exchange molecular dynamics simulations into mutation induced disordered-to-ordered transition in Hahellin, a  $\beta$ -crystallin.
- 267 Structure Biology of Peroxisomal Proteins, Peroxins. **2019**, 221-248 0
- 266 Biophysical Chemistry. **2019**,
- 265 Novel Interaction Mechanism between the Intrinsically Disordered Proteins. **2019**, 59, 202-204
- 264 Effective concentrations enforced by intrinsically disordered linkers are governed by polymer physics. 4
- 263 Myelin Basic Protein dynamics from out-of-equilibrium functional state to degraded state in myelin.
- 262 Intrinsically disordered proteins and structured proteins with intrinsically disordered regions have different functional roles in the cell. 1
- 261 Novel Small Molecules Targeting the Intrinsically Disordered Structural Ensemble of  $\beta$ Synuclein Protect Against Diverse  $\beta$ Synuclein Mediated Dysfunctions.
- 260 Role of Pre-molten Globule Structure in Protein Amyloid Fibril Formation. **2019**, 7, 35-42
- 259 Phosphorylation of multiple proteins involved in ciliogenesis by Tau Tubulin kinase 2. 0
- 258 Controlling Structural Bias in Intrinsically Disordered Proteins Using Solution Space Scanning.
- 257 Investigations of the Underlying Mechanisms of HIF-1 $\alpha$  and CITED2 Binding to TAZ1.
- 256 Disorder and interfaces in proteins are two sides of the same coin.
- 255 Enhanced Molecular Dynamics Simulations of Intrinsically Disordered Proteins. **2020**, 2141, 391-411 1
- 254 Strategies for identifying dynamic regions in protein complexes: flexibility changes accompany methylation in chemotaxis receptor signaling states.
- 253 Bifurcated Hydrogen Bonds and the Fold Switching of Lymphotactin.
- 252 High resolution ensemble description of metamorphic and intrinsically disordered proteins using an efficient hybrid parallel tempering scheme.
- 251 Chlamydomonas ARMC2/PF27 is an obligate cargo adapter for IFT of radial spokes.

250	Computational Prediction of Intrinsic Disorder in Protein Sequences with the disCoP Meta-predictor. <b>2020</b> , 2141, 21-35	3
249	RELT stains prominently in B-cell lymphomas and binds the hematopoietic transcription factor MDFIC. <b>2020</b> , 24, 100868	0
248	Intrinsic Disorder in Plant Transcription Factor Systems: Functional Implications. <b>2020</b> , 21,	2
247	Cancer-Associated Mutations Perturb the Structure and Interactions of the Intrinsically Disordered p53 Transactivation Domain.	
246	A novel mode of interaction between intrinsically disordered proteins. <b>2020</b> , 17, 86-93	5
245	Determining the Protective Activity of IDPs Under Partial Dehydration and Freeze-Thaw Conditions. <b>2020</b> , 2141, 519-528	0
244	NeProc predicts binding segments in intrinsically disordered regions without learning binding region sequences. <b>2020</b> , 17, 147-154	1
243	Using Paramagnetic Probes to Study Structural Transitions in Proteins. <b>2020</b> , 219-246	
242	Evolution of an interaction between disordered proteins resulted in increased heterogeneity of the binding transition state.	
241	Lipid membrane templated misfolding and self-assembly of intrinsically disordered tau protein.	
240	DeepCLD: An efficient sequence-based predictor of intrinsically disordered proteins. <b>2021</b> , PP,	1
239	Criticality in the conformational phase transition among self-similar groups in intrinsically disordered proteins: probed by salt-bridge dynamics.	
238	The protein disorder cycle.. <b>2021</b> , 13, 1155-1162	3
237	Molecular insights into the Y-domain of hepatitis E virus using computational analyses. <b>2021</b> , 10,	
236	Conformational dynamics of $\beta$ -synuclein during the interaction with phospholipid nanodiscs by Millisecond Hydrogen Deuterium Exchange Mass Spectrometry.	
235	Splicing modulators elicit global translational repression by condensate-prone proteins translated from introns.	
234	Network of inter-basin traffic in intrinsically disordered PUMA protein. <b>2020</b> , 132, 28002	
233	Identification of seven novel mutations in keratoconus patients in a Han Chinese population. <b>2017</b> , 23, 296-305	10

