

Harsha Vardhan Doddapaneni

List of Publications by Year in descending order

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Version: 2024-02-01

143
papers

54,302
citations

8159

76
h-index

8835

145
g-index

166
all docs

166
docs citations

166
times ranked

81876
citing authors

#	ARTICLE	IF	CITATIONS
1	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
2	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	6.6	3,706
3	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018, 173, 400-416.e11.	13.5	2,277
4	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	13.5	2,111
5	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	13.7	1,966
6	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	13.5	1,794
7	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018, 173, 291-304.e6.	13.5	1,718
8	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	13.5	1,670
9	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	13.5	1,417
10	Temporal development of the gut microbiome in early childhood from the TEDDY study. <i>Nature</i> , 2018, 562, 583-588.	13.7	1,220
11	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	2.9	801
12	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	7.7	750
13	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018, 23, 181-193.e7.	2.9	683
14	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	7.7	665
15	Trans-ancestry mutational landscape of hepatocellular carcinoma genomes. <i>Nature Genetics</i> , 2014, 46, 1267-1273.	9.4	655
16	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	7.7	623
17	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.	13.5	620
18	The 8q24 cancer risk variant rs6983267 shows long-range interaction with MYC in colorectal cancer. <i>Nature Genetics</i> , 2009, 41, 882-884.	9.4	616

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19	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018, 6, 271-281.e7.	2.9	605
20	Genome, transcriptome, and secretome analysis of wood decay fungus <i>Postia placenta</i> supports unique mechanisms of lignocellulose conversion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1954-1959.	3.3	530
21	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018, 23, 313-326.e5.	2.9	523
22	Mutational Landscape of Aggressive Cutaneous Squamous Cell Carcinoma. <i>Clinical Cancer Research</i> , 2014, 20, 6582-6592.	3.2	493
23	Complete Genome Sequence of Citrus Huanglongbing Bacterium, <i>Candidatus Liberibacter asiaticus</i> ™ Obtained Through Metagenomics. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 1011-1020.	1.4	485
24	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.	7.7	482
25	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	7.7	478
26	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	2.9	407
27	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. <i>Cancer Cell</i> , 2018, 33, 706-720.e9.	7.7	400
28	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	7.7	396
29	<i>Cyanophora paradoxa</i> Genome Elucidates Origin of Photosynthesis in Algae and Plants. <i>Science</i> , 2012, 335, 843-847.	6.0	371
30	Genome sequence of the button mushroom <i>Agaricus bisporus</i> reveals mechanisms governing adaptation to a humic-rich ecological niche. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17501-17506.	3.3	359
31	Mutually exclusive recurrent somatic mutations in MAP2K1 and BRAF support a central role for ERK activation in LCH pathogenesis. <i>Blood</i> , 2014, 124, 3007-3015.	0.6	352
32	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018, 23, 282-296.e4.	2.9	333
33	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018, 25, 1304-1317.e5.	2.9	329
34	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.	2.9	324
35	The house spider genome reveals an ancient whole-genome duplication during arachnid evolution. <i>BMC Biology</i> , 2017, 15, 62.	1.7	286
36	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , 2018, 6, 282-300.e2.	2.9	284

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37	Rise and fall of subclones from diagnosis to relapse in pediatric B-acute lymphoblastic leukaemia. <i>Nature Communications</i> , 2015, 6, 6604.	5.8	281
38	Genomic profiling of SÅ©zary syndrome identifies alterations of key T cell signaling and differentiation genes. <i>Nature Genetics</i> , 2015, 47, 1426-1434.	9.4	276
39	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	13.5	272
40	Comparative genomics of <i>Ceriporiopsis subvermispora</i> and <i>Phanerochaete chrysosporium</i> provide insight into selective ligninolysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5458-5463.	3.3	259
41	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018, 23, 194-212.e6.	2.9	245
42	Exonuclease mutations in DNA polymerase epsilon reveal replication strand specific mutation patterns and human origins of replication. <i>Genome Research</i> , 2014, 24, 1740-1750.	2.4	244
43	Genome of the Asian longhorned beetle (<i>Anoplophora glabripennis</i>), a globally significant invasive species, reveals key functional and evolutionary innovations at the beetleâ€‘plant interface. <i>Genome Biology</i> , 2016, 17, 227.	3.8	244
44	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018, 173, 386-399.e12.	13.5	228
45	Hemimetabolous genomes reveal molecular basis of termite eusociality. <i>Nature Ecology and Evolution</i> , 2018, 2, 557-566.	3.4	223
46	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. <i>Cell Reports</i> , 2018, 23, 297-312.e12.	2.9	205
47	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018, 23, 255-269.e4.	2.9	204
48	Mapping and characterization of structural variation in 17,795 human genomes. <i>Nature</i> , 2020, 583, 83-89.	13.7	194
49	Unique features of a global human ectoparasite identified through sequencing of the bed bug genome. <i>Nature Communications</i> , 2016, 7, 10165.	5.8	184
50	Lessons learned from additional research analyses of unsolved clinical exome cases. <i>Genome Medicine</i> , 2017, 9, 26.	3.6	184
51	Novel somatic and germline mutations in intracranial germ cell tumours. <i>Nature</i> , 2014, 511, 241-245.	13.7	181
52	Whole-exome sequencing points to considerable genetic heterogeneity of cerebral palsy. <i>Molecular Psychiatry</i> , 2015, 20, 176-182.	4.1	178
53	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018, 23, 270-281.e3.	2.9	177
54	Germline Mutations in Shelterin Complex Genes Are Associated With Familial Glioma. <i>Journal of the National Cancer Institute</i> , 2015, 107, 384.	3.0	172

