

# Gonzalo de Prat Gay

## List of Publications by Year in descending order

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91  
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44  
g-index

94  
all docs

94  
docs citations

94  
times ranked

2262  
citing authors

#	ARTICLE	IF	CITATIONS
1	Deconstructing virus condensation. PLoS Pathogens, 2021, 17, e1009926.	4.7	48
2	The structure of the extended E2 DNA-binding domain of the bovine papillomavirus E1. Proteins: Structure, Function and Bioinformatics, 2020, 88, 106-112.	2.6	1
3	A conformational switch balances viral RNA accessibility and protection in a nucleocapsid ring model. Archives of Biochemistry and Biophysics, 2019, 671, 77-86.	3.0	7
4	Conformational Isomerization Involving Conserved Proline Residues Modulates Oligomerization of the NS1 Interferon Response Inhibitor from the Syncytial Respiratory Virus. Biochemistry, 2019, 58, 2883-2892.	2.5	2
5	Topology Dictates Evolution of Regulatory Cysteines in a Family of Viral Oncoproteins. Molecular Biology and Evolution, 2019, 36, 1521-1532.	8.9	6
6	Hidden Structural Codes in Protein Intrinsic Disorder. Biophysical Journal, 2018, 114, 592a.	0.5	0
7	Cooperative RNA Recognition by a Viral Transcription Antiterminator. Journal of Molecular Biology, 2018, 430, 777-792.	4.2	10
8	Structure and stability of the Human respiratory syncytial virus M1 RNA-binding core domain reveals a compact and cooperative folding unit. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 23-30.	0.8	5
9	Mechanism of Tetramer Dissociation, Unfolding, and Oligomer Assembly of Pneumovirus M2-1 Transcription Antiterminators. ACS Omega, 2018, 3, 14732-14745.	3.5	4
10	Cooperative RNA Recognition by a Viral Transcription Antiterminator. Biophysical Journal, 2018, 114, 252a.	0.5	0
11	Interplay between sequence, structure and linear motifs in the adenovirus E1A hub protein. Virology, 2018, 525, 117-131.	2.4	17
12	Degenerate cysteine patterns mediate two redox sensing mechanisms in the papillomavirus E7 oncoprotein. Redox Biology, 2017, 11, 38-50.	9.0	6
13	Hidden Structural Codes in Protein Intrinsic Disorder. Biochemistry, 2017, 56, 5560-5569.	2.5	30
14	Intrinsic Disorder to Order Transitions in the Scaffold Phosphoprotein P from the Respiratory Syncytial Virus RNA Polymerase Complex. Biochemistry, 2016, 55, 1441-1454.	2.5	17
15	Conformational Heterogeneity Determined by Folding and Oligomer Assembly Routes of the Interferon Response Inhibitor NS1 Protein, Unique to Human Respiratory Syncytial Virus. Biochemistry, 2015, 54, 5136-5146.	2.5	7
16	Convergent evolution and mimicry of protein linear motifs in host-pathogen interactions. Current Opinion in Structural Biology, 2015, 32, 91-101.	5.7	43
17	Cysteine-Rich Positions Outside the Structural Zinc Motif of Human Papillomavirus E7 Provide Conformational Modulation and Suggest Functional Redox Roles. Biochemistry, 2014, 53, 1680-1696.	2.5	17
18	Argentophilic nucleolus organizer region as a proliferation marker in cervical intraepithelial neoplasia grade 1 of the uterine cervix. Journal of Obstetrics and Gynaecology Research, 2014, 40, 1717-1724.	1.3	5