232	Quasi-anharmonic analysis reveals intermediate states in the nuclear co-activator receptor binding domain ensemble. <b>2012</b> , 70-81	6
231	Modulation of p53 Transactivation Domain Conformations by Ligand Binding and Cancer-Associated Mutations. <b>2020</b> , 25, 195-206	4
230	Prediction of secondary structure population and intrinsic disorder of proteins using multitask deep learning. <b>2020</b> , 2020, 1325-1334	
229	Molecular Simulations of Intrinsically Disordered Proteins and Their Binding Mechanisms. <b>2022</b> , 2376, 343-362	
228	Physics of biomolecular recognition and conformational dynamics. <b>2021</b> , 84,	2
227	Structural Characterization of the Interaction of Hypoxia Inducible Factor-1 with Its Hypoxia Responsive Element at the -964G > A Variation Site of the Promoter Region. <b>2021</b> , 22,	1
226	Reversible Kinetic Trapping of FUS Biomolecular Condensates. <b>2021</b> , e2104247	1
225	ARMC2/PF27 is an obligate cargo adapter for IFT of radial spokes.. <b>2022</b> , 11,	3
224	The Mysterious Multitude: Structural Perspective on the Accessory Subunits of Respiratory Complex I.. <b>2021</b> , 8, 798353	7
223	Potential of rescue and reactivation of tumor suppressor p53 for cancer therapy.. <b>2022</b> , 14, 267-275	2
222	Targeting disorders in unstructured and structured proteins in various diseases.. <b>2021</b> , 281, 106742	2
221	Macromolecular Crowding Induces a Binding Competent Transient Structure in Intrinsically Disordered Gab1.. <b>2021</b> , 434, 167407	1
220	Ubiquitination of Alzheimer's-related tau protein affects liquid-liquid phase separation in a site- and cofactor-dependent manner.. <b>2022</b> , 201, 173-181	1
219	Co-opting disorder into order: Intrinsically disordered proteins and the early evolution of complex multicellularity.. <b>2022</b> , 201, 29-36	1
218	Modular peptide binders development of a predictive technology as alternative for reagent antibodies.. <b>2022</b> ,	0
217	Intrinsically Disordered Proteins (IDP): Purification Under Denaturing Conditions.. <b>2022</b> , 2406, 359-370	1
216	The intrinsically disordered TSSC4 protein acts as a helicase inhibitor, placeholder and multi-interaction coordinator during snRNP assembly and recycling.. <b>2022</b> ,	0
215	DisEnrich: Database of Enriched Regions in Human Dark Proteome.. <b>2022</b> ,	

214	Systematic Modeling, Prediction, and Comparison of Domain-Peptide Affinities: Does it Work Effectively With the Peptide QSAR Methodology?. <b>2021</b> , 12, 800857	5
213	Rational design of a helical peptide inhibitor targeting c-Myb-KIX interaction.. <b>2022</b> , 12, 816	2
212	Conformational dynamics promotes disordered regions from function-dispensable to essential in evolved site-specific DNA recombinases.. <b>2022</b> , 20, 989-1001	0
211	The Intrinsically Disordered Region of Coronins Fine-tunes Oligomerization and Actin Polymerization.	
210	Databases for intrinsically disordered proteins.. <b>2022</b> , 78, 144-151	
209	Identification and functional characterization of transcriptional activators in human cells.. <b>2022</b> ,	4
208	Multiscale relaxation dynamics and diffusion of myelin basic protein in solution studied by quasielastic neutron scattering.. <b>2022</b> , 156, 025102	0
207	Conformational and Solvation Dynamics of an Amyloidogenic Intrinsically Disordered Domain of a Melanosomal Protein.. <b>2022</b> ,	0
206	Oxidative Stress-Induced Misfolding and Inclusion Formation of Nrf2 and Keap1.. <b>2022</b> , 11,	0
205	The importance of the compact disordered state in the fuzzy interactions between intrinsically disordered proteins.. <b>2022</b> , 13, 2363-2377	2
204	Self-Diffusive Properties of the Intrinsically Disordered Protein Histatin 5 and the Impact of Crowding Thereon: A Combined Neutron Spectroscopy and Molecular Dynamics Simulation Study.. <b>2022</b> ,	1
203	Dual-Inhibition of Human N-Myristoyltransferase Subtypes Halts Common Cold Pathogenesis: Atomistic Perspectives from The Case Of IMP-1088.. <b>2021</b> ,	1
202	Analysis of structure and dynamics of intrinsically disordered regions in proteins using solution NMR methods. <b>2022</b> , 535-550	
201	Multiple in vivo roles for the C-terminal domain of the RNA chaperone Hfq.. <b>2022</b> ,	2
200	Intrinsically disordered proteins/regions and insight into their biomolecular interactions.. <b>2022</b> , 283, 106769	5
199	Structures of highly flexible intracellular domain of human $\alpha 7$ nicotinic acetylcholine receptor.. <b>2022</b> , 13, 793	2
198	Barcoded Bulk QTL mapping reveals highly polygenic and epistatic architecture of complex traits in yeast.. <b>2022</b> , 11,	3
197	Rules of Physical Mathematics Govern Intrinsically Disordered Proteins.. <b>2022</b> ,	1



