

Lincoln Stein

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11477145/publications.pdf>

Version: 2024-02-01

81
papers

28,891
citations

25034

57
h-index

62596

80
g-index

81
all docs

81
docs citations

81
times ranked

45569
citing authors

#	ARTICLE	IF	CITATIONS
1	The reactome pathway knowledgebase 2022. <i>Nucleic Acids Research</i> , 2022, 50, D687-D692.	14.5	924
2	WormBase in 2022â€”data, processes, and tools for analyzing <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2022, 220, .	2.9	128
3	Harmonizing model organism data in the Alliance of Genome Resources. <i>Genetics</i> , 2022, 220, .	2.9	52
4	Using Reactome to build an autophagy mechanism knowledgebase. <i>Autophagy</i> , 2021, 17, 1543-1554.	9.1	5
5	The Dockstore: enhancing a community platform for sharing reproducible and accessible computational protocols. <i>Nucleic Acids Research</i> , 2021, 49, W624-W632.	14.5	10
6	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334.	14.5	2,416
7	WormBase: a modern Model Organism Information Resource. <i>Nucleic Acids Research</i> , 2020, 48, D762-D767.	14.5	213
8	Plant Reactome: a knowledgebase and resource for comparative pathway analysis. <i>Nucleic Acids Research</i> , 2020, 48, D1093-D1103.	14.5	44
9	The reactome pathway knowledgebase. <i>Nucleic Acids Research</i> , 2020, 48, D498-D503.	14.5	1,570
10	JBrowse Connect: A server API to connect JBrowse instances and users. <i>PLoS Computational Biology</i> , 2020, 16, e1007261.	3.2	1
11	Detection of Circulating Tumor DNA in Plasma: A Potential Biomarker for Esophageal Adenocarcinoma. <i>Annals of Thoracic Surgery</i> , 2019, 108, 343-349.	1.3	36
12	<p>Combined EsophaCap cytology and MUC2 immunohistochemistry for screening of intestinal metaplasia, dysplasia and carcinoma</p>. <i>Clinical and Experimental Gastroenterology</i> , 2019, Volume 12, 219-229.	2.3	13
13	Reactome and ORCIDâ€™fine-grained credit attribution for community curation. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	12
14	Interleukins and their signaling pathways in the Reactome biological pathway database. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 1411-1416.	2.9	11
15	WormBase 2017: molting into a new stage. <i>Nucleic Acids Research</i> , 2018, 46, D869-D874.	14.5	172
16	The Reactome Pathway Knowledgebase. <i>Nucleic Acids Research</i> , 2018, 46, D649-D655.	14.5	2,388
17	Reactome graph database: Efficient access to complex pathway data. <i>PLoS Computational Biology</i> , 2018, 14, e1005968.	3.2	202
18	Simple multiplexed PCR-based barcoding of DNA for ultrasensitive mutation detection by next-generation sequencing. <i>Nature Protocols</i> , 2017, 12, 664-682.	12.0	93

