Catherine Etchebest

List of Publications by Year
in descending order

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93 papers	3,974 citations	126907 33 h-index	128289 60 g-index
96 all docs	96 docs citations	96 times ranked	3743 citing authors

#	Article	IF	Citations
1	VHH Structural Modelling Approaches: A Critical Review. International Journal of Molecular Sciences, 2022, 23, 3721.	4.1	9
2	Self-association features of NS1 proteins from different flaviviruses. Virus Research, 2022, 318, 198838.	2.2	6
3	How the Strain Origin of Zika Virus NS1 Protein Impacts Its Dynamics and Implications to Their Differential Virulence. Journal of Chemical Information and Modeling, 2021, 61, 1516-1530.	5.4	15
4	Discrete analyses of protein dynamics. Journal of Biomolecular Structure and Dynamics, 2020, 38, 2988-3002.	3.5	20
5	Identification of Electrostatic Epitopes in Flavivirus by Computer Simulations: The PROCEEDpKa Method. Journal of Chemical Information and Modeling, 2020, 60, 944-963.	5.4	20
6	Versatile Dimerisation Process of Translocator Protein (TSPO) Revealed by an Extensive Sampling Based on a Coarse-Grained Dynamics Study. Journal of Chemical Information and Modeling, 2020, 60, 3944-3957.	5.4	7
7	In silico prediction of protein flexibility with local structure approach. Biochimie, 2019, 165, 150-155.	2.6	15
8	New insights into GluT1 mechanics during glucose transfer. Scientific Reports, 2019, 9, 998.	3.3	60
9	Repository of Enriched Structures of Proteins Involved in the Red Blood Cell Environment (RESPIRE). PLoS ONE, 2019, 14, e0211043.	2.5	5
10	The C Terminus of Rotavirus VP4 Protein Contains an Actin Binding Domain Which Requires Cooperation with the Coiled-Coil Domain for Actin Remodeling. Journal of Virology, 2019, 93, .	3.4	8
11	Dynamics and deformability of Î±-, 310- and Ï€-helices. Archives of Biological Sciences, 2018, 70, 21-31.	0.5	10
12	Insights into the ZIKV NS1 Virology from Different Strains through a Fine Analysis of Physicochemical Properties. ACS Omega, 2018, 3, 16212-16229.	3.5	22
13	Antioxidant and Membrane Binding Properties of Serotonin Protect Lipids from Oxidation. Biophysical Journal, 2017, 112, 1863-1873.	0.5	66
14	TMPL: a database of experimental and theoretical transmembrane protein models positioned in the lipid bilayer. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	2
15	Molecular Modeling of Transporters: From Low Resolution Cryo-Electron Microscopy Map to Conformational Exploration. The Example of TSPO. Methods in Molecular Biology, 2017, 1635, 383-416.	0.9	0
16	An Isozyme-specific Redox Switch in Human Brain Glycogen Phosphorylase Modulates Its Allosteric Activation by AMP. Journal of Biological Chemistry, 2016, 291, 23842-23853.	3.4	20
17	Insights into Brain Glycogen Metabolism. Journal of Biological Chemistry, 2016, 291, 18072-18083.	3.4	43
18	Protein flexibility in the light of structural alphabets. Frontiers in Molecular Biosciences, 2015, 2, 20.	3.5	71

