

Resource Summary Report

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CGSC

RRID:SCR_002303

Type: Tool

Proper Citation

CGSC (RRID:SCR_002303)

Resource Information

URL: <http://cgsc.biology.yale.edu/index.php>

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Description: The CGSC Collection contains only non-pathogenic BSL-1 laboratory strains, primarily genetic derivatives of Escherichia coli K-12, the laboratory strain widely used in genetic and molecular studies, but a few B strains. The CGSC Database of E. coli genetic information includes genotypes and reference information for the strains in the CGSC collection, the names, synonyms, properties, and map position for genes, gene product information, and information on specific mutations and references to primary literature. The public version of the database includes this information and can be queried directly via this CGSC DB WebServer. The collection includes cultures of wild-type contributed from a number of laboratories and a few thousand derivatives carrying one or up to 29 mutations from among 3500 mutations in (or included in deletions spanning) more than 1300 different loci. Some combinations were constructed particularly for mapping purposes and are still used for teaching and for rapid localization, some for manifestation of a particular phenotype, some strains for transferring a particular region or for complementation analysis. Some plasmids, e.g., the Clarke and Carbon collection, F-primes, a number of toolkit plasmids, and a few classic plasmids are included, but it is not a comprehensive collection of plasmids. Additionally, we have recently acquired most of the strains from the Keio Collection of systematic individual gene knockout (deletion/kan insertion) strains.

Abbreviations: CGSC

Synonyms: The Coli Genetic Stock Center, E. coli Genetic Stock Center, CGSC - The Coli Genetic Stock Center, Coli Genetic Stock Center

Resource Type: biomaterial supply resource, material resource

Keywords: e. coli. escherichia coli, chromosome, culture, genotype, interval, k-12, linkage map, locus, mutation, non-pathogenic, phenotype, plasmid, prokaryote, strain, wild-type, auxotrophic, amino acids, wanner lambda red, gene disruption, keio knockout

Funding: NSF DBI-0742708;
User fees

Resource Name: CGSC

Resource ID: SCR_002303

Alternate IDs: nif-0000-21083

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260725T191224+0000

Ratings and Alerts

No rating or validation information has been found for CGSC.

No alerts have been found for CGSC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 26 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Stindt KR, et al. (2024) Tuning interdomain conjugation to enable in situ population modification in yeasts. *mSystems*, 9(6), e0005024.

Saunders SH, et al. (2024) ORBIT for E. coli: kilobase-scale oligonucleotide recombineering at high throughput and high efficiency. *Nucleic acids research*, 52(8), e43.

Suzuki H, et al. (2024) A Dementia-Friendly Educational Program Using Virtual Reality for the General Public in Japan: A Randomized Controlled Trial for DRIVE. *The Gerontologist*, 64(11).

Otoupal PB, et al. (2021) Potentiating antibiotic efficacy via perturbation of non-essential gene expression. *Communications biology*, 4(1), 1267.

Niblett D, et al. (2021) Mutations in domain IV of elongation factor EF-G confer -1 frameshifting. *RNA (New York, N.Y.)*, 27(1), 40.

Maeda G, et al. (2021) Oxygenated Cyclohexene Derivatives from the Stem and Root Barks of *Uvaria pandensis*. *Journal of natural products*, 84(12), 3080.

Verma K, et al. (2020) Distinct metabolic states of a cell guide alternate fates of mutational buffering through altered proteostasis. *Nature communications*, 11(1), 2926.

Sadat A, et al. (2020) GROEL/ES Buffers Entropic Traps in Folding Pathway during Evolution of a Model Substrate. *Journal of molecular biology*, 432(20), 5649.

Boundy-Mills K, et al. (2020) Preserving US microbe collections sparks future discoveries. *Journal of applied microbiology*, 129(2), 162.

Malkowski SN, et al. (2020) A rare bacterial RNA motif is implicated in the regulation of the purF gene whose encoded enzyme synthesizes phosphoribosylamine. *RNA (New York, N.Y.)*, 26(12), 1838.

Kim JM, et al. (2020) Stochastic transcriptional pulses orchestrate flagellar biosynthesis in *Escherichia coli*. *Science advances*, 6(6), eaax0947.

Batta V, et al. (2020) Early neurodevelopmental outcomes of congenital gastrointestinal surgical conditions: a single-centre retrospective study. *BMJ paediatrics open*, 4(1), e000736.

Zhang H, et al. (2019) The Chinese Glaucoma Study Consortium for Patients With Glaucoma: Design, Rationale and Baseline Patient Characteristics. *Journal of glaucoma*, 28(11), 974.

Lee J, et al. (2019) Cytosolic Copper Binding by a Bacterial Storage Protein and Interplay with Copper Efflux. *International journal of molecular sciences*, 20(17).

Morin M, et al. (2018) Changes in the genetic requirements for microbial interactions with increasing community complexity. *eLife*, 7.

Sánchez-Osuna M, et al. (2018) Origin of the Mobile Di-Hydro-Pterate Synthase Gene Determining Sulfonamide Resistance in Clinical Isolates. *Frontiers in microbiology*, 9, 3332.

Schretter CE, et al. (2018) A gut microbial factor modulates locomotor behaviour in *Drosophila*. *Nature*, 563(7731), 402.

Ramkissoon CM, et al. (2018) Unannounced Meals in the Artificial Pancreas: Detection Using Continuous Glucose Monitoring. *Sensors (Basel, Switzerland)*, 18(3).

Swings T, et al. (2017) Adaptive tuning of mutation rates allows fast response to lethal stress in *Escherichia coli*. *eLife*, 6.

Kwong WK, et al. (2017) Convergent evolution of a modified, acetate-driven TCA cycle in bacteria. *Nature microbiology*, 2, 17067.