Resource Summary Report

Generated by dkNET on Apr 16, 2025

Codon and Codon-Pair Usage Tables

RRID:SCR_018504
Type: Tool

Proper Citation

Codon and Codon-Pair Usage Tables (RRID:SCR_018504)

Resource Information

URL:
https://hive.biochemistry.gwu.edu/dna.cgi?cmd=tissue_codon_usage&id=586358&mode=cocoputs

Proper Citation: Codon and Codon-Pair Usage Tables (RRID:SCR_018504)

Description: Database includes genomic codon-pair and dinucleotide statistics of all organisms with sequenced genome. Facilitates genetic variation analyses and recombinant gene design. Derived from all available GenBank and RefSeq data.

Abbreviations: CoCoPUTs

Resource Type: database, data or information resource

Defining Citation: PMID:31029701

Keywords: Codon-pair, codon, nucleotide, gene, genomic codon pair, dinucleotide statistic, sequence, genetic variation, recombinant gene design, data

Funding:

Availability: Free, Freely available

Resource Name: Codon and Codon-Pair Usage Tables

Resource ID: SCR_018504

Record Creation Time: 20220129T080340+0000

Record Last Update: 20250412T060233+0000

Ratings and Alerts

No rating or validation information has been found for Codon and Codon-Pair Usage Tables.

No alerts have been found for Codon and Codon-Pair Usage Tables.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Holcomb DD, et al. (2022) Protocol to identify host-viral protein interactions between coagulation-related proteins and their genetic variants with SARS-CoV-2 proteins. STAR protocols, 3(3), 101648.

Fay EJ, et al. (2022) Natural rodent model of viral transmission reveals biological features of virus population dynamics. The Journal of experimental medicine, 219(2).

Ata G, et al. (2021) Edging on Mutational Bias, Induced Natural Selection From Host and Natural Reservoirs Predominates Codon Usage Evolution in Hantaan Virus. Frontiers in microbiology, 12, 699788.

Kames J, et al. (2020) Sequence analysis of SARS-CoV-2 genome reveals features important for vaccine design. Scientific reports, 10(1), 15643.