

Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

ESRseq score

RRID:SCR_022270

Type: Tool

Proper Citation

ESRseq score (RRID:SCR_022270)

Resource Information

URL: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3149502/>

Proper Citation: ESRseq score (RRID:SCR_022270)

Description: Software for comprehensive quantitative measure of splicing impact of complete set of RNA 6-mer sequences by deep sequencing successfully spliced transcripts.

Resource Type: software application, software resource

Defining Citation: [PMID:21659425](#)

Keywords: Splicing impact quantitative measure, set of RNA 6-mer sequences, deep sequencing, successfully spliced transcripts

Funding: NIGMS GM072740

Resource Name: ESRseq score

Resource ID: SCR_022270

Record Creation Time: 20220511T050132+0000

Record Last Update: 20260805T044503+0000

Ratings and Alerts

No rating or validation information has been found for ESRseq score.

No alerts have been found for ESRseq score.

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 [RRID](#) .

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.

Barbosa P, et al. (2022) Computational prediction of human deep intronic variation. GigaScience, 12.