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259	Selecting proteins with improved stability by a phage-based method. 1998 , 16, 955-60		176
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257	Purification and characterization of papaya glutamine cyclotransferase, a plant enzyme highly resistant to chemical, acid and thermal denaturation. 1998 , 1387, 275-90		29
256	Proteolytic selection for protein folding using filamentous bacteriophages. <i>Folding & Design</i> , 1998 , 3, 321-8		217
255	Proteolysis as a measure of the free energy difference between cytochrome c and its derivatives. <i>Protein Science</i> , 1998 , 7, 2460-4	6.3	33
254	Selective and asymmetric action of trypsin on the dimeric forms of seminal RNase. <i>Protein Science</i> , 1998 , 7, 2653-8	6.3	6
253	Identification of the binding surface on beta-lactamase for GroEL by limited proteolysis and MALDI-mass spectrometry. <i>Biochemistry</i> , 1998 , 37, 11660-9	3.2	23
252	Early steps in the unfolding of thermolysin-like proteases. 1998 , 273, 35074-7		26
251	Limited Proteolysis of Proteins by Thermolysin in Trifluoroethanol. 1998 , 15, 381-392		1
250	Proteolysis of native proteins. Trapping of a reaction intermediate. 1999 , 274, 1108-15		18
249	Importance of the carboxyl terminus in the folding and function of alpha-hemolysin of Staphylococcus aureus. 1999 , 274, 9193-9		12
248	Mutational and structural analyses of the regulatory protein B of soluble methane monooxygenase from Methylococcus capsulatus (Bath). 1999 , 6, 441-9		29
247	Structural features of a chimeric peptide inducing cytotoxic T lymphocyte responses in saline. 1999 , 265, 336-45		4
246	Denaturant mediated unfolding of both native and molten globule states of maltose binding protein are accompanied by large deltaCp@. <i>Protein Science</i> , 1999 , 8, 1689-95	6.3	29
245	Micellar electrokinetic chromatography as a complementary method to sodium dodecyl sulfate-polyacrylamide gel electrophoresis for studying limited proteolysis of proteins. 1999 , 20, 2400-	-6	1

(2001-1999)

244	Probing the modelled structure of Wheatwin1 by controlled proteolysis and sequence analysis of unfractionated digestion mixtures. 1999 , 36, 192-204		11
243	Cooperative folding units of escherichia coli tryptophan repressor. 1999 , 77, 1619-26		4
242	Unfolding and refolding of human glyoxalase II and its single-tryptophan mutants. 1999 , 291, 481-90		9
241	Autonomous protein folding units. 2000 , 53, 1-47		31
240	A new alternative method to quantify residual structure in QnfoldedQroteins. 2000, 1479, 155-65		26
239	Engineering a compact non-native state of intestinal fatty acid-binding protein. 2000, 1476, 203-18		18
238	Predicting protein function from structure: unique structural features of proteases. 2000 , 97, 3954-8		36
237	Trypsin sheds light on the singular case of seminal RNase, a dimer with two quaternary conformations. 2000 , 275, 8000-6		9
236	The interconversion of isoforms of seminal ribonuclease: modelling key intermediates and trypsin effects. 2000 , 301, 775-82		2
235	Mass spectrometry in viral proteomics. 2000 , 33, 179-87		59
234	Tryptophan mutants of intestinal fatty acid-binding protein: ultraviolet absorption and circular dichroism studies. <i>Archives of Biochemistry and Biophysics</i> , 2001 , 395, 215-24	4.1	21
233	A serpin-induced extensive proteolytic susceptibility of urokinase-type plasminogen activator implicates distortion of the proteinase substrate-binding pocket and oxyanion hole in the serpin inhibitory mechanism. 2001 , 268, 673-85		44
232	Incomplete refolding of a fragment of the N-terminal domain of pig muscle 3-phosphoglycerate kinase that lacks a subdomain. 2001 , 268, 1851-1860		5
231	Probing the conformational state of a truncated staphylococcal nuclease R using time of flight mass spectrometry with limited proteolysis. 2001 , 268, 4227-32		11
230	Stepwise proteolytic removal of the beta subdomain in alpha-lactalbumin. The protein remains folded and can form the molten globule in acid solution. 2001 , 268, 4324-33		17
229	Structure of an intermediate in the unfolding of creatine kinase. 2001 , 42, 269-278		20
229	Structure of an intermediate in the unfolding of creatine kinase. 2001 , 42, 269-278 Folding/unfolding/refolding of proteins: present methodologies in comparison with capillary zone electrophoresis. 2001 , 22, 2359-74		53

