

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	Rare coding variants in 35 genes associate with circulating lipid levelsâ€”A multi-ancestry analysis of 170,000 exomes. <i>American Journal of Human Genetics</i> , 2022, 109, 81-96.	2.6	24
2	Centers for Mendelian Genomics: A decade of facilitating gene discovery. <i>Genetics in Medicine</i> , 2022, 24, 784-797.	1.1	44
3	Fully resolved assembly of <i>Cryptosporidium parvum</i> . <i>GigaScience</i> , 2022, 11, .	3.3	8
4	Abstract PD15-03: Overlapping molecular features (proliferation, immune signatures) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 627 Td (and Cancer Research, 2022, 82, PD15-03-PD15-03.	0.4	0
5	Implementation of preemptive DNA sequenceâ€”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
6	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
7	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
8	Genome Sequencing in the Parkinson Disease Clinic. <i>Neurology: Genetics</i> , 2022, 8, .	0.9	7
9	Molecular Features of Cancers Exhibiting Exceptional Responses to Treatment. <i>Cancer Cell</i> , 2021, 39, 38-53.e7.	7.7	65
10	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. <i>Nature Communications</i> , 2021, 12, 2182.	5.8	17
11	Genome sequencing unveils a regulatory landscape of platelet reactivity. <i>Nature Communications</i> , 2021, 12, 3626.	5.8	29
12	Variant-specific inflation factors for assessing population stratification at the phenotypic variance level. <i>Nature Communications</i> , 2021, 12, 3506.	5.8	1
13	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
14	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
15	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
16	PRINCESS: comprehensive detection of haplotype resolved SNVs, SVs, and methylation. <i>Genome Biology</i> , 2021, 22, 268.	3.8	28
17	Transmission event of SARS-CoV-2 delta variant reveals multiple vaccine breakthrough infections. <i>BMC Medicine</i> , 2021, 19, 255.	2.3	137
18	Drivers of transcriptional variance in human intestinal epithelial organoids. <i>Physiological Genomics</i> , 2021, 53, 486-508.	1.0	17

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19	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
20	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
21	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
22	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
23	A combined risk score enhances prediction of type 1 diabetes among susceptible children. <i>Nature Medicine</i> , 2020, 26, 1247-1255.	15.2	83
24	Genome-enabled insights into the biology of thrips as crop pests. <i>BMC Biology</i> , 2020, 18, 142.	1.7	54
25	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
26	Mapping and characterization of structural variation in 17,795 human genomes. <i>Nature</i> , 2020, 583, 83-89.	13.7	194
27	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
28	<sc>Wolffâ€“Parkinsonâ€“White</sc> 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
29	Gene content evolution in the arthropods. <i>Genome Biology</i> , 2020, 21, 15.	3.8	150
30	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
31	Beliefs in vaccine as causes of autism among SPARK cohort caregivers. <i>Vaccine</i> , 2020, 38, 1794-1803.	1.7	12
32	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	13.7	1,966
33	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
34	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
35	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
36	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

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37	The comparative genomics and complex population history of <i>Papio</i> baboons. <i>Science Advances</i> , 2019, 5, eaau6947.	4.7	115
38	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
39	Megabase Length Hypermutation Accompanies Human Structural Variation at 17p11.2. <i>Cell</i> , 2019, 176, 1310-1324.e10.	13.5	73
40	Bi-allelic Variants in TONSL Cause SPONASTRIME Dysplasia and a Spectrum of Skeletal Dysplasia Phenotypes. <i>American Journal of Human Genetics</i> , 2019, 104, 422-438.	2.6	27
41	Genetic architecture of laterality defects revealed by whole exome sequencing. <i>European Journal of Human Genetics</i> , 2019, 27, 563-573.	1.4	44
42	Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. <i>Human Molecular Genetics</i> , 2019, 28, 1212-1224.	1.4	12
43	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
44	Chemistry-First Approach for Nomination of Personalized Treatment in Lung Cancer. <i>Cell</i> , 2018, 173, 864-878.e29.	13.5	102
45	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
46	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	13.5	1,670
47	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
48	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018, 173, 386-399.e12.	13.5	228
49	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	13.5	272
50	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	13.5	1,417
51	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	13.5	2,111
52	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.	13.5	620
53	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
54	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

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55	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	2.9	245
56	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12.	2.9	205
57	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	2.9	523
58	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	2.9	683
59	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	6.6	3,706
60	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	2.9	119
61	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3.	2.9	83
62	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	2.9	801
63	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	2.9	204
64	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	2.9	177
65	The Toxicogenome of <i>Hyalella azteca</i> : A Model for Sediment Ecotoxicology and Evolutionary Toxicology. Environmental Science & Technology, 2018, 52, 6009-6022.	4.6	79
66	Hemimetabolous genomes reveal molecular basis of termite eusociality. Nature Ecology and Evolution, 2018, 2, 557-566.	3.4	223
67	Novel CYP2A6 diplotypes identified through next-generation sequencing are associated with in-vitro and in-vivo nicotine metabolism. Pharmacogenetics and Genomics, 2018, 28, 7-16.	0.7	20
68	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	2.9	605
69	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	2.9	284
70	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. Cancer Cell, 2018, 33, 706-720.e9.	7.7	400
71	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	7.7	750
72	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	7.7	396