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55	Evolutionary History of Chemosensory-Related Gene Families across the Arthropoda. <i>Molecular Biology and Evolution</i> , 2017, 34, 1838-1862.	3.5	157
56	Gene content evolution in the arthropods. <i>Genome Biology</i> , 2020, 21, 15.	3.8	150
57	Transmission event of SARS-CoV-2 delta variant reveals multiple vaccine breakthrough infections. <i>BMC Medicine</i> , 2021, 19, 255.	2.3	137
58	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- β Superfamily. <i>Cell Systems</i> , 2018, 7, 422-437.e7.	2.9	134
59	Genome-based PCR Primers for Specific and Sensitive Detection and Quantification of <i>Xylella fastidiosa</i> . <i>European Journal of Plant Pathology</i> , 2006, 115, 203-213.	0.8	133
60	Identification of a single-stranded DNA virus associated with citrus chlorotic dwarf disease, a new member in the family Geminiviridae. <i>Virology</i> , 2012, 432, 162-172.	1.1	130
61	The whole genome sequence of the Mediterranean fruit fly, <i>Ceratitis capitata</i> (Wiedemann), reveals insights into the biology and adaptive evolution of a highly invasive pest species. <i>Genome Biology</i> , 2016, 17, 192.	3.8	130
62	The Complete Genome Sequence of <i>Candidatus Liberibacter solanacearum</i> TM , the Bacterium Associated with Potato Zebra Chip Disease. <i>PLoS ONE</i> , 2011, 6, e19135.	1.1	127
63	Recurrent internal tandem duplications of BCOR in clear cell sarcoma of the kidney. <i>Nature Communications</i> , 2015, 6, 8891.	5.8	126
64	BCOR-CCNB3 fusions are frequent in undifferentiated sarcomas of male children. <i>Modern Pathology</i> , 2015, 28, 575-586.	2.9	122
65	Molecular profiling predicts meningioma recurrence and reveals loss of DREAM complex repression in aggressive tumors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21715-21726.	3.3	122
66	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 172-180.e3.	2.9	119
67	The comparative genomics and complex population history of <i>Papio</i> baboons. <i>Science Advances</i> , 2019, 5, eaau6947.	4.7	115
68	Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. <i>Genome Biology</i> , 2019, 20, 64.	3.8	114
69	Genome-to-function characterization of novel fungal P450 monooxygenases oxidizing polycyclic aromatic hydrocarbons (PAHs). <i>Biochemical and Biophysical Research Communications</i> , 2010, 399, 492-497.	1.0	107
70	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. <i>Cell Reports</i> , 2016, 14, 907-919.	2.9	107
71	Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. <i>Cell Reports</i> , 2019, 29, 1675-1689.e9.	2.9	103
72	Chemistry-First Approach for Nomination of Personalized Treatment in Lung Cancer. <i>Cell</i> , 2018, 173, 864-878.e29.	13.5	102