196	Molecular Basis of Small-Molecule Binding to Synuclein.. <b>2022</b> ,	2
195	Identification of Catechins Binding Pockets in Monomeric A $\beta$ 42 Through Ensemble Docking and MD Simulations.	1
194	DeepIDP-2L: protein intrinsically disordered region prediction by combining convolutional attention network and hierarchical attention network. <b>2021</b> ,	1
193	Ultrafast dynamics-driven biomolecular recognition where fast activities dictate slow events. <b>2018</b> , 43, 485-498	
192	Contact-Based Analysis of Aggregation of Intrinsically Disordered Proteins.. <b>2022</b> , 2340, 105-120	
191	The auto-inhibition mechanism of transcription factor Ets-1 induced by phosphorylation on the intrinsically disordered region.. <b>2022</b> , 20, 1132-1141	0
190	Intrinsically Disordered Proteins: Perspective on COVID-19 Infection and Drug Discovery.. <b>2022</b> ,	4
189	The ankyrin repeat protein RARP-1 is a periplasmic factor that supports Rickettsia parkeri growth and host cell invasion.	
188	Identifying Intrinsically Disordered Protein Regions through a Deep Neural Network with Three Novel Sequence Features.. <b>2022</b> , 12,	
187	Intrinsically Disordered Proteins: Critical Components of the Wetware.. <b>2022</b> ,	4
186	Cognate DNA Recognition by Engrailed Homeodomain Involves a Conformational Change Controlled via an Electrostatic-Spring-Loaded Latch.. <b>2022</b> , 23,	
185	Salt Induced Transitions in the Conformational Ensembles of Intrinsically Disordered Proteins.	0
184	The dark proteome of rodent hepatitis E virus: Analysis of intrinsically disordered regions. <b>2022</b> , 8, 005-011	0
183	Regulatory Roles of the N-Terminal Intrinsically Disordered Region of Modular Src.. <b>2022</b> , 23,	0
182	Intrinsically disordered proteins play diverse roles in cell signaling.. <b>2022</b> , 20, 20	8
181	Conformational Dynamics of Intrinsically Disordered Proteins Regulate Biomolecular Condensate Chemistry.. <b>2022</b> , 122, 6719-6748	5
180	Soft disorder modulates the assembly path of protein complexes.	
179	A multi-factor trafficking site on the spliceosome remodeling enzyme BRR2 recruits C9ORF78 to regulate alternative splicing.. <b>2022</b> , 13, 1132	2

