## veronique receveur-brechot or veronique

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A new type of flexible CP12 protein in the marine diatom Thalassiosira pseudonana. Cell Communication and Signaling, 2021, 19, 38.	6.5	9
2	Flexibility of Oxidized and Reduced States of the Chloroplast Regulatory Protein CP12 in Isolation and in Cell Extracts. Biomolecules, 2021, 11, 701.	4.0	4
3	Orchestration of algal metabolism by protein disorder. Archives of Biochemistry and Biophysics, 2019, 672, 108070.	3.0	13
4	Cryptic Disorder Out of Disorder: Encounter between Conditionally Disordered CP12 and Glyceraldehyde-3-Phosphate Dehydrogenase. Journal of Molecular Biology, 2018, 430, 1218-1234.	4.2	19
5	Absence of residual structure in the intrinsically disordered regulatory protein CP12 in its reduced state. Biochemical and Biophysical Research Communications, 2016, 477, 20-26.	2.1	14
6	Saccharification of thermochemically pretreated cellulosic biomass using native and engineered cellulosomal enzyme systems. Reaction Chemistry and Engineering, 2016, 1, 616-628.	3.7	8
7	How Random are Intrinsically Disordered Proteins? A Small Angle Scattering Perspective. Current Protein and Peptide Science, 2012, 13, 55-75.	1.4	287
8	Small-Angle X-ray Scattering and Crystallography. Methods in Enzymology, 2012, 510, 183-210.	1.0	16
9	Understanding the structural ensembles of a highly extended disordered protein. Molecular BioSystems, 2012, 8, 308-319.	2.9	37
10	Synergy, Structure and Conformational Flexibility of Hybrid Cellulosomes Displaying Various Inter-cohesins Linkers. Journal of Molecular Biology, 2011, 405, 143-157.	4.2	33
11	Antitumoral activity of allosteric inhibitors of protein kinase CK2. Oncotarget, 2011, 2, 997-1010.	1.8	39
12	UV and Xâ€ray structural studies of a 101â€residue long Tat protein from a HIVâ€1 primary isolate and of its mutated, detoxified, vaccine candidate. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1441-1456.	2.6	30
13	Crystal structure at 1.45-à resolution of the major allergen endo-β-1,3-glucanase of banana as a molecular basis for the latex-fruit syndrome. Proteins: Structure, Function and Bioinformatics, 2006, 63, 235-242.	2.6	40
14	An Archaeal Peptidase Assembles into Two Different Quaternary Structures. Journal of Biological Chemistry, 2006, 281, 36327-36337.	3.4	35
15	Structural Basis of Cellulosome Efficiency Explored by Small Angle X-ray Scattering. Journal of Biological Chemistry, 2005, 280, 38562-38568.	3.4	95
16	The intrinsically disordered C-terminal domain of the measles virus nucleoprotein interacts with the C-terminal domain of the phosphoprotein via two distinct sites and remains predominantly unfolded. Protein Science, 2005, 14, 1975-1992.	7.6	139
17	Assessing protein disorder and induced folding. Proteins: Structure, Function and Bioinformatics, 2005, 62, 24-45.	2.6	388
18	Activation of the LicT Transcriptional Antiterminator Involves a Domain Swing/Lock Mechanism Provoking Massive Structural Changes. Journal of Biological Chemistry, 2005, 280, 14780-14789.	3.4	64

#	Article	IF	CITATIONS
19	Structure of a Full Length Psychrophilic Cellulase from Pseudoalteromonas haloplanktis revealed by X-ray Diffraction and Small Angle X-ray Scattering. Journal of Molecular Biology, 2005, 348, 1211-1224.	4.2	97
20	Protein Disorder: Conformational Distribution of the Flexible Linker in a Chimeric Double Cellulase. Biophysical Journal, 2005, 88, 2823-2832.	0.5	80
21	Structural Insights into the Mechanism of Formation of Cellulosomes Probed by Small Angle X-ray Scattering. Journal of Biological Chemistry, 2004, 279, 55985-55994.	3.4	48
22	The C-terminal domain of measles virus nucleoprotein belongs to the class of intrinsically disordered proteins that fold upon binding to their physiological partner. Virus Research, 2004, 99, 157-167.	2.2	156
23	Quaternary structure of alpha-crustacyanin from lobster as seen by small-angle X-ray scattering. FEBS Letters, 2003, 544, 189-193.	2.8	19
24	The C-terminal Domain of the Measles Virus Nucleoprotein Is Intrinsically Disordered and Folds upon Binding to the C-terminal Moiety of the Phosphoprotein. Journal of Biological Chemistry, 2003, 278, 18638-18648.	3.4	260