

Jay C Nix

List of Publications by Year in descending order

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Version: 2024-02-01

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	Structural basis of SARS-CoV-2 Omicron immune evasion and receptor engagement. <i>Science</i> , 2022, 375, 864-868.	12.6	394
2	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
3	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
4	SARS-CoV-2 RBD antibodies that maximize breadth and resistance to escape. <i>Nature</i> , 2021, 597, 97-102.	27.8	385
5	Coordination of Di-Acetylated Histone Ligands by the ATAD2 Bromodomain. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9128.	4.1	9
6	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
7	Structure, dynamics and function of the evolutionarily changing biliverdin reductase B family. <i>Journal of Biochemistry</i> , 2020, 168, 191-202.	1.7	9
8	<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
9	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
10	Evaluation of integrin α 26 cystine knot PET tracers to detect cancer and idiopathic pulmonary fibrosis. <i>Nature Communications</i> , 2019, 10, 4673.	12.8	73
11	2'- and N6'-functionalized adenosine 5'-diphosphate analogs for the inhibition of mortalin. <i>FEBS Letters</i> , 2019, 593, 2030-2039.	2.8	4
12	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
13	Structural and dynamical description of the enzymatic reaction of a phosphohexomutase. <i>Structural Dynamics</i> , 2019, 6, 024703.	2.3	8
14	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
15	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
16	Specific Recognition of Arginine Methylated Histone Tails by JMJD5 and JMJD7. <i>Scientific Reports</i> , 2018, 8, 3275.	3.3	23
17	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
18	Targeted Delivery of Cytotoxic NAMPT Inhibitors Using Antibody-Drug Conjugates. <i>Molecular Cancer Therapeutics</i> , 2018, 17, 2633-2642.	4.1	33

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19	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
20	A Noncanonical Metal Center Drives the Activity of the <i>Sediminispirochaeta smaragdinae</i> Metallo- β -lactamase SPS-1. <i>Biochemistry</i> , 2018, 57, 5218-5229.	2.5	11
21	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
22	Clinical Variants of New Delhi Metallo- β -Lactamase Are Evolving To Overcome Zinc Scarcity. <i>ACS Infectious Diseases</i> , 2017, 3, 927-940.	3.8	49
23	New Delhi Metallo- β -Lactamase Variants NDM-4 and NDM-12 from <i>E. coli</i> Clinical Isolates Exhibit Increased Activity and Stability. <i>FASEB Journal</i> , 2017, 31, 777.21.	0.5	0
24	Shifting Sands: Modulating Interactions and Outputs of the CHIP-Hsp70/HOP-Hsp70 Protein Quality Control Complexes. <i>FASEB Journal</i> , 2017, 31, .	0.5	1
25	Structural Insights into Substrate Recognition by <i>Clostridium difficile</i> Sortase. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 160.	3.9	4
26	Synchrotron-based macromolecular crystallography module for an undergraduate biochemistry laboratory course. <i>Journal of Applied Crystallography</i> , 2016, 49, 2235-2243.	4.5	4
27	Individual Ion Binding Sites in the K ⁺ Channel Play Distinct Roles in C-type Inactivation and in Recovery from Inactivation. <i>Structure</i> , 2016, 24, 750-761.	3.3	41
28	The Sampling of Conformational Dynamics in Ambient-Temperature Crystal Structures of Arginine Kinase. <i>Structure</i> , 2016, 24, 1658-1667.	3.3	5
29	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
30	Defining NADH-Driven Allosteric Regulating Apoptosis-Inducing Factor. <i>Structure</i> , 2016, 24, 2067-2079.	3.3	39
31	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
32	A Bipartite Interaction between Hsp70 and CHIP Regulates Ubiquitination of Chaperoned Client Proteins. <i>Structure</i> , 2015, 23, 472-482.	3.3	78
33	Protein gRAFTing: a RAFT Polymerization Strategy for Grafting-to and Grafting-from Proteins. <i>FASEB Journal</i> , 2015, 29, 723.1.	0.5	1
34	Modulation of Hsp70 Interactions with Co-chaperones via Phosphorylation. <i>FASEB Journal</i> , 2015, 29, 713.1.	0.5	0
35	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
36	The Structural Basis of Pathogenic Subgenomic Flavivirus RNA (sfRNA) Production. <i>Science</i> , 2014, 344, 307-310.	12.6	223

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37	Crystal structure of the nucleotide-binding domain of mortalin, the mitochondrial Hsp70 chaperone. <i>Protein Science</i> , 2014, 23, 833-842.	7.6	40
38	The structural basis of transfer RNA mimicry and conformational plasticity by a viral RNA. <i>Nature</i> , 2014, 511, 366-369.	27.8	85
39	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
40	Nuclear localization of clathrin involves a labile helix outside the trimerization domain. <i>FEBS Letters</i> , 2013, 587, 142-149.	2.8	8
41	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
42	Inelastic X-ray Scattering of a Transition-Metal Complex (FeCl_4^-): Vibrational Spectroscopy for All Normal Modes. <i>Inorganic Chemistry</i> , 2013, 52, 6767-6769.	4.0	7
43	Pyrrolopyrimidine 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
44	Nuclear resonance vibrational spectroscopy (NRVS) of rubredoxin and MoFe protein crystals. <i>Hyperfine Interactions</i> , 2013, 222, 77-90.	0.5	10
45	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
46	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
47	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
48	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
49	Crystal Structures of Progressive Ca^{2+} Binding States of the Ca^{2+} Sensor Ca^{2+} Binding Domain 1 (CBD1) from the CALX $\text{Na}^+/\text{Ca}^{2+}$ Exchanger Reveal Incremental Conformational Transitions. <i>Journal of Biological Chemistry</i> , 2010, 285, 2554-2561.	3.4	36
50	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
51	Structural Insight into p53 Recognition by the 53BP1 Tandem Tudor Domain. <i>Journal of Molecular Biology</i> , 2010, 398, 489-496.	4.2	50
52	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
53	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
54	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

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55	Crystal Structure of CBD2 from the Drosophila Na ⁺ /Ca ²⁺ Exchanger: Diversity of Ca ²⁺ Regulation and Its Alternative Splicing Modification. <i>Journal of Molecular Biology</i> , 2009, 387, 104-112.	4.2	43
56	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
57	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
58	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
59	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
60	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
61	Entrapment of Phosphoryl Intermediates by SAICAR Synthetase. <i>FASEB Journal</i> , 2008, 22, 233-233.	0.5	1
62	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
63	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
64	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
65	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
66	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
67	Preliminary crystallographic characterization of an in vitro evolved biotin-binding RNA pseudoknot. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 323-325.	2.5	2