- 178 Stereochemistry of transient protein-protein interactions in a signaling hub: exploring G3BP1-mediated regulation of CFTR deubiquitination.
- 177 Hornerin deposits in neuronal intranuclear inclusion disease: direct identification of proteins with compositionally biased regions in inclusions.. **2022**, 10, 28 ○
- 176 Molecular Modeling is an Enabling Approach to Complement and Enhance Channelopathy Research.. **2022**, 12, 3141-3166
- 175 Contiguously hydrophobic sequences are functionally significant throughout the human exome.. **2022**, 119, e2116267119 ○
- 174 The PentUnFOLD algorithm as a tool to distinguish the dark and the light sides of the structural instability of proteins.. **2022**, 1 ○
- 173 Prediction of Intrinsically Disordered Proteins Using Machine Learning Based on Low Complexity Methods. **2022**, 15, 86
- 172 Proteomic analysis of heat-stable proteins revealed an increased proportion of proteins with compositionally biased regions.. **2022**, 12, 4347 ○
- 171 Intrinsically disordered proteins: Ensembles at the limits of Anfinsen's dogma. **2022**, 3, 011306 1
- 170 Integrative conformational ensembles of Sic1 using different initial pools and optimization methods.
- 169 Inferring bound structure and residue specific contributions to binding energetics in the Intrinsically Disordered Protein, CcdA. 1
- 168 Acquired disorder and asymmetry in a domain-swapped model for  $\beta$ -crystallin aggregation.. **2022**, 167559
- 167 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 ○
- 166 Small Molecules Targeting the Disordered Transactivation Domain of the Androgen Receptor Induce the Formation of Collapsed Helical States. ○
- 165 Tracing the genetics of neurological disease to the mutation-directed addition of single hydrogen bonds.
- 164 Predicting Protein-Peptide Complex Structures by Accounting for Peptide Flexibility and the Physicochemical Environment.. **2021**, 1
- 163 Examining the Ensembles of Amyloid- $\beta$  Monomer Variants and Their Propensities to Form Fibers Using an Energy Landscape Visualization Method.. **2021**, 4
- 162 IFP35 Is a Relevant Factor in Innate Immunity, Multiple Sclerosis, and Other Chronic Inflammatory Diseases: A Review.. **2021**, 10, ○
- 161 Synergies of Single Molecule Fluorescence and NMR for the Study of Intrinsically Disordered Proteins.. **2021**, 12, 1

160	Spatial covariance analysis reveals the residue-by-residue thermodynamic contribution of variation to the CFTR fold.. <b>2022</b> , 5, 356	2
159	Identification of Intrinsically Disordered Proteins and Regions in a Non-Model Insect Species (Hbn.).. <b>2022</b> , 12,	0
158	Liquid-liquid phase separation as an organizing principle of intracellular space: overview of the evolution of the cell compartmentalization concept.. <b>2022</b> , 79, 251	9
157	Macromolecular crowding and intrinsically disordered proteins: a polymer physics perspective..	1
156	Chapter 12. Molecular Modelling and Simulations Applied to Challenging Drug Discovery Targets. 317-348	
155	DataSheet_1.docx. <b>2019</b> ,	
154	presentation_1.PDF. <b>2018</b> ,	
153	Data_Sheet_1.PDF. <b>2019</b> ,	
152	Data_Sheet_1.docx. <b>2019</b> ,	
151	Table_2.XLSX. <b>2019</b> ,	
150	Image_1.JPEG. <b>2019</b> ,	
149	Image_2.JPEG. <b>2019</b> ,	
148	Image_3.jpg. <b>2019</b> ,	
147	Table_1.DOCX. <b>2019</b> ,	
146	Data_Sheet_1.docx. <b>2020</b> ,	
145	Image_1.TIF. <b>2018</b> ,	
144	Image_2.TIF. <b>2018</b> ,	
143	Image_3.TIF. <b>2018</b> ,	

