

Jean-Luc Pellequer

List of Publications by Year in descending order

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83
papers

3,200
citations

230014

27
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53
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docs citations

86
times ranked

5197
citing authors

#	ARTICLE	IF	CITATIONS
1	Intrinsically Disordered Tardigrade Proteins Self-Assemble into Fibrous Gels in Response to Environmental Stress. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	7.2	28
2	Intrinsically Disordered Tardigrade Proteins Self-Assemble into Fibrous Gels in Response to Environmental Stress. <i>Angewandte Chemie</i> , 2022, 134, e202109961.	1.6	2
3	Special collection for the ninth AFM BioMed conference. <i>Journal of Molecular Recognition</i> , 2022, 35, e2954.	1.1	1
4	Frontispiece: Intrinsically Disordered Tardigrade Proteins Self-Assemble into Fibrous Gels in Response to Environmental Stress. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	7.2	0
5	Frontispiz: Intrinsically Disordered Tardigrade Proteins Self-Assemble into Fibrous Gels in Response to Environmental Stress. <i>Angewandte Chemie</i> , 2022, 134, .	1.6	0
6	Structural and functional characterization of DdrC, a novel DNA damage-induced nucleoid associated protein involved in DNA compaction. <i>Nucleic Acids Research</i> , 2022, 50, 7680-7696.	6.5	8
7	Insertion and activation of functional Bacteriorhodopsin in a floating bilayer. <i>Journal of Colloid and Interface Science</i> , 2021, 597, 370-382.	5.0	4
8	Nanoscale surface structures of DNA bound to <i>Deinococcus radiodurans</i> HU unveiled by atomic force microscopy. <i>Nanoscale</i> , 2020, 12, 22628-22638.	2.8	9
9	Exolysin (ExLA) from <i>Pseudomonas aeruginosa</i> Punctures Holes into Target Membranes Using a Molten Globule Domain. <i>Journal of Molecular Biology</i> , 2020, 432, 4466-4480.	2.0	8
10	Serial femtosecond crystallography on in vivo-grown crystals drives elucidation of mosquitocidal Cyt1Aa bioactivation cascade. <i>Nature Communications</i> , 2020, 11, 1153.	5.8	31
11	The Importance of Characterizing the Hemoglobin Instability of New Variants: The Case of Hb Dompierre [²²⁹ (B11)Gly ⁺ Arg, <i>HBB</i> : c.88G>C]. <i>Hemoglobin</i> , 2020, 44, 13-16.	0.4	0
12	Visualizing the functional 3D shape and topography of long noncoding RNAs by single-particle atomic force microscopy and in-solution hydrodynamic techniques. <i>Nature Protocols</i> , 2020, 15, 2107-2139.	5.5	14
13	Conserved Pseudoknots in lncRNA MEG3 Are Essential for Stimulation of the p53 Pathway. <i>Molecular Cell</i> , 2019, 75, 982-995.e9.	4.5	138
14	Structural and Functional Characterization of the Type Three Secretion System (T3SS) Needle of <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 573.	1.5	37
15	Externalized histone H4 orchestrates chronic inflammation by inducing lytic cell death. <i>Nature</i> , 2019, 569, 236-240.	13.7	268
16	The Plasma Factor XIII Heterotetrameric Complex Structure: Unexpected Unequal Pairing within a Symmetric Complex. <i>Biomolecules</i> , 2019, 9, 765.	1.8	13
17	On the Operational Aspects of Measuring Nanoparticle Sizes. <i>Nanomaterials</i> , 2019, 9, 18.	1.9	41
18	Fifteen years of <i>Servitude et Grandeur</i> to the application of a biophysical technique in medicine: The tale of AFMBioMed. <i>Journal of Molecular Recognition</i> , 2019, 32, e2773.	1.1	4

