

Piotr Sliz

List of Publications by Year in descending order

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Version: 2024-02-01

68
papers

7,651
citations

109321

35
h-index

98798

67
g-index

77
all docs

77
docs citations

77
times ranked

12403
citing authors

#	ARTICLE	IF	CITATIONS
1	A synonymous coding variant that alters <i>ALAS2</i> splicing and causes X-linked sideroblastic anemia. <i>Pediatric Blood and Cancer</i> , 2022, 69, e29309.	1.5	1
2	Mendelian etiologies identified with whole exome sequencing in cerebral palsy. <i>Annals of Clinical and Translational Neurology</i> , 2022, 9, 193-205.	3.7	23
3	Single-cell transcriptome profile of mouse skin undergoing antigen-driven allergic inflammation recapitulates findings in atopic dermatitis skin lesions. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 150, 373-384.	2.9	14
4	Clinical Phenotypes and Outcomes in Monogenic Versus Non-monogenic Very Early Onset Inflammatory Bowel Disease. <i>Journal of Crohn's and Colitis</i> , 2022, 16, 1380-1396.	1.3	19
5	Structural and functional impact by SARS-CoV-2 Omicron spike mutations. <i>Cell Reports</i> , 2022, 39, 110729.	6.4	102
6	International comparisons of laboratory values from the 4CE collaborative to predict COVID-19 mortality. <i>Npj Digital Medicine</i> , 2022, 5, .	10.9	7
7	Maternal Iron Deficiency Modulates Placental Transcriptome and Proteome in Mid-Gestation of Mouse Pregnancy. <i>Journal of Nutrition</i> , 2021, 151, 1073-1083.	2.9	16
8	What Every Reader Should Know About Studies Using Electronic Health Record Data but May Be Afraid to Ask. <i>Journal of Medical Internet Research</i> , 2021, 23, e22219.	4.3	61
9	Structural impact on SARS-CoV-2 spike protein by D614G substitution. <i>Science</i> , 2021, 372, 525-530.	12.6	344
10	International Analysis of Electronic Health Records of Children and Youth Hospitalized With COVID-19 Infection in 6 Countries. <i>JAMA Network Open</i> , 2021, 4, e2112596.	5.9	33
11	A data-driven architecture using natural language processing to improve phenotyping efficiency and accelerate genetic diagnoses of rare disorders. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100035.	1.7	4
12	Mechanisms underlying genetic susceptibility to multisystem inflammatory syndrome in children (MIS-C). <i>Journal of Allergy and Clinical Immunology</i> , 2021, 148, 732-738.e1.	2.9	84
13	Congenital X-linked Neutropenia with Myelodysplasia and Somatic Tetraploidy due to a Germline Mutation in <i>SEPT6</i> . <i>American Journal of Hematology</i> , 2021, , .	4.1	1
14	Multinational characterization of neurological phenotypes in patients hospitalized with COVID-19. <i>Scientific Reports</i> , 2021, 11, 20238.	3.3	10
15	Molecular Dissection of the Primase and Polymerase Activities of Deep-Sea Phage NrS-1 Primase-Polymerase. <i>Frontiers in Microbiology</i> , 2021, 12, 766612.	3.5	2
16	Children's rare disease cohorts: an integrative research and clinical genomics initiative. <i>Npj Genomic Medicine</i> , 2020, 5, 29.	3.8	38
17	Virtual Screening for Ligand Discovery at the β_1 Receptor. <i>ACS Medicinal Chemistry Letters</i> , 2020, 11, 1555-1561.	2.8	14
18	International electronic health record-derived COVID-19 clinical course profiles: the 4CE consortium. <i>Npj Digital Medicine</i> , 2020, 3, 109.	10.9	128

