

Nicolas Tarbouriech

List of Publications by Year in descending order

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34
papers

1,608
citations

304743

22
h-index

395702

33
g-index

34
all docs

34
docs citations

34
times ranked

1866
citing authors

#	ARTICLE	IF	CITATIONS
1	Selection of Primer-Template Sequences That Bind with Enhanced Affinity to Vaccinia Virus E9 DNA Polymerase. <i>Viruses</i> , 2022, 14, 369.	3.3	0
2	Structural Dynamics of the C-terminal X Domain of Nipah and Hendra Viruses Controls the Attachment to the C-terminal Tail of the Nucleocapsid Protein. <i>Journal of Molecular Biology</i> , 2022, 434, 167551.	4.2	3
3	Solution Structure of the C-terminal Domain of A20, the Missing Brick for the Characterization of the Interface between Vaccinia Virus DNA Polymerase and its Processivity Factor. <i>Journal of Molecular Biology</i> , 2021, 433, 167009.	4.2	14
4	Structural Description of the Nipah Virus Phosphoprotein and Its Interaction with STAT1. <i>Biophysical Journal</i> , 2020, 118, 2470-2488.	0.5	28
5	The vaccinia virus DNA polymerase structure provides insights into the mode of processivity factor binding. <i>Nature Communications</i> , 2017, 8, 1455.	12.8	31
6	Structural analysis of point mutations at the <i>Vaccinia virus</i> A20/D4 interface. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 687-691.	0.8	7
7	Domain Organization of Vaccinia Virus Helicase-Primase D5. <i>Journal of Virology</i> , 2016, 90, 4604-4613.	3.4	22
8	Crystal Structure of the Vaccinia Virus Uracil-DNA Glycosylase in Complex with DNA. <i>Journal of Biological Chemistry</i> , 2015, 290, 17923-17934.	3.4	24
9	Crystal Structure of the Vaccinia Virus DNA Polymerase Holoenzyme Subunit D4 in Complex with the A20 N-Terminal Domain. <i>PLoS Pathogens</i> , 2014, 10, e1003978.	4.7	27
10	Structure of Nipah virus unassembled nucleoprotein in complex with its viral chaperone. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 754-759.	8.2	119
11	Structural and functional characterization of the single-chain Fv fragment from a unique HCV E1E2-specific monoclonal antibody. <i>FEBS Letters</i> , 2013, 587, 3335-3340.	2.8	1
12	Atomic Resolution Description of the Interaction between the Nucleoprotein and Phosphoprotein of Hendra Virus. <i>PLoS Pathogens</i> , 2013, 9, e1003631.	4.7	68
13	Structure of the C-Terminal Domain of Lettuce Necrotic Yellow Virus Phosphoprotein. <i>Journal of Virology</i> , 2013, 87, 9569-9578.	3.4	10
14	Low-Resolution Structure of Vaccinia Virus DNA Replication Machinery. <i>Journal of Virology</i> , 2013, 87, 1679-1689.	3.4	37
15	Epstein-Barr Virus-Encoded BARF1 Protein is a Decoy Receptor for Macrophage Colony Stimulating Factor and Interferes with Macrophage Differentiation and Activation. <i>Viral Immunology</i> , 2012, 25, 461-470.	1.3	26
16	Allosteric competitive inactivation of hematopoietic CSF-1 signaling by the viral decoy receptor BARF1. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 938-947.	8.2	39
17	Structure of the Vesicular Stomatitis Virus N0-P Complex. <i>PLoS Pathogens</i> , 2011, 7, e1002248.	4.7	111
18	The Flexible Motif V of Epstein-Barr Virus Deoxyuridine 5'-Triphosphate Pyrophosphatase Is Essential for Catalysis. <i>Journal of Biological Chemistry</i> , 2009, 284, 25280-25289.	3.4	27

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19	A Bridge Crosses the Active-Site Canyon of the Epstein-Barr Virus Nuclease with DNase and RNase Activities. <i>Journal of Molecular Biology</i> , 2009, 391, 717-728.	4.2	46
20	Interaction of the C-Terminal Domains of Sendai Virus N and P Proteins: Comparison of Polymerase-Nucleocapsid Interactions within the Paramyxovirus Family. <i>Journal of Virology</i> , 2007, 81, 6807-6816.	3.4	111
21	New Insights on the Role of the $\hat{3}$ -Herpesvirus Uracil-DNA Glycosylase Leucine Loop Revealed by the Structure of the Epstein-Barr Virus Enzyme in Complex with an Inhibitor Protein. <i>Journal of Molecular Biology</i> , 2007, 366, 117-131.	4.2	28
22	Structure of the Epstein-Barr Virus Oncogene BARF1. <i>Journal of Molecular Biology</i> , 2006, 359, 667-678.	4.2	43
23	Structural genomics of the Epstein-Barr virus. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1276-1285.	2.5	34
24	Application of the use of high-throughput technologies to the determination of protein structures of bacterial and viral pathogens. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1196-1207.	2.5	23
25	The Monomeric dUTPase from Epstein-Barr Virus Mimics Trimeric dUTPases. <i>Structure</i> , 2005, 13, 1299-1310.	3.3	49
26	Molecular determinants of substrate specificity in the feruloyl esterase module of xylanase 10B from <i>Clostridium thermocellum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 194-197.	2.5	22
27	Crystal structure of levansucrase from the Gram-negative bacterium <i>Gluconacetobacter diazotrophicus</i> . <i>Biochemical Journal</i> , 2005, 390, 19-27.	3.7	135
28	Ab Initio Structure Determination and Functional Characterization Of CBM36. <i>Structure</i> , 2004, 12, 1177-1187.	3.3	76
29	Structure and dynamics of the nucleocapsid-binding domain of the Sendai virus phosphoprotein in solution. <i>Virology</i> , 2004, 319, 201-211.	2.4	73
30	Crystallization and preliminary X-ray diffraction analysis of levansucrase (LsdA) from <i>Gluconacetobacter diazotrophicus</i> SRT4. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 181-183.	2.5	4
31	Three-dimensional structures of the Mn and Mg dTDP complexes of the family GT-2 glycosyltransferase SpsA: a comparison with related NDP-sugar glycosyltransferases 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 314, 655-661.	4.2	118
32	Assignment of the ^1H , ^{15}N and ^{13}C resonances of the nucleocapsid-binding domain of the Sendai virus phosphoprotein. <i>Journal of Biomolecular NMR</i> , 2001, 21, 75-76.	2.8	17
33	Tetrameric coiled coil domain of Sendai virus phosphoprotein. <i>Nature Structural Biology</i> , 2000, 7, 777-781.	9.7	154
34	On the Domain Structure and the Polymerization State of the Sendai Virus P Protein. <i>Virology</i> , 2000, 266, 99-109.	2.4	81