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73	Reproductive Longevity Predicts Mutation Rates in Primates. <i>Current Biology</i> , 2018, 28, 3193-3197.e5.	1.8	94
74	Genome-wide structural and evolutionary analysis of the P450 monooxygenase genes (P450ome) in the white rot fungus <i>Phanerochaete chrysosporium</i> : Evidence for gene duplications and extensive gene clustering. <i>BMC Genomics</i> , 2005, 6, 92.	1.2	90
75	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018, 23, 213-226.e3.	2.9	83
76	A combined risk score enhances prediction of type 1 diabetes among susceptible children. <i>Nature Medicine</i> , 2020, 26, 1247-1255.	15.2	83
77	Exome sequencing in mostly consanguineous Arab families with neurologic disease provides a high potential molecular diagnosis rate. <i>BMC Medical Genomics</i> , 2016, 9, 42.	0.7	80
78	The Toxicogenome of <i>Hyalella azteca</i> : A Model for Sediment Ecotoxicology and Evolutionary Toxicology. <i>Environmental Science & Technology</i> , 2018, 52, 6009-6022.	4.6	79
79	The Genomics of Arthrogyrosis, a Complex Trait: Candidate Genes and Further Evidence for Oligogenic Inheritance. <i>American Journal of Human Genetics</i> , 2019, 105, 132-150.	2.6	74
80	Megabase Length Hypermutation Accompanies Human Structural Variation at 17p11.2. <i>Cell</i> , 2019, 176, 1310-1324.e10.	13.5	73
81	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. <i>Nature Genetics</i> , 2021, 53, 1504-1516.	9.4	69
82	Molecular Features of Cancers Exhibiting Exceptional Responses to Treatment. <i>Cancer Cell</i> , 2021, 39, 38-53.e7.	7.7	65
83	Brown marmorated stink bug, <i>Halyomorpha halys</i> (Stål), genome: putative underpinnings of polyphagy, insecticide resistance potential and biology of a top worldwide pest. <i>BMC Genomics</i> , 2020, 21, 227.	1.2	60
84	Comparative genomics of the miniature wasp and pest control agent <i>Trichogramma pretiosum</i> . <i>BMC Biology</i> , 2018, 16, 54.	1.7	57
85	Differential regulation and xenobiotic induction of tandem P450 monooxygenase genes <i>pc-1</i> (CYP63A1) and <i>pc-2</i> (CYP63A2) in the white-rot fungus <i>Phanerochaete chrysosporium</i> . <i>Applied Microbiology and Biotechnology</i> , 2004, 65, 559-65.	1.7	56
86	Novel patient-derived xenograft and cell line models for therapeutic testing of pediatric liver cancer. <i>Journal of Hepatology</i> , 2016, 65, 325-333.	1.8	56
87	Genome-enabled insights into the biology of thrips as crop pests. <i>BMC Biology</i> , 2020, 18, 142.	1.7	54
88	OikoBase: a genomics and developmental transcriptomics resource for the urochordate <i>Oikopleura dioica</i> . <i>Nucleic Acids Research</i> , 2013, 41, D845-D853.	6.5	53
89	A new diagnostic system for ultra-sensitive and specific detection and quantification of <i>Candidatus Liberibacter asiaticus</i> , the bacterium associated with citrus Huanglongbing. <i>Journal of Microbiological Methods</i> , 2010, 81, 17-25.	0.7	49
90	Paternal age in rhesus macaques is positively associated with germline mutation accumulation but not with measures of offspring sociability. <i>Genome Research</i> , 2020, 30, 826-834.	2.4	48

