

Resource Summary Report

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RECODE- The database of the translational recoding events

RRID:SCR_007887

Type: Tool

Proper Citation

RECODE- The database of the translational recoding events (RRID:SCR_007887)

Resource Information

URL: <http://recode.genetics.utah.edu>

Proper Citation: RECODE- The database of the translational recoding events (RRID:SCR_007887)

Description: A compilation of programmed; translational recoding events taken from the scientific literature and personal communications. The database deals with programmed ribosomal frameshifting, codon redefinition and translational bypass occurring in a variety of organisms. The entries for each event include the sequences of the corresponding genes, their encoded proteins for both the normal and alternate decoding, the types of the recoding events involved, trans-factors and cis-elements that influence recoding.

Synonyms: RECODE

Resource Type: data or information resource, database

Resource Name: RECODE- The database of the translational recoding events

Resource ID: SCR_007887

Alternate IDs: r3d100011305

Alternate URLs: <https://doi.org/10.17616/R3ND0T>

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260729T044158+0000

Ratings and Alerts

No rating or validation information has been found for RECODE- The database of the translational recoding events.

No alerts have been found for RECODE- The database of the translational recoding events.

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 [dkNET](#) .

Okoye C, et al. (2025) Multicomponent interventions and technologies to reduce the burden of frailty, functional, and cognitive decline: insights from the Age-It Research Program. The journals of gerontology. Series B, Psychological sciences and social sciences, 80(Supplement_2), S180.

Imoto Y, et al. (2025) Comprehensive noise reduction in single-cell data with the RECODE platform. Cell reports methods, 5(10), 101178.

Treanor CA, et al. (2025) Protocol for the development of enhanced recovery after surgery (ERAS) recommendations for individuals undergoing surgery for degenerative cervical myelopathy. Spinal cord, 63(12), 674.

Nakamura F, et al. (2024) Fine construction of gene coexpression network analysis using GTOM and RECODE detected a critical module of neuroblastoma stages 4 and 4S. Hereditas, 161(1), 44.

Smirnova AM, et al. (2024) Stem-loop-induced ribosome queuing in the uORF2/ATF4 overlap fine-tunes stress-induced human ATF4 translational control. Cell reports, 43(4), 113976.

McNair K, et al. (2024) PRFect: a tool to predict programmed ribosomal frameshifts in prokaryotic and viral genomes. BMC bioinformatics, 25(1), 82.

Murase Y, et al. (2024) In vitro reconstitution of epigenetic reprogramming in the human germ line. Nature, 631(8019), 170.

Imoto Y, et al. (2022) Resolution of the curse of dimensionality in single-cell RNA sequencing data analysis. Life science alliance, 5(12).

Murtagh S, et al. (2021) Integrating Primary and Secondary Care to Enhance Chronic Disease Management: A Scoping Review. International journal of integrated care, 21(1), 4.

Schlick T, et al. (2021) To knot or not to knot: Multiple conformations of the SARS-CoV-2 frameshifting RNA element. *bioRxiv : the preprint server for biology*.

Meijer E, et al. (2020) Exploring characteristics of COPD patients with clinical improvement after integrated disease management or usual care: post-hoc analysis of the RECODE study. *BMC pulmonary medicine*, 20(1), 176.

Boland MR, et al. (2015) Exploring the variation in implementation of a COPD disease management programme and its impact on health outcomes: a post hoc analysis of the RECODE cluster randomised trial. *NPJ primary care respiratory medicine*, 25, 15071.

Kruis AL, et al. (2014) Primary care COPD patients compared with large pharmaceutically-sponsored COPD studies: an UNLOCK validation study. *PloS one*, 9(3), e90145.

Ego A, et al. (2013) Stillbirth classification in population-based data and role of fetal growth restriction: the example of RECODE. *BMC pregnancy and childbirth*, 13, 182.

Ketteler R, et al. (2012) On programmed ribosomal frameshifting: the alternative proteomes. *Frontiers in genetics*, 3, 242.

Palti Y, et al. (2011) A first generation integrated map of the rainbow trout genome. *BMC genomics*, 12, 180.

Palti Y, et al. (2009) A first generation BAC-based physical map of the rainbow trout genome. *BMC genomics*, 10, 462.

Sánchez CC, et al. (2009) Single nucleotide polymorphism discovery in rainbow trout by deep sequencing of a reduced representation library. *BMC genomics*, 10, 559.

Rexroad CE, et al. (2009) Estimates of linkage disequilibrium and effective population size in rainbow trout. *BMC genetics*, 10, 83.

Theis C, et al. (2008) KnotInFrame: prediction of -1 ribosomal frameshift events. *Nucleic acids research*, 36(18), 6013.