

Nuria Verdaguer

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1833580/publications.pdf>

Version: 2024-02-01

87
papers

3,860
citations

109137

35
h-index

133063

59
g-index

94
all docs

94
docs citations

94
times ranked

3421
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 Point Mutation and Deletion Spectra and Their Association with Different Disease Outcomes. <i>Microbiology Spectrum</i> , 2022, 10, e0022122.	1.2	10
2	Symmetry disruption commits vault particles to disassembly. <i>Science Advances</i> , 2022, 8, eabj7795.	4.7	9
3	SARS-CoV-2 Mutant Spectra at Different Depth Levels Reveal an Overwhelming Abundance of Low Frequency Mutations. <i>Pathogens</i> , 2022, 11, 662.	1.2	16
4	Structure and Double-Stranded RNA-Binding Activity of the Birnavirus <i>Drosophila X</i> Virus VP3 Protein. <i>Journal of Virology</i> , 2021, 95, .	1.5	2
5	Snapshots of a Non-Canonical RdRP in Action. <i>Viruses</i> , 2021, 13, 1260.	1.5	5
6	Amino Acid Substitutions Associated with Treatment Failure for Hepatitis C Virus Infection. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	15
7	Multimerization of Zika Virus-NS5 Causes Ciliopathy and Forces Premature Neurogenesis. <i>Cell Stem Cell</i> , 2020, 27, 920-936.e8.	5.2	18
8	(F)uridylylated Peptides Linked to VPg1 of Foot-and- Mouth Disease Virus (FMDV): Design, Synthesis and X-Ray Crystallography of the Complexes with FMDV RNA-Dependent RNA Polymerase. <i>Molecules</i> , 2019, 24, 2360.	1.7	2
9	Cryo-EM structure of pleconaril-resistant rhinovirus-B5 complexed to the antiviral OBR-5-340 reveals unexpected binding site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19109-19115.	3.3	22
10	Supramolecular arrangement of the full-length Zika virus NS5. <i>PLoS Pathogens</i> , 2019, 15, e1007656.	2.1	38
11	Contribution of a Multifunctional Polymerase Region of Foot-and-Mouth Disease Virus to Lethal Mutagenesis. <i>Journal of Virology</i> , 2018, 92, .	1.5	5
12	Viral RNA-Dependent RNA Polymerases: A Structural Overview. <i>Sub-Cellular Biochemistry</i> , 2018, 88, 39-71.	1.0	38
13	Structure of eIF4E in Complex with an eIF4G Peptide Supports a Universal Bipartite Binding Mode for Protein Translation. <i>Plant Physiology</i> , 2017, 174, 1476-1491.	2.3	32
14	Structural characterization of the Rabphilin-3A-SNAP25 interaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5343-E5351.	3.3	37
15	Molecular and Functional Bases of Selection against a Mutation Bias in an RNA Virus. <i>Genome Biology and Evolution</i> , 2017, 9, 1212-1228.	1.1	13
16	Structural basis for biologically relevant mechanical stiffening of a virus capsid by cavity-creating or spacefilling mutations. <i>Scientific Reports</i> , 2017, 7, 4101.	1.6	23
17	Both <i>cis</i> and <i>trans</i> Activities of Foot-and-Mouth Disease Virus 3D Polymerase Are Essential for Viral RNA Replication. <i>Journal of Virology</i> , 2016, 90, 6864-6883.	1.5	17
18	Decrease in pH destabilizes individual vault nanocages by weakening the inter-protein lateral interaction. <i>Scientific Reports</i> , 2016, 6, 34143.	1.6	17