226	Conformational analysis of putative regulatory subunit D of the toluene/o-xylene-monooxygenase complex from Pseudomonas stutzeri OX1. <i>Protein Science</i> , 2001 , 10, 482-90	6.3	12
225	Ca(2+)-induced structural changes in rat m-calpain revealed by partial proteolysis. 2001 , 1545, 245-54		20
224	Patterns of adaptation in a laboratory evolved thermophilic enzyme. 2001 , 1549, 1-8		44
223	The cost of exposing a hydrophobic loop and implications for the functional role of 4.5 S RNA in the Escherichia coli signal recognition particle. 2001 , 276, 19327-31		10
222	Osmolytes stabilize ribonuclease S by stabilizing its fragments S protein and S peptide to compact folding-competent states. 2001 , 276, 28789-98		59
221	A histidine-rich metal binding domain at the N terminus of Cu,Zn-superoxide dismutases from pathogenic bacteria: a novel strategy for metal chaperoning. 2001 , 276, 30315-25		48
220	Ribonuclease L proteolysis in peripheral blood mononuclear cells of chronic fatigue syndrome patients. 2002 , 277, 35746-51		37
219	Metal ions restore the proteolytic resistance of denatured conglutin gamma, a lupin seed glycoprotein, by promoting its refolding. 2002 , 50, 2029-33		11
218	Protein secondary structure and stability determined by combining exoproteolysis and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. 2002 , 37, 974-84		14
217	Proteolysis of bovine beta-lactoglobulin during thermal treatment in subdenaturing conditions highlights some structural features of the temperature-modified protein and yields fragments with low immunoreactivity. 2002 , 269, 1362-72		41
216	Local dynamic properties of the heme pocket in native and solvent-induced molten-globule-like states of cytochrome c. <i>Biophysical Chemistry</i> , 2002 , 97, 121-8	3.5	3
215	Flexibility in monomeric Cu,Zn superoxide dismutase detected by limited proteolysis and molecular dynamics simulation. 2002 , 47, 513-20		19
214	Molten globule of bovine alpha-lactalbumin at neutral pH induced by heat, trifluoroethanol, and oleic acid: a comparative analysis by circular dichroism spectroscopy and limited proteolysis. 2002 , 49, 385-97		64
213	Energetic landscape of alpha-lytic protease optimizes longevity through kinetic stability. 2002 , 415, 34	3-6	154
212	The N-terminal domain of the phosphoprotein of Morbilliviruses belongs to the natively unfolded class of proteins. 2002 , 296, 251-62		87
211	Thermodynamics of single peptide bond cleavage in bovine pancreatic trypsin inhibitor (BPTI). <i>Protein Science</i> , 2002 , 11, 924-32	6.3	24
2 10	Reducing the computational complexity of protein folding via fragment folding and assembly. <i>Protein Science</i> , 2003 , 12, 1177-87	6.3	41
209	Extended disordered proteins: targeting function with less scaffold. 2003 , 28, 81-5		286

208	The functional benefits of protein disorder. 2003 , 666-667, 361-371		68
207	Effects of arginine on rabbit muscle creatine kinase and salt-induced molten globule-like state. 2003 , 1652, 7-16		3
206	Hierarchical protein folding pathways: a computational study of protein fragments. 2003, 51, 203-15		25
205	Protein aggregation and amyloid fibril formation by an SH3 domain probed by limited proteolysis. 2003 , 334, 129-41		93
204	The voltage-dependent calcium channel beta subunit contains two stable interacting domains. 2003 , 278, 52323-32		68
203	Investigating Viral Proteins and Intact Viruses with Mass Spectrometry. 2003, 265-282		12
202	Protein structure characterization with mass spectrometry. 2004 , 18, 37-47		9
201	Rapid subunit exchange in dimeric lipoprotein lipase and properties of the inactive monomer. 2004 , 279, 49964-72		49
200	On the sequential determinants of calpain cleavage. 2004 , 279, 20775-85		245
199	Hydrogen/deuterium exchange studies of native rabbit MM-CK dynamics. <i>Protein Science</i> , 2004 , 13, 476	-863	3
198	Potential folding-function interrelationship in proteins. 2004 , 56, 635-49		4
197	Combinatorial approaches to novel proteins. 2004 , 5, 177-82		11
196	Conformational dynamics of the GdmHCl-induced molten globule state of creatine kinase monitored by hydrogen exchange and mass spectrometry. <i>Biochemistry</i> , 2004 , 43, 5045-54	3.2	21
195	Modulation of the structural integrity of helix F in apomyoglobin by single amino acid replacements. <i>Protein Science</i> , 2004 , 13, 1572-85	6.3	27
194	Use of the phase diagram method to analyze the protein unfolding-refolding reactions: fishing out the "invisible" intermediates. 2004 , 3, 485-94		120
193	The effects of amino acid replacements of glycine 20 on conformational stability and catalysis of staphylococcal nuclease. 2004 , 86, 893-901		2
192	Comparative studies on trifluoroethanol (TFE) state of a thermophilic alpha-amylase and its mesophilic counterpart: limited proteolysis, conformational analysis, aggregation and reactivation of the enzymes. <i>International Journal of Biological Macromolecules</i> , 2004 , 34, 173-9	7.9	11
191	A highly amyloidogenic region of hen lysozyme. 2004 , 340, 1153-65		228