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19	Sequenceâ€“structure relationship study in all-Î± transmembrane proteins using an unsupervised learning approach. Amino Acids, 2015, 47, 2303-2322.	2.7	8
20	Direct minimization: Alternative to the traditional L2 norm to derive partial atomic charges. Computational and Theoretical Chemistry, 2015, 1074, 50-57.	2.5	1
21	Construction and validation of an atomic model for bacterial TSPO from electron microscopy density, evolutionary constraints, and biochemical and biophysical data. Biochimica Et Biophysica Acta - Biomembranes, 2015, 1848, 568-580.	2.6	14
22	Decoding the structural events in substrateâ€gating mechanism of eukaryotic prolyl oligopeptidase using normal mode analysis and molecular dynamics simulations. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1428-1443.	2.6	20
23	Efficient Protein Structure Alignment Methods Based on a Structural Alphabet. Biophysical Journal, 2014, 106, 54a.	0.5	0
24	Effect of Serotonin on Membranes Properties Studied by Molecular Dynamics Simulations. Biophysical Journal, 2014, 106, 805a.	0.5	0
25	Urea and Water Permeation across the Human Red Blood Cell Membrane. New Insights into Transport Mechanisms. Biophysical Journal, 2013, 104, 112a-113a.	0.5	1
26	Molecular Dynamics Study of a Protein Motif that Senses Packing Defects Induced by Membrane Curvature. Biophysical Journal, 2013, 104, 662a.	0.5	1
27	Structural Model of the Anion Exchanger 1 (SLC4A1) and Identification of Transmembrane Segments Forming the Transport Site. Journal of Biological Chemistry, 2013, 288, 26372-26384.	3.4	40
28	Conical Lipids in Flat Bilayers Induce Packing Defects Similar to that Induced by Positive Curvature. Biophysical Journal, 2013, 104, 585-593.	0.5	149
29	Amphipathic Lipid Packing Sensor Motifs: Probing Bilayer Defects with Hydrophobic Residues. Biophysical Journal, 2013, 104, 575-584.	0.5	171
30	Energetic and Molecular Water Permeation Mechanisms of the Human Red Blood Cell Urea Transporter B. PLoS ONE, 2013, 8, e82338.	2.5	27
31	PredyFlexy: flexibility and local structure prediction from sequence. Nucleic Acids Research, 2012, 40, W317-W322.	14.5	78
32	Mg2+ in the Major Groove Modulates B-DNA Structure and Dynamics. PLoS ONE, 2012, 7, e41704.	2.5	37
33	Mutation in the substrate-binding site of aminopeptidase B confers new enzymatic properties. Biochimie, 2011, 93, 730-741.	2.6	10
34	Amphipathic-Lipid-Packing-Sensor interactions with lipids assessed by atomistic molecular dynamics. Biochimica Et Biophysica Acta - Biomembranes, 2011, 1808, 2119-2127.	2.6	35
35	The Reconstruction of Condition-Specific Transcriptional Modules Provides New Insights in the Evolution of Yeast AP-1 Proteins. PLoS ONE, 2011, 6, e20924.	2.5	14
36	Predicting protein flexibility through the prediction of local structures. Proteins: Structure, Function and Bioinformatics, 2011, 79, 839-852.	2.6	107

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37	Influence of assignment on the prediction of transmembrane helices in protein structures. Amino Acids, 2010, 39, 1241-1254.	2.7	6
38	A short survey on protein blocks. Biophysical Reviews, 2010, 2, 137-145.	3.2	107
39	Structural and Dynamical Insights into the Opening Mechanism of P. aeruginosa OprM Channel. Structure, 2010, 18, 507-517.	3.3	53
40	Multiple interests in structural models of DARC transmembrane protein. Transfusion Clinique Et Biologique, 2010, 17, 184-196.	0.4	13
41	Critical Review of General Guidelines for Membrane Proteins Model Building and Analysis. Methods in Molecular Biology, 2010, 654, 363-385.	0.9	3
42	Clustering of protein domains for functional and evolutionary studies. BMC Bioinformatics, 2009, 10, 335.	2.6	6
43	Multisensory VR interaction for protein-docking in the CoRSAIRe project. Virtual Reality, 2009, 13, 273-293.	6.1	42
44	A new prediction strategy for long local protein structures using an original description. Proteins: Structure, Function and Bioinformatics, 2009, 76, 570-587.	2.6	29
45	Extension of a local backbone description using a structural alphabet: A new approach to the sequence-structure relationship. Protein Science, 2009, 11, 2871-2886.	7.6	54
46	In Silico Studies on DARC. Infectious Disorders - Drug Targets, 2009, 9, 289-303.	0.8	18
47	New insights of membrane environment effects on MscL channel mechanics from theoretical approaches. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1183-1196.	2.6	18
48	Taking advantage of local structure descriptors to analyze interresidue contacts in protein structures and protein complexes. Proteins: Structure, Function and Bioinformatics, 2008, 73, 672-689.	2.6	10
49	Genome adaptation to chemical stress: clues from comparative transcriptomics in Saccharomyces cerevisiae and Candida glabrata. Genome Biology, 2008, 9, R164.	9.6	48
50	On the Orientation of a Designed Transmembrane Peptide:â€‰ Toward the Right Tilt Angle?. Journal of the American Chemical Society, 2007, 129, 15174-15181.	13.7	96
51	Aminopeptidase B, a glucagon-processing enzyme: site directed mutagenesis of the Zn2+-binding motif and molecular modelling. BMC Biochemistry, 2007, 8, 21.	4.4	25
52	Determining membrane protein structures: still a challenge!. Trends in Biochemical Sciences, 2007, 32, 259-270.	7.5	164
53	A reduced amino acid alphabet for understanding and designing protein adaptation to mutation. European Biophysics Journal, 2007, 36, 1059-1069.	2.2	78
54	â€œPinning strategyâ€: a novel approach for predicting the backbone structure in terms of protein blocks from sequence. Journal of Biosciences, 2007, 32, 51-70.	1.1	28

