Jay C Nix

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4330803/publications.pdf

Version: 2024-02-01

67
papers

5,395
citations

126708

33
h-index

106150

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. Science, 2022, 375, 864-868.	6.0	394
2	The intrinsically disordered protein TgIST from Toxoplasma gondii inhibits STAT1 signaling by blocking cofactor recruitment. Nature Communications, 2022, 13, .	5.8	15
3	Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity. Cell, 2021, 184, 1171-1187.e20.	13.5	541
4	SARS-CoV-2 RBD antibodies that maximize breadth and resistance to escape. Nature, 2021, 597, 97-102.	13.7	385
5	Coordination of Di-Acetylated Histone Ligands by the ATAD2 Bromodomain. International Journal of Molecular Sciences, 2021, 22, 9128.	1.8	9
6	Mapping Neutralizing and Immunodominant Sites on the SARS-CoV-2 Spike Receptor-Binding Domain by Structure-Guided High-Resolution Serology. Cell, 2020, 183, 1024-1042.e21.	13.5	1,195
7	Structure, dynamics and function of the evolutionarily changing biliverdin reductase B family. Journal of Biochemistry, 2020, 168, 191-202.	0.9	9
8	Aedes aegypti Odorant Binding Protein 22 selectively binds fatty acids through a conformational change in its C-terminal tail. Scientific Reports, 2020, 10, 3300.	1.6	21
9	The crystal structure of a Polerovirus exoribonuclease-resistant RNA shows how diverse sequences are integrated into a conserved fold. Rna, 2020, 26, 1767-1776.	1.6	15
10	Evaluation of integrin Î±vÎ²6 cystine knot PET tracers to detect cancer and idiopathic pulmonary fibrosis. Nature Communications, 2019, 10, 4673.	5.8	73
11	2â€•and N6â€•functionalized adenosineâ€•5â€²â€•diphosphate analogs for the inhibition of mortalin. FEBS Letters, 2019, 593, 2030-2039.	1.3	4
12	Biophysical Consequences of EVEN-PLUS Syndrome Mutations for the Function of Mortalin. Journal of Physical Chemistry B, 2019, 123, 3383-3396.	1.2	10
13	Structural and dynamical description of the enzymatic reaction of a phosphohexomutase. Structural Dynamics, 2019, 6, 024703.	0.9	8
14	Interleukin-37 monomer is the active form for reducing innate immunity. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5514-5522.	3.3	38
15	A Single Salt Bridge in VIM-20 Increases Protein Stability and Antibiotic Resistance under Low-Zinc Conditions. MBio, 2019, 10, .	1.8	16
16	Specific Recognition of Arginine Methylated Histone Tails by JMJD5 and JMJD7. Scientific Reports, 2018, 8, 3275.	1.6	23
17	Ribosome-induced RNA conformational changes in a viral 3â€²-UTR sense and regulate translation levels. Nature Communications, 2018, 9, 5074.	5.8	19
18	Targeted Delivery of Cytotoxic NAMPT Inhibitors Using Antibodyâ€"Drug Conjugates. Molecular Cancer Therapeutics, 2018, 17, 2633-2642.	1.9	33

