## Kim D Pruitt

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11336006/publications.pdf

Version: 2024-02-01

69 papers 33,640 citations

51
h-index

102304 66 g-index

70 all docs

70 docs citations

70 times ranked

49516 citing authors

#	Article	IF	CITATIONS
1	Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Research, 2016, 44, D733-D745.	6.5	4,739
2	NCBI prokaryotic genome annotation pipeline. Nucleic Acids Research, 2016, 44, 6614-6624.	6.5	4,711
3	NCBI reference sequences (RefSeq): a curated non-redundant sequence database of genomes, transcripts and proteins. Nucleic Acids Research, 2007, 35, D61-D65.	6.5	3,236
4	NCBI Reference Sequence (RefSeq): a curated non-redundant sequence database of genomes, transcripts and proteins. Nucleic Acids Research, 2004, 33, D501-D504.	6.5	1,407
5	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2018, 46, D8-D13.	6.5	1,291
6	Entrez Gene: gene-centered information at NCBI. Nucleic Acids Research, 2011, 39, D52-D57.	6.5	1,194
7	NCBI Reference Sequences (RefSeq): current status, new features and genome annotation policy. Nucleic Acids Research, 2012, 40, D130-D135.	6.5	1,027
8	RefSeq: an update on mammalian reference sequences. Nucleic Acids Research, 2014, 42, D756-D763.	6.5	892
9	Database resources of the national center for biotechnology information. Nucleic Acids Research, 2022, 50, D20-D26.	6.5	887
10	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2009, 37, D5-D15.	6.5	797
11	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2007, 36, D13-D21.	6.5	757
12	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2007, 35, D5-D12.	6.5	757
13	RefSeq: an update on prokaryotic genome annotation and curation. Nucleic Acids Research, 2018, 46, D851-D860.	6.5	749
14	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. Genome Research, 2017, 27, 849-864.	2.4	728
15	NCBI Reference Sequences: current status, policy and new initiatives. Nucleic Acids Research, 2009, 37, D32-D36.	6.5	672
16	GenBank. Nucleic Acids Research, 2018, 46, D41-D47.	6.5	607
17	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2011, 39, D38-D51.	6.5	582
18	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2021, 49, D10-D17.	6.5	545

#	Article	IF	CITATIONS
19	Gene: a gene-centered information resource at NCBI. Nucleic Acids Research, 2015, 43, D36-D42.	6.5	534
20	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2012, 40, D13-D25.	6.5	510
21	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2019, 47, D23-D28.	6.5	502
22	Entrez Gene: gene-centered information at NCBI. Nucleic Acids Research, 2007, 35, D26-D31.	6.5	497
23	The consensus coding sequence (CCDS) project: Identifying a common protein-coding gene set for the human and mouse genomes. Genome Research, 2009, 19, 1316-1323.	2.4	476
24	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2006, 34, D173-D180.	6.5	435
25	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2020, 48, D9-D16.	6.5	381
26	GenBank. Nucleic Acids Research, 2019, 47, D94-D99.	6.5	373
27	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2004, 33, D39-D45.	6.5	369
28	Assembly: a resource for assembled genomes at NCBI. Nucleic Acids Research, 2016, 44, D73-D80.	6.5	292
29	Data management and analysis for gene expression arrays. Nature Genetics, 1998, 20, 19-23.	9.4	290
30	GenBank. Nucleic Acids Research, 2020, 48, D84-D86.	6.5	269
31	BioProject and BioSample databases at NCBI: facilitating capture and organization of metadata. Nucleic Acids Research, 2012, 40, D57-D63.	6.5	268
32	Human immunodeficiency virus type $1$ , human protein interaction database at NCBI. Nucleic Acids Research, 2009, 37, D417-D422.	6.5	230
33	A New Chicken Genome Assembly Provides Insight into Avian Genome Structure. G3: Genes, Genomes, Genetics, 2017, 7, 109-117.	0.8	228
34	Introducing RefSeq and LocusLink: curated human genome resources at the NCBI. Trends in Genetics, 2000, 16, 44-47.	2.9	227
35	GenBank. Nucleic Acids Research, 2021, 49, D92-D96.	6.5	199
36	A joint NCBI and EMBL-EBI transcript set for clinical genomics and research. Nature, 2022, 604, 310-315.	13.7	162

