

Pau BernadÃ³

List of Publications by Year in descending order

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108
papers

6,899
citations

61857

43
h-index

64668

79
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118
all docs

118
docs citations

118
times ranked

7041
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Characterization of Flexible Proteins Using Small-Angle X-ray Scattering. <i>Journal of the American Chemical Society</i> , 2007, 129, 5656-5664.	6.6	1,080
2	A structural model for unfolded proteins from residual dipolar couplings and small-angle x-ray scattering. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 17002-17007.	3.3	413
3	<i>Flexible-meccano:</i> a tool for the generation of explicit ensemble descriptions of intrinsically disordered proteins and their associated experimental observables. <i>Bioinformatics</i> , 2012, 28, 1463-1470.	1.8	324
4	Structural analysis of intrinsically disordered proteins by small-angle X-ray scattering. <i>Molecular BioSystems</i> , 2012, 8, 151-167.	2.9	291
5	Defining Long-Range Order and Local Disorder in Native Î±-Synuclein Using Residual Dipolar Couplings. <i>Journal of the American Chemical Society</i> , 2005, 127, 17968-17969.	6.6	223
6	Identification of slow correlated motions in proteins using residual dipolar and hydrogen-bond scalar couplings. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 13885-13890.	3.3	220
7	Highly Populated Turn Conformations in Natively Unfolded Tau Protein Identified from Residual Dipolar Couplings and Molecular Simulation. <i>Journal of the American Chemical Society</i> , 2007, 129, 5235-5243.	6.6	208
8	Domain Conformation of Tau Protein Studied by Solution Small-Angle X-ray Scattering. <i>Biochemistry</i> , 2008, 47, 10345-10353.	1.2	187
9	Human mitochondrial transcription factor A induces a U-turn structure in the light strand promoter. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1281-1289.	3.6	168
10	Quantitative Determination of the Conformational Properties of Partially Folded and Intrinsically Disordered Proteins Using NMR Dipolar Couplings. <i>Structure</i> , 2009, 17, 1169-1185.	1.6	160
11	Interaction of Human Complement with Sbi, a Staphylococcal Immunoglobulin-binding Protein. <i>Journal of Biological Chemistry</i> , 2008, 283, 17579-17593.	1.6	139
12	A Self-Consistent Description of the Conformational Behavior of Chemically Denatured Proteins from NMR and Small Angle Scattering. <i>Biophysical Journal</i> , 2009, 97, 2839-2845.	0.2	120
13	Dynamic interactions of proteins in complex networks: a more structured view. <i>FEBS Journal</i> , 2009, 276, 5390-5405.	2.2	104
14	Effect of interdomain dynamics on the structure determination of modular proteins by small-angle scattering. <i>European Biophysics Journal</i> , 2010, 39, 769-780.	1.2	102
15	Structural characterization of Î±-synuclein in an aggregation prone state. <i>Protein Science</i> , 2009, 18, 1840-1846.	3.1	97
16	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. <i>Nucleic Acids Research</i> , 2021, 49, D404-D411.	6.5	95
17	Peptide Binding Induces Large Scale Changes in Inter-domain Mobility in Human Pin1. <i>Journal of Biological Chemistry</i> , 2003, 278, 26174-26182.	1.6	87
18	Lipid binding by the Unique and SH3 domains of c-Src suggests a new regulatory mechanism. <i>Scientific Reports</i> , 2013, 3, 1295.	1.6	84