142	Table_1.pdf. <b>2018,</b>	
141	DataSheet_1.xlsx. <b>2019,</b>	
140	Presentation_1.pdf. <b>2019,</b>	
139	DataSheet_1.pdf. <b>2019,</b>	
138	Table_1.xlsx. <b>2019,</b>	
137	Insights into Membrane Curvature Sensing and Membrane Remodeling by Intrinsically Disordered Proteins and Protein Regions.. <b>2022,</b> 1	2
136	NMR Provides Unique Insight into the Functional Dynamics and Interactions of Intrinsically Disordered Proteins.. <b>2022,</b>	4
135	Allostery in the dynamic coactivator domain KIX occurs through minor conformational micro-states.. <b>2022,</b> 18, e1009977	
134	Post-translational modifications in liquid-liquid phase separation: a comprehensive review.. <b>2022,</b> 3, 13	2
133	Comprehensive Folding Variations for Protein Folding.. <b>2022,</b>	0
132	Comparative Analysis of Structural Features in SLiMs from Eukaryotes, Bacteria, and Viruses with Importance for Host-Pathogen Interactions. <b>2022,</b> 11, 583	0
131	The Role of Nonapoptotic Programmed Cell Death [Ferroptosis, Necroptosis, and Pyroptosis] in Pancreatic Ductal Adenocarcinoma Treatment. <b>2022,</b> 12,	0
130	Predicting protein-peptide binding residues via interpretable deep learning.	2
129	Insights into the client protein release mechanism of the ATP-independent chaperone Spy. <b>2022,</b> 13,	1
128	Molecular Gymnastics Required for Mdmx Inhibition of P53 DNA Binding Activity.	
127	Acidic dileucine motifs in the cylindrical inclusion protein of turnip mosaic virus are crucial for endosomal targeting and viral replication.	1
126	Plant phase extraction (PPE): A novel method for enhanced discovery of RNA-binding proteome in plants.	1
125	The RGG motif proteins: Interactions, functions, and regulations.	0

- 124 The Ankyrin Repeat Protein RARP-1 Is a Periplasmic Factor That Supports *Rickettsia parkeri* Growth and Host Cell Invasion. 0
- 123 Variation of Structural and Dynamical Flexibility of Myelin Basic Protein in Response to Guanidinium Chloride. **2022**, 23, 6969 1
- 122 TransDFL: Identification of Disordered Flexible Linkers in Proteins by Transfer Learning. 0
- 121 Electronic Polarization at the Interface between the p53 Transactivation Domain and Two Binding Partners. 0
- 120 HIV-1 mutants expressing B cell clonogenic matrix protein p17 variants are increasing their prevalence worldwide. **2022**, 119, 0
- 119 SETH predicts nuances of residue disorder from protein embeddings. 0
- 118 Zinc finger structure determination by NMR: why zinc fingers can be a handful. **2022**, 0
- 117 Activation of p53: How phosphorylated Ser15 triggers sequential phosphorylation of p53 at Thr18 by CK1 $\beta$ . 0
- 116 Integrative Conformational Ensembles of Sic1 Using Different Initial Pools and Optimization Methods. 9, 2
- 115 Negative Thermal Expansion and Disorder-to-Order Collapse of an Intrinsically Disordered Protein under Marginally Denaturing Conditions. **2022**, 126, 5055-5065 0
- 114 Membrane cholesterol modulates the dynamics and depth of penetration of  $\beta$ -casein. **2022**, 119849 0
- 113 Deciphering the conformations and dynamics of FG-nucleoporins in situ. 0
- 112 Enhancing and inhibitory motifs regulate CD4 activity. 11, 1
- 111 Hepatitis C Virus Infection and Intrinsic Disorder in the Signaling Pathways Induced by Toll-Like Receptors. **2022**, 11, 1091 0
- 110 A unified model for the surveillance of translation in diverse noncoding sequences. 0
- 109 Foreword. **2009**, v-vi 0
- 108 Copyright Page. **2009**, iv-iv 0
- 107 Contributors. **2009**, xi-xii 0

106 Introduction. **2009**, xiii-xvi

105 Critical roles for Housekeeping Nucleases in Type III CRISPR-Cas immunity. 0

104 Remodeling of the Plasma Membrane by Surface-Bound Protein Monomers and Oligomers: The Critical Role of Intrinsically Disordered Regions. 0

103 PSICalc: A novel approach to identifying and ranking critical non-proximal interdependencies within the overall protein structure.

102 Graph-based Automated Macro-Molecule Assembly. **2022**, 62, 3714-3723

101 Salt-Induced Transitions in the Conformational Ensembles of Intrinsically Disordered Proteins. **2022**, 126, 5959-5971 2

100 Specific phosphorylation of microtubule-associated protein 2c by extracellular signal-regulated kinase reduces interactions at its Pro-rich regions. **2022**, 102384

99 Predicting molecular properties of Synuclein using force fields for intrinsically disordered proteins. 0

98 A context-dependent and disordered ubiquitin-binding motif. **2022**, 79, 0

97 Flexible Target Recognition of the Intrinsically Disordered DNA-Binding Domain of CytR Monitored by Single-Molecule Fluorescence Spectroscopy. **2022**, 126, 6136-6147

