

Gonzalo de Prat Gay

List of Publications by Year in descending order

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172457

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94
docs citations

94
times ranked

2262
citing authors

#	ARTICLE	IF	CITATIONS
1	UDP-Glc:glycoprotein glucosyltransferase recognizes structured and solvent accessible hydrophobic patches in molten globule-like folding intermediates. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 86-91.	7.1	164
2	The Endoplasmic Reticulum Glucosyltransferase Recognizes Nearly Native Glycoprotein Folding Intermediates. Journal of Biological Chemistry, 2004, 279, 46280-46285.	3.4	105
3	Circular Dichroism Techniques for the Analysis of Intrinsically Disordered Proteins and Domains. Methods in Molecular Biology, 2012, 895, 387-404.	0.9	93
4	Equilibrium dissociation and unfolding of the dimeric human papillomavirus strain HPV16 E2 DNA-binding domain. Protein Science, 1996, 5, 310-319.	7.6	77
5	Folding of a nascent polypeptide chain in vitro: cooperative formation of structure in a protein module.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 3683-3686.	7.1	75
6	Search for Nucleation Sites in Smaller Fragments of Chymotrypsin Inhibitor 2. Journal of Molecular Biology, 1995, 254, 289-304.	4.2	72
7	Molecular Basis for Phosphorylation-Dependent, PEST-Mediated Protein Turnover. Structure, 2006, 14, 309-319.	3.3	68
8	Conformational Pathway of the Polypeptide Chain of Chymotrypsin Inhibitor-2 Growing from its N Terminus in vitro. Parallels with the Protein Folding Pathway. Journal of Molecular Biology, 1995, 254, 968-979.	4.2	66
9	The HPV16 E7 Viral Oncoprotein Self-Assembles into Defined Spherical Oligomers. Biochemistry, 2004, 43, 3310-3317.	2.5	59
10	High-Risk (HPV16) Human Papillomavirus E7 Oncoprotein Is Highly Stable and Extended, with Conformational Transitions that Could Explain Its Multiple Cellular Binding Partners. Biochemistry, 2002, 41, 10510-10518.	2.5	58
11	Folding of a pressure-denatured model protein. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 7888-7893.	7.1	55
12	The N-Terminal Module of HPV16 E7 Is an Intrinsically Disordered Domain That Confers Conformational and Recognition Plasticity to the Oncoprotein. Biochemistry, 2007, 46, 10405-10412.	2.5	55
13	Casein Kinase II Phosphorylation-induced Conformational Switch Triggers Degradation of the Papillomavirus E2 Protein. Journal of Biological Chemistry, 2004, 279, 22430-22439.	3.4	52
14	Targeting mechanism of the retinoblastoma tumor suppressor by a prototypical viral oncoprotein. FEBS Journal, 2010, 277, 973-988.	4.7	52
15	Complementation of peptide fragments of the single domain protein chymotrypsin inhibitor 2. Journal of Molecular Biology, 1997, 273, 317-329.	4.2	49
16	Deconstructing virus condensation. PLoS Pathogens, 2021, 17, e1009926.	4.7	48
17	Convergent evolution and mimicry of protein linear motifs in host-pathogen interactions. Current Opinion in Structural Biology, 2015, 32, 91-101.	5.7	43
18	The structure of the transition state for the association of two fragments of the barley chymotrypsin inhibitor 2 to generate native-like protein: implications for mechanisms of protein folding.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 10943-10946.	7.1	41