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73	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	7.7	478
74	Whole-Exome Sequencing Identifies Novel Variants for Tooth Agenesis. <i>Journal of Dental Research</i> , 2018, 97, 49-59.	2.5	44
75	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
76	Reproductive Longevity Predicts Mutation Rates in Primates. <i>Current Biology</i> , 2018, 28, 3193-3197.e5.	1.8	94
77	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
78	Temporal development of the gut microbiome in early childhood from the TEDDY study. <i>Nature</i> , 2018, 562, 583-588.	13.7	1,220
79	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018, 25, 1304-1317.e5.	2.9	329
80	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	7.7	623
81	Comparative genomics of the miniature wasp and pest control agent <i>Trichogramma pretiosum</i> . <i>BMC Biology</i> , 2018, 16, 54.	1.7	57
82	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
83	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.	2.9	324
84	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
85	Evolutionary History of Chemosensory-Related Gene Families across the Arthropoda. <i>Molecular Biology and Evolution</i> , 2017, 34, 1838-1862.	3.5	157
86	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	13.5	1,794
87	Lessons learned from additional research analyses of unsolved clinical exome cases. <i>Genome Medicine</i> , 2017, 9, 26.	3.6	184
88	The house spider genome reveals an ancient whole-genome duplication during arachnid evolution. <i>BMC Biology</i> , 2017, 15, 62.	1.7	286
89	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
90	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.	7.7	482

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91	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
92	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
93	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
94	Genome of the Asian longhorned beetle (<i>Anoplophora glabripennis</i>), a globally significant invasive species, reveals key functional and evolutionary innovations at the beetle-plant interface. <i>Genome Biology</i> , 2016, 17, 227.	3.8	244
95	An open access pilot freely sharing cancer genomic data from participants in Texas. <i>Scientific Data</i> , 2016, 3, 160010.	2.4	19
96	Ampullary Cancers Harbor <i>ELF3</i> Tumor Suppressor Gene Mutations and Exhibit Frequent <i>WNT</i> Dysregulation. <i>Cell Reports</i> , 2016, 14, 907-919.	2.9	107
97	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
98	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
99	Whole-exome sequencing points to considerable genetic heterogeneity of cerebral palsy. <i>Molecular Psychiatry</i> , 2015, 20, 176-182.	4.1	178
100	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
101	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
102	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
103	Recurrent internal tandem duplications of <i>BCOR</i> in clear cell sarcoma of the kidney. <i>Nature Communications</i> , 2015, 6, 8891.	5.8	126
104	Genomic profiling of <i>SÄ©zary</i> syndrome identifies alterations of key T cell signaling and differentiation genes. <i>Nature Genetics</i> , 2015, 47, 1426-1434.	9.4	276
105	<i>BCOR</i> - <i>CCNB3</i> fusions are frequent in undifferentiated sarcomas of male children. <i>Modern Pathology</i> , 2015, 28, 575-586.	2.9	122
106	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
107	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
108	Mutational Landscape of Aggressive Cutaneous Squamous Cell Carcinoma. <i>Clinical Cancer Research</i> , 2014, 20, 6582-6592.	3.2	493

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109	The relationship of JAK2V617F and acquired UPD at chromosome 9p in polycythemia vera. <i>Leukemia</i> , 2014, 28, 938-941.	3.3	18
110	Trans-ancestry mutational landscape of hepatocellular carcinoma genomes. <i>Nature Genetics</i> , 2014, 46, 1267-1273.	9.4	655
111	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
112	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
113	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	7.7	665
114	Novel somatic and germline mutations in intracranial germ cell tumours. <i>Nature</i> , 2014, 511, 241-245.	13.7	181
115	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
116	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
117	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
118	Identification of a response regulator involved in surface attachment, cell-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
119	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
120	Characterization of transcriptomes from sexual and asexual lineages of a New Zealand snail (<i>Tj ETQq0 0 0 rgBT /Oyerlock 1Q Tf 50 302</i>)	2.2	14
121	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
122	<i>Cyanophora paradoxa</i> Genome Elucidates Origin of Photosynthesis in Algae and Plants. <i>Science</i> , 2012, 335, 843-847.	6.0	371
123	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
124	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
125	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
126	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

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127	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
128	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
129	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
130	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
131	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
132	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
133	VitisExpDB: A database resource for grape functional genomics. <i>BMC Plant Biology</i> , 2008, 8, 23.	1.6	16
134	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
135	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
136	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
137	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
138	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
139	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
140	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
141	Physiological Regulation, Xenobiotic Induction, and Heterologous Expression of P450 Monooxygenase Gene pc-3 (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
142	Differential regulation and xenobiotic induction of tandem P450 monooxygenase genes pc-1 (CYP63A1) and pc-2 (CYP63A2) in the white-rot fungus <i>Phanerochaete chrysosporium</i> . <i>Applied Microbiology and Biotechnology</i> , 2004, 65, 559-65.	1.7	56
143	Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0