

# Jay C Nix

## List of Publications by Year in descending order

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67  
papers

5,395  
citations

126907

33  
h-index

106344

65  
g-index

70  
all docs

70  
docs citations

70  
times ranked

9741  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping Neutralizing and Immunodominant Sites on the SARS-CoV-2 Spike Receptor-Binding Domain by Structure-Guided High-Resolution Serology. <i>Cell</i> , 2020, 183, 1024-1042.e21.	28.9	1,195
2	Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity. <i>Cell</i> , 2021, 184, 1171-1187.e20.	28.9	541
3	Structural basis of SARS-CoV-2 Omicron immune evasion and receptor engagement. <i>Science</i> , 2022, 375, 864-868.	12.6	394
4	SARS-CoV-2 RBD antibodies that maximize breadth and resistance to escape. <i>Nature</i> , 2021, 597, 97-102.	27.8	385
5	The Structural Basis of Pathogenic Subgenomic Flavivirus RNA (sfRNA) Production. <i>Science</i> , 2014, 344, 307-310.	12.6	223
6	Zika virus produces noncoding RNAs using a multi-pseudoknot structure that confounds a cellular exonuclease. <i>Science</i> , 2016, 354, 1148-1152.	12.6	212
7	Structural basis for dsRNA recognition and interferon antagonism by Ebola VP35. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 165-172.	8.2	177
8	Structure of the Ebola VP35 interferon inhibitory domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 411-416.	7.1	149
9	Pyrolopyrimidine inhibitors of DNA gyrase B (GyrB) and topoisomerase IV (ParE). Part I: Structure guided discovery and optimization of dual targeting agents with potent, broad-spectrum enzymatic activity. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2013, 23, 1529-1536.	2.2	112
10	Investigating the Impact of Polymer Functional Groups on the Stability and Activity of Lysozyme-Polymer Conjugates. <i>Biomacromolecules</i> , 2016, 17, 1123-1134.	5.4	92
11	The structural basis for molecular recognition by the vitamin B 12 RNA aptamer. <i>Nature Structural Biology</i> , 2000, 7, 53-57.	9.7	91
12	Structural evidence for consecutive Hel308-like modules in the spliceosomal ATPase Brr2. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 731-739.	8.2	87
13	Tricyclic GyrB/ParE (TriBE) Inhibitors: A New Class of Broad-Spectrum Dual-Targeting Antibacterial Agents. <i>PLoS ONE</i> , 2013, 8, e84409.	2.5	86
14	Structural basis of nucleotide exchange and client binding by the Hsp70 cochaperone Bag2. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 1309-1317.	8.2	85
15	The structural basis of transfer RNA mimicry and conformational plasticity by a viral RNA. <i>Nature</i> , 2014, 511, 366-369.	27.8	85
16	Structural analysis and DNA binding of the HMG domains of the human mitochondrial transcription factor A. <i>Nucleic Acids Research</i> , 2009, 37, 3153-3164.	14.5	83
17	A folded viral noncoding RNA blocks host cell exoribonucleases through a conformationally dynamic RNA structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6404-6409.	7.1	82
18	A Bipartite Interaction between Hsp70 and CHIP Regulates Ubiquitination of Chaperoned Client Proteins. <i>Structure</i> , 2015, 23, 472-482.	3.3	78