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19	ProtSA: a web application for calculating sequence specific protein solvent accessibilities in the unfolded ensemble. <i>BMC Bioinformatics</i> , 2009, 10, 104.	1.2	77
20	Structural characterization of intrinsically disordered proteins by the combined use of NMR and SAXS. <i>Biochemical Society Transactions</i> , 2012, 40, 955-962.	1.6	77
21	Dynamic interplay between catalytic and lectin domains of GalNAc-transferases modulates protein O-glycosylation. <i>Nature Communications</i> , 2015, 6, 6937.	5.8	77
22	Interpretation of ¹⁵ N NMR relaxation data of globular proteins using hydrodynamic calculations with HYDRONMR. <i>Journal of Biomolecular NMR</i> , 2002, 23, 139-150.	1.6	76
23	Small-angle scattering studies of intrinsically disordered proteins and their complexes. <i>Current Opinion in Structural Biology</i> , 2017, 42, 15-23.	2.6	76
24	Structural Characterization of the Natively Unfolded N-Terminal Domain of Human c-Src Kinase: Insights into the Role of Phosphorylation of the Unique Domain. <i>Journal of Molecular Biology</i> , 2009, 391, 136-148.	2.0	74
25	Proteins in dynamic equilibrium. <i>Nature</i> , 2010, 468, 1046-1048.	13.7	74
26	The Unique Domain Forms a Fuzzy Intramolecular Complex in Src Family Kinases. <i>Structure</i> , 2017, 25, 630-640.e4.	1.6	72
27	Disentangling the complexity of low complexity proteins. <i>Briefings in Bioinformatics</i> , 2020, 21, 458-472.	3.2	70
28	Structure and Dynamics of Ribosomal Protein L12: An Ensemble Model Based on SAXS and NMR Relaxation. <i>Biophysical Journal</i> , 2010, 98, 2374-2382.	0.2	67
29	Structure of p15PAF-PCNA complex and implications for clamp sliding during DNA replication and repair. <i>Nature Communications</i> , 2015, 6, 6439.	5.8	65
30	Anisotropic Small Amplitude Peptide Plane Dynamics in Proteins from Residual Dipolar Couplings. <i>Journal of the American Chemical Society</i> , 2004, 126, 4907-4920.	6.6	64
31	Structural Characterization of Protein-Protein Complexes by Integrating Computational Docking with Small-angle Scattering Data. <i>Journal of Molecular Biology</i> , 2010, 403, 217-230.	2.0	64
32	Amino Acid Bulkiness Defines the Local Conformations and Dynamics of Natively Unfolded α -Synuclein and Tau. <i>Journal of the American Chemical Society</i> , 2007, 129, 3032-3033.	6.6	61
33	pyDockSAXS: protein-protein complex structure by SAXS and computational docking. <i>Nucleic Acids Research</i> , 2015, 43, W356-W361.	6.5	61
34	Low-Resolution Structures of Transient Protein-Protein Complexes Using Small-Angle X-ray Scattering. <i>Journal of the American Chemical Society</i> , 2009, 131, 4378-4386.	6.6	59
35	Residual Dipolar Couplings in Short Peptides Reveal Systematic Conformational Preferences of Individual Amino Acids. <i>Journal of the American Chemical Society</i> , 2006, 128, 13508-13514.	6.6	55
36	An Analytical Solution to the Problem of the Orientation of Rigid Particles by Planar Obstacles. Application to Membrane Systems and to the Calculation of Dipolar Couplings in Protein NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2001, 123, 12037-12047.	6.6	54

