# Harsha Vardhan Doddapaneni

List of Publications by Year
in descending order



| | | | |
|---|---|---|---|
| 143 papers | 54,302 citations | 8181 76 h-index | 8866 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. American Journal of Human Genetics, 2022, 109, 81-96. | 6.2 | 24 |
| 2 | Centers for Mendelian Genomics: A decade of facilitating gene discovery. Genetics in Medicine, 2022, 24, 784-797. | 2.4 | 44 |
| 3 | Fully resolved assembly of Cryptosporidium parvum. GigaScience, 2022, 11, . | 6.4 | 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. | 0.9 | 0 |
| 5 | Implementation of preemptive DNA sequenceâ€"based pharmacogenomics testing across a large academic medical center: The Mayo-Baylor RIGHT 10K Study. Genetics in Medicine, 2022, 24, 1062-1072. | 2.4 | 28 |
| 6 | Multiple Respiratory Syncytial Virus (RSV) Strains Infecting HEp-2 and A549 Cells Reveal Cell Line-Dependent Differences in Resistance to RSV Infection. Journal of Virology, 2022, , e0190421. | 3.4 | 17 |
| 7 | Polygenic transcriptome risk scores for COPD and lung function improve cross-ethnic portability of prediction in the NHLBI TOPMed program. American Journal of Human Genetics, 2022, 109, 857-870. | 6.2 | 7 |
| 8 | Genome Sequencing in the Parkinson Disease Clinic. Neurology: Genetics, 2022, 8, . | 1.9 | 7 |
| 9 | Molecular Features of Cancers Exhibiting Exceptional Responses to Treatment. Cancer Cell, 2021, 39, 38-53.e7. | 16.8 | 65 |
| 10 | Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182. | 12.8 | 17 |
| 11 | Genome sequencing unveils a regulatory landscape of platelet reactivity. Nature Communications, 2021, 12, 3626. | 12.8 | 29 |
| 12 | Variant-specific inflation factors for assessing population stratification at the phenotypic variance level. Nature Communications, 2021, 12, 3506. | 12.8 | 1 |
| 13 | Sequencing of a central nervous system tumor demonstrates cancer transmission in an organ transplant. Life Science Alliance, 2021, 4, e202000941. | 2.8 | 1 |
| 14 | Oligonucleotide capture sequencing of the SARS-CoV-2 genome and subgenomic fragments from COVID-19 individuals. PLoS ONE, 2021, 16, e0244468. | 2.5 | 20 |
| 15 | High prevalence of multilocus pathogenic variation in neurodevelopmental disorders in the Turkish population. American Journal of Human Genetics, 2021, 108, 1981-2005. | 6.2 | 38 |
| 16 | PRINCESS: comprehensive detection of haplotype resolved SNVs, SVs, and methylation. Genome Biology, 2021, 22, 268. | 8.8 | 28 |
| 17 | Transmission event of SARS-CoV-2 delta variant reveals multiple vaccine breakthrough infections. BMC Medicine, 2021, 19, 255. | 5.5 | 137 |
| 18 | Drivers of transcriptional variance in human intestinal epithelial organoids. Physiological Genomics, 2021, 53, 486-508. | 2.3 | 17 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. Nature Genetics, 2021, 53, 1504-1516. | 21.4 | 69 |
| 20 | Transcriptional Reprogramming Differentiates Active from Inactive ESR1 Fusions in Endocrine Therapy-Refractory Metastatic Breast Cancer. Cancer Research, 2021, 81, 6259-6272. | 0.9 | 10 |
| 21 | Cohort Profile: The Right Drug, Right Dose, Right Time: Using Genomic Data to Individualize Treatment Protocol (RIGHT Protocol). International Journal of Epidemiology, 2020, 49, 23-24k. | 1.9 | 34 |
| 22 | Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182. | 12.8 | 32 |
| 23 | A combined risk score enhances prediction of type 1 diabetes among susceptible children. Nature Medicine, 2020, 26, 1247-1255. | 30.7 | 83 |
| 24 | Genome-enabled insights into the biology of thrips as crop pests. BMC Biology, 2020, 18, 142. | 3.8 | 54 |
| 25 | Paternal age in rhesus macaques is positively associated with germline mutation accumulation but not with measures of offspring sociability. Genome Research, 2020, 30, 826-834. | 5.5 | 48 |
| 26 | Mapping and characterization of structural variation in 17,795 human genomes. Nature, 2020, 583, 83-89. | 27.8 | 194 |
| 27 | Brown marmorated stink bug, Halyomorpha halys (StÃ¥l), genome: putative underpinnings of polyphagy, insecticide resistance potential and biology of a top worldwide pest. BMC Genomics, 2020, 21, 227. | 2.8 | 60 |