190	Probing the high energy states in proteins by proteolysis. 2004 , 343, 1467-76	108
189	Effect of Na+ binding on the conformation, stability and molecular recognition properties of thrombin. <i>Biochemical Journal</i> , 2005 , 390, 485-92	42
188	The Amyloid Protein. 384-491	2
187	Directed evolution of enzyme stability. 2005 , 22, 21-30	334
186	Protein dissection enhances the amyloidogenic properties of alpha-lactalbumin. 2005, 272, 2176-88	32
185	Flexible nets. The roles of intrinsic disorder in protein interaction networks. 2005 , 272, 5129-48	895
184	Showing your ID: intrinsic disorder as an ID for recognition, regulation and cell signaling. 2005, 18, 343-84	660
183	The folding landscape of an alpha-lytic protease variant reveals the role of a conserved beta-hairpin in the development of kinetic stability. 2005 , 61, 105-14	12
182	Intrinsic unstructuredness and abundance of PEST motifs in eukaryotic proteomes. 2006 , 62, 309-15	79
181	Assessing protein disorder and induced folding. 2006 , 62, 24-45	347
180	Recent developments in structural proteomics for protein structure determination. 2005, 5, 2056-68	57
179	A prokaryotic superoxide dismutase paralog lacking two Cu ligands: from largely unstructured in solution to ordered in the crystal. 2005 , 102, 7541-6	21
178	A folding-dependent mechanism of antimicrobial peptide resistance to degradation unveiled by solution structure of distinctin. 2005 , 102, 6309-14	64
177	The essential role of the flexible termini in the temperature-responsiveness of the oligomeric state and chaperone-like activity for the polydisperse small heat shock protein IbpB from Escherichia coli. 2005 , 347, 871-84	58
176	Comprehensive analysis of protein folding activation thermodynamics reveals a universal behavior violated by kinetically stable proteases. 2005 , 347, 355-66	49
175	Effects of nitration on the structure and aggregation of alpha-synuclein. 2005, 134, 84-102	127
174	Analysis of the peanut agglutinin molten globule-like intermediate by limited proteolysis. 2005 , 1725, 283-9	5
173	Maturation efficiency, trypsin sensitivity, and optical properties of Arg96, Glu222, and Gly67 variants of green fluorescent protein. <i>Biochemical and Biophysical Research Communications</i> , 2005 , 3.4 332, 657-63	60

172	The interplay between structure and function in intrinsically unstructured proteins. 2005, 579, 3346-54		563
171	Probing the subtle conformational state of N138ND2-Q106O hydrogen bonding deletion mutant (Asn138Asp) of staphylococcal nuclease using time of flight mass spectrometry with limited proteolysis. <i>Archives of Biochemistry and Biophysics</i> , 2005 , 434, 86-92	4.1	5
170	Contribution of the copper ions in the dinuclear active site to the stability of Carcinus aestuarii hemocyanin. <i>Archives of Biochemistry and Biophysics</i> , 2005 , 439, 42-52	4.1	5
169	Nanotools for megaproblems: probing protein misfolding diseases using nanomedicine modus operandi. 2006 , 5, 2505-22		24
168	Identification of the core structure of lysozyme amyloid fibrils by proteolysis. 2006, 361, 551-61		121
167	Proteolysis of bovine 🛭 actalbumin by thermolysin during thermal denaturation. 2006 , 16, 1157-1167		15
166	Limited proteolysis of human histone deacetylase 1. 2006 , 7, 22		6
165	Role of lysine versus arginine in enzyme cold-adaptation: modifying lysine to homo-arginine stabilizes the cold-adapted alpha-amylase from Pseudoalteramonas haloplanktis. 2006 , 64, 486-501		55
164	Intrinsically unstructured N-terminal domain of bZIP transcription factor HY5. 2006, 65, 856-66		28
	N. I. I. S. I. B. S. I. I. I. I. B. B. S. I. B.		
163	Molecular analysis of a human PAX6 homeobox mutant. 2006 , 14, 744-51		7
163	Identification of cysteinylation of a free cysteine in the Fab region of a recombinant monoclonal IgG1 antibody using Lys-C limited proteolysis coupled with LC/MS analysis. 2006 , 355, 165-74		7
	Identification of cysteinylation of a free cysteine in the Fab region of a recombinant monoclonal		
162	Identification of cysteinylation of a free cysteine in the Fab region of a recombinant monoclonal IgG1 antibody using Lys-C limited proteolysis coupled with LC/MS analysis. 2006 , 355, 165-74 Acidic and proteolytic digestion of Emylases from Bacillus licheniformis and Bacillus		108
162	Identification of cysteinylation of a free cysteine in the Fab region of a recombinant monoclonal IgG1 antibody using Lys-C limited proteolysis coupled with LC/MS analysis. 2006, 355, 165-74 Acidic and proteolytic digestion of Emylases from Bacillus licheniformis and Bacillus amyloliquefaciens: Stability and flexibility analysis. 2006, 38, 422-428		108
162 161 160	Identification of cysteinylation of a free cysteine in the Fab region of a recombinant monoclonal IgG1 antibody using Lys-C limited proteolysis coupled with LC/MS analysis. 2006, 355, 165-74 Acidic and proteolytic digestion of the mylases from Bacillus licheniformis and Bacillus amyloliquefaciens: Stability and flexibility analysis. 2006, 38, 422-428 Structural characterization of pollen allergens. 2006, 30, 73-95 Assessment of the conformational features of vasoactive intestinal peptide in solution by limited		108 13 10
162 161 160	Identification of cysteinylation of a free cysteine in the Fab region of a recombinant monoclonal IgG1 antibody using Lys-C limited proteolysis coupled with LC/MS analysis. 2006, 355, 165-74 Acidic and proteolytic digestion of Emylases from Bacillus licheniformis and Bacillus amyloliquefaciens: Stability and flexibility analysis. 2006, 38, 422-428 Structural characterization of pollen allergens. 2006, 30, 73-95 Assessment of the conformational features of vasoactive intestinal peptide in solution by limited proteolysis experiments. 2006, 81, 110-9 Investigation of de novo totally random biosequences, Part I: A general method for in vitro		108 13 10 7
162 161 160 159	Identification of cysteinylation of a free cysteine in the Fab region of a recombinant monoclonal IgG1 antibody using Lys-C limited proteolysis coupled with LC/MS analysis. 2006, 355, 165-74 Acidic and proteolytic digestion of the mylases from Bacillus licheniformis and Bacillus amyloliquefaciens: Stability and flexibility analysis. 2006, 38, 422-428 Structural characterization of pollen allergens. 2006, 30, 73-95 Assessment of the conformational features of vasoactive intestinal peptide in solution by limited proteolysis experiments. 2006, 81, 110-9 Investigation of de novo totally random biosequences, Part I: A general method for in vitro selection of folded domains from a random polypeptide library displayed on phage. 2006, 3, 827-39 Investigation of de novo totally random biosequences, Part II: On the folding frequency in a totally		108 13 10 7 20