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37	p15PAF Is an Intrinsically Disordered Protein with Nonrandom Structural Preferences at Sites of Interaction with Other Proteins. <i>Biophysical Journal</i> , 2014, 106, 865-874.	0.2	54
38	Indirect DNA Readout by an H-NS Related Protein: Structure of the DNA Complex of the C-Terminal Domain of Ler. <i>PLoS Pathogens</i> , 2011, 7, e1002380.	2.1	53
39	Molecular basis for fibroblast growth factor 23 O-glycosylation by GalNAc-T3. <i>Nature Chemical Biology</i> , 2020, 16, 351-360.	3.9	52
40	Interplay of Protein Disorder in Retinoic Acid Receptor Heterodimer and Its Corepressor Regulates Gene Expression. <i>Structure</i> , 2019, 27, 1270-1285.e6.	1.6	50
41	Structural Characterization of the Active and Inactive States of Src Kinase in Solution by Small-Angle X-ray Scattering. <i>Journal of Molecular Biology</i> , 2008, 376, 492-505.	2.0	49
42	Structural Analysis of Multi-component Amyloid Systems by Chemometric SAXS Data Decomposition. <i>Structure</i> , 2017, 25, 5-15.	1.6	49
43	Realistic Ensemble Models of Intrinsically Disordered Proteins Using a Structure-Encoding Coil Database. <i>Structure</i> , 2019, 27, 381-391.e2.	1.6	49
44	Sequence-Specific Solvent Accessibilities of Protein Residues in Unfolded Protein Ensembles. <i>Biophysical Journal</i> , 2006, 91, 4536-4543.	0.2	48
45	Macromolecular crowding in biological systems: hydrodynamics and NMR methods. <i>Journal of Molecular Recognition</i> , 2004, 17, 397-407.	1.1	47
46	Local Dynamic Amplitudes on the Protein Backbone from Dipolar Couplings: Toward the Elucidation of Slower Motions in Biomolecules. <i>Journal of the American Chemical Society</i> , 2004, 126, 7760-7761.	6.6	46
47	Structural Relationships Among the Ribosomal Stalk Proteins from the Three Domains of Life. <i>Journal of Molecular Evolution</i> , 2008, 67, 154-167.	0.8	46
48	Human mitochondrial mTERF wraps around DNA through a left-handed superhelical tandem repeat. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 891-893.	3.6	46
49	Oncogenic mutations at the EGFR ectodomain structurally converge to remove a steric hindrance on a kinase-coupled cryptic epitope. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10009-10018.	3.3	46
50	Flanking Regions Determine the Structure of the Poly-Glutamine in Huntingtin through Mechanisms Common among Glutamine-Rich Human Proteins. <i>Structure</i> , 2020, 28, 733-746.e5.	1.6	45
51	The hexameric structure of the human mitochondrial replicative helicase Twinkle. <i>Nucleic Acids Research</i> , 2015, 43, 4284-4295.	6.5	40
52	Solution scattering approaches to dynamical ordering in biomolecular systems. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 253-274.	1.1	39
53	Combined Use of NMR Relaxation Measurements and Hydrodynamic Calculations To Study Protein Association. Evidence for Tetramers of Low Molecular Weight Protein Tyrosine Phosphatase in Solution. <i>Journal of the American Chemical Society</i> , 2003, 125, 916-923.	6.6	38
54	Analysis of Intrinsically Disordered Proteins by Small-Angle X-ray Scattering. , 2012, 896, 107-122.		38

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55	The Dimeric Structure and the Bivalent Recognition of H3K4me3 by the Tumor Suppressor ING4 Suggests a Mechanism for Enhanced Targeting of the HBO1 Complex to Chromatin. <i>Journal of Molecular Biology</i> , 2010, 396, 1117-1127.	2.0	36
56	Disentangling polydispersity in the PCNA [~] p15PAF complex, a disordered, transient and multivalent macromolecular assembly. <i>Nucleic Acids Research</i> , 2017, 45, 1501-1515.	6.5	33
57	A General Strategy to Access Structural Information at Atomic Resolution in Polyglutamine Homorepeats. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 3598-3601.	7.2	30
58	Structural Characterization of Highly Flexible Proteins by Small-Angle Scattering. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1009, 107-129.	0.8	29
59	Interpretation of NMR relaxation properties of Pin1, a two-domain protein, based on Brownian dynamic simulations. <i>Journal of Biomolecular NMR</i> , 2004, 29, 21-35.	1.6	27
60	Structural Analysis of an Equilibrium Folding Intermediate in the Apoflavodoxin Native Ensemble by Small-Angle X-ray Scattering. <i>Journal of Molecular Biology</i> , 2011, 406, 604-619.	2.0	27
61	NMR measurement of the off rate from the first calcium-binding site of the synaptotagmin I C2A domain. <i>FEBS Letters</i> , 2002, 516, 93-96.	1.3	26
62	Structural characterization of unphosphorylated STAT5a oligomerization equilibrium in solution by small \angle X \AA ray scattering. <i>Protein Science</i> , 2009, 18, 716-726.	3.1	26
63	Protein backbone dynamics from N \AA HN dipolar couplings in partially aligned systems: a comparison of motional models in the presence of structural noise. <i>Journal of Magnetic Resonance</i> , 2005, 173, 328-338.	1.2	25
64	Structural Characterization of the Ribosomal P1A \AA P2B Protein Dimer by Small-Angle X-ray Scattering and NMR Spectroscopy. <i>Biochemistry</i> , 2007, 46, 1988-1998.	1.2	25
65	Structural Disorder within Sendai Virus Nucleoprotein and Phosphoprotein: Insight into the Structural Basis of Molecular Recognition. <i>Protein and Peptide Letters</i> , 2010, 17, 952-960.	0.4	25
66	Design and Structure of an Equilibrium Protein Folding Intermediate: A Hint into Dynamical Regions of Proteins. <i>Journal of Molecular Biology</i> , 2010, 400, 922-934.	2.0	25
67	A Three-protein Charge Zipper Stabilizes a Complex Modulating Bacterial Gene Silencing. <i>Journal of Biological Chemistry</i> , 2015, 290, 21200-21212.	1.6	18
68	The importance of definitions in the study of polyQ regions: A tale of thresholds, impurities and sequence context. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 306-313.	1.9	18
69	Evidence of the Reduced Abundance of Proline cis Conformation in Protein Poly Proline Tracts. <i>Journal of the American Chemical Society</i> , 2020, 142, 7976-7986.	6.6	18
70	Protein Tyrosine Phosphatase Oligomerization Studied by a Combination of ¹⁵ N NMR Relaxation and ¹²⁹ Xe NMR. Effect of Buffer Containing Arginine and Glutamic Acid. <i>Journal of the American Chemical Society</i> , 2007, 129, 5946-5953.	6.6	16
71	Ensemble Structure of the Highly Flexible Complex Formed between Vesicular Stomatitis Virus Unassembled Nucleoprotein and its Phosphoprotein Chaperone. <i>Journal of Molecular Biology</i> , 2016, 428, 2671-2694.	2.0	16
72	Protein Flexibility and Synergy of HMG Domains Underlie U-Turn Bending of DNA by TFAM in Solution. <i>Biophysical Journal</i> , 2018, 114, 2386-2396.	0.2	16