96 Correlating multi-functional role of cold shock domain proteins with intrinsically disordered regions. **2022**, 220, 743-753 0

95 The role of NUPR1 in response to stress and cancer development. **2022**, 454, 116244 0

94 Drugging the Undruggable: Targeting the N-Terminal Domain of Nuclear Hormone Receptors. **2022**, 311-326 1

93 Proteomic and Transcriptomic Analyses in the Slipper Snail *Crepidula fornicata* Uncover Shell Matrix Genes Expressed During Adult and Larval Biomineralization. **2022**, 4, 1

92 Cryo-electron Microscopy to Analyze the Structure of Bacterial Amyloids In Vitro. **2022**, 13-23 0

91 A Novel SPR Based Method for Measuring Diffusion Coefficients: From Small Molecules to Supramolecular Aggregates. 0

90 Tryptophan mutations in G3BP1 tune the stability of a cellular signaling hub by weakening transient interactions with Caprin1 and USP10. **2022**, 102552 0

89 Carboxyl terminus of HOATZ is intrinsically disordered and interacts with heat shock protein A families. **2022**, 29, 0

88	Simulating Polyproline II-Helix-Rich Peptides with the Latest KirkwoodBuff Force Field: A Direct Comparison with AMBER and CHARMM.	0
87	Functional benefit of structural disorder for the replication of measles, Nipah and Hendra viruses.	2
86	Toward Accurate Coarse-Grained Simulations of Disordered Proteins and Their Dynamic Interactions. <b>2022</b> , 62, 4523-4536	1
85	Convergent views on disordered protein dynamics from NMR and computational approaches. <b>2022</b> ,	1
84	Two short linear motifs in the MDMX acidic domain bind overlapping sites on MDMX and p53. <b>2022</b> , 167844	0
83	Comparative and evolutionary analysis of Arabidopsis RIN4-like/NOI proteins induced by herbivory. <b>2022</b> , 17, e0270791	0
82	Alternative proteoforms and proteoform-dependent assemblies in humans and plants.	0
81	AMBRA1 and its role as a target for anticancer therapy. 12,	0
80	Studies on the Escherichia coli ExbD Transmembrane Domain, Residue L132, and an Inhibitory Cyclic Peptide.	0
79	Accurate Prediction for ProteinPeptide Binding Based on High-Temperature Molecular Dynamics Simulations.	0
78	Lineage-specific protein repeat expansions and contractions reveal malleable regions of immune genes.	0
77	pH Induced Switch in the Conformational Ensemble of Intrinsically Disordered Protein Prothymosin- $\beta$ and Its Implications for Amyloid Fibril Formation. 9589-9598	0
76	P311 promotes type II transforming growth factor- $\beta$ receptor mediated fibroblast activation and granulation tissue formation in wound healing. <b>2022</b> , 10,	0
75	Cross-Linking Mass Spectrometry Analysis of Metastable Compact Structures in Intrinsically Disordered Proteins. <b>2023</b> , 189-201	0
74	Prediction of Intrinsic Disorder Using Rosetta ResidueDisorder and AlphaFold2. <b>2022</b> , 126, 8439-8446	2
73	Small molecules targeting the disordered transactivation domain of the androgen receptor induce the formation of collapsed helical states. <b>2022</b> , 13,	3
72	DPCfam: Unsupervised protein family classification by Density Peak Clustering of large sequence datasets. <b>2022</b> , 18, e1010610	0
71	SETH predicts nuances of residue disorder from protein embeddings. 2,	0