154	Chaperones activate hepadnavirus reverse transcriptase by transiently exposing a C-proximal region in the terminal protein domain that contributes to epsilon RNA binding. 2007 , 81, 13354-64		52
153	Protein Crystallization. 2007, 433-446		
152	Modeling Protein Aggregate Assembly and Structure. 2007 , 279-317		3
151	Histone deacetylase 1 phosphorylation at S421 and S423 is constitutive in vivo, but dispensable in vitro. <i>Biochemical and Biophysical Research Communications</i> , 2007 , 361, 349-55	3.4	14
150	Amyloid fibril formation and disaggregation of fragment 1-29 of apomyoglobin: insights into the effect of pH on protein fibrillogenesis. 2007 , 367, 1237-45		57
149	Comparison of proteolytic susceptibility in phosphoglycerate kinases from yeast and E. coli: modulation of conformational ensembles without altering structure or stability. 2007 , 368, 1438-47		32
148	Energetics-based protein profiling on a proteomic scale: identification of proteins resistant to proteolysis. 2007 , 368, 1426-37		63
147	Structure-function studies of Murraya koenigii trypsin inhibitor revealed a stable core beta sheet structure surrounded by alpha-helices with a possible role for alpha-helix in inhibitory function. <i>International Journal of Biological Macromolecules</i> , 2007 , 41, 410-4	7.9	12
146	Intrinsic disorder and functional proteomics. 2007 , 92, 1439-56		571
145	Comparative studies of wild type Escherichia coli 5-enolpyruvylshikimate 3-phosphate synthase with three glyphosate-insensitive mutated forms: activity, stability and structural characterization. 2008 , 1784, 1167-75		10
144	Limited proteolysis of bovine alpha-lactalbumin: isolation and characterization of protein domains. <i>Protein Science</i> , 1999 , 8, 2290-303	6.3	44
143	Site-specific modification and PEGylation of pharmaceutical proteins mediated by transglutaminase. 2008 , 60, 13-28		205
142	Structural prediction and mutational analysis of the Gifsy-I Xis protein. 2008, 8, 199		1
141	Characterization of linear forms of the circular enterocin AS-48 obtained by limited proteolysis. 2008 , 582, 3237-42		26
140	Effects of familial Alzheimer@ disease mutations on the folding nucleation of the amyloid beta-protein. 2008 , 381, 221-8		88
139	Scrapie prion protein structural constraints obtained by limited proteolysis and mass spectrometry. 2008 , 382, 88-98		43
138	Structural features of distinctin affecting peptide biological and biochemical properties. <i>Biochemistry</i> , 2008 , 47, 7888-99	3.2	26
137	Substrate-binding model of the chlorophyll biosynthetic magnesium chelatase BchH subunit. 2008 , 283, 11652-60		40

(2010-2008)

