

Dominique Durand

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

1,198
citations

567281

15
h-index

477307

29
g-index

31
all docs

31
docs citations

31
times ranked

2470
citing authors

#	ARTICLE	IF	CITATIONS
1	The apo-form of the <i>Vibrio cholerae</i> replicative helicase DnaB is a labile and inactive planar trimer of dimers. FEBS Letters, 2022, , .	2.8	2
2	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
3	The cooperative binding of TDP-43 to GU-rich RNA repeats antagonizes TDP-43 aggregation. ELife, 2021, 10, .	6.0	35
4	Structural ensemble and biological activity of DciA intrinsically disordered region. Journal of Structural Biology, 2020, 212, 107573.	2.8	11
5	Defects in t6A tRNA modification due to GON7 and YRDC mutations lead to Galloway-Mowat syndrome. Nature Communications, 2019, 10, 3967.	12.8	66
6	Investigation into Early Steps of Actin Recognition by the Intrinsically Disordered N-WASP Domain V. International Journal of Molecular Sciences, 2019, 20, 4493.	4.1	3
7	Quantitative live-cell imaging and 3D modeling reveal critical functional features in the cytosolic complex of phagocyte NADPH oxidase. Journal of Biological Chemistry, 2019, 294, 3824-3836.	3.4	25
8	Ligand-induced conformational switch in an artificial bidomain protein scaffold. Scientific Reports, 2019, 9, 1178.	3.3	16
9	Molecular Dynamics Simulations Combined with Nuclear Magnetic Resonance and/or Small-Angle X-ray Scattering Data for Characterizing Intrinsically Disordered Protein Conformational Ensembles. Journal of Chemical Information and Modeling, 2019, 59, 1743-1758.	5.4	40
10	Structural Characterization of N-WASP Domain V Using MD Simulations with NMR and SAXS Data. Biophysical Journal, 2019, 116, 1216-1227.	0.5	18
11	YB-1, an abundant core mRNA-binding protein, has the capacity to form an RNA nucleoprotein filament: a structural analysis. Nucleic Acids Research, 2019, 47, 3127-3141.	14.5	32
12	Translocation and calmodulin-activation of the adenylate cyclase toxin (CyaA) of <i>Bordetella pertussis</i> . Pathogens and Disease, 2018, 76, .	2.0	11
13	Dissociation of the Dimer of the Intrinsically Disordered Domain of RNase Y upon Antibody Binding. Biophysical Journal, 2018, 115, 2102-2113.	0.5	5
14	The structure of the TsaB/TsaD/TsaE complex reveals an unexpected mechanism for the bacterial t6A tRNA-modification. Nucleic Acids Research, 2018, 46, 5850-5860.	14.5	28
15	High affinity anchoring of the decoration protein pb10 onto the bacteriophage T5 capsid. Scientific Reports, 2017, 7, 41662.	3.3	21
16	The crystal structure of Trz1, the long form RNase Z from yeast. Nucleic Acids Research, 2017, 45, 6209-6216.	14.5	16
17	Trz1, the long form RNase Z from yeast, forms a stable heterohexamer with endonuclease Nuc1 and mutarotase. Biochemical Journal, 2017, 474, 3599-3613.	3.7	3
18	Conformational switch of harmonin, a submembrane scaffold protein of the hair cell mechanoelectrical transduction machinery. FEBS Letters, 2017, 591, 2299-2310.	2.8	9

#	ARTICLE	IF	CITATIONS
19	2017 publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution: an update. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 710-728.	2.3	205
20	Calmodulin fishing with a structurally disordered bait triggers CyaA catalysis. <i>PLoS Biology</i> , 2017, 15, e2004486.	5.6	31
21	The unexpected structure of the designed protein Octarellin V.1 forms a challenge for protein structure prediction tools. <i>Journal of Structural Biology</i> , 2016, 195, 19-30.	2.8	15
22	Can Changes in Temperature or Ionic Conditions Modify the DNA Organization in the Full Bacteriophage Capsid?. <i>Journal of Physical Chemistry B</i> , 2016, 120, 5975-5986.	2.6	14
23	A Brief Survey of State-of-the-Art BioSAXS. <i>Protein and Peptide Letters</i> , 2016, 23, 217-231.	0.9	46
24	Crystal structures of the Gon7/Pcc1 and Bud32/Cgi121 complexes provide a model for the complete yeast KEOPS complex. <i>Nucleic Acids Research</i> , 2015, 43, 3358-3372.	14.5	43
25	Structural and functional analysis of the fibronectin-binding protein <sc>FNE</sc> from <i>Streptococcus equi</i> spp. <i>equi</i>. <i>FEBS Journal</i> , 2014, 281, 5513-5531.	4.7	17
26	How Random are Intrinsically Disordered Proteins? A Small Angle Scattering Perspective. <i>Current Protein and Peptide Science</i> , 2012, 13, 55-75.	1.4	287
27	Design, Production and Molecular Structure of a New Family of Artificial Alpha-helical Repeat Proteins (Î±Rep) Based on Thermostable HEAT-like Repeats. <i>Journal of Molecular Biology</i> , 2010, 404, 307-327.	4.2	85
28	Structure of the Yeast tRNA m7G Methylation Complex. <i>Structure</i> , 2008, 16, 52-61.	3.3	95