

Francoise Ochsenbein

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6715388/publications.pdf>

Version: 2024-02-01

36
papers

1,614
citations

430874

18
h-index

377865

34
g-index

39
all docs

39
docs citations

39
times ranked

2234
citing authors

#	ARTICLE	IF	CITATIONS
1	PP2C Phosphatases Ptc2 and Ptc3 Are Required for DNA Checkpoint Inactivation after a Double-Strand Break. <i>Molecular Cell</i> , 2003, 11, 827-835.	9.7	184
2	Structural and Functional Analysis of SGT1 Reveals That Its Interaction with HSP90 Is Required for the Accumulation of Rx, an R Protein Involved in Plant Immunity. <i>Plant Cell</i> , 2007, 19, 3791-3804.	6.6	168
3	Prediction of homoprotein and heteroprotein complexes by protein docking and template-based modeling: A CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 323-348.	2.6	148
4	Structural basis for the interaction of Asf1 with histone H3 and its functional implications. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5975-5980.	7.1	127
5	Structural insight into how the human helicase subunit MCM2 may act as a histone chaperone together with ASF1 at the replication fork. <i>Nucleic Acids Research</i> , 2015, 43, 1905-1917.	14.5	108
6	The histone chaperone Asf1 at the crossroads of chromatin and DNA checkpoint pathways. <i>Chromosoma</i> , 2007, 116, 79-93.	2.2	102
7	Targeting protein-protein interactions, a wide open field for drug design. <i>Comptes Rendus Chimie</i> , 2016, 19, 19-27.	0.5	96
8	A New Consensus Sequence for Phosphatidylserine Recognition by Annexins. <i>Journal of Biological Chemistry</i> , 2002, 277, 24684-24693.	3.4	62
9	Mechanisms of Checkpoint Kinase Rad53 Inactivation after a Double-Strand Break in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2007, 27, 3378-3389.	2.3	62
10	Subfunctionalization via Adaptive Evolution Influenced by Genomic Context: The Case of Histone Chaperones ASF1a and ASF1b. <i>Molecular Biology and Evolution</i> , 2013, 30, 1853-1866.	8.9	60
11	Structural and functional analysis of SGT1-HSP90 core complex required for innate immunity in plants. <i>EMBO Reports</i> , 2008, 9, 1209-1215.	4.5	59
12	Dual functions of the Hsm3 protein in chaperoning and scaffolding regulatory particle subunits during the proteasome assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1001-E1010.	7.1	54
13	Insights into the molecular architecture and histone H3-H4 deposition mechanism of yeast Chromatin assembly factor 1. <i>ELife</i> , 2017, 6, .	6.0	47
14	Structure of the Histone Chaperone Asf1 Bound to the Histone H3 C-Terminal Helix and Functional Insights. <i>Structure</i> , 2007, 15, 191-199.	3.3	43
15	Lessons from (co)evolution in the docking of proteins and peptides for CAPRI Rounds 28-35. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 378-390.	2.6	39
16	In Vivo Study of the Nucleosome Assembly Functions of ASF1 Histone Chaperones in Human Cells. <i>Molecular and Cellular Biology</i> , 2008, 28, 3672-3685.	2.3	37
17	The Chromatin Assembly Factor 1 Promotes Rad51-Dependent Template Switches at Replication Forks by Counteracting D-Loop Disassembly by the RecQ-Type Helicase Rqh1. <i>PLoS Biology</i> , 2014, 12, e1001968.	5.6	30
18	Dynamical characterization of residual and non-native structures in a partially folded protein by 15N NMR relaxation using a model based on a distribution of correlation times. <i>Protein Science</i> , 2002, 11, 957-964.	7.6	26

#	ARTICLE	IF	CITATIONS
19	Disentangling the molecular determinants for Cenpâ€F localization to nuclear pores and kinetochores. EMBO Reports, 2018, 19, .	4.5	26
20	Hug1 is an intrinsically disordered protein that inhibits ribonucleotide reductase activity by directly binding Rnr2 subunit. Nucleic Acids Research, 2014, 42, 13174-13185.	14.5	19
21	Study of the DnaB:DciA interplay reveals insights into the primary mode of loading of the bacterial replicative helicase. Nucleic Acids Research, 2021, 49, 6569-6586.	14.5	18
22	Surprising complexity of the Asf1 histone chaperone-Rad53 kinase interaction. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2866-2871.	7.1	17
23	Solution NMR Structure and Backbone Dynamics of the PsaE Subunit of Photosystem I from Synechocystis sp. PCC 6803,. Biochemistry, 2002, 41, 13902-13914.	2.5	15
24	Design on a Rational Basis of High-Affinity Peptides Inhibiting the Histone Chaperone ASF1. Cell Chemical Biology, 2019, 26, 1573-1585.e10.	5.2	11
25	Optimal anchoring of a foldamer inhibitor of ASF1 histone chaperone through backbone plasticity. Science Advances, 2021, 7, .	10.3	11
26	A Strategy for Interaction Site Prediction between Phospho-binding Modules and their Partners Identified from Proteomic Data. Molecular and Cellular Proteomics, 2010, 9, 2745-2759.	3.8	9
27	Sak4 of Phage HK620 Is a RecA Remote Homolog With Single-Strand Annealing Activity Stimulated by Its Cognate SSB Protein. Frontiers in Microbiology, 2018, 9, 743.	3.5	9
28	Recognition of ASF1 by Using Hydrocarbonâ€Constrained Peptides. ChemBioChem, 2019, 20, 891-895.	2.6	7
29	The Xer activation factor of TLCI ₁ expands the possibilities for Xer recombination. Nucleic Acids Research, 2022, 50, 6368-6383.	14.5	6
30	Letter to the Editor:1H,13C and15N Resonance Assignments of the Conserved Core of hAsf1. Journal of Biomolecular NMR, 2004, 29, 413-414.	2.8	5
31	Footprinting of Protein Interactions by Tritium Labeling. Biochemistry, 2010, 49, 4297-4299.	2.5	3
32	Structural Analysis of the Hanks-Type Protein Kinase YabT From Bacillus subtilis Provides New Insights in its DNA-Dependent Activation. Frontiers in Microbiology, 2018, 9, 3014.	3.5	3
33	PP2C Phosphatases Ptc2 and Ptc3 Are Required for DNA Checkpoint Inactivation after a Double-Strand Break. Molecular Cell, 2003, 11, 1119.	9.7	2
34	The Câ€Cterminal domain of HpDprA is a DNAâ€Cbinding winged helix domain that does not bind doubleâ€Cstranded DNA. FEBS Journal, 2019, 286, 1941-1958.	4.7	1
35	Analysis of slow motions in the microâ€Cmillisecond range on domain 1 of annexin I. Comptes Rendus Chimie, 2004, 7, 253-258.	0.5	0
36	Editorial. Progress in Biophysics and Molecular Biology, 2015, 119, 1.	2.9	0