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19	RiboToolkit: an integrated platform for analysis and annotation of ribosome profiling data to decode mRNA translation at codon resolution. <i>Nucleic Acids Research</i> , 2020, 48, W218-W229.	14.5	53
20	A nanobody targeting the LIN28:let-7 interaction fragment of TUT4 blocks uridylation of let-7. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 4653-4663.	7.1	15
21	MightyScreen: An Open-Source Visualization Application for Screening Data Analysis. <i>SLAS Discovery</i> , 2018, 23, 218-223.	2.7	2
22	In silico Screening and Evaluation of <i>Plasmodium falciparum</i> Protein Kinase...5 (PK5) Inhibitors. <i>ChemMedChem</i> , 2018, 13, 2479-2483.	3.2	6
23	mRNA circularization by METTL3...eIF3h enhances translation and promotes oncogenesis. <i>Nature</i> , 2018, 561, 556-560.	27.8	498
24	Small-Molecule Inhibitors Disrupt let-7 Oligouridylation and Release the Selective Blockade of let-7 Processing by LIN28. <i>Cell Reports</i> , 2018, 23, 3091-3101.	6.4	81
25	Extension of research data repository system to support direct compute access to biomedical datasets: enhancing DataVerse to support large datasets. <i>Annals of the New York Academy of Sciences</i> , 2017, 1387, 95-104.	3.8	5
26	Cryo-EM structure of the replisome reveals multiple interactions coordinating DNA synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1848-E1856.	7.1	26
27	LIN28 Zinc Knuckle Domain Is Required and Sufficient to Induce let-7 Oligouridylation. <i>Cell Reports</i> , 2017, 18, 2664-2675.	6.4	66
28	Comparative analysis of LIN28-RNA binding sites identified at single nucleotide resolution. <i>RNA Biology</i> , 2017, 14, 1756-1765.	3.1	10
29	Pulmonary Vasculopathy Associated with FIGF Gene Mutation. <i>American Journal of Pathology</i> , 2017, 187, 25-32.	3.8	8
30	Development of the Precision Link Biobank at Boston Children's Hospital: Challenges and Opportunities. <i>Journal of Personalized Medicine</i> , 2017, 7, 21.	2.5	20
31	Data publication with the structural biology data grid supports live analysis. <i>Nature Communications</i> , 2016, 7, 10882.	12.8	113
32	LIN28 Regulates Stem Cell Metabolism and Conversion to Primed Pluripotency. <i>Cell Stem Cell</i> , 2016, 19, 66-80.	11.1	278
33	Science and technology consortia in U.S. biomedical research: A paradigm shift in response to unsustainable academic growth. <i>BioEssays</i> , 2015, 37, 119-122.	2.5	10
34	A Biogenesis Step Upstream of Microprocessor Controls miR-17...492 Expression. <i>Cell</i> , 2015, 162, 885-899.	28.9	85
35	AppCiter: A Web Application for Increasing Rates and Accuracy of Scientific Software Citation. <i>Structure</i> , 2015, 23, 807-808.	3.3	3
36	Pinpointing RNA-Protein Cross-Links with Site-Specific Stable Isotope-Labeled Oligonucleotides. <i>Journal of the American Chemical Society</i> , 2015, 137, 15378-15381.	13.7	15