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91	The genome of the water strider <i>Gerris buenoi</i> reveals expansions of gene repertoires associated with adaptations to life on the water. <i>BMC Genomics</i> , 2018, 19, 832.	1.2	47
92	Whole-Exome Sequencing Identifies Novel Variants for Tooth Agenesis. <i>Journal of Dental Research</i> , 2018, 97, 49-59.	2.5	44
93	Genetic architecture of laterality defects revealed by whole exome sequencing. <i>European Journal of Human Genetics</i> , 2019, 27, 563-573.	1.4	44
94	Centers for Mendelian Genomics: A decade of facilitating gene discovery. <i>Genetics in Medicine</i> , 2022, 24, 784-797.	1.1	44
95	High prevalence of multilocus pathogenic variation in neurodevelopmental disorders in the Turkish population. <i>American Journal of Human Genetics</i> , 2021, 108, 1981-2005.	2.6	38
96	Comparative analysis of ESTs involved in grape responses to <i>Xylella fastidiosa</i> infection. <i>BMC Plant Biology</i> , 2007, 7, 8.	1.6	36
97	Physiological Regulation, Xenobiotic Induction, and Heterologous Expression of P450 Monooxygenase Gene <i>pc-3</i> (CYP63A3), a New Member of the CYP63 Gene Cluster in the White-rot Fungus <i>Phanerochaete chrysosporium</i> . <i>Current Microbiology</i> , 2005, 50, 292-298.	1.0	34
98	Cohort Profile: The Right Drug, Right Dose, Right Time: Using Genomic Data to Individualize Treatment Protocol (RIGHT Protocol). <i>International Journal of Epidemiology</i> , 2020, 49, 23-24k.	0.9	34
99	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. <i>Nature Communications</i> , 2020, 11, 5182.	5.8	32
100	Postmortem genetic screening for the identification, verification, and reporting of genetic variants contributing to the sudden death of the young. <i>Genome Research</i> , 2016, 26, 1170-1177.	2.4	29
101	Genome sequencing unveils a regulatory landscape of platelet reactivity. <i>Nature Communications</i> , 2021, 12, 3626.	5.8	29
102	Analysis of the genome-wide variations among multiple strains of the plant pathogenic bacterium <i>Xylella fastidiosa</i> . <i>BMC Genomics</i> , 2006, 7, 225.	1.2	28
103	PRINCESS: comprehensive detection of haplotype resolved SNVs, SVs, and methylation. <i>Genome Biology</i> , 2021, 22, 268.	3.8	28
104	Implementation of preemptive DNA sequence-based pharmacogenomics testing across a large academic medical center: The Mayo-Baylor RIGHT 10K Study. <i>Genetics in Medicine</i> , 2022, 24, 1062-1072.	1.1	28
105	Bi-allelic Variants in <i>TONSL</i> Cause <i>SPONASTRIME</i> Dysplasia and a Spectrum of Skeletal Dysplasia Phenotypes. <i>American Journal of Human Genetics</i> , 2019, 104, 422-438.	2.6	27
106	Acquisition of uncharacterized sequences from <i>Candidatus Liberibacter</i> , an unculturable bacterium, using an improved genomic walking method. <i>Molecular and Cellular Probes</i> , 2008, 22, 30-37.	0.9	24
107	Rare coding variants in 35 genes associate with circulating lipid levels—A multi-ancestry analysis of 170,000 exomes. <i>American Journal of Human Genetics</i> , 2022, 109, 81-96.	2.6	24
108	A comparative genomic analysis of the oxidative enzymes potentially involved in lignin degradation by <i>Agaricus bisporus</i> . <i>Fungal Genetics and Biology</i> , 2013, 55, 22-31.	0.9	22

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109	Whole-exome sequencing of polycythemia vera revealed novel driver genes and somatic mutation shared by T cells and granulocytes. <i>Leukemia</i> , 2014, 28, 935-938.	3.3	22
110	Novel CYP2A6 diplotypes identified through next-generation sequencing are associated with in-vitro and in-vivo nicotine metabolism. <i>Pharmacogenetics and Genomics</i> , 2018, 28, 7-16.	0.7	20
111	Oligonucleotide capture sequencing of the SARS-CoV-2 genome and subgenomic fragments from COVID-19 individuals. <i>PLoS ONE</i> , 2021, 16, e0244468.	1.1	20
112	An open access pilot freely sharing cancer genomic data from participants in Texas. <i>Scientific Data</i> , 2016, 3, 160010.	2.4	19
113	The relationship of JAK2V617F and acquired UPD at chromosome 9p in polycythemia vera. <i>Leukemia</i> , 2014, 28, 938-941.	3.3	18
114	Mismatch repair gene mutations lead to lynch syndrome colorectal cancer in rhesus macaques. <i>Genes and Cancer</i> , 2018, 9, 142-152.	0.6	18
115	Identification of a response regulator involved in surface attachment, cell aggregation, exopolysaccharide production and virulence in the plant pathogen <i>Xylella fastidiosa</i> . <i>Molecular Plant Pathology</i> , 2013, 14, 256-264.	2.0	17
116	Evidence for Stabilizing Selection on Codon Usage in Chromosomal Rearrangements of <i>Drosophila pseudoobscura</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2433-2449.	0.8	17
117	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. <i>Nature Communications</i> , 2021, 12, 2182.	5.8	17
118	Sawfly Genomes Reveal Evolutionary Acquisitions That Fostered the Mega-Radiation of Parasitoid and Eusocial Hymenoptera. <i>Genome Biology and Evolution</i> , 2020, 12, 1099-1188.	1.1	17
119	Drivers of transcriptional variance in human intestinal epithelial organoids. <i>Physiological Genomics</i> , 2021, 53, 486-508.	1.0	17
120	Multiple Respiratory Syncytial Virus (RSV) Strains Infecting HEp-2 and A549 Cells Reveal Cell Line-Dependent Differences in Resistance to RSV Infection. <i>Journal of Virology</i> , 2022, , e0190421.	1.5	17
121	VitisExpDB: A database resource for grape functional genomics. <i>BMC Plant Biology</i> , 2008, 8, 23.	1.6	16
122	Improved Real-Time PCR Diagnosis of Citrus Stubborn Disease by Targeting Prophage Genes of <i>Spiroplasma citri</i> . <i>Plant Disease</i> , 2015, 99, 149-154.	0.7	16
123	Characterization of transcriptomes from sexual and asexual lineages of a New Zealand snail (<i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 T</i>)	2.2	14
124	Wolffâ€“Parkinsonâ€“White syndrome: De novo variants and evidence for mutational burden in genes associated with atrial fibrillation. <i>American Journal of Medical Genetics, Part A</i> , 2020, 182, 1387-1399.	0.7	14
125	Comparative phylogenomics and multi-gene cluster analyses of the Citrus Huanglongbing (HLB)-associated bacterium <i>Candidatus Liberibacter</i> . <i>BMC Research Notes</i> , 2008, 1, 72.	0.6	13
126	Elucidating the molecular pathogenesis of glioma: integrated germline and somatic profiling of a familial glioma case series. <i>Neuro-Oncology</i> , 2018, 20, 1625-1633.	0.6	12