#	Article	IF	Citations
37	NCBI Reference Sequence Project: update and current status. Nucleic Acids Research, 2003, 31, 34-37.	6.5	153
38	Current status and new features of the Consensus Coding Sequence database. Nucleic Acids Research, 2014, 42, D865-D872.	6.5	140
39	<i>Short Communication: </i> Cataloguing the HIV Type 1 Human Protein Interaction Network. AIDS Research and Human Retroviruses, 2008, 24, 1497-1502.	0.5	126
40	The completion of the Mammalian Gene Collection (MGC). Genome Research, 2009, 19, 2324-2333.	2.4	125
41	GenBank. Nucleic Acids Research, 2022, 50, D161-D164.	6.5	119
42	Clonal polymorphism and high heterozygosity in the celibate genome of the Amazon molly. Nature Ecology and Evolution, 2018, 2, 669-679.	3.4	117
43	RNAcentral: an international database of ncRNA sequences. Nucleic Acids Research, 2015, 43, D123-D129.	6.5	103
44	Consensus coding sequence (CCDS) database: a standardized set of human and mouse protein-coding regions supported by expert curation. Nucleic Acids Research, 2018, 46, D221-D228.	6.5	97
45	Meeting report: GenBank microbial genomic taxonomy workshop ( $12\hat{a}$ $\in$ "13 May, 2015). Standards in Genomic Sciences, 2016, 11, .	1.5	81
46	Transcription of the Petunia mitochondrial CMS-associated Pcf locus in male sterile and fertility-restored lines. Molecular Genetics and Genomics, 1991, 227, 348-355.	2.4	79
47	HIV-1, human interaction database: current status and new features. Nucleic Acids Research, 2015, 43, D566-D570.	6.5	79
48	Cytochrome oxidase subunit II sequences in Petunia mitochondria: two intron-containing genes and an intron-less pseudogene associated with cytoplasmic male sterility. Current Genetics, 1989, 16, 281-291.	0.8	75
49	RNAcentral: A vision for an international database of RNA sequences. Rna, 2011, 17, 1941-1946.	1.6	67
50	Solving the Problem: Genome Annotation Standards before the Data Deluge. Standards in Genomic Sciences, 2011, 5, 168-193.	1.5	61
51	Genome assembly and transcriptome resource for river buffalo, Bubalus bubalis (2n = 50). GigaScience, 2017, 6, 1-6.	3.3	55
52	Tracking and coordinating an international curation effort for the CCDS Project. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas008-bas008.	1.4	48
53	What everybody should know about the rat genome and its online resources. Nature Genetics, 2008, 40, 523-527.	9.4	43
54	RefSeq curation and annotation of stop codon recoding in vertebrates. Nucleic Acids Research, 2019, 47, 594-606.	6.5	37

#	Article	IF	Citations
55	Standards recommendations for the Earth BioGenome Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	33
56	Comparison of RefSeq protein-coding regions in human and vertebrate genomes. BMC Genomics, 2013, 14, 654.	1.2	27
57	Editing of rps3/rpl16 transcripts creates a premature truncation of the rpl16 open reading frame. Current Genetics, 1993, 23, 472-476.	0.8	26
58	Splicing of the Petunia cytochrome oxidase subunit II intron. Current Genetics, 1991, 19, 191-197.	0.8	22
59	A curated catalog of canine and equine keratin genes. PLoS ONE, 2017, 12, e0180359.	1.1	19
60	Mouse genome annotation by the RefSeq project. Mammalian Genome, 2015, 26, 379-390.	1.0	17
61	Key challenges for the creation and maintenance of specialist protein resources. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1005-1013.	1.5	13
62	Cytoplasmic Male Sterility in Petunia. , 1991, , 383-399.		10
63	WebWise: Navigating the Human Genome Project: Table 1 Genome Research, 1997, 7, 1038-1039.	2.4	8
64	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat: Figure 1 Database: the Journal of Biological Databases and Curation, 2015, 2015, bav063.	1.4	8
65	RefSeq Functional Elements as experimentally assayed nongenic reference standards and functional interactions in human and mouse. Genome Research, 2022, 32, 175-188.	2.4	7
66	RefSeq curation and annotation of antizyme and antizyme inhibitor genes in vertebrates. Nucleic Acids Research, 2015, 43, 7270-7279.	6.5	4
67	WebWise: Guide to the University of Washington Genome Center Web Site. Genome Research, 1998, 8, 572-575.	2.4	1
68	WebWise: Guide to McDermott Center for Human Growth and Development at University of Texas Southwest Web Site. Genome Research, 1998, 8, 422-426.	2.4	0
69	Accessing the Human Genome. Current Protocols in Human Genetics, 2002, 34, Unit 6.9.	3.5	0