

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

%MinMax

RRID:SCR_022268

Type: Tool

Proper Citation

%MinMax (RRID:SCR_022268)

Resource Information

URL: <http://www.codons.org/calc.html>

Proper Citation: %MinMax (RRID:SCR_022268)

Description: Software tool for calculating and comparing synonymous codon usage and its impact on protein folding. Used to harmonize codon usage frequencies for heterologous gene expression. Codon usage calculator that evaluates relative usage frequencies of synonymous codons used to encode protein sequence of interest and compares these results to rigorous null mode. Evaluates synonymous codon usage patterns for any coding sequence from any fully sequenced genome.

Resource Type: data access protocol, software resource, web service

Defining Citation: [PMID:29090506](#)

Keywords: Calculating and comparing synonymous codon usage, impact on protein folding, harmonize codon usage frequencies, heterologous gene expression, codon usage calculator, encode protein sequence

Availability: Free, Freely available

Resource Name: %MinMax

Resource ID: SCR_022268

Record Creation Time: 20220511T050132+0000

Record Last Update: 20260905T133013+0000

Ratings and Alerts

No rating or validation information has been found for %MinMax.

No alerts have been found for %MinMax.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Frei Y, et al. (2024) Upstream open reading frames repress the translation from the iab-8 RNA. PLoS genetics, 20(9), e1011214.

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.