# Resource Summary Report

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## Baylor College of Medicine Human Genome Sequencing Center

RRID:SCR_013605
Type: Tool

### Proper Citation

Baylor College of Medicine Human Genome Sequencing Center (RRID:SCR_013605)

### Resource Information

**URL:** http://www.hgsc.bcm.tmc.edu/

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**Description:** Center for high-throughput DNA sequence generation and the accompanying analysis. The sequence data generated by the center's machines are analyzed in a complex bioinformatics pipeline, and the data are deposited regularly in the public databases at the National Center for Biotechnology Information (NCBI).

**Abbreviations:** BCM-HGSC

**Synonyms:** Human Genome Sequencing Center, BCM HGSC

**Resource Type:** production service resource, analysis service resource, service resource

**Keywords:** next-generation sequencing, genetic variation, genome, dna sequence, FASEB list

**Funding:** NIH Office of the Director R24 OD011173

**Resource Name:** Baylor College of Medicine Human Genome Sequencing Center

**Resource ID:** SCR_013605

**Alternate IDs:** nif-0000-10162

**Record Creation Time:** 20220129T080317+0000

**Record Last Update:** 20250423T060729+0000

## Ratings and Alerts

No rating or validation information has been found for Baylor College of Medicine Human Genome Sequencing Center.

No alerts have been found for Baylor College of Medicine Human Genome Sequencing Center.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 65 mentions in open access literature.

**Listed below are recent publications.** The full list is available at dkNET.

?opie?ska-Biernat E, et al. (2018) Developmental changes in gene expression and enzyme activities of anabolic and catabolic enzymes for storage carbohydrates in the honeybee, Apis mellifera. Insectes sociaux, 65(4), 571.

Karaca E, et al. (2015) Genes that Affect Brain Structure and Function Identified by Rare Variant Analyses of Mendelian Neurologic Disease. Neuron, 88(3), 499.

Qu Z, et al. (2015) How Did Arthropod Sesquiterpenoids and Ecdysteroids Arise? Comparison of Hormonal Pathway Genes in Noninsect Arthropod Genomes. Genome biology and evolution, 7(7), 1951.

Yuan D, et al. (2014) Ancestral genetic complexity of arachidonic acid metabolism in Metazoa. Biochimica et biophysica acta, 1841(9), 1272.

Dubreuil G, et al. (2014) Diversification of MIF immune regulators in aphids: link with agonistic and antagonistic interactions. BMC genomics, 15(1), 762.

Riddell CE, et al. (2014) Differential gene expression and alternative splicing in insect immune specificity. BMC genomics, 15(1), 1031.

Manson McGuire A, et al. (2014) Evolution of invasion in a diverse set of Fusobacterium species. mBio, 5(6), e01864.

Du Q, et al. (2014) The cyclic AMP phosphodiesterase RegA critically regulates encystation in social and pathogenic amoebas. Cellular signalling, 26(2), 453.

Krishnan A, et al. (2013) Remarkable similarities between the hemichordate (Saccoglossus kowalevskii) and vertebrate GPCR repertoire. Gene, 526(2), 122.

Leger MM, et al. (2013) Evidence for a hydrogenosomal-type anaerobic ATP generation pathway in Acanthamoeba castellanii. PloS one, 8(9), e69532.

Behura SK, et al. (2013) Association of microsatellite pairs with segmental duplications in insect genomes. BMC genomics, 14, 907.

Tirumalai MR, et al. (2013) Candidate genes that may be responsible for the unusual resistances exhibited by Bacillus pumilus SAFR-032 spores. PloS one, 8(6), e66012.

Dellas N, et al. (2013) Discovery of a metabolic alternative to the classical mevalonate pathway. eLife, 2, e00672.

McCarthy CB, et al. (2013) First comparative transcriptomic analysis of wild adult male and female Lutzomyia longipalpis, vector of visceral leishmaniasis. PloS one, 8(3), e58645.

Rao SA, et al. (2013) Proteomic profiling of cereal aphid saliva reveals both ubiquitous and adaptive secreted proteins. PloS one, 8(2), e57413.

Odon V, et al. (2013) APE-type non-LTR retrotransposons of multicellular organisms encode virus-like 2A oligopeptide sequences, which mediate translational recoding during protein synthesis. Molecular biology and evolution, 30(8), 1955.

De Maio N, et al. (2013) Estimating empirical codon hidden Markov models. Molecular biology and evolution, 30(3), 725.

Klinger EG, et al. (2013) A multi-gene phylogeny provides additional insight into the relationships between several Ascosphaera species. Journal of invertebrate pathology, 112(1), 41.

Diaz MA, et al. (2013) Identification of Lactobacillus strains with probiotic features from the bottlenose dolphin (Tursiops truncatus). Journal of applied microbiology, 115(4), 1037.

Kumar A, et al. (2012) Molecular phylogeny of OVOL genes illustrates a conserved C2H2 zinc finger domain coupled by hypervariable unstructured regions. PloS one, 7(6), e39399.