#	ARTICLE	IF	CITATIONS
19	Reactome enhanced pathway visualization. <i>Bioinformatics</i> , 2017, 33, 3461-3467.	4.1	140
20	Reactome pathway analysis: a high-performance in-memory approach. <i>BMC Bioinformatics</i> , 2017, 18, 142.	2.6	600
21	The Dockstore: enabling modular, community-focused sharing of Docker-based genomics tools and workflows. <i>F1000Research</i> , 2017, 6, 52.	1.6	82
22	JBrowse: a dynamic web platform for genome visualization and analysis. <i>Genome Biology</i> , 2016, 17, 66.	8.8	690
23	The Reactome pathway Knowledgebase. <i>Nucleic Acids Research</i> , 2016, 44, D481-D487.	14.5	3,319
24	Simple, multiplexed, PCR-based barcoding of DNA enables sensitive mutation detection in liquid biopsies using sequencing. <i>Nucleic Acids Research</i> , 2016, 44, e105-e105.	14.5	108
25	Gramene 2016: comparative plant genomics and pathway resources. <i>Nucleic Acids Research</i> , 2016, 44, D1133-D1140.	14.5	138
26	WormBase 2016: expanding to enable helminth genomic research. <i>Nucleic Acids Research</i> , 2016, 44, D774-D780.	14.5	329
27	Cross-organism analysis using InterMine. <i>Genesis</i> , 2015, 53, 547-560.	1.6	31
28	A genome-wide association study platform built on iPlant cyberinfrastructure. <i>Concurrency Computation Practice and Experience</i> , 2015, 27, 420-432.	2.2	5
29	Glucocorticoid-Induced Reversal of Interleukin-1 β -Stimulated Inflammatory Gene Expression in Human Oviductal Cells. <i>PLoS ONE</i> , 2014, 9, e97997.	2.5	9
30	ReactomeFIViz: a Cytoscape app for pathway and network-based data analysis. <i>F1000Research</i> , 2014, 3, 146.	1.6	155
31	The Reactome pathway knowledgebase. <i>Nucleic Acids Research</i> , 2014, 42, D472-D477.	14.5	1,448
32	Next-generation sequencing identifies rare variants associated with Noonan syndrome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11473-11478.	7.1	158
33	WormBase 2014: new views of curated biology. <i>Nucleic Acids Research</i> , 2014, 42, D789-D793.	14.5	149
34	Gramene 2013: comparative plant genomics resources. <i>Nucleic Acids Research</i> , 2014, 42, D1193-D1199.	14.5	163
35	ReactomeFIViz: the Reactome FI Cytoscape app for pathway and network-based data analysis. <i>F1000Research</i> , 2014, 3, 146.	1.6	129
36	Web Apollo: a web-based genomic annotation editing platform. <i>Genome Biology</i> , 2013, 14, R93.	9.6	329

#	ARTICLE	IF	CITATIONS
37	InterMOD: integrated data and tools for the unification of model organism research. Scientific Reports, 2013, 3, 1802.	3.3	25
38	Annotating Cancer Variants and Anti-Cancer Therapeutics in Reactome. Cancers, 2012, 4, 1180-1211.	3.7	270
39	WormBase 2012: more genomes, more data, new website. Nucleic Acids Research, 2012, 40, D735-D741.	14.5	175
40	Bile Exposure Inhibits Expression of Squamous Differentiation Genes in Human Esophageal Epithelial Cells. Annals of Surgery, 2012, 255, 1113-1120.	4.2	16
41	PeakRanger: A cloud-enabled peak caller for ChIP-seq data. BMC Bioinformatics, 2011, 12, 139.	2.6	142
42	Reactome: a database of reactions, pathways and biological processes. Nucleic Acids Research, 2011, 39, D691-D697.	14.5	1,391
43	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. Frontiers in Plant Science, 2011, 2, 34.	3.6	396
44	Identification of a Therapeutic Strategy Targeting Amplified FGF19 in Liver Cancer by Oncogenomic Screening. Cancer Cell, 2011, 19, 347-358.	16.8	379
45	Reactome pathway analysis to enrich biological discovery in proteomics data sets. Proteomics, 2011, 11, 3598-3613.	2.2	89
46	Phylogenomic Analysis of BAC-end Sequence Libraries in <i>Oryza</i> (Poaceae). Systematic Botany, 2010, 35, 512-523.	0.5	8
47	Dynamic <i>Oryza</i> Genomes: Repetitive DNA Sequences as Genome Modeling Agents. Rice, 2010, 3, 251-269.	4.0	15
48	Rice structural variation: a comparative analysis of structural variation between rice and three of its closest relatives in the genus <i>Oryza</i> . Plant Journal, 2010, 63, 990-1003.	5.7	47
49	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. Science, 2010, 330, 1775-1787.	12.6	912
50	The systematic annotation of the three main GPCR families in Reactome. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq018-baq018.	3.0	24
51	A human functional protein interaction network and its application to cancer data analysis. Genome Biology, 2010, 11, R53.	9.6	591
52	Evidence-based gene predictions in plant genomes. Genome Research, 2009, 19, 1912-1923.	5.5	44
53	Gramene QTL database: development, content and applications. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap005.	3.0	95
54	Species Trees from Highly Incongruent Gene Trees in Rice. Systematic Biology, 2009, 58, 489-500.	5.6	98