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73	Protein loop compaction and the origin of the effect of arginine and glutamic acid mixtures on solubility, stability and transient oligomerization of proteins. <i>European Biophysics Journal</i> , 2011, 40, 1327-1338.	1.2	15
74	Defining the Nature of Thermal Intermediate in 3 State Folding Proteins: Apoflavodoxin, a Study Case. <i>PLoS Computational Biology</i> , 2012, 8, e1002647.	1.5	14
75	Active-Site-Directed Inhibitors of Prolyl Oligopeptidase Abolish Its Conformational Dynamics. <i>ChemBioChem</i> , 2016, 17, 913-917.	1.3	14
76	Disulfide driven folding for a conditionally disordered protein. <i>Scientific Reports</i> , 2017, 7, 16994.	1.6	14
77	Structural Insights into the Interaction of the Intrinsically Disordered Co-activator TIF2 with Retinoic Acid Receptor Heterodimer (RXR/RAR). <i>Journal of Molecular Biology</i> , 2021, 433, 166899.	2.0	14
78	Comment on the Optimal Parameters to Derive Intrinsically Disordered Protein Conformational Ensembles from Small-Angle X-ray Scattering Data Using the Ensemble Optimization Method. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 2014-2021.	2.3	13
79	Tailoring the NIR-Photoluminescence of Single Thiolated Au ₂₅ Nanoclusters by Selective Binding to Proteins**. <i>Chemistry - A European Journal</i> , 2022, 28, .	1.7	13
80	Lanthanide Modulation of the Orientation of Macromolecules Induced by Purple Membrane. <i>Journal of the American Chemical Society</i> , 2002, 124, 374-375.	6.6	12
81	Double Monoubiquitination Modifies the Molecular Recognition Properties of p15PAF Promoting Binding to the Reader Module of Dnmt1. <i>ACS Chemical Biology</i> , 2019, 14, 2315-2326.	1.6	12
82	Site-Specific Isotopic Labeling (SSIL): Access to High-Resolution Structural and Dynamic Information in Low-Complexity Proteins. <i>ChemBioChem</i> , 2020, 21, 769-775.	1.3	12
83	Measurement and Analysis of NMR Residual Dipolar Couplings for the Study of Intrinsically Disordered Proteins. <i>Methods in Molecular Biology</i> , 2012, 895, 115-125.	0.4	11
84	Conformational transitions in human translin enable nucleic acid binding. <i>Nucleic Acids Research</i> , 2013, 41, 9956-9966.	6.5	11
85	Robust Cell-Free Expression of Sub-Pathological and Pathological Huntingtin Exon-1 for NMR Studies. General Approaches for the Isotopic Labeling of Low-Complexity Proteins. <i>Biomolecules</i> , 2020, 10, 1458.	1.8	11
86	Predicting Secondary Structure Propensities in IDPs Using Simple Statistics from Three-Residue Fragments. <i>Journal of Molecular Biology</i> , 2020, 432, 5447-5459.	2.0	10
87	Hybrid parallelization of a multi-tree path search algorithm: Application to highly-flexible biomolecules. <i>Parallel Computing</i> , 2018, 77, 84-100.	1.3	9
88	Weak oligomerization of low-molecular-weight protein tyrosine phosphatase is conserved from mammals to bacteria. <i>FEBS Journal</i> , 2009, 276, 4346-4357.	2.2	8
89	A General Strategy to Access Structural Information at Atomic Resolution in Polyglutamine Homorepeats. <i>Angewandte Chemie</i> , 2018, 130, 3660-3663.	1.6	8
90	Structural Analyses of Intrinsically Disordered Proteins by Small-Angle X-Ray Scattering. <i>Methods in Molecular Biology</i> , 2020, 2141, 249-269.	0.4	8