#	Article	IF	Citations
19	YbtT is a low-specificity type II thioesterase that maintains production of the metallophore yersiniabactin in pathogenic enterobacteria. Journal of Biological Chemistry, 2018, 293, 19572-19585.	1.6	14
20	A Noncanonical Metal Center Drives the Activity of the <i>Sediminispirochaeta smaragdinae</i> Metallo-Î²-lactamase SPS-1. Biochemistry, 2018, 57, 5218-5229.	1.2	11
21	A folded viral noncoding RNA blocks host cell exoribonucleases through a conformationally dynamic RNA structure. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 6404-6409.	3.3	82
22	Clinical Variants of New Delhi Metallo-Î²-Lactamase Are Evolving To Overcome Zinc Scarcity. ACS Infectious Diseases, 2017, 3, 927-940.	1.8	49
23	New Delhi Metalloâ€Betaâ€Lactamase Variants NDMâ€4 and NDMâ€12 from E. coli Clinical Isolates Exhibit Increased Activity and Stability. FASEB Journal, 2017, 31, 777.21.	0.2	0
24	Shifting Sands: Modulating Interactions and Outputs of the CHIPâ€Hsp70/HOPâ€Hsp70 Protein Quality Control Complexes. FASEB Journal, 2017, 31, .	0.2	1
25	Structural Insights into Substrate Recognition by Clostridium difficile Sortase. Frontiers in Cellular and Infection Microbiology, 2016, 6, 160.	1.8	4
26	Synchrotron-based macromolecular crystallography module for an undergraduate biochemistry laboratory course. Journal of Applied Crystallography, 2016, 49, 2235-2243.	1.9	4
27	Individual Ion Binding Sites in the K+ Channel Play Distinct Roles in C-type Inactivation and in Recovery from Inactivation. Structure, 2016, 24, 750-761.	1.6	41
28	The Sampling of Conformational Dynamics in Ambient-Temperature Crystal Structures of Arginine Kinase. Structure, 2016, 24, 1658-1667.	1.6	5
29	Zika virus produces noncoding RNAs using a multi-pseudoknot structure that confounds a cellular exonuclease. Science, 2016, 354, 1148-1152.	6.0	212
30	Defining NADH-Driven Allostery Regulating Apoptosis-Inducing Factor. Structure, 2016, 24, 2067-2079.	1.6	39
31	Investigating the Impact of Polymer Functional Groups on the Stability and Activity of Lysozymeâ€“Polymer Conjugates. Biomacromolecules, 2016, 17, 1123-1134.	2.6	92
32	A Bipartite Interaction between Hsp70 and CHIP Regulates Ubiquitination of Chaperoned Client Proteins. Structure, 2015, 23, 472-482.	1.6	78
33	Protein gRAFTing: a RAFT Polymerization Strategy for Graftingâ€to and Graftingâ€from Proteins. FASEB Journal, 2015, 29, 723.1.	0.2	1
34	Modulation of Hsp70 Interactions with Coâ€chaperones via Phosphorylation. FASEB Journal, 2015, 29, 713.1.	0.2	0
35	Structure of human peptidylâ€prolyl <i>cisâ€“trans</i> isomerase FKBP22 containing two EFâ€hand motifs. Protein Science, 2014, 23, 67-75.	3.1	22
36	The Structural Basis of Pathogenic Subgenomic Flavivirus RNA (sfRNA) Production. Science, 2014, 344, 307-310.	6.0	223

#	ARTICLE	IF	CITATIONS
37	Crystal structure of the nucleotideâ€binding domain of mortalin, the mitochondrial Hsp70 chaperone. Protein Science, 2014, 23, 833-842.	3.1	40
38	The structural basis of transfer RNA mimicry and conformational plasticity by a viral RNA. Nature, 2014, 511, 366-369.	13.7	85
39	Distinct Structural Features of the Peroxide Response Regulator from Group A Streptococcus Drive DNA Binding. PLoS ONE, 2014, 9, e89027.	1.1	13
40	Nuclear localization of clathrin involves a labile helix outside the trimerization domain. FEBS Letters, 2013, 587, 142-149.	1.3	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). Journal of Biological Chemistry, 2013, 288, 20499-20509.	1.6	46
42	Inelastic X-ray Scattering of a Transition-Metal Complex (FeCl₄^{â€“}): Vibrational Spectroscopy for All Normal Modes. Inorganic Chemistry, 2013, 52, 6767-6769.	1.9	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. Bioorganic and Medicinal Chemistry Letters, 2013, 23, 1529-1536.	1.0	112
44	Nuclear resonance vibrational spectroscopy (NRVS) of rubredoxin and MoFe protein crystals. Hyperfine Interactions, 2013, 222, 77-90.	0.2	10
45	Tricyclic GyrB/ParE (TriBE) Inhibitors: A New Class of Broad-Spectrum Dual-Targeting Antibacterial Agents. PLoS ONE, 2013, 8, e84409.	1.1	86
46	Structures of Coxsackievirus, Rhinovirus, and Poliovirus Polymerase Elongation Complexes Solved by Engineering RNA Mediated Crystal Contacts. PLoS ONE, 2013, 8, e60272.	1.1	60
47	Crystal Structures and Small-angle X-ray Scattering Analysis of UDP-galactopyranose Mutase from the Pathogenic Fungus Aspergillus fumigatus. Journal of Biological Chemistry, 2012, 287, 9041-9051.	1.6	33
48	Structural basis for dsRNA recognition and interferon antagonism by Ebola VP35. Nature Structural and Molecular Biology, 2010, 17, 165-172.	3.6	177
49	Crystal Structures of Progressive Ca2+ Binding States of the Ca2+ Sensor Ca2+ Binding Domain 1 (CBD1) from the CALX Na+/Ca2+ Exchanger Reveal Incremental Conformational Transitions. Journal of Biological Chemistry, 2010, 285, 2554-2561.	1.6	36
50	Biochemical Basis of the Interaction between Cystic Fibrosis Transmembrane Conductance Regulator and Immunoglobulin-like Repeats of Filamin. Journal of Biological Chemistry, 2010, 285, 17166-17176.	1.6	20
51	Structural Insight into p53 Recognition by the 53BP1 Tandem Tudor Domain. Journal of Molecular Biology, 2010, 398, 489-496.	2.0	50
52	Structure of the Ebola VP35 interferon inhibitory domain. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 411-416.	3.3	149
53	Structural analysis and DNA binding of the HMG domains of the human mitochondrial transcription factor A. Nucleic Acids Research, 2009, 37, 3153-3164.	6.5	83
54	Structural evidence for consecutive Hel308-like modules in the spliceosomal ATPase Brr2. Nature Structural and Molecular Biology, 2009, 16, 731-739.	3.6	87