#	ARTICLE	IF	CITATIONS
19	RNA-Dependent RNA Polymerases of Picornaviruses: From the Structure to Regulatory Mechanisms. <i>Viruses</i> , 2015, 7, 4438-4460.	1.5	53
20	The Structure of the RNA-Dependent RNA Polymerase of a Permutotetrahavirus Suggests a Link between Primer-Dependent and Primer-Independent Polymerases. <i>PLoS Pathogens</i> , 2015, 11, e1005265.	2.1	25
21	The RNA Template Channel of the RNA-Dependent RNA Polymerase as a Target for Development of Antiviral Therapy of Multiple Genera within a Virus Family. <i>PLoS Pathogens</i> , 2015, 11, e1004733.	2.1	55
22	Multifunctionality of a Picornavirus Polymerase Domain: Nuclear Localization Signal and Nucleotide Recognition. <i>Journal of Virology</i> , 2015, 89, 6848-6859.	1.5	22
23	Structural Basis for Host Membrane Remodeling Induced by Protein 2B of Hepatitis A Virus. <i>Journal of Virology</i> , 2015, 89, 3648-3658.	1.5	16
24	Infectious Bursal Disease Virus VP3 Upregulates VP1-Mediated RNA-Dependent RNA Replication. <i>Journal of Virology</i> , 2015, 89, 11165-11168.	1.5	27
25	The Crystal Structure of a Cardiovirus RNA-Dependent RNA Polymerase Reveals an Unusual Conformation of the Polymerase Active Site. <i>Journal of Virology</i> , 2014, 88, 5595-5607.	1.5	24
26	A novel benzonitrile analogue inhibits rhinovirus replication. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 2723-2732.	1.3	27
27	Cryo-EM near-atomic structure of a dsRNA fungal virus shows ancient structural motifs preserved in the dsRNA viral lineage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7641-7646.	3.3	32
28	Mechanical Stability and Reversible Fracture of Vault Particles. <i>Biophysical Journal</i> , 2014, 106, 687-695.	0.2	36
29	Viruses and viral proteins. <i>IUCr</i> , 2014, 1, 492-504.	1.0	24
30	Uncoating of common cold virus is preceded by RNA switching as determined by X-ray and cryo-EM analyses of the subviral A-particle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20063-20068.	3.3	51
31	Role of Motif B Loop in Allosteric Regulation of RNA-Dependent RNA Polymerization Activity. <i>Journal of Molecular Biology</i> , 2013, 425, 2279-2287.	2.0	55
32	X-Ray Crystallography of Viruses. <i>Sub-Cellular Biochemistry</i> , 2013, 68, 117-144.	1.0	8
33	New features of vault architecture and dynamics revealed by novel refinement using the deformable elastic network approach. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1054-1061.	2.5	12
34	Structural insights into the Ca ²⁺ and PI(4,5)P ₂ binding modes of the C2 domains of rabphilin 3A and synaptotagmin 1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20503-20508.	3.3	64
35	Insights into Minor Group Rhinovirus Uncoating: The X-ray Structure of the HRV2 Empty Capsid. <i>PLoS Pathogens</i> , 2012, 8, e1002473.	2.1	98
36	Purification, crystallization and preliminary X-ray diffraction analysis of the RNA-dependent RNA polymerase from <i>Thossea assignavirus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1263-1266.	0.7	3