| 28 | <scp>Wolffâ€“Parkinsonâ€“White</scp> syndrome: De novo variants and evidence for mutational burden in genes associated with atrial fibrillation. American Journal of Medical Genetics, Part A, 2020, 182, 1387-1399. | 1.2 | 14 |
| 29 | Gene content evolution in the arthropods. Genome Biology, 2020, 21, 15. | 8.8 | 150 |
| 30 | Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. American Journal of Human Genetics, 2020, 106, 112-120. | 6.2 | 9 |
| 31 | Beliefs in vaccine as causes of autism among SPARK cohort caregivers. Vaccine, 2020, 38, 1794-1803. | 3.8 | 12 |
| 32 | Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93. | 27.8 | 1,966 |
| 33 | Sawfly Genomes Reveal Evolutionary Acquisitions That Fostered the Mega-Radiation of Parasitoid and Eusocial Hymenoptera. Genome Biology and Evolution, 2020, 12, 1099-1188. | 2.5 | 17 |
| 34 | The Genomics of Arthrogryposis, a Complex Trait: Candidate Genes and Further Evidence for Oligogenic Inheritance. American Journal of Human Genetics, 2019, 105, 132-150. | 6.2 | 74 |
| 35 | Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. Cell Reports, 2019, 29, 1675-1689.e9. | 6.4 | 103 |
| 36 | Molecular profiling predicts meningioma recurrence and reveals loss of DREAM complex repression in aggressive tumors. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 21715-21726. | 7.1 | 122 |

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|---|---|---|---|
| 37 | The comparative genomics and complex population history of Papio baboons. Science Advances, 2019, 5, eaau6947. | 10.3 | 115 |
| 38 | Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. Genome Biology, 2019, 20, 64. | 8.8 | 114 |
| 39 | Megabase Length Hypermutation Accompanies Human Structural Variation at 17p11.2. Cell, 2019, 176, 1310-1324.e10. | 28.9 | 73 |
| 40 | Bi-allelic Variants in TONSL Cause SPONASTRIME Dysplasia and a Spectrum of Skeletal Dysplasia Phenotypes. American Journal of Human Genetics, 2019, 104, 422-438. | 6.2 | 27 |
| 41 | Genetic architecture of laterality defects revealed by whole exome sequencing. European Journal of Human Genetics, 2019, 27, 563-573. | 2.8 | 44 |
| 42 | Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. Human Molecular Genetics, 2019, 28, 1212-1224. | 2.9 | 12 |
| 43 | A biallelic ANTXR1 variant expands the anthrax toxin receptor associated phenotype to tooth agenesis. American Journal of Medical Genetics, Part A, 2018, 176, 1015-1022. | 1.2 | 11 |
| 44 | Chemistry-First Approach for Nomination of Personalized Treatment in Lung Cancer. Cell, 2018, 173, 864-878.e29. | 28.9 | 102 |
| 45 | An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11. | 28.9 | 2,277 |
| 46 | Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18. | 28.9 | 1,670 |
| 47 | Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6. | 28.9 | 1,718 |
| 48 | A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12. | 28.9 | 228 |
| 49 | Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10. | 28.9 | 272 |
| 50 | Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15. | 28.9 | 1,417 |
| 51 | Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10. | 28.9 | 2,111 |
| 52 | Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14. | 28.9 | 620 |
| 53 | Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4. | 6.4 | 333 |
| 54 | Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3. | 6.4 | 407 |

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|---|---|---|---|
| 55 | Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6. | 6.4 | 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. | 6.4 | 205 |
| 57 | The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5. | 6.4 | 523 |
| 58 | Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7. | 6.4 | 683 |
| 59 | The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14. | 14.3 | 3,706 |
| 60 | Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3. | 6.4 | 119 |
| 61 | Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3. | 6.4 | 83 |
| 62 | Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6. | 6.4 | 801 |
| 63 | Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4. | 6.4 | 204 |
| 64 | Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3. | 6.4 | 177 |