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19	Modification of the amino acid specificity of tyrosyl-tRNA synthetase by protein engineering. <i>FEBS Letters</i> , 1993, 318, 167-171.	2.8	39
20	Kinetic Recognition of the Retinoblastoma Tumor Suppressor by a Specific Protein Target. <i>Journal of Molecular Biology</i> , 2011, 412, 267-284.	4.2	38
21	Towards the complete structural characterization of a protein folding pathway: the structures of the denatured, transition and native states for the association/folding of two complementary fragments of cleaved chymotrypsin inhibitor 2. Direct evidence for a nucleation-condensation mechanism. <i>Folding & Design</i> , 1996, 1, 189-208.	4.5	37
22	Distinctive Cognate Sequence Discrimination, Bound DNA Conformation, and Binding Modes in the E2 C-Terminal Domains from Prototype Human and Bovine Papillomaviruses. <i>Biochemistry</i> , 2000, 39, 14692-14701.	2.5	37
23	A Proteinâ€™DNA Binding Mechanism Proceeds Through Multi-state or Two-state Parallel Pathways. <i>Journal of Molecular Biology</i> , 2003, 331, 89-99.	4.2	37
24	The dimeric DNA binding domain of the human papillomavirus E2 protein folds through a monomeric intermediate which cannot be native-like. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 711-717.	8.2	35
25	The Catalytic Domain of Insulin-degrading Enzyme Forms a Denaturant-resistant Complex with Amyloid Î² Peptide. <i>Journal of Biological Chemistry</i> , 2008, 283, 17039-17048.	3.4	34
26	Comprehensive comparison of the interaction of the E2 master regulator with its cognate target DNA sites in 73 human papillomavirus types by sequence statistics. <i>Nucleic Acids Research</i> , 2008, 36, 756-769.	14.5	32
27	Conformational Changes and Stabilization Induced by Ligand Binding in the DNA-binding Domain of the E2 Protein from Human Papillomavirus. <i>Journal of Biological Chemistry</i> , 1997, 272, 19295-19303.	3.4	30
28	Following co-operative formation of secondary and tertiary structure in a single protein module. <i>Journal of Molecular Biology</i> , 1997, 268, 185-197.	4.2	30
29	Characterization of a Partially Folded Monomer of the DNA-binding Domain of Human Papillomavirus E2 Protein Obtained at High Pressure. <i>Journal of Biological Chemistry</i> , 1998, 273, 9050-9057.	3.4	30
30	Hidden Structural Codes in Protein Intrinsic Disorder. <i>Biochemistry</i> , 2017, 56, 5560-5569.	2.5	30
31	Association of complementary fragments and the elucidation of protein folding pathways. <i>Protein Engineering, Design and Selection</i> , 1996, 9, 843-847.	2.1	29
32	Free Energy Contributions to Direct Readout of a DNA Sequence. <i>Journal of Biological Chemistry</i> , 2005, 280, 32480-32484.	3.4	29
33	Cytosolic accumulation of HPV16 E7 oligomers supports different transformation routes for the prototypic viral oncoprotein: The amyloidâ€™cancer connection. <i>International Journal of Cancer</i> , 2009, 125, 1902-1911.	5.1	29
34	Transition state for protein-DNA recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 10797-10802.	7.1	28
35	Insulin-degrading enzyme degrades amyloid peptides associated with British and Danish familial dementia. <i>Biochemical and Biophysical Research Communications</i> , 2005, 332, 808-816.	2.1	27
36	Evolution of Linear Motifs within the Papillomavirus E7 Oncoprotein. <i>Journal of Molecular Biology</i> , 2012, 422, 336-346.	4.2	27

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37	Modular Unfolding and Dissociation of the Human Respiratory Syncytial Virus Phosphoprotein P and Its Interaction with the M ₂ Antiterminator: A Singular Tetramer-Tetramer Interface Arrangement. <i>Biochemistry</i> , 2012, 51, 8100-8110.	2.5	27
38	Generation of Sequence-specific, High Affinity Anti-DNA Antibodies. <i>Journal of Biological Chemistry</i> , 2001, 276, 12769-12773.	3.4	26
39	Protein Folding in the Absence of Chemical Denaturants. <i>Journal of Biological Chemistry</i> , 1999, 274, 7732-7740.	3.4	25
40	Letter to Editor: Solution structure of the HPV-16 E2 DNA binding domain, a transcriptional regulator with a dimeric β -barrel fold. <i>Journal of Biomolecular NMR</i> , 2004, 30, 211-214.	2.8	25
41	Sequence Evolution of the Intrinsically Disordered and Globular Domains of a Model Viral Oncoprotein. <i>PLoS ONE</i> , 2012, 7, e47661.	2.5	25
42	Structural and Thermodynamic Basis for the Enhanced Transcriptional Control by the Human Papillomavirus Strain-16 E2 Protein. <i>Biochemistry</i> , 2006, 45, 6551-6560.	2.5	23
43	A viral DNA-binding domain elicits anti-DNA antibodies of different specificities. <i>Molecular Immunology</i> , 2005, 42, 327-333.	2.2	21
44	Chaperone Holdase Activity of Human Papillomavirus E7 Oncoprotein. <i>Biochemistry</i> , 2006, 45, 657-667.	2.5	20
45	Experimental snapshots of a protein-DNA binding landscape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7751-7756.	7.1	19
46	The Folding Mechanism of a Dimeric β -Barrel Domain. <i>Journal of Molecular Biology</i> , 2005, 351, 672-682.	4.2	18
47	High-Risk HPV E6 Oncoproteins Assemble into Large Oligomers that Allow Localization of Endogenous Species in Prototypic HPV-Transformed Cell Lines. <i>Biochemistry</i> , 2007, 46, 341-349.	2.5	18
48	The Non-Structural NS1 Protein Unique to Respiratory Syncytial Virus: A Two-State Folding Monomer in Quasi-Equilibrium with a Stable Spherical Oligomer. <i>PLoS ONE</i> , 2013, 8, e74338.	2.5	18
49	Folding of a Cyclin Box. <i>Journal of Biological Chemistry</i> , 2013, 288, 18923-18938.	3.4	17
50	Conformational Dissection of a Viral Intrinsically Disordered Domain Involved in Cellular Transformation. <i>PLoS ONE</i> , 2013, 8, e72760.	2.5	17
51	Cysteine-Rich Positions Outside the Structural Zinc Motif of Human Papillomavirus E7 Provide Conformational Modulation and Suggest Functional Redox Roles. <i>Biochemistry</i> , 2014, 53, 1680-1696.	2.5	17
52	Intrinsic Disorder to Order Transitions in the Scaffold Phosphoprotein P from the Respiratory Syncytial Virus RNA Polymerase Complex. <i>Biochemistry</i> , 2016, 55, 1441-1454.	2.5	17
53	Interplay between sequence, structure and linear motifs in the adenovirus E1A hub protein. <i>Virology</i> , 2018, 525, 117-131.	2.4	17
54	Folding of a dimeric β -barrel: Residual structure in the urea denatured state of the human papillomavirus E2 DNA binding domain. <i>Protein Science</i> , 2000, 9, 799-811.	7.6	16