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55	Theoretical model of human apolipoprotein B100 tertiary structure. Proteins: Structure, Function and Bioinformatics, 2006, 66, 342-358.	2.6	22
56	Protein Peeling 2: a web server to convert protein structures into series of protein units. Nucleic Acids Research, 2006, 34, W75-W78.	14.5	16
57	A structural alphabet for local protein structures: Improved prediction methods. Proteins: Structure, Function and Bioinformatics, 2005, 59, 810-827.	2.6	98
58	Assessing a novel approach for predicting local 3D protein structures from sequence. Proteins: Structure, Function and Bioinformatics, 2005, 62, 865-880.	2.6	40
59	A structural model of a seven-transmembrane helix receptor: The Duffy antigen/receptor for chemokine (DARC). Biochimica Et Biophysica Acta - General Subjects, 2005, 1724, 288-306.	2.4	68
60	Local backbone structure prediction of proteins. In Silico Biology, 2004, 4, 381-6.	0.9	29
61	Dynamical Properties of the MscL of Escherichia coli: A Normal Mode Analysis. Journal of Molecular Biology, 2003, 332, 657-674.	4.2	101
62	A Procedure for Refining a Coiled Coil Protein Structure Using X-Ray Fiber Diffraction and Modeling. Biophysical Journal, 2002, 83, 1774-1783.	0.5	12
63	Cloning and modeling of CD8 Î² in the amphibian ambystoma Mexicanum. Evolutionary conserved structures for interactions with major histocompatibility complex (MHC) class I molecules. Gene, 2002, 288, 95-102.	2.2	10
64	Bayesian probabilistic approach for predicting backbone structures in terms of protein blocks. Proteins: Structure, Function and Bioinformatics, 2000, 41, 271-287.	2.6	254
65	Unraveling Proteins: A Molecular Mechanics Study. Biophysical Journal, 1999, 76, 2760-2768.	0.5	103
66	Prediction of protein side chain conformations: a study on the influence of backbone accuracy on conformation stability in the rotamer space. Protein Engineering, Design and Selection, 1997, 10, 361-372.	2.1	49
67	A Model for the Photosystem II Reaction Center Core Including the Structure of the Primary Donor P680â€,â€¡. Biochemistry, 1996, 35, 14486-14502.	2.5	209
68	Modelling of transmembrane ?-helix bundles. Molecular Engineering, 1995, 5, 1-9.	0.2	0
69	Modelling of Transmembrane Î±-Helix Bundles. Jerusalem Symposia on Quantum Chemistry and Biochemistry, 1995, , 1-9.	0.2	0
70	Hydrophobic neighboring homology (HNH) dotplot: an approach for assessing structurally similar motifs in proteins. Computer Methods and Programs in Biomedicine, 1994, 45, 265-282.	4.7	0
71	Rotational orientation of transmembrane Î±-helices in bacteriorhodopsin. Journal of Molecular Biology, 1994, 236, 1093-1104.	4.2	17
72	Prediction of the positioning of the seven transmembrane Î±-helices of bacteriorhodopsin. Journal of Molecular Biology, 1994, 236, 1105-1122.	4.2	32