#	ARTICLE	IF	CITATIONS
55	Crystal Structure of CBD2 from the Drosophila Na+/Ca2+ Exchanger: Diversity of Ca2+ Regulation and Its Alternative Splicing Modification. Journal of Molecular Biology, 2009, 387, 104-112.	2.0	43
56	Crystal Structure of Human Collagen XVIII Trimerization Domain: A Novel Collagen Trimerization Fold. Journal of Molecular Biology, 2009, 392, 787-802.	2.0	45
57	Structural basis of nucleotide exchange and client binding by the Hsp70 cochaperone Bag2. Nature Structural and Molecular Biology, 2008, 15, 1309-1317.	3.6	85
58	Structures of the Rare-Cutting Restriction Endonuclease NotI Reveal a Unique Metal Binding Fold Involved in DNA Binding. Structure, 2008, 16, 558-569.	1.6	33
59	The Role of Multiple Hydrogen-Bonding Groups in Specific Alcohol Binding Sites in Proteins: Insights from Structural Studies of LUSH. Journal of Molecular Biology, 2008, 376, 1360-1376.	2.0	72
60	Structural Basis of the Transcriptional Regulation of the Proline Utilization Regulon by Multifunctional PutA. Journal of Molecular Biology, 2008, 381, 174-188.	2.0	62
61	Entrapment of Phosphoryl Intermediates by SAICAR Synthetase. FASEB Journal, 2008, 22, 233-233.	0.2	1
62	Crystal Structure at 2.8ÂÅ... of the DLLRKN-containing Coiled-coil Domain of Huntingtin-interacting Protein 1 (HIP1) Reveals a Surface Suitable for Clathrin Light Chain Binding. Journal of Molecular Biology, 2007, 367, 8-15.	2.0	20
63	Structures of Mammalian and Bacterial Fructose-1,6-bisphosphatase Reveal the Basis for Synergism in AMP/Fructose 2,6-Bisphosphate Inhibition. Journal of Biological Chemistry, 2007, 282, 36121-36131.	1.6	18
64	Structural basis for the inhibition of Aurora A kinase by a novel class of high affinity disubstituted pyrimidine inhibitors. Bioorganic and Medicinal Chemistry Letters, 2007, 17, 688-691.	1.0	36
65	The structural basis for molecular recognition by the vitamin B 12 RNA aptamer. Nature Structural Biology, 2000, 7, 53-57.	9.7	91
66	The 1.3 Ã¥ crystal structure of a biotin-binding pseudoknot and the basis for RNA molecular recognition 1 1Edited by I. Tinoco. Journal of Molecular Biology, 2000, 296, 1235-1244.	2.0	52
67	Preliminary crystallographic characterization of anin vitroevolved biotin-binding RNA pseudoknot. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 323-325.	2.5	2