<table>
<thead>
<tr>
<th><strong>Aragorn</strong></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>RRID:SCR_015974</td>
<td>Type: Tool</td>
</tr>
</tbody>
</table>

**Proper Citation**

Aragorn (RRID:SCR_015974)

**Resource Information**

**URL:** [http://mbio-serv2.mbioekol.lu.se/ARAGORN/](http://mbio-serv2.mbioekol.lu.se/ARAGORN/)

**Proper Citation:** Aragorn (RRID:SCR_015974)

**Description:** Software that detects tRNA genes and tmRNA genes in nucleotide sequences. The program employs heuristic algorithms to predict tRNA secondary structure, based on homology with recognized tRNA consensus sequences and ability to form a base-paired cloverleaf.

**Resource Type:** Resource, software resource, data processing software, data analysis software, sequence analysis software, software application

**References:** [PMID:14704338](https://www.ncbi.nlm.nih.gov/pubmed/14704338)

**Keywords:** software, program, nucleotide, sequence, detect, tmRNA, tRNA

**Availability:** Free, Freely available, Available for download

**Website Status:** Last checked up

**Resource Name:** Aragorn

**Resource ID:** SCR_015974

**Ratings and Alerts**

No rating or validation information has been found for Aragorn.

No alerts have been found for Aragorn.
Usage and Citation Metrics

We found 269 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](https://www.FDI Lab - SciCrunch.org).


Park S, et al. (2020) Recurrent gene duplication in the angiosperm tribe Delphinieae (Ranunculaceae) inferred from intracellular gene transfer events and heteroplasmic mutations in the plastid matK gene. Scientific reports, 10(1), 2720.


Zhang L, et al. (2020) A comprehensive investigation of metagenome assembly by linked-read sequencing. Microbiome, 8(1), 156.

Herold M, et al. (2020) Integration of time-series meta-omics data reveals how microbial
ecosystems respond to disturbance. Nature communications, 11(1), 5281.

Putintseva YA, et al. (2020) Siberian larch (Larix sibirica Ledeb.) mitochondrial genome assembled using both short and long nucleotide sequence reads is currently the largest known mitogenome. BMC genomics, 21(1), 654.