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37	Selective microRNA uridylation by Zcchc6 (TUT7) and Zcchc11 (TUT4). <i>Nucleic Acids Research</i> , 2014, 42, 11777-11791.	14.5	87
38	Chemical Interrogation of the Malaria Kinome. <i>ChemBioChem</i> , 2014, 15, 1920-1930.	2.6	29
39	Structural biology computing: Lessons for the biomedical research sciences. <i>Biopolymers</i> , 2013, 99, 809-816.	2.4	6
40	Optimizing Peer Review of Software Code. <i>Science</i> , 2013, 341, 236-237.	12.6	3
41	Collaboration gets the most out of software. <i>ELife</i> , 2013, 2, e01456.	6.0	869
42	A Quick Guide to Software Licensing for the Scientist-Programmer. <i>PLoS Computational Biology</i> , 2012, 8, e1002598.	3.2	62
43	Shining Light into Black Boxes. <i>Science</i> , 2012, 336, 159-160.	12.6	154
44	An integrated science portal for collaborative compute and data intensive protein structure studies. , 2012, , .		2
45	A neutral diphosphate mimic crosslinks the active site of human O-GlcNAc transferase. <i>Nature Chemical Biology</i> , 2012, 8, 72-77.	8.0	87
46	A grid-enabled web service for low-resolution crystal structure refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 261-267.	2.5	17
47	Conformational Locking upon Cooperative Assembly of Notch Transcription Complexes. <i>Structure</i> , 2012, 20, 340-349.	3.3	60
48	Adapting federated cyberinfrastructure for shared data collection facilities in structural biology. <i>Journal of Synchrotron Radiation</i> , 2012, 19, 462-467.	2.4	4
49	Molecular Basis for Interaction of let-7 MicroRNAs with Lin28. <i>Cell</i> , 2011, 147, 1080-1091.	28.9	335
50	Structure of human O-GlcNAc transferase and its complex with a peptide substrate. <i>Nature</i> , 2011, 469, 564-567.	27.8	385
51	Protein structure determination by exhaustive search of Protein Data Bank derived databases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21476-21481.	7.1	42
52	Functional and Structural Analysis of a Key Region of the Cell Wall Inhibitor Moenomycin. <i>ACS Chemical Biology</i> , 2010, 5, 701-711.	3.4	46
53	Compute and data management strategies for grid deployment of high throughput protein structure studies. , 2010, , .		1
54	Structural Analysis of the Contacts Anchoring Moenomycin to Peptidoglycan Glycosyltransferases and Implications for Antibiotic Design. <i>ACS Chemical Biology</i> , 2008, 3, 429-436.	3.4	82

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55	Determinants of MicroRNA Processing Inhibition by the Developmentally Regulated RNA-binding Protein Lin28. <i>Journal of Biological Chemistry</i> , 2008, 283, 21310-21314.	3.4	301
56	Identification and Characterization of Small Molecule Inhibitors of Plasmodium falciparum Dihydroorotate Dehydrogenase. <i>Journal of Biological Chemistry</i> , 2008, 283, 35078-35085.	3.4	78
57	Structure and Function of an Essential Component of the Outer Membrane Protein Assembly Machine. <i>Science</i> , 2007, 317, 961-964.	12.6	327
58	Crystal structure of a peptidoglycan glycosyltransferase suggests a model for processive glycan chain synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5348-5353.	7.1	135
59	Cooperative assembly of higher-order Notch complexes functions as a switch to induce transcription. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2103-2108.	7.1	145
60	Structural Basis for Cooperativity in Recruitment of MAML Coactivators to Notch Transcription Complexes. <i>Cell</i> , 2006, 124, 973-983.	28.9	390
61	Activity of dual SRC-ABL inhibitors highlights the role of BCR/ABL kinase dynamics in drug resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 9244-9249.	7.1	104
62	Lipid-protein interactions in double-layered two-dimensional AQP0 crystals. <i>Nature</i> , 2005, 438, 633-638.	27.8	617
63	Aquaporin-0 membrane junctions reveal the structure of a closed water pore. <i>Nature</i> , 2004, 429, 193-197.	27.8	347
64	Molecular model for a complete clathrin lattice from electron cryomicroscopy. <i>Nature</i> , 2004, 432, 573-579.	27.8	464
65	How does Radiation Damage in Protein Crystals Depend on X-Ray Dose?. <i>Structure</i> , 2003, 11, 13-19.	3.3	102
66	An asymmetric NFAT1 dimer on a pseudo-palindromic β -like DNA site. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 807-811.	8.2	56
67	Crystal Structures of Two Closely Related but Antigenically Distinct HLA-A2/Melanocyte-Melanoma Tumor-Antigen Peptide Complexes. <i>Journal of Immunology</i> , 2001, 167, 3276-3284.	0.8	75
68	Crystallization and preliminary structural studies of lactose-specific enzyme IIA from <i>Lactococcus lactis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996, 52, 1199-1201.	2.5	2