

Francoise Ochsenbein

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

1,614
citations

430874

18
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377865

34
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39
all docs

39
docs citations

39
times ranked

2234
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | The Xer activation factor of <i>TLCI</i> expands the possibilities for Xer recombination. <i>Nucleic Acids Research</i> , 2022, 50, 6368-6383. | 14.5 | 6 |
| 2 | Optimal anchoring of a foldamer inhibitor of ASF1 histone chaperone through backbone plasticity. <i>Science Advances</i> , 2021, 7, . | 10.3 | 11 |
| 3 | Study of the DnaB:DciA interplay reveals insights into the primary mode of loading of the bacterial replicative helicase. <i>Nucleic Acids Research</i> , 2021, 49, 6569-6586. | 14.5 | 18 |
| 4 | Design on a Rational Basis of High-Affinity Peptides Inhibiting the Histone Chaperone ASF1. <i>Cell Chemical Biology</i> , 2019, 26, 1573-1585.e10. | 5.2 | 11 |
| 5 | The C-terminal domain of HpDprA is a DNA-binding winged helix domain that does not bind double-stranded DNA. <i>FEBS Journal</i> , 2019, 286, 1941-1958. | 4.7 | 1 |
| 6 | Recognition of ASF1 by Using Hydrocarbon-Constrained Peptides. <i>ChemBioChem</i> , 2019, 20, 891-895. | 2.6 | 7 |
| 7 | Disentangling the molecular determinants for CenP localization to nuclear pores and kinetochores. <i>EMBO Reports</i> , 2018, 19, . | 4.5 | 26 |
| 8 | Sak4 of Phage HK620 Is a RecA Remote Homolog With Single-Strand Annealing Activity Stimulated by Its Cognate SSB Protein. <i>Frontiers in Microbiology</i> , 2018, 9, 743. | 3.5 | 9 |
| 9 | Structural Analysis of the Hanks-Type Protein Kinase YabT From <i>Bacillus subtilis</i> Provides New Insights in its DNA-Dependent Activation. <i>Frontiers in Microbiology</i> , 2018, 9, 3014. | 3.5 | 3 |
| 10 | 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 |
| 11 | 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 |
| 12 | Prediction of homoprotein and heteroprotein complexes by protein docking and template-based modeling: A CASP-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 323-348. | 2.6 | 148 |
| 13 | Targeting protein-protein interactions, a wide open field for drug design. <i>Comptes Rendus Chimie</i> , 2016, 19, 19-27. | 0.5 | 96 |
| 14 | 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 |
| 15 | Editorial. <i>Progress in Biophysics and Molecular Biology</i> , 2015, 119, 1. | 2.9 | 0 |
| 16 | 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 |
| 17 | Hug1 is an intrinsically disordered protein that inhibits ribonucleotide reductase activity by directly binding Rnr2 subunit. <i>Nucleic Acids Research</i> , 2014, 42, 13174-13185. | 14.5 | 19 |
| 18 | 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 |

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|----|---|-----|-----------|
| 19 | 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 |
| 20 | Dual functions of the Hsm3 protein in chaperoning and scaffolding regulatory particle subunits during the proteasome assembly. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1001-E1010. | 7.1 | 54 |
| 21 | 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 |
| 22 | Footprinting of Protein Interactions by Tritium Labeling. Biochemistry, 2010, 49, 4297-4299. | 2.5 | 3 |
| 23 | Structural and functional analysis of SGT1-HSP90 core complex required for innate immunity in plants. EMBO Reports, 2008, 9, 1209-1215. | 4.5 | 59 |
| 24 | In Vivo Study of the Nucleosome Assembly Functions of ASF1 Histone Chaperones in Human Cells. Molecular and Cellular Biology, 2008, 28, 3672-3685. | 2.3 | 37 |
| 25 | Mechanisms of Checkpoint Kinase Rad53 Inactivation after a Double-Strand Break in Saccharomyces cerevisiae. Molecular and Cellular Biology, 2007, 27, 3378-3389. | 2.3 | 62 |
| 26 | 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. Plant Cell, 2007, 19, 3791-3804. | 6.6 | 168 |
| 27 | Structure of the Histone Chaperone Asf1 Bound to the Histone H3 C-Terminal Helix and Functional Insights. Structure, 2007, 15, 191-199. | 3.3 | 43 |
| 28 | The histone chaperone Asf1 at the crossroads of chromatin and DNA checkpoint pathways. Chromosoma, 2007, 116, 79-93. | 2.2 | 102 |
| 29 | Structural basis for the interaction of Asf1 with histone H3 and its functional implications. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 5975-5980. | 7.1 | 127 |
| 30 | Letter to the Editor: ¹ H, ¹³ C and ¹⁵ N Resonance Assignments of the Conserved Core of hAsf1. Journal of Biomolecular NMR, 2004, 29, 413-414. | 2.8 | 5 |
| 31 | Analysis of slow motions in the micro-millisecond range on domain 1 of annexin I. Comptes Rendus Chimie, 2004, 7, 253-258. | 0.5 | 0 |
| 32 | PP2C Phosphatases Ptc2 and Ptc3 Are Required for DNA Checkpoint Inactivation after a Double-Strand Break. Molecular Cell, 2003, 11, 827-835. | 9.7 | 184 |
| 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 | A New Consensus Sequence for Phosphatidylserine Recognition by Annexins. Journal of Biological Chemistry, 2002, 277, 24684-24693. | 3.4 | 62 |
| 35 | 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 |
| 36 | Dynamical characterization of residual and non-native structures in a partially folded protein by ¹⁵ N NMR relaxation using a model based on a distribution of correlation times. Protein Science, 2002, 11, 957-964. | 7.6 | 26 |