| 65 | The Toxicogenome of Hyalella azteca: A Model for Sediment Ecotoxicology and Evolutionary Toxicology. Environmental Science & Technology, 2018, 52, 6009-6022. | 10.0 | 79 |
| 66 | Hemimetabolous genomes reveal molecular basis of termite eusociality. Nature Ecology and Evolution, 2018, 2, 557-566. | 7.8 | 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. | 1.5 | 20 |
| 68 | Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7. | 6.2 | 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. | 6.2 | 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. | 16.8 | 400 |
| 71 | Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3. | 16.8 | 750 |
| 72 | Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8. | 16.8 | 396 |

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|---|---|---|---|
| 73 | A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9. | 16.8 | 478 |
| 74 | Whole-Exome Sequencing Identifies Novel Variants for Tooth Agenesis. Journal of Dental Research, 2018, 97, 49-59. | 5.2 | 44 |
| 75 | The genome of the water strider Gerris buenoi reveals expansions of gene repertoires associated with adaptations to life on the water. BMC Genomics, 2018, 19, 832. | 2.8 | 47 |
| 76 | Reproductive Longevity Predicts Mutation Rates in Primates. Current Biology, 2018, 28, 3193-3197.e5. | 3.9 | 94 |
| 77 | A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-Î² Superfamily. Cell Systems, 2018, 7, 422-437.e7. | 6.2 | 134 |
| 78 | Temporal development of the gut microbiome in early childhood from the TEDDY study. Nature, 2018, 562, 583-588. | 27.8 | 1,220 |
| 79 | Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. Cell Reports, 2018, 25, 1304-1317.e5. | 6.4 | 329 |
| 80 | Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6. | 16.8 | 623 |
| 81 | Comparative genomics of the miniature wasp and pest control agent Trichogramma pretiosum. BMC Biology, 2018, 16, 54. | 3.8 | 57 |
| 82 | Elucidating the molecular pathogenesis of glioma: integrated germline and somatic profiling of a familial glioma case series. Neuro-Oncology, 2018, 20, 1625-1633. | 1.2 | 12 |
| 83 | Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406. | 6.4 | 324 |
| 84 | Mismatch repair gene mutations lead to lynch syndrome colorectal cancer in rhesus macaques. Genes and Cancer, 2018, 9, 142-152. | 1.9 | 18 |
| 85 | Evolutionary History of Chemosensory-Related Gene Families across the Arthropoda. Molecular Biology and Evolution, 2017, 34, 1838-1862. | 8.9 | 157 |
| 86 | Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23. | 28.9 | 1,794 |
| 87 | Lessons learned from additional research analyses of unsolved clinical exome cases. Genome Medicine, 2017, 9, 26. | 8.2 | 184 |
| 88 | The house spider genome reveals an ancient whole-genome duplication during arachnid evolution. BMC Biology, 2017, 15, 62. | 3.8 | 286 |
| 89 | Novel patient-derived xenograft and cell line models for therapeutic testing of pediatric liver cancer. Journal of Hepatology, 2016, 65, 325-333. | 3.7 | 56 |
| 90 | Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736. | 16.8 | 482 |

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| 91 | The whole genome sequence of the Mediterranean fruit fly, Ceratitis capitata (Wiedemann), reveals insights into the biology and adaptive evolution of a highly invasive pest species. Genome Biology, 2016, 17, 192. | 8.8 | 130 |
| 92 | Exome sequencing in mostly consanguineous Arab families with neurologic disease provides a high potential molecular diagnosis rate. BMC Medical Genomics, 2016, 9, 42. | 1.5 | 80 |
| 93 | Postmortem genetic screening for the identification, verification, and reporting of genetic variants contributing to the sudden death of the young. Genome Research, 2016, 26, 1170-1177. | 5.5 | 29 |
| 94 | Genome of the Asian longhorned beetle (Anoplophora glabripennis), a globally significant invasive species, reveals key functional and evolutionary innovations at the beetleâ€“plant interface. Genome Biology, 2016, 17, 227. | 8.8 | 244 |
| 95 | An open access pilot freely sharing cancer genomic data from participants in Texas. Scientific Data, 2016, 3, 160010. | 5.3 | 19 |
| 96 | Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. Cell Reports, 2016, 14, 907-919. | 6.4 | 107 |