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19	Evaluation of integrin $\alpha_6$ cystine knot PET tracers to detect cancer and idiopathic pulmonary fibrosis. <i>Nature Communications</i> , 2019, 10, 4673.	12.8	73
20	The Role of Multiple Hydrogen-Bonding Groups in Specific Alcohol Binding Sites in Proteins: Insights from Structural Studies of LUSH. <i>Journal of Molecular Biology</i> , 2008, 376, 1360-1376.	4.2	72
21	Structural Basis of the Transcriptional Regulation of the Proline Utilization Regulon by Multifunctional PutA. <i>Journal of Molecular Biology</i> , 2008, 381, 174-188.	4.2	62
22	Structures of Coxsackievirus, Rhinovirus, and Poliovirus Polymerase Elongation Complexes Solved by Engineering RNA Mediated Crystal Contacts. <i>PLoS ONE</i> , 2013, 8, e60272.	2.5	60
23	The 1.3 Å crystal structure of a biotin-binding pseudoknot and the basis for RNA molecular recognition 1 Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 2000, 296, 1235-1244.	4.2	52
24	Structural Insight into p53 Recognition by the 53BP1 Tandem Tudor Domain. <i>Journal of Molecular Biology</i> , 2010, 398, 489-496.	4.2	50
25	Clinical Variants of New Delhi Metallo- $\beta$ -Lactamase Are Evolving To Overcome Zinc Scarcity. <i>ACS Infectious Diseases</i> , 2017, 3, 927-940.	3.8	49
26	Structural Characterization of Carbohydrate Binding by LMAN1 Protein Provides New Insight into the Endoplasmic Reticulum Export of Factors V (FV) and VIII (FVIII). <i>Journal of Biological Chemistry</i> , 2013, 288, 20499-20509.	3.4	46
27	Crystal Structure of Human Collagen XVIII Trimerization Domain: A Novel Collagen Trimerization Fold. <i>Journal of Molecular Biology</i> , 2009, 392, 787-802.	4.2	45
28	Crystal Structure of CBD2 from the <i>Drosophila</i> Na <sup>+</sup> /Ca <sup>2+</sup> Exchanger: Diversity of Ca <sup>2+</sup> Regulation and Its Alternative Splicing Modification. <i>Journal of Molecular Biology</i> , 2009, 387, 104-112.	4.2	43
29	Individual Ion Binding Sites in the K <sup>+</sup> Channel Play Distinct Roles in C-type Inactivation and in Recovery from Inactivation. <i>Structure</i> , 2016, 24, 750-761.	3.3	41
30	Crystal structure of the nucleotide-binding domain of mortalin, the mitochondrial Hsp70 chaperone. <i>Protein Science</i> , 2014, 23, 833-842.	7.6	40
31	Defining NADH-Driven Allostery Regulating Apoptosis-Inducing Factor. <i>Structure</i> , 2016, 24, 2067-2079.	3.3	39
32	Interleukin-37 monomer is the active form for reducing innate immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5514-5522.	7.1	38
33	Structural basis for the inhibition of Aurora A kinase by a novel class of high affinity disubstituted pyrimidine inhibitors. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2007, 17, 688-691.	2.2	36
34	Crystal Structures of Progressive Ca <sup>2+</sup> Binding States of the Ca <sup>2+</sup> Sensor Ca <sup>2+</sup> Binding Domain 1 (CBD1) from the CALX Na <sup>+</sup> /Ca <sup>2+</sup> Exchanger Reveal Incremental Conformational Transitions. <i>Journal of Biological Chemistry</i> , 2010, 285, 2554-2561.	3.4	36
35	Structures of the Rare-Cutting Restriction Endonuclease NotI Reveal a Unique Metal Binding Fold Involved in DNA Binding. <i>Structure</i> , 2008, 16, 558-569.	3.3	33
36	Crystal Structures and Small-angle X-ray Scattering Analysis of UDP-galactopyranose Mutase from the Pathogenic Fungus <i>Aspergillus fumigatus</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 9041-9051.	3.4	33