136	The dramatically increased chaperone activity of small heat-shock protein IbpB is retained for an extended period of time after the stress condition is removed. <i>Biochemical Journal</i> , 2008 , 410, 63-70	3.8	20
135	Catecholaminergic polymorphic ventricular tachycardia-related mutations R33Q and L167H alter calcium sensitivity of human cardiac calsequestrin. <i>Biochemical Journal</i> , 2008 , 413, 291-303	3.8	41
134	Limited proteolysis analysis of the ribosome is affected by subunit association. 2009 , 91, 410-22		3
133	Order propensity of an intrinsically disordered protein, the cyclin-dependent-kinase inhibitor Sic1. 2009 , 76, 731-46		58
132	On the use of hydrogen/deuterium exchange mass spectrometry data to improve de novo protein structure prediction. 2009 , 23, 459-61		2
131	Unusual stability of human neuroglobin at low pHmolecular mechanisms and biological significance. 2009 , 276, 7027-39		12
130	Limited proteolysis of luciferase as a reporter in nanosystem biology: a comparative study. 2009 , 85, 1162-7		12
129	Comparison of protein fragments identified by limited proteolysis and by computational cutting of proteins. <i>Protein Science</i> , 2002 , 11, 1753-70	6.3	24
128	Intrinsic Disorder in Proteins Associated with Neurodegenerative Diseases. 2009 , 21-75		6
127	Characterization of oligomeric species on the aggregation pathway of human lysozyme. 2009 , 387, 17-2	27	77
126	Mapping transient partial unfolding by protein engineering and native-state proteolysis. 2009 , 393, 543	-56	17
125	The site-specific TGase-mediated PEGylation of proteins occurs at flexible sites. 2009 , 89-112		4
124	Partly folded states of members of the lysozyme/lactalbumin superfamily: a comparative study by circular dichroism spectroscopy and limited proteolysis. <i>Protein Science</i> , 2002 , 11, 2932-46	6.3	79
123	On the nucleation of amyloid beta-protein monomer folding. <i>Protein Science</i> , 2005 , 14, 1581-96	6.3	270
122	In silico protein design by combinatorial assembly of protein building blocks. <i>Protein Science</i> , 2004 , 13, 2753-65	6.3	34
121	References. 2009 , 265-312		
120	The importance of being flexible: the case of basic region leucine zipper transcriptional regulators. 2009 , 10, 244-69		72
119	且actalbumin forms with oleic acid a high molecular weight complex displaying cytotoxic activity. <i>Biochemistry</i> , 2010 , 49, 8658-67	3.2	51

118	Detecting Disordered Regions in Proteins by Limited Proteolysis. 2010 , 569-626		7
117	Understanding protein non-folding. 2010 , 1804, 1231-64		875
116	Structural disorder within Henipavirus nucleoprotein and phosphoprotein: from predictions to experimental assessment. <i>PLoS ONE</i> , 2010 , 5, e11684	3.7	63
115	Viral disorder or disordered viruses: do viral proteins possess unique features?. <i>Protein and Peptide Letters</i> , 2010 , 17, 932-51	1.9	96
114	An analysis of the solution structure and signaling mechanism of LovK, a sensor histidine kinase integrating light and redox signals. <i>Biochemistry</i> , 2010 , 49, 6761-70	3.2	58
113	Physicochemical studies on peroxynitrite-modified H3 histone. <i>International Journal of Biological Macromolecules</i> , 2010 , 46, 20-6	7.9	25
112	Conformational role for the C-terminal tail of the intrinsically disordered high mobility group A (HMGA) chromatin factors. 2011 , 10, 3283-91		25
111	Intrinsically Disordered Chaperones and Neurodegeneration. 2011 , 1-63		1
110	Zn2+@ ability to alter the distribution of Cu2+ among the available binding sites of A[11-16)-polyethylenglycol-ylated peptide: implications in Alzheimer@ disease. 2011 , 50, 5342-50		41
109	Flexible nets of malleable guardians: intrinsically disordered chaperones in neurodegenerative diseases. 2011 , 111, 1134-66		59
108	Folding of AcrB Subunit Precedes Trimerization. 2011 , 411, 264-74		24
107	. 2011,		1
106	Do Viral Proteins Possess Unique Features?. 2011 , 1-34		4
105	Identification of a novel effector domain of BIN1 for cancer suppression. 2011 , 112, 2992-3001		9
104	Characterization of the interactions between the nucleoprotein and the phosphoprotein of Henipavirus. 2011 , 286, 13583-602		51
103	Cleavage of the vesicular GABA transporter under excitotoxic conditions is followed by accumulation of the truncated transporter in nonsynaptic sites. 2011 , 31, 4622-35		38
102	High-throughput characterization of intrinsic disorder in proteins from the Protein Structure Initiative. 2012 , 180, 201-15		31
101	Relationship between stability and flexibility in the most flexible region of Photinus pyralis luciferase. 2012 , 1824, 350-8		28

(2014-2012)

100	Molecular basis for the Kallmann syndrome-linked fibroblast growth factor receptor mutation. <i>Biochemical and Biophysical Research Communications</i> , 2012 , 425, 673-8	3.4	7
99	3.9 Intrinsically Disordered Proteins. 2012 , 170-211		О
98	Local unfolding is required for the site-specific protein modification by transglutaminase. <i>Biochemistry</i> , 2012 , 51, 8679-89	3.2	50
97	GCK-MODY diabetes associated with protein misfolding, cellular self-association and degradation. 2012 , 1822, 1705-15		12
96	Identifying disordered regions in proteins by limited proteolysis. <i>Methods in Molecular Biology</i> , 2012 , 896, 297-318	1.4	31
95	Probing protein stability and proteolytic resistance by loop scanning: a comprehensive mutational analysis. <i>Protein Science</i> , 2012 , 21, 433-46	6.3	59
94	Molecular properties of lysozyme-microbubbles: towards the protein and nucleic acid delivery. 2012 , 43, 885-96		14
93	Approaches to chemical synthetic biology. 2012 , 586, 2138-45		13
92	Hydrogen exchange and proteolytic degradation of ribonuclease A. The local splitting of the native structure and the conformation of loop segments. 2012 , 57, 35-54		
91	Enhancement of thermal stability of chondroitinase ABC I by site-directed mutagenesis: an insight from Ramachandran plot. 2013 , 1834, 479-86		37
90	Utilization of protein intrinsic disorder knowledge in structural proteomics. 2013, 1834, 487-98		46
89	The interplay between protein stability and dynamics in conformational diseases: the case of hPGK1 deficiency. 2013 , 1834, 2502-11		10
88	Getting intimate with trypsin, the leading protease in proteomics. 2013, 32, 453-65		127
87	Digested disorder: Quarterly intrinsic disorder digest (April-May-June, 2013). 2013 , 1, e27454		6
86	Disorder in the lifetime of a protein. 2013 , 1, e26782		2
85	A critical evaluation of in silico methods for detection of membrane protein intrinsic disorder. 2014 , 106, 1638-49		15
84	Structural disorder in viral proteins. 2014 , 114, 6880-911		133
83	The intrinsic disorder status of the human hepatitis C virus proteome. 2014 , 10, 1345-63		52