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127	Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. <i>Human Molecular Genetics</i> , 2019, 28, 1212-1224.	1.4	12
128	Beliefs in vaccine as causes of autism among SPARK cohort caregivers. <i>Vaccine</i> , 2020, 38, 1794-1803.	1.7	12
129	A biallelic <i>ANTXR1</i> variant expands the anthrax toxin receptor associated phenotype to tooth agenesis. <i>American Journal of Medical Genetics, Part A</i> , 2018, 176, 1015-1022.	0.7	11
130	Expression of a β -glucosidase gene results in increased accumulation of salicylic acid in transgenic <i>Nicotiana tabacum</i> cv. Xanthi-nc NN genotype. <i>Plant Cell Reports</i> , 2007, 26, 291-301.	2.8	10
131	Transcriptional Reprogramming Differentiates Active from Inactive ESR1 Fusions in Endocrine Therapy-Refractory Metastatic Breast Cancer. <i>Cancer Research</i> , 2021, 81, 6259-6272.	0.4	10
132	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. <i>American Journal of Human Genetics</i> , 2020, 106, 112-120.	2.6	9
133	Fully resolved assembly of <i>Cryptosporidium parvum</i> . <i>GigaScience</i> , 2022, 11, .	3.3	8
134	P450 Redox Enzymes in the White Rot Fungus <i>Phanerochaete chrysosporium</i> : Gene Transcription, Heterologous Expression, and Activity Analysis on the Purified Proteins. <i>Current Microbiology</i> , 2010, 61, 306-314.	1.0	7
135	Polygenic transcriptome risk scores for COPD and lung function improve cross-ethnic portability of prediction in the NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2022, 109, 857-870.	2.6	7
136	Genome Sequencing in the Parkinson Disease Clinic. <i>Neurology: Genetics</i> , 2022, 8, .	0.9	7
137	Draft genome sequences and description of <i>Lactobacillus rhamnosus</i> strains L31, L34, and L35. <i>Standards in Genomic Sciences</i> , 2014, 9, 744-754.	1.5	5
138	PrimerSNP: a web tool for whole-genome selection of allele-specific and common primers of phylogenetically-related bacterial genomic sequences. <i>BMC Microbiology</i> , 2008, 8, 185.	1.3	1
139	Variant-specific inflation factors for assessing population stratification at the phenotypic variance level. <i>Nature Communications</i> , 2021, 12, 3506.	5.8	1
140	Sequencing of a central nervous system tumor demonstrates cancer transmission in an organ transplant. <i>Life Science Alliance</i> , 2021, 4, e202000941.	1.3	1
141	Integrated Genomic Analysis of Down Syndrome Acute Lymphoblastic Leukemia Reveals Recurrent Cancer Gene Alterations and Evidence of Frequent Subclonal Driver Events. <i>Blood</i> , 2016, 128, 4083-4083.	0.6	0
142	Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
143	Abstract PD15-03: Overlapping molecular features (proliferation, immune signatures) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 107 Cancer Research, 2022, 82, PD15-03-PD15-03.	0.4	0