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19	Fine Modulation of the Respiratory Syncytial Virus M <sub>2</sub> Protein Quaternary Structure by Reversible Zinc Removal from Its Cys <sub>3</sub> -His <sub>1</sub> Motif. <i>Biochemistry</i> , 2013, 52, 6779-6789.	2.5	12
20	Folding of a Cyclin Box. <i>Journal of Biological Chemistry</i> , 2013, 288, 18923-18938.	3.4	17
21	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
22	Conformational Dissection of a Viral Intrinsically Disordered Domain Involved in Cellular Transformation. <i>PLoS ONE</i> , 2013, 8, e72760.	2.5	17
23	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
24	Evolution of Linear Motifs within the Papillomavirus E7 Oncoprotein. <i>Journal of Molecular Biology</i> , 2012, 422, 336-346.	4.2	27
25	Modular Unfolding and Dissociation of the Human Respiratory Syncytial Virus Phosphoprotein P and Its Interaction with the M <sub>2</sub> Antiterminator: A Singular Tetramer-Tetramer Interface Arrangement. <i>Biochemistry</i> , 2012, 51, 8100-8110.	2.5	27
26	Circular Dichroism Techniques for the Analysis of Intrinsically Disordered Proteins and Domains. <i>Methods in Molecular Biology</i> , 2012, 895, 387-404.	0.9	93
27	Sequence Evolution of the Intrinsically Disordered and Globular Domains of a Model Viral Oncoprotein. <i>PLoS ONE</i> , 2012, 7, e47661.	2.5	25
28	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
29	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
30	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
31	The Respiratory Syncytial Virus Transcription Antiterminator M2 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
32	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
33	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
34	Targeting mechanism of the retinoblastoma tumor suppressor by a prototypical viral oncoprotein. <i>FEBS Journal</i> , 2010, 277, 973-988.	4.7	52
35	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
36	Thermodynamics of Cooperative DNA Recognition at a Replication Origin and Transcription Regulatory Site. <i>Biochemistry</i> , 2010, 49, 10277-10286.	2.5	8

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37	Cytosolic accumulation of HPV16 E7 oligomers supports different transformation routes for the prototypic viral oncoprotein: The amyloid-like cancer connection. <i>International Journal of Cancer</i> , 2009, 125, 1902-1911.	5.1	29
38	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
39	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
40	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
41	Kinetically driven refolding of the hyperstable EBNA1 origin DNA-binding dimeric $\beta$ -barrel domain into amyloid-like spherical oligomers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 450-461.	2.6	11
42	The Catalytic Domain of Insulin-degrading Enzyme Forms a Denaturant-resistant Complex with Amyloid $\beta$ Peptide. <i>Journal of Biological Chemistry</i> , 2008, 283, 17039-17048.	3.4	34
43	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
44	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
45	The papillomavirus E2 DNA binding domain. <i>Frontiers in Bioscience - Landmark</i> , 2008, Volume, 6006.	3.0	14
46	Specific Recognition of a DNA Immunogen by its Elicited Antibody. <i>Journal of Molecular Biology</i> , 2007, 370, 183-195.	4.2	13
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 N-Terminal Module of HPV16 E7 Is an Intrinsically Disordered Domain That Confers Conformational and Recognition Plasticity to the Oncoprotein. <i>Biochemistry</i> , 2007, 46, 10405-10412.	2.5	55
49	Increased Stability and DNA Site Discrimination of $\alpha$ -Single Chain Variants of the Dimeric $\beta$ -Barrel DNA Binding Domain of the Human Papillomavirus E2 Transcriptional Regulator. <i>Biochemistry</i> , 2007, 46, 12441-12450.	2.5	11
50	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
51	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
52	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
53	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
54	Chaperone Holdase Activity of Human Papillomavirus E7 Oncoprotein. <i>Biochemistry</i> , 2006, 45, 657-667.	2.5	20