82	Purification and biophysical characterization of the CapA membrane protein FTT0807 from Francisella tularensis. <i>Biochemistry</i> , 2014 , 53, 1958-70	3.2	8
81	Open questions in origin of life: experimental studies on the origin of nucleic acids and proteins with specific and functional sequences by a chemical synthetic biology approach. 2014 , 9, e201402004		14
80	Partial unfolding of a monoclonal antibody: role of a single domain in driving protein aggregation. <i>Biochemistry</i> , 2014 , 53, 3367-77	3.2	22
79	Physicochemical properties of cells and their effects on intrinsically disordered proteins (IDPs). 2014 , 114, 6661-714		301
78	Wrecked regulation of intrinsically disordered proteins in diseases: pathogenicity of deregulated regulators. 2014 , 1, 6		68
77	Substrate Phage Display. 2015 , 222-245		
76	Unstructural biology of the Dengue virus proteins. 2015 , 282, 3368-94		43
75	Bioanalytical approaches to assess the proteolytic stability of therapeutic fusion proteins. 2015 , 7, 303	5-51	20
74	Thrombin inhibits the anti-myeloperoxidase and ferroxidase functions of ceruloplasmin: relevance in rheumatoid arthritis. 2015 , 86, 279-94		24
73	Biophysical Methods to Investigate Intrinsically Disordered Proteins: Avoiding an "Elephant and Blind Men" Situation. 2015 , 870, 215-60		26
7 ²	How disordered is my protein and what is its disorder for? A guide through the "dark side" of the protein universe. 2016 , 4, e1259708		66
71	Hydrophobic Interactions Contribute to Conformational Stabilization of Endoglycoceramidase II by Mechanism-Based Probes. <i>Biochemistry</i> , 2016 , 55, 4823-35	3.2	6
70	Nickel impact on human health: An intrinsic disorder perspective. 2016 , 1864, 1714-1731		98
69	Resolution of protein structure by mass spectrometry. 2016 , 35, 653-665		14
68	Degree of hydrolysis and antigenicity of buffalo alpha S1 casein and its hydrolysates in children with cow milk allergy. 2016 , 27, 87-98		4
67	Differential effects of zinc binding on structured and disordered regions in the multidomain STIL protein. 2016 , 7, 4140-4147		2
66	Antimicrobial potentials and structural disorder of human and animal defensins. 2016, 28, 95-111		45
65	Rigidifying flexible sites: An approach to improve stability of chondroitinase ABC I. <i>International Journal of Biological Macromolecules</i> , 2017 , 97, 270-278	7.9	19

64	Cell-wide analysis of protein thermal unfolding reveals determinants of thermostability. 2017, 355,		198
63	Bioinformatics Approaches to the Structure and Function of Intrinsically Disordered Proteins. 2017 , 16	7-203	2
62	Improvement of activity and stability of Chondroitinase ABC I by introducing an aromatic cluster at the surface of protein. 2017 , 105, 38-44		13
61	Disulfide bonds and disorder in granulin-3: An unusual handshake between structural stability and plasticity. <i>Protein Science</i> , 2017 , 26, 1759-1772	6.3	10
60	Expression and Purification of ZASP Subdomains and Clinically Important Isoforms: High-Affinity Binding to G-Actin. <i>Biochemistry</i> , 2017 , 56, 2061-2070	3.2	5
59	Onset of disorder and protein aggregation due to oxidation-induced intermolecular disulfide bonds: case study of RRM2 domain from TDP-43. <i>Scientific Reports</i> , 2017 , 7, 11161	4.9	19
58	Structural plasticity of T4 transcription co-activator gp33 revealed by a protease-resistant unfolded state. <i>Biochemical and Biophysical Research Communications</i> , 2017 , 492, 61-66	3.4	
57	How to Predict Disorder in a Protein of Interest. <i>Methods in Molecular Biology</i> , 2017 , 1484, 137-158	1.4	11
56	Computational Modeling of Stapled Peptides toward a Treatment Strategy for CML and Broader Implications in the Design of Lengthy Peptide Therapeutics. <i>Journal of Physical Chemistry B</i> , 2018 , 122, 3864-3875	3.4	6
55	Impact of the dairy product structure and protein nature on the proteolysis and amino acid bioaccessiblity during in vitro digestion. <i>Food Hydrocolloids</i> , 2018 , 82, 399-411	10.6	57
54	Structural insights into the molecular mechanism of mouse TRPA1 activation and inhibition. <i>Journal of General Physiology</i> , 2018 , 150, 751-762	3.4	22
53	Pulsed electric field: Role in protein digestion of beef Biceps femoris. <i>Innovative Food Science and Emerging Technologies</i> , 2018 , 50, 132-138	6.8	38
52	The Longest Amyloid-Precursor Protein Intracellular Domain Produced with AB2 Forms Esheet-Containing Monomers That Self-Assemble and Are Proteolyzed by Insulin-Degrading Enzyme. ACS Chemical Neuroscience, 2018, 9, 2892-2897	5.7	2
51	An arsenal of methods for the experimental characterization of intrinsically disordered proteins - How to choose and combine them?. <i>Archives of Biochemistry and Biophysics</i> , 2019 , 676, 108055	4.1	21
50	Role of the bolus degree of structure on the protein digestibility during in vitro digestion of a pea protein-fortified sponge cake chewed by elderly. <i>Journal of Texture Studies</i> , 2020 , 51, 134-143	3.6	6
49	Structural modeling and role of HAX-1 as a positive allosteric modulator of human serine protease HtrA2. <i>Biochemical Journal</i> , 2019 , 476, 2965-2980	3.8	3
48	Native peptide mapping - A simple method to routinely monitor higher order structure changes and relation to functional activity. <i>MAbs</i> , 2019 , 11, 1391-1401	6.6	3
47	Effect of barrel temperature and feed moisture on the physical properties of chickpealorghum and chickpealhaize extrudates, and the functionality and nutritional value of their resultant flours Part II. Cereal Chemistry, 2019, 96, 621-633	2.4	6

