Resource Summary Report

Generated by nidm-terms on Aug 14, 2026

C321.?A

RRID:Addgene_48998
Type: Plasmid

Proper Citation

RRID:Addgene_48998

Plasmid Information

URL: http://www.addgene.org/48998

Proper Citation: RRID:Addgene_48998

Insert Name: Recoded E. coli genome with all instances of the UAG codon and RF1 removed (UAG termination function removed)

Organism: E. coli

Bacterial Resistance: Ampicillin

Defining Citation: PMID:24136966

Vector Backbone Description: Vector Backbone:E. coli genome; Vector Types:Bacterial Expression; Bacterial Resistance:Ampicillin

Comments: E. coli MG1655 Delta(ybhB-bioAB)::[lcI857 N(cro-ea59)::tetR-bla] Delta prfA Delta mutS::zeoR; all 321 UAG codons changed to UAA This strain is mutS-, which causes a spontaneous mutation frequency of ~2E-8. This strain is auxotrophic for d-biotin. A mutS+ version of this strain will be deposited with addgene soon. Genome sequence deposited at NCBI (accession # CP006698)

Plasmid Name: C321.?A

Relevant Mutation: See genbank file

Record Creation Time: 20220422T222252+0000

Record Last Update: 20260808T081744+0000

Ratings and Alerts

No rating or validation information has been found for C321.?A.

No alerts have been found for C321.?A.

Data and Source Information

Source: Addgene

Usage and Citation Metrics

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Hemez C, et al. (2024) Genomically recoded Escherichia coli with optimized functional phenotypes. bioRxiv : the preprint server for biology.

Arranz-Gibert P, et al. (2022) Chemoselective restoration of para-azido-phenylalanine at multiple sites in proteins. Cell chemical biology, 29(6), 1046.

Vanderschuren K, et al. (2022) Tuning protein half-life in mouse using sequence-defined biopolymers functionalized with lipids. Proceedings of the National Academy of Sciences of the United States of America, 119(4).

Yi H, et al. (2021) Comparative Analyses of the Transcriptome and Proteome of Escherichia coli C321.?A and Further Improving Its Noncanonical Amino Acids Containing Protein Expression Ability by Integration of T7 RNA Polymerase. Frontiers in microbiology, 12, 744284.

Cheng Q, et al. (2021) Production and purification of homogenous recombinant human selenoproteins reveals a unique codon skipping event in E. coli and GPX4-specific affinity to bromosulfophthalein. Redox biology, 46, 102070.

Prum S, et al. (2020) Characterization and in vitro functional analysis of thioredoxin glutathione reductase from the liver fluke Opisthorchis viverrini. Acta tropica, 210, 105621.

Swiecicki JM, et al. (2020) A Strategic Approach for Fluorescence Imaging of Membrane Proteins in a Native-like Environment. Cell chemical biology, 27(2), 245.

Chemla Y, et al. (2019) Simplified methodology for a modular and genetically expanded protein synthesis in cell-free systems. Synthetic and systems biotechnology, 4(4), 189.

Li X, et al. (2018) Site-Specific Incorporation of Sulfotyrosine Using an Expanded Genetic Code. Methods in molecular biology (Clifton, N.J.), 1728, 191.

Ozer E, et al. (2017) In vitro suppression of two different stop codons. Biotechnology and bioengineering, 114(5), 1065.

Ostrov N, et al. (2016) Design, synthesis, and testing toward a 57-codon genome. Science (New York, N.Y.), 353(6301), 819.

Hammerling MJ, et al. (2016) Expanded Genetic Codes Create New Mutational Routes to Rifampicin Resistance in Escherichia coli. Molecular biology and evolution, 33(8), 2054.

Wang N, et al. (2016) Systematic Evolution and Study of UAGN Decoding tRNAs in a Genomically Recoded Bacteria. Scientific reports, 6, 21898.