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55	Molecular Basis for Phosphorylation-Dependent, PEST-Mediated Protein Turnover. <i>Structure</i> , 2006, 14, 309-319.	3.3	68
56	Mechanism of DNA Recognition at a Viral Replication Origin. <i>Journal of Biological Chemistry</i> , 2006, 281, 26893-26903.	3.4	10
57	Free Energy Contributions to Direct Readout of a DNA Sequence. <i>Journal of Biological Chemistry</i> , 2005, 280, 32480-32484.	3.4	29
58	The Folding Mechanism of a Dimeric $\beta^2$ -Barrel Domain. <i>Journal of Molecular Biology</i> , 2005, 351, 672-682.	4.2	18
59	A viral DNA-binding domain elicits anti-DNA antibodies of different specificities. <i>Molecular Immunology</i> , 2005, 42, 327-333.	2.2	21
60	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
61	Casein Kinase II Phosphorylation-induced Conformational Switch Triggers Degradation of the Papillomavirus E2 Protein. <i>Journal of Biological Chemistry</i> , 2004, 279, 22430-22439.	3.4	52
62	The Endoplasmic Reticulum Glucosyltransferase Recognizes Nearly Native Glycoprotein Folding Intermediates. <i>Journal of Biological Chemistry</i> , 2004, 279, 46280-46285.	3.4	105
63	Letter to Editor: Solution structure of the HPV-16 E2 DNA binding domain, a transcriptional regulator with a dimeric $\beta^2$ -barrel fold. <i>Journal of Biomolecular NMR</i> , 2004, 30, 211-214.	2.8	25
64	The HPV16 E7 Viral Oncoprotein Self-Assembles into Defined Spherical Oligomers. <i>Biochemistry</i> , 2004, 43, 3310-3317.	2.5	59
65	Specific Antibody-DNA Interaction: A Novel Strategy for Tight DNA Recognition. <i>Biochemistry</i> , 2003, 42, 6218-6227.	2.5	15
66	A Protein's 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
67	Antibody response to a viral transcriptional regulator. <i>FEBS Letters</i> , 2003, 534, 202-206.	2.8	5
68	UDP-Glc:glycoprotein glucosyltransferase recognizes structured and solvent accessible hydrophobic patches in molten globule-like folding intermediates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 86-91.	7.1	164
69	High-Risk (HPV16) Human Papillomavirus E7 Oncoprotein Is Highly Stable and Extended, with Conformational Transitions that Could Explain Its Multiple Cellular Binding Partners. <i>Biochemistry</i> , 2002, 41, 10510-10518.	2.5	58
70	Three-Dimensional Solution Structure and Stability of Thioredoxin m from Spinach. <i>Biochemistry</i> , 2001, 40, 15246-15256.	2.5	13
71	Generation of Sequence-specific, High Affinity Anti-DNA Antibodies. <i>Journal of Biological Chemistry</i> , 2001, 276, 12769-12773.	3.4	26
72	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

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73	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
74	Folding of a dimeric $\beta$ -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
75	Protein Folding in the Absence of Chemical Denaturants. <i>Journal of Biological Chemistry</i> , 1999, 274, 7732-7740.	3.4	25
76	Folding of a pressure-denatured model protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 7888-7893.	7.1	55
77	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
78	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
79	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
80	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
81	Complementation of peptide fragments of the single domain protein chymotrypsin inhibitor 2. <i>Journal of Molecular Biology</i> , 1997, 273, 317-329.	4.2	49
82	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
83	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 &amp; Design</i> , 1996, 1, 189-208.	4.5	37
84	Equilibrium dissociation and unfolding of the dimeric human papillomavirus strain 16 E2 DNA-binding domain. <i>Protein Science</i> , 1996, 5, 310-319.	7.6	77
85	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
86	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
87	Folding of a nascent polypeptide chain in vitro: cooperative formation of structure in a protein module.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 3683-3686.	7.1	75
88	Search for Nucleation Sites in Smaller Fragments of Chymotrypsin Inhibitor 2. <i>Journal of Molecular Biology</i> , 1995, 254, 289-304.	4.2	72
89	Conformational Pathway of the Polypeptide Chain of Chymotrypsin Inhibitor-2 Growing from its N Terminus in vitro. Parallels with the Protein Folding Pathway. <i>Journal of Molecular Biology</i> , 1995, 254, 968-979.	4.2	66
90	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.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 10943-10946.	7.1	41

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91	Modification of the amino acid specificity of tyrosyl-tRNA synthetase by protein engineering. FEBS Letters, 1993, 318, 167-171.	2.8	39