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19	Low phosphate activates STOP1-ALMT1 to rapidly inhibit root cell elongation. <i>Nature Communications</i> , 2017, 8, 15300.	5.8	268
20	Conditions to minimize soft single biomolecule deformation when imaging with atomic force microscopy. <i>Journal of Structural Biology</i> , 2017, 197, 322-329.	1.3	18
21	Standardized Nanomechanical Atomic Force Microscopy Procedure (SNAP) for Measuring Soft and Biological Samples. <i>Scientific Reports</i> , 2017, 7, 5117.	1.6	195
22	Seventh International AFMBioMed Conference on AFM in Life Sciences and Medicine, April 11 to 15, 2016, Porto, Portugal. <i>Journal of Molecular Recognition</i> , 2017, 30, e2681.	1.1	3
23	Factor VII variants: which thromboplastin is the most relevant for FVII activity measurement?. <i>Hematologie</i> , 2017, 23, 181-187.	0.0	1
24	Sixth International AFM BioMed Conference on AFM in life sciences and medicine, December 13 to 17, 2014, San Diego, California. <i>Journal of Molecular Recognition</i> , 2016, 29, 404-405.	1.1	4
25	Combined small angle X-ray solution scattering with atomic force microscopy for characterizing radiation damage on biological macromolecules. <i>BMC Structural Biology</i> , 2016, 16, 18.	2.3	13
26	Safety, Stability and Pharmacokinetic Properties of superFactor Va, a Novel Engineered Coagulation Factor V for Treatment of Severe Bleeding. <i>Pharmaceutical Research</i> , 2016, 33, 1517-1526.	1.7	18
27	Atomic force microscope, molecular imaging, and analysis. <i>Journal of Molecular Recognition</i> , 2016, 29, 51-55.	1.1	14
28	Factor Va alternative conformation reconstruction using atomic force microscopy. <i>Thrombosis and Haemostasis</i> , 2014, 112, 1167-1173.	1.8	15
29	Effect of hydration and thermal treatment on ceria surface using non-intrusive techniques. <i>Journal of Nuclear Materials</i> , 2014, 444, 359-367.	1.3	8
30	The sodium/iodide symporter: State of the art of its molecular characterization. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014, 1838, 244-253.	1.4	68
31	Virus particle assembly into crystalline domains enabled by the coffee ring effect. <i>Soft Matter</i> , 2014, 10, 5458-5462.	1.2	24
32	Self-assembled monolayer for AFM measurements of Tobacco Mosaic Virus (TMV) at the atomic level. <i>RSC Advances</i> , 2014, 4, 11927.	1.7	9
33	Fifth International AFMBioMed Conference on AFM in Life Sciences and Medicine, 7-11 May 2013, Shanghai, China. <i>Journal of Molecular Recognition</i> , 2014, 27, 1-2.	1.1	5
34	Nanoscale structural features determined by AFM for single virus particles. <i>Nanoscale</i> , 2013, 5, 10877.	2.8	40
35	DockAFM: benchmarking protein structures by docking under AFM topographs. <i>Bioinformatics</i> , 2013, 29, 3230-3231.	1.8	17
36	Adepth: new representation and its implications for atomic depths of macromolecules. <i>Nucleic Acids Research</i> , 2013, 41, W412-W416.	6.5	17