46	Empirical and Computational Comparison of Alternative Therapeutic Exon Skip Repairs for Duchenne Muscular Dystrophy. <i>Biochemistry</i> , 2019 , 58, 2061-2076	3.2	3
45	NB9 and CI74 Truncated Enzymes of Chondroitinase ABC I Regain More Imperturbable Microenvironments Around Structural Components in Comparison to their Wild Type. <i>Protein Journal</i> , 2019 , 38, 151-159	3.9	1
44	Structural disorder in the proteome and interactome of Alkhurma virus (ALKV). <i>Cellular and Molecular Life Sciences</i> , 2019 , 76, 577-608	10.3	13
43	Pulsed electric field: Effect on in-vitro simulated gastrointestinal protein digestion of deer Longissimus dorsi. <i>Food Research International</i> , 2019 , 120, 793-799	7	22
42	Insulin fibrillation: toward strategies for attenuating the process. <i>Chemical Communications</i> , 2020 , 56, 11354-11373	5.8	19
41	A serine protease secreted from Bacillus subtilis cleaves human plasma transthyretin to generate an amyloidogenic fragment. <i>Communications Biology</i> , 2020 , 3, 764	6.7	6
40	Intrinsic disorder perspective of an interplay between the renin-angiotensin-aldosterone system and SARS-CoV-2. <i>Infection, Genetics and Evolution</i> , 2020 , 85, 104510	4.5	6
39	Calcium ions modulate the structure of the intrinsically disordered Nucleobindin-2 protein. <i>International Journal of Biological Macromolecules</i> , 2020 , 154, 1091-1104	7.9	4
38	Thermostabilization of VPR, a kinetically stable cold adapted subtilase, via multiple proline substitutions into surface loops. <i>Scientific Reports</i> , 2020 , 10, 1045	4.9	4
37	Intrinsically Disordered Proteins. 2020 , 587-612		4
37 36	Intrinsically Disordered Proteins. 2020 , 587-612 Intrinsically disordered proteins of viruses: Involvement in the mechanism of cell regulation and pathogenesis. <i>Progress in Molecular Biology and Translational Science</i> , 2020 , 174, 1-78	4	22
	Intrinsically disordered proteins of viruses: Involvement in the mechanism of cell regulation and	15.3	
36	Intrinsically disordered proteins of viruses: Involvement in the mechanism of cell regulation and pathogenesis. <i>Progress in Molecular Biology and Translational Science</i> , 2020 , 174, 1-78 Emerging processing technologies for improved digestibility of muscle proteins. <i>Trends in Food</i>		22
36 35	Intrinsically disordered proteins of viruses: Involvement in the mechanism of cell regulation and pathogenesis. <i>Progress in Molecular Biology and Translational Science</i> , 2020 , 174, 1-78 Emerging processing technologies for improved digestibility of muscle proteins. <i>Trends in Food Science and Technology</i> , 2021 , 110, 226-239 Progress of tubulin polymerization activity detection methods. <i>Bioorganic and Medicinal Chemistry</i>	15.3	22 18 9
36 35 34	Intrinsically disordered proteins of viruses: Involvement in the mechanism of cell regulation and pathogenesis. <i>Progress in Molecular Biology and Translational Science</i> , 2020 , 174, 1-78 Emerging processing technologies for improved digestibility of muscle proteins. <i>Trends in Food Science and Technology</i> , 2021 , 110, 226-239 Progress of tubulin polymerization activity detection methods. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2021 , 37, 127698 Non-thermal processing has an impact on the digestibility of the muscle proteins. <i>Critical Reviews in</i>	15.3 2.9	22 18 9
36 35 34 33	Intrinsically disordered proteins of viruses: Involvement in the mechanism of cell regulation and pathogenesis. <i>Progress in Molecular Biology and Translational Science</i> , 2020 , 174, 1-78 Emerging processing technologies for improved digestibility of muscle proteins. <i>Trends in Food Science and Technology</i> , 2021 , 110, 226-239 Progress of tubulin polymerization activity detection methods. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2021 , 37, 127698 Non-thermal processing has an impact on the digestibility of the muscle proteins. <i>Critical Reviews in Food Science and Nutrition</i> , 2021 , 1-28	15.3 2.9	22 18 9
36 35 34 33 32	Intrinsically disordered proteins of viruses: Involvement in the mechanism of cell regulation and pathogenesis. <i>Progress in Molecular Biology and Translational Science</i> , 2020 , 174, 1-78 Emerging processing technologies for improved digestibility of muscle proteins. <i>Trends in Food Science and Technology</i> , 2021 , 110, 226-239 Progress of tubulin polymerization activity detection methods. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2021 , 37, 127698 Non-thermal processing has an impact on the digestibility of the muscle proteins. <i>Critical Reviews in Food Science and Nutrition</i> , 2021 , 1-28 Systems-wide analysis of glycoprotein conformational changes by limited deglycosylation assay. Thermostability of Ctenophore and Coelenterate Ca-Regulated Apo-photoproteins: A Comparative	15.3 2.9 11.5	22 18 9