| 97 | Unique features of a global human ectoparasite identified through sequencing of the bed bug genome. Nature Communications, 2016, 7, 10165. | 12.8 | 184 |
| 98 | Integrated Genomic Analysis of Down Syndrome Acute Lymphoblastic Leukemia Reveals Recurrent Cancer Gene Alterations and Evidence of Frequent Subclonal Driver Events. Blood, 2016, 128, 4083-4083. | 1.4 | 0 |
| 99 | Whole-exome sequencing points to considerable genetic heterogeneity of cerebral palsy. Molecular Psychiatry, 2015, 20, 176-182. | 7.9 | 178 |
| 100 | Germline Mutations in Shelterin Complex Genes Are Associated With Familial Glioma. Journal of the National Cancer Institute, 2015, 107, 384. | 6.3 | 172 |
| 101 | Rise and fall of subclones from diagnosis to relapse in pediatric B-acute lymphoblastic leukaemia. Nature Communications, 2015, 6, 6604. | 12.8 | 281 |
| 102 | A global reference for human genetic variation. Nature, 2015, 526, 68-74. | 27.8 | 13,998 |
| 103 | Recurrent internal tandem duplications of BCOR in clear cell sarcoma of the kidney. Nature Communications, 2015, 6, 8891. | 12.8 | 126 |
| 104 | Genomic profiling of SÃ©zary syndrome identifies alterations of key T cell signaling and differentiation genes. Nature Genetics, 2015, 47, 1426-1434. | 21.4 | 276 |
| 105 | BCORâ€“CCNB3 fusions are frequent in undifferentiated sarcomas of male children. Modern Pathology, 2015, 28, 575-586. | 5.5 | 122 |
| 106 | Improved Real-Time PCR Diagnosis of Citrus Stubborn Disease by Targeting Prophage Genes of Spiroplasma citri. Plant Disease, 2015, 99, 149-154. | 1.4 | 16 |
| 107 | Evidence for Stabilizing Selection on Codon Usage in Chromosomal Rearrangements ofDrosophila pseudoobscura. G3: Genes, Genomes, Genetics, 2014, 4, 2433-2449. | 1.8 | 17 |
| 108 | Mutational Landscape of Aggressive Cutaneous Squamous Cell Carcinoma. Clinical Cancer Research, 2014, 20, 6582-6592. | 7.0 | 493 |

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| 109 | The relationship of JAK2V617F and acquired UPD at chromosome 9p in polycythemia vera. Leukemia, 2014, 28, 938-941. | 7.2 | 18 |
| 110 | Trans-ancestry mutational landscape of hepatocellular carcinoma genomes. Nature Genetics, 2014, 46, 1267-1273. | 21.4 | 655 |
| 111 | Whole-exome sequencing of polycythemia vera revealed novel driver genes and somatic mutation shared by T cells and granulocytes. Leukemia, 2014, 28, 935-938. | 7.2 | 22 |
| 112 | Exonuclease mutations in DNA polymerase epsilon reveal replication strand specific mutation patterns and human origins of replication. Genome Research, 2014, 24, 1740-1750. | 5.5 | 244 |
| 113 | The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330. | 16.8 | 665 |
| 114 | Novel somatic and germline mutations in intracranial germ cell tumours. Nature, 2014, 511, 241-245. | 27.8 | 181 |
| 115 | Mutually exclusive recurrent somatic mutations in MAP2K1 and BRAF support a central role for ERK activation in LCH pathogenesis. Blood, 2014, 124, 3007-3015. | 1.4 | 352 |
| 116 | Draft genome sequences and description of Lactobacillus rhamnosus strains L31, L34, and L35. Standards in Genomic Sciences, 2014, 9, 744-754. | 1.5 | 5 |
| 117 | A comparative genomic analysis of the oxidative enzymes potentially involved in lignin degradation by Agaricus bisporus. Fungal Genetics and Biology, 2013, 55, 22-31. | 2.1 | 22 |
| 118 | Identification of a response regulator involved in surface attachment, cellâ€“cell aggregation, exopolysaccharide production and virulence in the plant pathogen <scp>X</scp>ylella fastidiosa. Molecular Plant Pathology, 2013, 14, 256-264. | 4.2 | 17 |
| 119 | OikoBase: a genomics and developmental transcriptomics resource for the urochordate Oikopleura dioica. Nucleic Acids Research, 2013, 41, D845-D853. | 14.5 | 53 |
| 120 | Characterization of transcriptomes from sexual and asexual lineages of a New Zealand snail () Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 302 | 4.8 | 14 |
| 121 | Genome sequence of the button mushroom Agaricus bisporus reveals mechanisms governing adaptation to a humic-rich ecological niche. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17501-17506. | 7.1 | 359 |