#	ARTICLE	IF	CITATIONS
37	Vault particles: a new generation of delivery nanodevices. <i>Current Opinion in Biotechnology</i> , 2012, 23, 972-977.	3.3	19
38	Conformational Changes in Motif D of RdRPs as Fidelity Determinant. <i>Structure</i> , 2012, 20, 1448-1450.	1.6	8
39	Epitope Insertion at the N-Terminal Molecular Switch of the Rabbit Hemorrhagic Disease Virus T=3 Capsid Protein Leads to Larger T=4 Capsids. <i>Journal of Virology</i> , 2012, 86, 6470-6480.	1.5	25
40	Structural Dynamics of Picornaviral RdRP Complexes. Implications for the Design of Antivirals. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2012, , 183-193.	0.5	0
41	Cloning, purification and preliminary crystallographic studies of the 2AB protein from hepatitis A virus. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1224-1227.	0.7	3
42	Structure of Foot-and-Mouth Disease Virus Mutant Polymerases with Reduced Sensitivity to Ribavirin. <i>Journal of Virology</i> , 2010, 84, 6188-6199.	1.5	50
43	A Multi-Step Process of Viral Adaptation to a Mutagenic Nucleoside Analogue by Modulation of Transition Types Leads to Extinction-Escape. <i>PLoS Pathogens</i> , 2010, 6, e1001072.	2.1	83
44	The T=1 Capsid Protein of <i>Penicillium chrysogenum</i> Virus Is Formed by a Repeated Helix-Rich Core Indicative of Gene Duplication. <i>Journal of Virology</i> , 2010, 84, 7256-7266.	1.5	39
45	Autoproteolytic Activity Derived from the Infectious Bursal Disease Virus Capsid Protein. <i>Journal of Biological Chemistry</i> , 2009, 284, 8064-8072.	1.6	40
46	Structural and mechanistic insights into the association of PKC ζ -C2 domain to PtdIns(4,5)P ₂ . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6603-6607.	3.3	99
47	Structural insights into replication initiation and elongation processes by the FMDV RNA-dependent RNA polymerase. <i>Current Opinion in Structural Biology</i> , 2009, 19, 752-758.	2.6	56
48	Minor group human rhinovirus α receptor interactions: Geometry of multimodular attachment and basis of recognition. <i>FEBS Letters</i> , 2009, 583, 235-240.	1.3	26
49	The mechanism of vault opening from the high resolution structure of the N-terminal repeats of MVP. <i>EMBO Journal</i> , 2009, 28, 3450-3457.	3.5	30
50	RNA Virus Polymerases. , 2009, , 383-401.		3
51	Structural Insights into the Multifunctional Protein VP3 of Birnaviruses. <i>Structure</i> , 2008, 16, 29-37.	1.6	37
52	Sequential structures provide insights into the fidelity of RNA replication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 9463-9468.	3.3	113
53	Activation mechanism of a noncanonical RNA-dependent RNA polymerase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 20540-20545.	3.3	80
54	Infectious Bursal Disease Virus Capsid Assembly and Maturation by Structural Rearrangements of a Transient Molecular Switch. <i>Journal of Virology</i> , 2007, 81, 6869-6878.	1.5	45

#	ARTICLE	IF	CITATIONS
55	The structure of a protein primer-polymerase complex in the initiation of genome replication. <i>EMBO Journal</i> , 2006, 25, 880-888.	3.5	124
56	A comparison of viral RNA-dependent RNA polymerases. <i>Current Opinion in Structural Biology</i> , 2006, 16, 27-34.	2.6	205
57	The 2.6-Angstrom Structure of Infectious Bursal Disease Virus-Derived T=1 Particles Reveals New Stabilizing Elements of the Virus Capsid. <i>Journal of Virology</i> , 2006, 80, 6895-6905.	1.5	60
58	X-ray crystallography of virus-receptor complexes: structure of a minor group rhinovirus bound to its cellular receptor protein. <i>Crystallography Reviews</i> , 2005, 11, 73-81.	0.4	1
59	Mutant Viral Polymerase in the Transition of Virus to Error Catastrophe Identifies a Critical Site for RNA Binding. <i>Journal of Molecular Biology</i> , 2005, 353, 1021-1032.	2.0	42
60	Preliminary analysis of two and three dimensional crystals of vault ribonucleoprotein particles. <i>Journal of Structural Biology</i> , 2005, 151, 111-115.	1.3	4
61	X-ray structure of a minor group human rhinovirus bound to a fragment of its cellular receptor protein. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 429-434.	3.6	143
62	The coat protein of Rabbit hemorrhagic disease virus contains a molecular switch at the N-terminal region facing the inner surface of the capsid. <i>Virology</i> , 2004, 322, 118-134.	1.1	49
63	Structure of Foot-and-Mouth Disease Virus RNA-dependent RNA Polymerase and Its Complex with a Template-Primer RNA. <i>Journal of Biological Chemistry</i> , 2004, 279, 47212-47221.	1.6	198
64	Functional and Structural Aspects of the Interaction of Foot-and-Mouth Disease Virus with Antibodies. , 2004, , 224-260.		5
65	Crystallization and preliminary X-ray analysis of swine vesicular disease virus (SVDV). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 541-543.	2.5	3
66	Crystallization and preliminary X-ray analysis of the glycogen synthase from <i>Pyrococcus abyssi</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2322-2324.	2.5	6
67	Retinoic Acid Binds to the C2-Domain of Protein Kinase C α . <i>Biochemistry</i> , 2003, 42, 8774-8779.	1.2	76
68	Structure of Swine Vesicular Disease Virus: Mapping of Changes Occurring during Adaptation of Human Coxsackie B5 Virus To Infect Swine. <i>Journal of Virology</i> , 2003, 77, 9780-9789.	1.5	21
69	Evolution of Cell Recognition by Viruses: A Source of Biological Novelty with Medical Implications. <i>Advances in Virus Research</i> , 2003, 62, 19-111.	0.9	58
70	Additional Binding Sites for Anionic Phospholipids and Calcium Ions in the Crystal Structures of Complexes of the C2 Domain of Protein Kinase C β . <i>Journal of Molecular Biology</i> , 2002, 320, 277-291.	2.0	74
71	Structure of the C2 domain from novel protein kinase C μ . A membrane binding model for Ca $^{2+}$ -independent C2 domains. <i>Journal of Molecular Biology</i> , 2001, 311, 837-849.	2.0	97
72	Crystallization and preliminary X-ray analysis of clade I catalases from <i>Pseudomonas syringae</i> and <i>Listeria seeligeri</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1184-1186.	2.5	6