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37	Conformational dynamics of individual antibodies using computational docking and AFM. <i>Journal of Molecular Recognition</i> , 2013, 26, 596-604.	1.1	25
38	Piezoelectric tuning fork probe for atomic force microscopy imaging and specific recognition force spectroscopy of an enzyme and its ligand. <i>Journal of Molecular Recognition</i> , 2013, 26, 521-531.	1.1	11
39	Mapping the Epitopes of a Neutralizing Antibody Fragment Directed against the Lethal Factor of <i>Bacillus anthracis</i> and Cross-Reacting with the Homologous Edema Factor. <i>PLoS ONE</i> , 2013, 8, e65855.	1.1	10
40	Functional mapping of the A2 domain from human factor VIII. <i>Thrombosis and Haemostasis</i> , 2012, 107, 315-327.	1.8	9
41	Removal of Non-uniform Stripe Noises from AFM Images. , 2012, , .		2
42	Is the coexistence of thromboembolic events and Factor VII deficiency fortuitous?. <i>Thrombosis Research</i> , 2012, 130, S47-S49.	0.8	17
43	Pilot in vivo toxicological investigation of boron nitride nanotubes. <i>International Journal of Nanomedicine</i> , 2012, 7, 19.	3.3	76
44	AFMBioMed Conference: Paris, France, August 2011. <i>Journal of Molecular Recognition</i> , 2012, 25, 239-240.	1.1	7
45	Computational Reconstruction of Multidomain Proteins Using Atomic Force Microscopy Data. <i>Structure</i> , 2012, 20, 113-120.	1.6	28
46	Functional mapping of factor VIII C2 domain. <i>Thrombosis and Haemostasis</i> , 2011, 106, 121-131.	1.8	8
47	DeStripe: frequency-based algorithm for removing stripe noises from AFM images. <i>BMC Structural Biology</i> , 2011, 11, 7.	2.3	71
48	Single and multiple bonds in (strept)avidinâ€“biotin interactions. <i>Journal of Molecular Recognition</i> , 2011, 24, 490-502.	1.1	69
49	Tobacco mosaic virus as an AFM tip calibrator. <i>Journal of Molecular Recognition</i> , 2011, 24, 503-510.	1.1	30
50	On stabilization of a neutral aromatic ligand by π - π cation interactions in monoclonal antibodies. <i>Biophysical Chemistry</i> , 2011, 154, 35-40.	1.5	12
51	Predicting the disruption by UO_2^{2+} of a proteinâ€“ligand interaction. <i>Protein Science</i> , 2010, 19, 2219-2230.	3.1	32
52	Structure-Activity Relationships in Peptide-Antibody Complexes: Implications for Epitope Prediction and Development of Synthetic Peptide Vaccines. <i>Current Medicinal Chemistry</i> , 2009, 16, 953-964.	1.2	65
53	Second international <i>AFM BioMed Conference</i> on AFM in life sciences and medicine, 16â€“18 October 2008, Monterey, CA, USA. <i>Journal of Molecular Recognition</i> , 2009, 22, 345-346.	1.1	8
54	Interdomain engineered disulfide bond permitting elucidation of mechanisms of inactivation of coagulation factor Va by activated protein C. <i>Protein Science</i> , 2009, 11, 2091-2101.	3.1	45