| 122 | Cyanophora paradoxa Genome Elucidates Origin of Photosynthesis in Algae and Plants. Science, 2012, 335, 843-847. | 12.6 | 371 |
| 123 | Identification of a single-stranded DNA virus associated with citrus chlorotic dwarf disease, a new member in the family Geminiviridae. Virology, 2012, 432, 162-172. | 2.4 | 130 |
| 124 | Comparative genomics of Ceriporiopsis subvermispora and Phanerochaete chrysosporium provide insight into selective ligninolysis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5458-5463. | 7.1 | 259 |
| 125 | The Complete Genome Sequence of â€˜Candidatus Liberibacter solanacearumâ€™, the Bacterium Associated with Potato Zebra Chip Disease. PLoS ONE, 2011, 6, e19135. | 2.5 | 127 |
| 126 | P450 Redox Enzymes in the White Rot Fungus Phanerochaete chrysosporium: Gene Transcription, Heterologous Expression, and Activity Analysis on the Purified Proteins. Current Microbiology, 2010, 61, 306-314. | 2.2 | 7 |

| # | Article | IF | Citations |
|---|---|---|---|
| 127 | A new diagnostic system for ultra-sensitive and specific detection and quantification of Candidatus Liberibacter asiaticus, the bacterium associated with citrus Huanglongbing. Journal of Microbiological Methods, 2010, 81, 17-25. | 1.6 | 49 |
| 128 | Genome-to-function characterization of novel fungal P450 monooxygenases oxidizing polycyclic aromatic hydrocarbons (PAHs). Biochemical and Biophysical Research Communications, 2010, 399, 492-497. | 2.1 | 107 |
| 129 | The 8q24 cancer risk variant rs6983267 shows long-range interaction with MYC in colorectal cancer. Nature Genetics, 2009, 41, 882-884. | 21.4 | 616 |
| 130 | Genome, transcriptome, and secretome analysis of wood decay fungus Postia placenta supports unique mechanisms of lignocellulose conversion. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1954-1959. | 7.1 | 530 |
| 131 | Complete Genome Sequence of Citrus Huanglongbing Bacterium, â€˜CandidatusLiberibacter asiaticusâ€™ Obtained Through Metagenomics. Molecular Plant-Microbe Interactions, 2009, 22, 1011-1020. | 2.6 | 485 |
| 132 | PrimerSNP: a web tool for whole-genome selection of allele-specific and common primers of phylogenetically-related bacterial genomic sequences. BMC Microbiology, 2008, 8, 185. | 3.3 | 1 |
| 133 | VitisExpDB: A database resource for grape functional genomics. BMC Plant Biology, 2008, 8, 23. | 3.6 | 16 |
| 134 | Comparative phylogenomics and multi-gene cluster analyses of the Citrus Huanglongbing (HLB)-associated bacterium Candidatus Liberibacter. BMC Research Notes, 2008, 1, 72. | 1.4 | 13 |
| 135 | Acquisition of uncharacterized sequences from Candidatus Liberibacter, an unculturable bacterium, using an improved genomic walking method. Molecular and Cellular Probes, 2008, 22, 30-37. | 2.1 | 24 |
| 136 | Comparative analysis of ESTs involved in grape responses to Xylella fastidiosa infection. BMC Plant Biology, 2007, 7, 8. | 3.6 | 36 |
| 137 | Expression of a Î²-glucosidase gene results in increased accumulation of salicylic acid in transgenic Nicotiana tabacum cv. Xanthi-nc NN genotype. Plant Cell Reports, 2007, 26, 291-301. | 5.6 | 10 |
| 138 | Genome-based PCR Primers for Specific and Sensitive Detection and Quantification of Xylella fastidiosa. European Journal of Plant Pathology, 2006, 115, 203-213. | 1.7 | 133 |
| 139 | Analysis of the genome-wide variations among multiple strains of the plant pathogenic bacterium Xylella fastidiosa. BMC Genomics, 2006, 7, 225. | 2.8 | 28 |
| 140 | Genome-wide structural and evolutionary analysis of the P450 monooxygenase genes (P450ome) in the white rot fungus Phanerochaete chrysosporium : Evidence for gene duplications and extensive gene clustering. BMC Genomics, 2005, 6, 92. | 2.8 | 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 FungusPhanerochaete chrysosporium. Current Microbiology, 2005, 50, 292-298. | 2.2 | 34 |
| 142 | Differential regulation and xenobiotic induction of tandem P450 monooxygenase genes pc-1 (CYP63A1) and pc-2 (CYP63A2) in the white-rot fungus Phanerochaete chrysosporium. Applied Microbiology and Biotechnology, 2004, 65, 559-65. | 3.6 | 56 |
| 143 | Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. SSRN Electronic Journal, 0, , . | 0.4 | 0 |