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73	Steps Towards Predicting the Structure of Membrane Proteins. NATO ASI Series Series B: Physics, 1994, , 239-252.	0.2	0
74	A critical comparison of search algorithms applied to the optimization of protein side-chain conformations. Journal of Computational Chemistry, 1993, 14, 790-798.	3.3	66
75	Structure and dynamics of bacteriorhodopsin. FEBS Letters, 1993, 327, 256-260.	2.8	20
76	Comparison of three algorithms for the assignment of secondary structure in proteins: the advantages of a consensus assignment. Protein Engineering, Design and Selection, 1993, 6, 377-382.	2.1	117
77	A New Approach to the Rapid Determination of Protein Side Chain Conformations. Journal of Biomolecular Structure and Dynamics, 1991, 8, 1267-1289.	3.5	320
78	Conformational and helicoidal analysis of the molecular dynamics of proteins: â€œCurves,â€•dials and windows for a 50 psec dynamic trajectory of BPTI. Proteins: Structure, Function and Bioinformatics, 1990, 8, 179-193.	2.6	34
79	Describing protein structure: A general algorithm yielding complete helicoidal parameters and a unique overall axis. Proteins: Structure, Function and Bioinformatics, 1989, 6, 46-60.	2.6	129
80	Energy Profile of Cs+in Gramicidin A in the Presence of Water. Problem of the Ion Selectivity of the Channel. Journal of Biomolecular Structure and Dynamics, 1988, 5, 1111-1125.	3.5	7
81	Linear Gramicidins : Influence of the Nature of the Aromatic Side Chains of the Channel Conductance. Jerusalem Symposia on Quantum Chemistry and Biochemistry, 1988, , 147-165.	0.2	5
82	The Gramicidin a Channel: Left Versus Right-Handed Helix. Jerusalem Symposia on Quantum Chemistry and Biochemistry, 1988, , 167-185.	0.2	3
83	Experimental and theoretical study of gramicidin P, an analog of gramicidin A with a methylamine C-terminal. FEBS Letters, 1987, 216, 11-16.	2.8	15
84	The gramicidin A channel. FEBS Letters, 1986, 204, 261-265.	2.8	12
85	The Gramicidin A Channel: Energetics and Structural Characteristics of the Progression of a Sodium Ion in the Presence of Water. Journal of Biomolecular Structure and Dynamics, 1986, 3, 805-825.	3.5	29
86	The Effect of the Amino-Acid Side Chains on the Energy Profiles for Ion Transport in the Gramicidin A Channel. Journal of Biomolecular Structure and Dynamics, 1985, 2, 859-870.	3.5	36
87	The gramicidin A channel: theoretical energy profile computed for single occupancy by a divalent cation, Ca2+. Biochimica Et Biophysica Acta - Biomembranes, 1985, 818, 23-30.	2.6	15
88	The gramicidin A channel: comparison of the energy profiles of Na+ , K+ and Cs+. FEBS Letters, 1984, 173, 301-306.	2.8	42
89	The gramicidin A channel. FEBS Letters, 1984, 170, 191-195.	2.8	33
90	The gramicidin A channel: the energy profile for single and double occupancy in a head-to-head Î²6.3 3,3 -helical dimer backbone. FEBS Letters, 1983, 163, 199-202.	2.8	42

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91	Calculation of the molecular electrostatic potential from a multipole expansion based on localized orbitals. Chemical Physics Letters, 1982, 85, 266-270.	2.6	28
92	The calculation of molecular electrostatic potential from a multipole expansion based on localized orbitals and developed at their centroids: Accuracy and applicability for macromolecular computations. Theoretica Chimica Acta, 1982, 62, 17-28.	0.8	26
93	A theoretical study of the selective alkali and alkaline-earth cation binding properties of valinomycin. International Journal of Quantum Chemistry, 1981, 20, 109-116.	2.0	25