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55	Specific Antibody-DNA Interaction: A Novel Strategy for Tight DNA Recognition. <i>Biochemistry</i> , 2003, 42, 6218-6227.	2.5	15
56	A quasi-spontaneous amyloid route in a DNA binding gene regulatory domain: The papillomavirus HPV16 E2 protein. <i>Protein Science</i> , 2007, 16, 744-754.	7.6	15
57	The Human Papillomavirus E7-E2 Interaction Mechanism in Vitro Reveals a Finely Tuned System for Modulating Available E7 and E2 Proteins. <i>Biochemistry</i> , 2009, 48, 11939-11949.	2.5	15
58	Minute Time Scale Prolyl Isomerization Governs Antibody Recognition of an Intrinsically Disordered Immunodominant Epitope. <i>Journal of Biological Chemistry</i> , 2013, 288, 13110-13123.	3.4	15
59	Conformational Preferences of a Peptide Corresponding to the Major Antigenic Determinant of Foot-and-Mouth Disease Virus: Implications for Peptide-Vaccine Approaches. <i>Archives of Biochemistry and Biophysics</i> , 1997, 341, 360-369.	3.0	14
60	Indirect DNA Readout on the Protein Side: Coupling between Histidine Protonation, Global Structural Cooperativity, Dynamics, and DNA Binding of the Human Papillomavirus Type 16 E2C Domain. <i>Journal of Molecular Biology</i> , 2009, 388, 327-344.	4.2	14
61	Ordered Self-Assembly Mechanism of a Spherical Oncoprotein Oligomer Triggered by Zinc Removal and Stabilized by an Intrinsically Disordered Domain. <i>PLoS ONE</i> , 2012, 7, e36457.	2.5	14
62	The papillomavirus E2 DNA binding domain. <i>Frontiers in Bioscience - Landmark</i> , 2008, Volume, 6006.	3.0	14
63	Three-Dimensional Solution Structure and Stability of Thioredoxin m from Spinach. <i>Biochemistry</i> , 2001, 40, 15246-15256.	2.5	13
64	Specific Recognition of a DNA Immunogen by its Elicited Antibody. <i>Journal of Molecular Biology</i> , 2007, 370, 183-195.	4.2	13
65	Spectroscopic Characterization of the Growing Polypeptide Chain of the Barley Chymotrypsin Inhibitor-2. <i>Archives of Biochemistry and Biophysics</i> , 1996, 335, 1-7.	3.0	12
66	Fine Modulation of the Respiratory Syncytial Virus M ₁ Protein Quaternary Structure by Reversible Zinc Removal from Its Cys ₃ -His ₁ Motif. <i>Biochemistry</i> , 2013, 52, 6779-6789.	2.5	12
67	Increased Stability and DNA Site Discrimination of Single Chain Variants of the Dimeric β -Barrel DNA Binding Domain of the Human Papillomavirus E2 Transcriptional Regulator. <i>Biochemistry</i> , 2007, 46, 12441-12450.	2.5	11
68	Kinetically driven refolding of the hyperstable EBNA1 origin DNA-binding dimeric β -barrel domain into amyloid-like spherical oligomers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 450-461.	2.6	11
69	Molecular dynamics of the DNA-binding domain of the papillomavirus E2 transcriptional regulator uncover differential properties for DNA target accommodation. <i>FEBS Journal</i> , 2007, 274, 2385-2395.	4.7	11
70	Mechanism of DNA Recognition at a Viral Replication Origin. <i>Journal of Biological Chemistry</i> , 2006, 281, 26893-26903.	3.4	10
71	The Respiratory Syncytial Virus Transcription Antiterminator M ₁ is a Highly Stable, Zinc Binding Tetramer with Strong pH-Dependent Dissociation and a Monomeric Unfolding Intermediate. <i>Biochemistry</i> , 2011, 50, 8529-8539.	2.5	10
72	Cooperative RNA Recognition by a Viral Transcription Antiterminator. <i>Journal of Molecular Biology</i> , 2018, 430, 777-792.	4.2	10

