

# Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 28, 2026

## %MinMax

RRID:SCR\_022268

Type: Tool

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### Proper Citation

%MinMax (RRID:SCR\_022268)

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### 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:** web service, data access protocol, software resource

**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:** 20260728T043640+0000

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### Ratings and Alerts

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

No alerts have been found for %MinMax.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

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.