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37	Targeted Delivery of Cytotoxic NAMPT Inhibitors Using Antibody-Drug Conjugates. <i>Molecular Cancer Therapeutics</i> , 2018, 17, 2633-2642.	4.1	33
38	Specific Recognition of Arginine Methylated Histone Tails by JMJD5 and JMJD7. <i>Scientific Reports</i> , 2018, 8, 3275.	3.3	23
39	Structure of human peptidyl-prolyl <i>cis</i> - <i>trans</i> isomerase FKBP22 containing two EF-hand motifs. <i>Protein Science</i> , 2014, 23, 67-75.	7.6	22
40	<i>Aedes aegypti</i> Odorant Binding Protein 22 selectively binds fatty acids through a conformational change in its C-terminal tail. <i>Scientific Reports</i> , 2020, 10, 3300.	3.3	21
41	Crystal Structure at 2.8Å... of the DLLRKN-containing Coiled-coil Domain of Huntingtin-interacting Protein 1 (HIP1) Reveals a Surface Suitable for Clathrin Light Chain Binding. <i>Journal of Molecular Biology</i> , 2007, 367, 8-15.	4.2	20
42	Biochemical Basis of the Interaction between Cystic Fibrosis Transmembrane Conductance Regulator and Immunoglobulin-like Repeats of Filamin. <i>Journal of Biological Chemistry</i> , 2010, 285, 17166-17176.	3.4	20
43	Ribosome-induced RNA conformational changes in a viral 3'-UTR sense and regulate translation levels. <i>Nature Communications</i> , 2018, 9, 5074.	12.8	19
44	Structures of Mammalian and Bacterial Fructose-1,6-bisphosphatase Reveal the Basis for Synergism in AMP/Fructose 2,6-Bisphosphate Inhibition. <i>Journal of Biological Chemistry</i> , 2007, 282, 36121-36131.	3.4	18
45	A Single Salt Bridge in VIM-20 Increases Protein Stability and Antibiotic Resistance under Low-Zinc Conditions. <i>MBio</i> , 2019, 10, .	4.1	16
46	The crystal structure of a Poliovirus exoribonuclease-resistant RNA shows how diverse sequences are integrated into a conserved fold. <i>Rna</i> , 2020, 26, 1767-1776.	3.5	15
47	The intrinsically disordered protein TgIST from <i>Toxoplasma gondii</i> inhibits STAT1 signaling by blocking cofactor recruitment. <i>Nature Communications</i> , 2022, 13, .	12.8	15
48	YbtT is a low-specificity type II thioesterase that maintains production of the metallophore yersiniabactin in pathogenic enterobacteria. <i>Journal of Biological Chemistry</i> , 2018, 293, 19572-19585.	3.4	14
49	Distinct Structural Features of the Peroxide Response Regulator from Group A <i>Streptococcus</i> Drive DNA Binding. <i>PLoS ONE</i> , 2014, 9, e89027.	2.5	13
50	A Noncanonical Metal Center Drives the Activity of the <i>Sediminispirochaeta smaragdinae</i> Metallo- $\beta$ -lactamase SPS-1. <i>Biochemistry</i> , 2018, 57, 5218-5229.	2.5	11
51	Nuclear resonance vibrational spectroscopy (NRVS) of rubredoxin and MoFe protein crystals. <i>Hyperfine Interactions</i> , 2013, 222, 77-90.	0.5	10
52	Biophysical Consequences of EVEN-PLUS Syndrome Mutations for the Function of Mortalin. <i>Journal of Physical Chemistry B</i> , 2019, 123, 3383-3396.	2.6	10
53	Structure, dynamics and function of the evolutionarily changing biliverdin reductase B family. <i>Journal of Biochemistry</i> , 2020, 168, 191-202.	1.7	9
54	Coordination of Di-Acetylated Histone Ligands by the ATAD2 Bromodomain. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9128.	4.1	9

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55	Nuclear localization of clathrin involves a labile helix outside the trimerization domain. FEBS Letters, 2013, 587, 142-149.	2.8	8
56	Structural and dynamical description of the enzymatic reaction of a phosphohexomutase. Structural Dynamics, 2019, 6, 024703.	2.3	8
57	Inelastic X-ray Scattering of a Transition-Metal Complex ( $\text{FeCl}_4^{+}$ ): Vibrational Spectroscopy for All Normal Modes. Inorganic Chemistry, 2013, 52, 6767-6769.	4.0	7
58	The Sampling of Conformational Dynamics in Ambient-Temperature Crystal Structures of Arginine Kinase. Structure, 2016, 24, 1658-1667.	3.3	5
59	Structural Insights into Substrate Recognition by Clostridium difficile Sortase. Frontiers in Cellular and Infection Microbiology, 2016, 6, 160.	3.9	4
60	Synchrotron-based macromolecular crystallography module for an undergraduate biochemistry laboratory course. Journal of Applied Crystallography, 2016, 49, 2235-2243.	4.5	4
61	2'- and N6'-functionalized adenosine 5'-diphosphate analogs for the inhibition of mortalin. FEBS Letters, 2019, 593, 2030-2039.	2.8	4
62	Preliminary crystallographic characterization of an in vitro evolved biotin-binding RNA pseudoknot. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 323-325.	2.5	2
63	Entrapment of Phosphoryl Intermediates by SAICAR Synthetase. FASEB Journal, 2008, 22, 233-233.	0.5	1
64	Protein gRAFTing: a RAFT Polymerization Strategy for Grafting to and Grafting from Proteins. FASEB Journal, 2015, 29, 723.1.	0.5	1
65	Shifting Sands: Modulating Interactions and Outputs of the CHIP/Hsp70/HOP/Hsp70 Protein Quality Control Complexes. FASEB Journal, 2017, 31, .	0.5	1
66	Modulation of Hsp70 Interactions with Co-chaperones via Phosphorylation. FASEB Journal, 2015, 29, 713.1.	0.5	0
67	New Delhi Metallo- $\beta$ -Lactamase Variants NDM4 and NDM12 from E. coli Clinical Isolates Exhibit Increased Activity and Stability. FASEB Journal, 2017, 31, 777.21.	0.5	0