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73	Antibody Recognition of a Flexible Epitope at the DNA Binding Site of the Human Papillomavirus Transcriptional Regulator E2. <i>Biochemistry</i> , 2006, 45, 15520-15528.	2.5	9
74	A strained DNA binding helix is conserved for site recognition, folding nucleation, and conformational modulation. <i>Biopolymers</i> , 2009, 91, 432-443.	2.4	9
75	Thermodynamics of Cooperative DNA Recognition at a Replication Origin and Transcription Regulatory Site. <i>Biochemistry</i> , 2010, 49, 10277-10286.	2.5	8
76	Conformational Heterogeneity Determined by Folding and Oligomer Assembly Routes of the Interferon Response Inhibitor NS1 Protein, Unique to Human Respiratory Syncytial Virus. <i>Biochemistry</i> , 2015, 54, 5136-5146.	2.5	7
77	A conformational switch balances viral RNA accessibility and protection in a nucleocapsid ring model. <i>Archives of Biochemistry and Biophysics</i> , 2019, 671, 77-86.	3.0	7
78	E6*, the 50 Amino Acid Product of the Most Abundant Spliced Transcript of the E6 Oncoprotein in High-Risk Human Papillomavirus, Is a Promiscuous Folder and Binder. <i>Biochemistry</i> , 2011, 50, 1376-1383.	2.5	6
79	Long-lasting immunoprotective and therapeutic effects of a hyperstable E7 oligomer based vaccine in a murine human papillomavirus tumor model. <i>International Journal of Cancer</i> , 2012, 130, 1813-1820.	5.1	6
80	Degenerate cysteine patterns mediate two redox sensing mechanisms in the papillomavirus E7 oncoprotein. <i>Redox Biology</i> , 2017, 11, 38-50.	9.0	6
81	Topology Dictates Evolution of Regulatory Cysteines in a Family of Viral Oncoproteins. <i>Molecular Biology and Evolution</i> , 2019, 36, 1521-1532.	8.9	6
82	Antibody response to a viral transcriptional regulator. <i>FEBS Letters</i> , 2003, 534, 202-206.	2.8	5
83	Argentophilic nucleolus organizer region as a proliferation marker in cervical intraepithelial neoplasia grade 1 of the uterine cervix. <i>Journal of Obstetrics and Gynaecology Research</i> , 2014, 40, 1717-1724.	1.3	5
84	Structure and stability of the Human respiratory syncytial virus M2 RNA-binding core domain reveals a compact and cooperative folding unit. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 23-30.	0.8	5
85	Mechanism of Tetramer Dissociation, Unfolding, and Oligomer Assembly of Pneumovirus M2-1 Transcription Antiterminators. <i>ACS Omega</i> , 2018, 3, 14732-14745.	3.5	4
86	Mutational analysis of kinetic partitioning in protein folding and protein-DNA binding. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 179-184.	2.1	3
87	Conformational Isomerization Involving Conserved Proline Residues Modulates Oligomerization of the NS1 Interferon Response Inhibitor from the Syncytial Respiratory Virus. <i>Biochemistry</i> , 2019, 58, 2883-2892.	2.5	2
88	The structure of the extended E2 DNA-binding domain of the bovine papillomavirus 1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 106-112.	2.6	1
89	Crystallization and X-Ray Data Analysis of the Extended Dna-Binding Domain of the E2 Bovine Papillomavirus Type 1 Protein. <i>Protein and Peptide Letters</i> , 2001, 8, 323-326.	0.9	1
90	Hidden Structural Codes in Protein Intrinsic Disorder. <i>Biophysical Journal</i> , 2018, 114, 592a.	0.5	0

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91	Cooperative RNA Recognition by a Viral Transcription Antiterminator. Biophysical Journal, 2018, 114, 252a.	0.5	0