

# Resource Summary Report

Generated by [NIF](#) on Aug 12, 2026

## Coddle-Codons Optimized to Discover Deleterious LEsions

RRID:SCR\_003003

Type: Tool

### Proper Citation

Coddle-Codons Optimized to Discover Deleterious LEsions (RRID:SCR\_003003)

### Resource Information

**URL:** <http://www.proweb.org/coddle/>

**Proper Citation:** Coddle-Codons Optimized to Discover Deleterious LEsions (RRID:SCR\_003003)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE, documented August 22, 2016. Web-accessible program that identifies the region(s) of a user-selected gene and of its coding sequence (CDS) where the anticipated point mutations are most likely to result in deleterious effects on the gene's function. CODDLe separately handles 1) the prediction of changes which should truncate the protein and destabilize the RNA - nonsense changes and splice junction changes, and 2) the prediction of missense changes which should alter function of the gene product - those in conserved amino acid blocks in the CDS. Because the region(s) identified will be PCR amplified by the user and that amplicon will be used for polymorphism discovery, the application delivers primer pairs selected by Primer3 (Steve Rozen, Helen J. Skaletsky (1996,1997,1998)Primer3.) After selecting a primer pair, CODDLe returns a window with the selected amplicon and tabulates the effects of all possible polymorphisms which could be detected in that amplicon. CODDLe will not identify the regions of a gene where polymorphisms are most likely to be discovered. Others have shown that naturally occurring SNPs are found more often in the untranslated regions of a gene.

**Abbreviations:** CODDLE

**Synonyms:** Choosing codons to Optimize Discovery of Deleterious Lesions, Codons Optimized to Discover Deleterious LEsions

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

**Keywords:** codon, deleterious lesion, gene, coding, sequence, mutation, primer, protein sequence, cdna, sequence alignment, coding sequence

**Funding:** DOE ;  
Office of Energy Research

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** Coddle-Codons Optimized to Discover Deleterious LEsions

**Resource ID:** SCR\_003003

**Alternate IDs:** nif-0000-30262

**Record Creation Time:** 20220129T080216+0000

**Record Last Update:** 20260812T044039+0000

---

## Ratings and Alerts

No rating or validation information has been found for Coddle-Codons Optimized to Discover Deleterious LEsions.

No alerts have been found for Coddle-Codons Optimized to Discover Deleterious LEsions.

---

## Data and Source Information

**Source:** [SciCrunch Registry](#)

---

## Usage and Citation Metrics

We found 16 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [NIF](#) .

Collin A, et al. (2020) Barley ABI5 (Absciscic Acid INSENSITIVE 5) Is Involved in Absciscic Acid-Dependent Drought Response. *Frontiers in plant science*, 11, 1138.

Richaud D, et al. (2018) Identification of Lycopene epsilon cyclase (LCYE) gene mutants to potentially increase ??-carotene content in durum wheat (*Triticum turgidum* L.ssp. durum) through TILLING. *PloS one*, 13(12), e0208948.

Aslam U, et al. (2016) COTIP: Cotton TILLING Platform, a Resource for Plant Improvement and Reverse Genetic Studies. *Frontiers in plant science*, 7, 1863.

Stolarek M, et al. (2015) Alleles of newly identified barley gene HvPARP3 exhibit changes in efficiency of DNA repair. *DNA repair*, 28, 116.

Guo Y, et al. (2015) TILLING by sequencing to identify induced mutations in stress resistance genes of peanut (*Arachis hypogaea*). *BMC genomics*, 16(1), 157.

Dalmais M, et al. (2013) A TILLING Platform for Functional Genomics in *Brachypodium distachyon*. *PloS one*, 8(6), e65503.

Frerichmann SL, et al. (2013) EcoTILLING in *Beta vulgaris* reveals polymorphisms in the FLC-like gene BvFL1 that are associated with annuality and winter hardiness. *BMC plant biology*, 13, 52.

Chantreau M, et al. (2013) PT-Flax (phenotyping and TILLinG of flax): development of a flax (*Linum usitatissimum* L.) mutant population and TILLinG platform for forward and reverse genetics. *BMC plant biology*, 13, 159.

Chen L, et al. (2012) Development and characterization of a new TILLING population of common bread wheat (*Triticum aestivum* L.). *PloS one*, 7(7), e41570.

Botticella E, et al. (2011) High resolution melting analysis for the detection of EMS induced mutations in wheat SBEIIa genes. *BMC plant biology*, 11, 156.

Sikora P, et al. (2011) Mutagenesis as a tool in plant genetics, functional genomics, and breeding. *International journal of plant genomics*, 2011, 314829.

Stephenson P, et al. (2010) A rich TILLING resource for studying gene function in *Brassica rapa*. *BMC plant biology*, 10, 62.

Dahmani-Mardas F, et al. (2010) Engineering melon plants with improved fruit shelf life using the TILLING approach. *PloS one*, 5(12), e15776.

Dong C, et al. (2009) Simultaneous mutation detection of three homoeologous genes in wheat by High Resolution Melting analysis and Mutation Surveyor. *BMC plant biology*, 9, 143.

Dalmaï M, et al. (2008) UTILLdb, a *Pisum sativum* in silico forward and reverse genetics tool. *Genome biology*, 9(2), R43.

Hays JB, et al. (2002) *Arabidopsis thaliana*, a versatile model system for study of eukaryotic genome-maintenance functions. *DNA repair*, 1(8), 579.