#	ARTICLE	IF	CITATIONS
73	The need for a shared database infrastructure: combining X-ray crystallography and electron microscopy. <i>European Biophysics Journal</i> , 2000, 29, 457-462.	1.2	5
74	A multiply substituted Gâ€“H loop from foot-and-mouth disease virus in complex with a neutralizing antibody: a role for water molecules. <i>Journal of General Virology</i> , 2000, 81, 1495-1505.	1.3	37
75	Crystallization and preliminary X-ray analysis of human rhinovirus serotype 2 (HRV2). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1459-1461.	2.5	4
76	Flexibility of the Major Antigenic Loop of Foot-and-Mouth Disease Virus Bound to a Fab Fragment of a Neutralising Antibody: Structure and Neutralisation. <i>Virology</i> , 1999, 255, 260-268.	1.1	53
77	Ca ²⁺ bridges the C2 membrane-binding domain of protein kinase C β directly to phosphatidylserine. <i>EMBO Journal</i> , 1999, 18, 6329-6338.	3.5	323
78	A Similar Pattern of Interaction for Different Antibodies with a Major Antigenic Site of Foot-and-Mouth Disease Virus: Implications for Intratypic Antigenic Variation. <i>Journal of Virology</i> , 1998, 72, 739-748.	1.5	69
79	Rapid Selection in Modified BHK-21 Cells of a Foot-and-Mouth Disease Virus Variant Showing Alterations in Cell Tropism. <i>Journal of Virology</i> , 1998, 72, 10171-10179.	1.5	56
80	Multiple Virulence Determinants of Foot-and-Mouth Disease Virus in Cell Culture. <i>Journal of Virology</i> , 1998, 72, 6362-6372.	1.5	141
81	Structural Variability of A-DNA in Crystals of the Octamer d(pCpCpCpGpCpGpGpG). <i>Journal of Biomolecular Structure and Dynamics</i> , 1997, 15, 151-163.	2.0	14
82	Induced Pocket to Accommodate the Cell Attachment Arg-Gly-Asp Motif in a Neutralizing Antibody Against Foot-and-Mouth-Disease Virus. <i>Journal of Molecular Biology</i> , 1996, 256, 364-376.	2.0	69
83	Antigenically Profound Amino Acid Substitutions Occur during Large Population Passages of Foot-and-Mouth Disease Virus. <i>Virology</i> , 1996, 225, 400-405.	1.1	22
84	Crystal structure of catalase HPII from <i>Escherichia coli</i> . <i>Structure</i> , 1995, 3, 491-502.	1.6	99
85	Molecular evolution of aphthoviruses. <i>Virus Genes</i> , 1995, 11, 197-207.	0.7	37
86	Molecular structure of a complete turn of A-DNA. <i>Journal of Molecular Biology</i> , 1991, 221, 623-635.	2.0	51
87	Mutation, Quasispecies, and Lethal Mutagenesis. , 0, , 195-211.		0