

Resource Summary Report

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Coarse grained co-translational folding analysis

RRID:SCR_022271

Type: Tool

Proper Citation

Coarse grained co-translational folding analysis (RRID:SCR_022271)

Resource Information

URL: <https://faculty.chemistry.harvard.edu/shakhnovich/software/coarse-grained-co-translational-folding-analysis>

Proper Citation: Coarse grained co-translational folding analysis (RRID:SCR_022271)

Description: Software for statistical approach to identify loci within genes that are both significantly enriched in slowly translated codons and evolutionarily conserved, and also co-translational protein folding model.

Synonyms: Coarse-grained co-translational folding analysis

Resource Type: software application, software resource

Defining Citation: [PMID:29073068](#)

Keywords: statistical approach, identify loci within genes, significantly enriched in slowly translated codons, co-translational protein folding model evolutionarily conserved,

Funding: NIGMS F32GM116231;
NIGMS R01GM124044

Availability: Free, Freely available

Resource Name: Coarse grained co-translational folding analysis

Resource ID: SCR_022271

Record Creation Time: 20220511T050132+0000

Record Last Update: 20260912T200300+0000

Ratings and Alerts

No rating or validation information has been found for Coarse grained co-translational folding analysis.

No alerts have been found for Coarse grained co-translational folding analysis.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

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.