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91	Molecular and cellular insight into Escherichia coli SsE and its role during biofilm maturation. Npj Biofilms and Microbiomes, 2022, 8, 9.	2.9	8
92	On the Use of low-resolution Data to Improve Structure Prediction of Proteins and Protein Complexes. Journal of Chemical Theory and Computation, 2009, 5, 3129-3137.	2.3	7
93	Structure and thermodynamics of transient protein-protein complexes by chemometric decomposition of SAXS datasets. Structure, 2021, 29, 1074-1090.e4.	1.6	7
94	Structural Characterization of Protein-Protein Interactions with pyDockSAXS. Methods in Molecular Biology, 2020, 2112, 131-144.	0.4	7
95	Structural Insights into the Intrinsically Disordered GPCR C-Terminal Region, Major Actor in Arrestin-GPCR Interaction. Biomolecules, 2022, 12, 617.	1.8	7
96	The metastasis suppressor KISS1 is an intrinsically disordered protein slightly more extended than a random coil. PLoS ONE, 2017, 12, e0172507.	1.1	6
97	IDPs and their complexes in GPCR and nuclear receptor signaling. Progress in Molecular Biology and Translational Science, 2020, 174, 105-155.	0.9	6
98	The diversity of molecular interactions involving intrinsically disordered proteins: A molecular modeling perspective. Computational and Structural Biotechnology Journal, 2021, 19, 3817-3828.	1.9	6
99	Noninvasive Structural Analysis of Intermediate Species During Fibrillation: An Application of Small-Angle X-Ray Scattering. Methods in Molecular Biology, 2018, 1779, 209-239.	0.4	5
100	Conformational Characterization of Intrinsically Disordered Proteins and Its Biological Significance. , 2018, , 381-399.		5
101	Low-resolution structural approaches to study biomolecular assemblies. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2011, 1, 283-297.	6.2	4
102	Integrative Biophysics: Protein Interaction and Disorder. Journal of Molecular Biology, 2020, 432, 2843-2845.	2.0	3
103	An Integrative Structural Biology Analysis of Von Willebrand Factor Binding and Processing by ADAMTS-13 in Solution. Journal of Molecular Biology, 2021, 433, 166954.	2.0	3
104	Investigating the Formation of Structural Elements in Proteins Using Local Sequence-Dependent Information and a Heuristic Search Algorithm. Molecules, 2019, 24, 1150.	1.7	2
105	Interdomain linkers tailor the stability of immunoglobulin repeats in polyproteins. Biochemical and Biophysical Research Communications, 2021, 550, 43-48.	1.0	2
106	Conformational Characterization of Intrinsically Disordered Proteins and Its Biological Significance. , 2017, , 1-20.		2
107	A FRET-Based Biosensor for the Src N-Terminal Regulatory Element. Biosensors, 2022, 12, 96.	2.3	1
108	Cover Feature: Tailoring the NIR-Photoluminescence of Single Thiolated Au ₂₅ Nanoclusters by Selective Binding to Proteins (Chem. Eur. J. 39/2022). Chemistry - A European Journal, 2022, 28, .	1.7	0