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55	Deciphering the Energy Landscape of the Interaction Uranyl-DCP with Antibodies Using Dynamic Force Spectroscopy. <i>Biophysical Journal</i> , 2008, 95, L63-L65.	0.2	6
56	Characterization of a Factor Xa Binding Site on Factor Va near the Arg-506 Activated Protein C Cleavage Site. <i>Journal of Biological Chemistry</i> , 2007, 282, 21848-21855.	1.6	25
57	Energy Landscape of Chelated Uranyl: Antibody Interactions by Dynamic Force Spectroscopy. <i>Biophysical Journal</i> , 2007, 93, 645-654.	0.2	42
58	Towards a consensus on datasets and evaluation metrics for developing B-cell epitope prediction tools. <i>Journal of Molecular Recognition</i> , 2007, 20, 75-82.	1.1	209
59	On molecular recognition of an uranyl chelate by monoclonal antibodies. <i>Journal of Molecular Recognition</i> , 2007, 20, 508-515.	1.1	8
60	Past, present and future of atomic force microscopy in life sciences and medicine. <i>Journal of Molecular Recognition</i> , 2007, 20, 418-431.	1.1	165
61	Editorial. <i>Journal of Molecular Recognition</i> , 2007, 20, 417-417.	1.1	9
62	Multi-template approach to modeling engineered disulfide bonds. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 192-202.	1.5	33
63	Structural basis for preferential binding of non-ortho-substituted polychlorinated biphenyls by the monoclonal antibody S2B1. <i>Journal of Molecular Recognition</i> , 2005, 18, 282-294.	1.1	16
64	Deciphering structure and topology of conserved COG2042 orphan proteins. <i>BMC Structural Biology</i> , 2005, 5, 3.	2.3	7
65	INTERALIGN: interactive alignment editor for distantly related protein sequences. <i>Bioinformatics</i> , 2005, 21, 3166-3167.	1.8	8
66	Identification of Functionally Important Residues in Proteins Using Comparative Models. <i>Current Medicinal Chemistry</i> , 2004, 11, 595-605.	1.2	29
67	Two Distinct Binding Sites for High Potential Iron-Sulfur Protein and Cytochrome c on the Reaction Center-bound Cytochrome of <i>Rubrivivax gelatinosus</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 32545-32553.	1.6	8
68	BEPITOPE: predicting the location of continuous epitopes and patterns in proteins. <i>Journal of Molecular Recognition</i> , 2003, 16, 20-22.	1.1	156
69	Identification, Purification, and Characterization of an Eukaryotic-like Phosphopantetheine Adenylyltransferase (Coenzyme A Biosynthetic Pathway) in the Hyperthermophilic Archaeon <i>Pyrococcus abyssi</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 31078-31087.	1.6	27
70	Model of a Ternary Complex between Activated Factor VII, Tissue Factor and Factor IX. <i>Thrombosis and Haemostasis</i> , 2002, 88, 74-82.	1.8	35
71	Functional characterization of an anti-estradiol antibody by site-directed mutagenesis and molecular modelling: modulation of binding properties and prominent role of the VLdomain in estradiol recognition. <i>Journal of Molecular Recognition</i> , 2002, 15, 6-18.	1.1	9
72	Model of a ternary complex between activated factor VII, tissue factor and factor IX. <i>Thrombosis and Haemostasis</i> , 2002, 88, 74-82.	1.8	10

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73	F-Box Protein Grr1 Interacts with Phosphorylated Targets via the Cationic Surface of Its Leucine-Rich Repeat. <i>Molecular and Cellular Biology</i> , 2001, 21, 2506-2520.	1.1	67
74	Blood coagulation: The outstanding hydrophobic residues. <i>Current Biology</i> , 2000, 10, R237-R240.	1.8	5
75	Three-dimensional Model of Coagulation Factor Va Bound to Activated Protein C. <i>Thrombosis and Haemostasis</i> , 2000, 84, 849-857.	1.8	66
76	Structural Basis for Hemophilia A Caused by Mutations in the C Domains of Blood Coagulation Factor VIII. <i>Thrombosis and Haemostasis</i> , 2000, 83, 78-85.	1.8	26
77	Stabilization of bound polycyclic aromatic hydrocarbons by a π -cation interaction. <i>Journal of Molecular Biology</i> , 2000, 302, 691-699.	2.0	40
78	Architecture of Antibody Binding Sites for Polynuclear Aromatic Hydrocarbons. <i>ACS Symposium Series</i> , 2000, , 398-416.	0.5	0
79	Unraveling the effect of changes in conformation and compactness at the antibody VL-VH interface upon antigen binding. <i>Journal of Molecular Recognition</i> , 1999, 12, 267-275.	1.1	27
80	Substrate specificity of prostate-specific antigen (PSA). <i>Chemistry and Biology</i> , 1998, 5, 475-488.	6.2	86
81	Homology Models of the C Domains of Blood Coagulation Factors V and VIII: A Proposed Membrane Binding Mode for FV and FVIII C2 Domains. <i>Blood Cells, Molecules, and Diseases</i> , 1998, 24, 448-461.	0.6	52
82	A thermodynamic analysis discriminating loop backbone conformations. <i>Techniques in Protein Chemistry</i> , 1997, , 755-766.	0.3	0
83	Correlation between the location of antigenic sites and the prediction of turns in proteins. <i>Immunology Letters</i> , 1993, 36, 83-99.	1.1	159