70	The unstructured linker of Mlh1 contains a motif required for endonuclease function which is mutated in cancers. <b>2022</b> , 119,	0
69	Perspectives on evolutionary and functional importance of intrinsically disordered proteins. <b>2022</b> ,	0
68	TransDFL: Identification of Disordered Flexible Linkers in Proteins by Transfer Learning. <b>2022</b> ,	0
67	A sequence-based foldability score combined with AlphaFold2 predictions to disentangle the protein order/disorder continuum.	0
66	Looking at the Pathogenesis of the Rabies Lyssavirus Strain Pasteur Vaccins through a Prism of the Disorder-Based Bioinformatics. <b>2022</b> , 12, 1436	0
65	Evolution of the orthopoxvirus core genome. <b>2023</b> , 323, 198975	0
64	Rapid Prediction and Analysis of Protein Intrinsic Disorder.	2
63	Shapeshifting tau: from intrinsically disordered to paired-helical filaments.	1
62	Enrichment of charge-absent regions in phase separated proteins.	0
61	Intrinsically Disordered Proteins: An Overview. <b>2022</b> , 23, 14050	2
60	Clustering conformational ensembles of intrinsically disordered proteins with t-distributed stochastic neighbor embedding.	1
59	Soft disorder modulates the assembly path of protein complexes. <b>2022</b> , 18, e1010713	0
58	Twisting development, the birth of a potential new gene. <b>2022</b> , 105627	0
57	Universality and Identity Ordering in Heteropolymer Coil-Globule Transition.	1
56	Disordered protein networks as mechanistic drivers of membrane remodeling and endocytosis. <b>2023</b> , 427-454	0
55	Intrinsic disorder and posttranslational modification: an evolutionary perspective. <b>2023</b> , 377-396	0
54	Structure and disorder: protein functions depend on this new binary transforming lock-and-key into structure-function continuum. <b>2023</b> , 127-148	0
53	Prediction of protein structure and intrinsic disorder in the era of deep learning. <b>2023</b> , 199-224	0



52	Computer simulation of molecular recognition in biomolecular system: from in silico screening to generalized ensembles.	1
51	Aggregation propensities of proteins with varying degrees of disorder.	0
50	NMR insights into dynamic, multivalent interactions of intrinsically disordered regions: from discrete complexes to condensates. <b>2022</b> , 66, 863-873	2
49	Critical roles for Housekeeping nucleases in type III CRISPR-Cas immunity. 11,	0
48	Cargo adapters expand the transport range of intraflagellar transport. <b>2022</b> , 135,	0
47	The structure, binding and function of a Notch transcription complex involving RBPJ and the epigenetic reader protein L3MBTL3.	0
46	Dynamics and composition of small heat shock protein condensates and aggregates.	0
45	Microbial biofilms are shaped by the constant dialogue between biological and physical forces in the extracellular matrix.	0
44	Arabidopsis DXO1 activates RNMT1 to methylate the mRNA guanosine cap. <b>2023</b> , 14,	0
43	Acyl-CoA-dependent and acyl-CoA-independent avocado acyltransferases positively influence oleic acid content in nonseed triacylglycerols. 13,	0
42	The SARS-CoV-2 nucleocapsid protein: its role in the viral life cycle, structure and functions, and use as a potential target in the development of vaccines and diagnostics. <b>2023</b> , 20,	2
41	Enrichment of intrinsically disordered residues in ohnologs facilitates abiotic stress resilience in Brassica rapa.	0
40	Illuminating Intrinsically Disordered Proteins with Integrative Structural Biology. <b>2023</b> , 13, 124	0
39	APLF and long non-coding RNA NIHCOLE promote stable DNA synapsis in non-homologous end joining. <b>2023</b> , 42, 111917	0
38	Intact Transition Epitope Mapping Force Differences between Original and Unusual Residues (ITEM-FOUR). <b>2023</b> , 13, 187	1
37	Mechanical and Histological Characteristics of Human Tubular Bones after Hyperthermal Treatment. <b>2023</b> , 15, 156	0
36	Solution characterization of the dynamic conjugative entry exclusion protein TraG. <b>2022</b> , 9, 064702	0
35	A Guide to In Silico Drug Design. <b>2023</b> , 15, 49	0

