# Resource Summary Report

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# J. Craig Venter Institute

RRID:SCR_011269
Type: Tool

## Proper Citation

J. Craig Venter Institute (RRID:SCR_011269)

## Resource Information

**URL:** http://www.jcvi.org/

**Proper Citation:** J. Craig Venter Institute (RRID:SCR_011269)

**Description:** A large multidisciplinary world leader in genomic research with locations in Rockville, Maryland and San Diego, California. It was formed through the merger of several affiliated and legacy organizations - The Institute for Genomic Research (TIGR) and The Center for the Advancement of Genomics (TCAG), The J. Craig Venter Science Foundation, The Joint Technology Center, and the Institute for Biological Energy Alternatives (IBEA).

**Abbreviations:** JCVI

**Resource Type:** institution

**Funding:**

**Resource Name:** J. Craig Venter Institute

**Resource ID:** SCR_011269

**Alternate IDs:** grid.469946.0, nlx_42542, Wikidata: Q1439786

**Alternate URLs:** https://ror.org/049r1ts75

**Record Creation Time:** 20220129T080303+0000

**Record Last Update:** 20250410T070101+0000

## Ratings and Alerts

No rating or validation information has been found for J. Craig Venter Institute.

No alerts have been found for J. Craig Venter Institute.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 41 mentions in open access literature.

**Listed below are recent publications.** The full list is available at FDI Lab - SciCrunch.org.

Liu X, et al. (2024) Correlation between the gut microbiome and neurodegenerative diseases: a review of metagenomics evidence. Neural regeneration research, 19(4), 833.

Yang H, et al. (2024) Unraveling the metabolic potential of biocontrol fungi through omics data: a key to enhancing large-scaleapplication strategies. Acta biochimica et biophysica Sinica, 56(6), 825.

Khan YN, et al. (2024) Whole exome sequencing enables the correct diagnosis of Frank-Ter Haar syndrome in a Saudi family. Vavilovskii zhurnal genetiki i selektsii, 28(3), 326.

Li X, et al. (2024) Genome-wide identification of starch phosphorylase gene family in Rosa chinensis and expression in response to abiotic stress. Scientific reports, 14(1), 13917.

Yang H, et al. (2024) High-quality assembly of the T2T genome for Isodon rubescens f. lushanensis reveals genomic structure variations between 2 typical forms of Isodon rubescens. GigaScience, 13.

Yao L, et al. (2023) PLP1 gene mutations cause spastic paraplegia type 2 in three families. Annals of clinical and translational neurology, 10(3), 328.

Pieri V, et al. (2023) Aberrant L-Fucose Accumulation and Increased Core Fucosylation Are Metabolic Liabilities in Mesenchymal Glioblastoma. Cancer research, 83(2), 195.

Rakshit D, et al. (2020) Functional Insights Into the Role of gppA in (p)ppGpp Metabolism of Vibrio cholerae. Frontiers in microbiology, 11, 564644.

Wang L, et al. (2020) High Synteny and Sequence Identity between Genomes of Nitrosococcus oceani Strains Isolated from Different Oceanic Gyres Reveals Genome Economization and Autochthonous Clonal Evolution. Microorganisms, 8(5).

Chen J, et al. (2020) Cardio-facio-cutaneous syndrome-associated pathogenic MAP2K1 variants activate autophagy. Gene, 733, 144369.

Han G, et al. (2019) Differential regulation of mycelial growth and aflatoxin biosynthesis by Aspergillus flavus under different temperatures as revealed by strand-specific RNA-Seq. MicrobiologyOpen, 8(10), e897.

Bai JF, et al. (2019) Genomic identification and characterization of MYC family genes in wheat (Triticum aestivum L.). BMC genomics, 20(1), 1032.

Sacharow SJ, et al. (2018) Characterization of a novel variant in siblings with Asparagine Synthetase Deficiency. Molecular genetics and metabolism, 123(3), 317.

Astrea G, et al. (2018) Broad phenotypic spectrum and genotype-phenotype correlations in GMPPB-related dystroglycanopathies: an Italian cross-sectional study. Orphanet journal of rare diseases, 13(1), 170.

Singh D, et al. (2017) Insights of Lr28 mediated wheat leaf rust resistance: Transcriptomic approach. Gene, 637, 72.

Castella C, et al. (2017) Post-translational modifications of Medicago truncatula glutathione peroxidase 1 induced by nitric oxide. Nitric oxide : biology and chemistry, 68, 125.

Youssefian L, et al. (2017) A novel mutation in ST14 at a functionally significant amino acid residue expands the spectrum of ichthyosis-hypotrichosis syndrome. Orphanet journal of rare diseases, 12(1), 176.

Yost S, et al. (2017) Potassium is a key signal in host-microbiome dysbiosis in periodontitis. PLoS pathogens, 13(6), e1006457.

Maansson M, et al. (2016) An Integrated Metabolomic and Genomic Mining Workflow To Uncover the Biosynthetic Potential of Bacteria. mSystems, 1(3).

Simm S, et al. (2016) Survey of Genes Involved in Biosynthesis, Transport, and Signaling of Phytohormones with Focus on Solanum lycopersicum. Bioinformatics and biology insights, 10, 185.