(2021-2021)

28	Systems-wide analysis of glycoprotein conformational changes by limited deglycosylation assay. <i>Journal of Proteomics</i> , 2021 , 248, 104355	3.9	1
27	Statistical modeling of in vitro pepsin specificity. <i>Food Chemistry</i> , 2021 , 362, 130098	8.5	3
26	Bioinformatics Approaches to the Structure and Function of Intrinsically Disordered Proteins. 2009 , 11	3-140	1
25	Recombinant production of native proteins from Escherichia coli. <i>Pharmaceutical Biotechnology</i> , 2002 , 13, 27-60		2
24	Prediction of intrinsic disorder and its use in functional proteomics. <i>Methods in Molecular Biology</i> , 2007 , 408, 69-92	1.4	32
23	Target identification and validation of natural products with label-free methodology: A critical review from 2005 to 2020. <i>Pharmacology & Therapeutics</i> , 2020 , 216, 107690	13.9	12
22	CHIP protects against cardiac pressure overload through regulation of AMPK. <i>Journal of Clinical Investigation</i> , 2013 , 123, 3588-99	15.9	49
21	The interaction between the first transmembrane domain and the thumb of ASIC1a is critical for its N-glycosylation and trafficking. <i>PLoS ONE</i> , 2011 , 6, e26909	3.7	18
20	Peroxynitrite-Mediated Structural Changes in Histone H2A: Biochemical and Biophysical Analysis. <i>Protein and Peptide Letters</i> , 2020 , 27, 989-998	1.9	1
19	Evolution of multifunctionality through a pleiotropic substitution in the innate immune protein S100A9. <i>ELife</i> , 2020 , 9,	8.9	6
18	Molten Globule.		
17	Engineering Proteins for Stability and Efficient Folding. 1281		Ο
16	Thermostable Proteins. 1		
15	Empirical and Computational Comparison of Alternative Therapeutic Exon Skip Repairs for Duchenne Muscular Dystrophy.		
14	Personality Development of Prospective Mathemathics Teachers. 2019,		1
13	Evolution of multifunctionality through a pleiotropic substitution in the innate immune protein S100A9.		
12	The protein disorder cycle <i>Biophysical Reviews</i> , 2021 , 13, 1155-1162	3.7	3
11	Multiscale Model for Quantitative Prediction of Insulin Aggregation Nucleation Kinetics. <i>Journal of Chemical Theory and Computation</i> , 2021 ,	6.4	Ο

10	Myopathy-associated G154S mutation causes important changes in the conformational stability, amyloidogenic properties, and chaperone-like activity of human B -crystallin <i>Biophysical Chemistry</i> , 2021 , 282, 106744	3.5	1
9	Lessons from a quarter century of being human in protein science Protein Science, 2022,	6.3	1
8	In vitro gastro-small intestinal digestion of conventional and mildly processed pea protein ingredients <i>Food Chemistry</i> , 2022 , 387, 132894	8.5	2
7	Structural Analysis and Construction of a Thermostable Antifungal Chitinase. <i>Applied and Environmental Microbiology</i> ,	4.8	O
6	Calpain cleavage of Junctophilin-2 generates a spectrum of calcium-dependent cleavage products and DNA-rich NT1-fragment domains in cardiomyocytes. <i>Scientific Reports</i> , 2022 , 12,	4.9	
5	Conformational dynamics and target-dependent myristoyl switch of calcineurin B homologous protein 3.		O
4	Methods for measuring structural disorder in proteins. 2023 , 149-198		O
3	Molten globular enzymes. 2023 , 303-325		O
2	The Role of Proteolysis in Amyloidosis. 2023 , 24, 699		1
1	Pre-Molten, Wet, and Dry Molten Globules en Route to the Functional State of Proteins. 2023 , 24, 2424	4	О