- 34 How AlphaFold2 Predicts Conditionally Folding Regions Annotated in an Intrinsically Disordered Protein Database, IDEAL. **2023**, 12, 182 ○
- 33 Structural preferences shape the entropic force of disordered protein ensembles. ○
- 32 Heterochromatin organization and phase separation. **2023**, 14, ○
- 31 Recent Advances on Small-Molecule Bromodomain-Containing Histone Acetyltransferase Inhibitors. **2023**, 66, 1678-1699 ○
- 30 The coexistence region in the Van der Waals fluid and the liquid-liquid phase transitions. 10, ○
- 29 CRISPR/Cas9-Targeted Disruption of Two Highly Homologous Arabidopsis thaliana DSS1 Genes with Roles in Development and the Oxidative Stress Response. **2023**, 24, 2442 ○
- 28 A novel SPR based method for measuring diffusion coefficients: From small molecules to supramolecular aggregates. **2023**, 13, 100306 ○
- 27 Aggregation of Disordered Proteins Associated with Neurodegeneration. **2023**, 24, 3380 1
- 26 Molecular Mechanisms of Functional Modulation of Transcriptional Coactivator PC4 via Phosphorylation on Its Intrinsically Disordered Region. ○
- 25 Plasma surface functionalization: A comprehensive review of advances in the quest for bioinspired materials and interfaces. **2023**, 10, 021301 ○
- 24 Mutational scan inferred binding energetics and structure in intrinsically disordered protein CcdA. **2023**, 32, ○
- 23 How Can Static and Oscillating Electric Fields Serve in Decomposing Alzheimer's and Other Senile Plaques?. **2023**, 145, 3543-3553 ○
- 22 Evo-devo beyond development: Generalizing evo-devo to all levels of the phenotypic evolution. **2023**, 45, 2200205 ○
- 21 pH Effects Can Dominate Chemical Shift Perturbations in <sup>1</sup>H,<sup>15</sup>N-HSQC NMR Spectroscopy for Studies of Small Molecule/β-Synuclein Interactions. **2023**, 14, 800-808 ○
- 20 Aberrant phase separation and nucleolar dysfunction in rare genetic diseases. ○
- 19 Coupled binding and folding of disordered SPIN N-terminal region in myeloperoxidase inhibition. 10, ○
- 18 Computational Prediction of Protein Intrinsically Disordered Region Related Interactions and Functions. **2023**, 14, 432 ○
- 17 Expression, purification, and characterisation of the p53 binding domain of Retinoblastoma binding protein 6 (RBBP6). **2023**, 18, e0277478 ○

- 16 Benchmarking Molecular Dynamics Force Fields for All-Atom Simulations of Biological Condensates. ○
- 15 Condensate formation of the human RNA-binding protein SMAUG1 is controlled by its intrinsically disordered regions and interactions with 14-3-3 proteins. ○
- 14 Overview of myelin, major myelin lipids, and myelin-associated proteins. 10, ○
- 13 Uncovering the Interaction Interface Between Harpin (Hpa1) and Rice Aquaporin (OsPIP1;3) Through Protein-Protein Docking: An In Silico Approach. ○
- 12 Coronavirus accessory protein ORF3 biology and its contribution to viral behavior and pathogenesis. **2023**, 26, 106280 ○
- 11 Combining experiments and simulations to examine the temperature-dependent behaviour of a disordered protein. ○
- 10 Intrinsic disorder in the open reading frame 2 of hepatitis E virus: a protein with multiple functions beyond viral capsid. **2023**, 21, ○
- 9 Dynamics-Based Regulatory Switches of Type II Antitoxins: Insights into New Antimicrobial Discovery. **2023**, 12, 637 ○
- 8 Ab Initio Modelling of the Structure of ToxA-like and MAX Fungal Effector Proteins. **2023**, 24, 6262 ○
- 7 Simultaneous Prediction of Interaction Sites on the Protein and Peptide Sides of Complexes through Multilayer Graph Convolutional Networks. **2023**, 63, 2251-2262 ○
- 6 The Oligomerization Domains of the APC Protein Mediate Liquid-Liquid Phase Separation That Is Phosphorylation Controlled. **2023**, 24, 6478 ○
- 5 pH Induced Switch in the Conformational Ensemble of an Intrinsically Disordered Protein Prothymosin- $\beta$  and Its Implications to Amyloid Fibril Formation. ○
- 4 Noncoding translation mitigation. ○
- 3 Rational peptide design for inhibition of the KIX-MLL interaction. **2023**, 13, ○
- 2 Tailoring the Formation and Stability of Self-Assembled Structures from Precisely Engineered Intrinsically Disordered Protein Polymers: A Comprehensive Review. **2023**, 100158 ○
- 1 Visualizing the disordered nuclear transport machinery in situ. **2023**, 617, 162-169 ○