#	ARTICLE	IF	CITATIONS
55	Unlocking the secrets of the genome. <i>Nature</i> , 2009, 459, 927-930.	27.8	744
56	Reactome knowledgebase of human biological pathways and processes. <i>Nucleic Acids Research</i> , 2009, 37, D619-D622.	14.5	760
57	Construction, alignment and analysis of 12 framework physical maps that represent the 10 genome types of the genus <i>Oryza</i> . <i>Genome Biology</i> , 2008, 9, R45.	9.6	82
58	The Plant Ontology Database: a community resource for plant structure and developmental stages controlled vocabulary and annotations. <i>Nucleic Acids Research</i> , 2008, 36, D449-D454.	14.5	135
59	Interoperability with Moby 1.0--It's better than sharing your toothbrush!. <i>Briefings in Bioinformatics</i> , 2008, 9, 220-231.	6.5	91
60	The <i>Oryza</i> Map Alignment Project (OMAP): A New Resource for Comparative Genome Studies within <i>Oryza</i> . , 2007, , 395-409.		9
61	Reactome: a knowledge base of biologic pathways and processes. <i>Genome Biology</i> , 2007, 8, R39.	9.6	539
62	Gramene: a growing plant comparative genomics resource. <i>Nucleic Acids Research</i> , 2007, 36, D947-D953.	14.5	151
63	Gramene: a bird's eye view of cereal genomes. <i>Nucleic Acids Research</i> , 2006, 34, D717-D723.	14.5	177
64	Whole-Plant Growth Stage Ontology for Angiosperms and Its Application in Plant Biology. <i>Plant Physiology</i> , 2006, 142, 414-428.	4.8	56
65	Panzea: a database and resource for molecular and functional diversity in the maize genome. <i>Nucleic Acids Research</i> , 2006, 34, D752-D757.	14.5	89
66	Evolution of <i>Arabidopsis</i> microRNA families through duplication events. <i>Genome Research</i> , 2006, 16, 510-519.	5.5	328
67	Plant Ontology (PO): a Controlled Vocabulary of Plant Structures and Growth Stages. <i>Comparative and Functional Genomics</i> , 2005, 6, 388-397.	2.0	129
68	The <i>Oryza</i> Map Alignment Project: The Golden Path to Unlocking the Genetic Potential of Wild Rice Species. <i>Plant Molecular Biology</i> , 2005, 59, 53-62.	3.9	143
69	Site Preferences of Insertional Mutagenesis Agents in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2005, 137, 168-175.	4.8	47
70	SynBrowse: a synteny browser for comparative sequence analysis. <i>Bioinformatics</i> , 2005, 21, 3461-3468.	4.1	66
71	The Sequence Ontology: a tool for the unification of genome annotations. <i>Genome Biology</i> , 2005, 6, R44.	9.6	638
72	Applying Semantic Web Services to Bioinformatics: Experiences Gained, Lessons Learnt. <i>Lecture Notes in Computer Science</i> , 2004, , 350-364.	1.3	55

#	ARTICLE	IF	CITATIONS
73	A 3.9-Centimorgan-Resolution Human Single-Nucleotide Polymorphism Linkage Map and Screening Set. <i>American Journal of Human Genetics</i> , 2003, 73, 271-284.	6.2	112
74	ATIDB: Arabidopsis thaliana insertion database. <i>Nucleic Acids Research</i> , 2003, 31, 1245-1251.	14.5	36
75	Maize-targeted mutagenesis: A knockout resource for maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 11541-11546.	7.1	109
76	Gramene: Development and Integration of Trait and Gene Ontologies for Rice. <i>Comparative and Functional Genomics</i> , 2002, 3, 132-136.	2.0	341
77	Creating a bioinformatics nation. <i>Nature</i> , 2002, 417, 119-120.	27.8	298
78	Gramene: a resource for comparative grass genomics. <i>Nucleic Acids Research</i> , 2002, 30, 103-105.	14.5	213
79	Genome annotation: from sequence to biology. <i>Nature Reviews Genetics</i> , 2001, 2, 493-503.	16.3	324
80	Differential methylation of genes and retrotransposons facilitates shotgun sequencing of the maize genome. <i>Nature Genetics</i> , 1999, 23, 305-308.	21.4	237
81	Large-Scale Identification, Mapping, and Genotyping of Single-Nucleotide Polymorphisms in the Human Genome. <i>Science</i> , 1998, 280, 1077-1082.	12.6	1,993