

Ribosomal RNA methylation by GidB is a capacitor for discrimination of mischarged tRNA

What is the Manuscript Microscope Sentence Audit?

The Manuscript Microscope Sentence Audit is a research paper introspection system that parses the text of your manuscript into minimal sentence components for faster, more accurate, enhanced proofreading.

Why use a Sentence Audit to proofread your manuscript?

- **Accelerated Proofreading:** Examine long technical texts in a fraction of the usual time.
- **Superior Proofreading:** Detect subtle errors that are invisible to traditional methods.
- **Focused Proofreading:** Inspect each individual sentence component in isolation.
- **Reliable Proofreading:** Ensure every single word of your manuscript is correct.
- **Easier Proofreading:** Take the hardship out of crafting academic papers.

Bonus 1: **Improved Productivity:** Rapidly refine rough drafts to polished papers.

Bonus 2: **Improved Authorship:** Cultivate a clear, concise, consistent, writing style.

Bonus 3: **Improved Reputation:** Become known for rigorously precise publications.

Manuscript Source: <https://www.biorxiv.org/content/10.1101/2021.03.02.433644v2>

Manuscript Authors: Zhuo Bi, Hong-Wei Su, Jia-Yao Hong & Babak Javid

Features of the Sentence Audit:

The Sentence Audit combines two complementary proofreading approaches:

1. Each sentence of your text is parsed and displayed in isolation for focused inspection.
2. Each individual sentence is further parsed into Minimal Sentence Components for a deeper review of the clarity, composition and consistency of the language you used.

The Minimal Sentence Components shown are the smallest coherent elements of each sentence of your text as derived from it's conjunctions, prepositions and selected punctuation symbols (i.e. commas, semicolons, round and square brackets).

The combined approaches ensure easier, faster, more effective proofreading.

Comments and Caveats:

- The sentence parsing is achieved using a prototype natural language processing pipeline written in Python and may include occasional errors in sentence segmentation.
- Depending on the source of the input text, the Sentence Audit may contain occasional html artefacts that are parsed as sentences (E.g. "Download figure. Open in new tab").
- Always consult the original research paper as the true reference source for the text.

Contact Information:

To get a Manuscript Microscope Sentence Audit of any other research paper, simply forward any copy of the text to John.James@OxfordResearchServices.com.

All queries, feedback or suggestions are also very welcome.

Research Paper Sections:

The sections of the research paper input text parsed in this audit.

[illegible]

Title **Ribosomal RNA methylation by GidB is a capacitor for discrimination of mischarged tRNA**

S1 [001] Summary

S1 [002] Despite redundant cellular pathways to minimize translational errors, errors in protein synthesis are common.

Despite redundant cellular pathways ...
... to minimize translational errors, ...
... errors ...
... in protein synthesis are common.

S1 [003] Pathways and mechanisms to minimize errors are classified as pre-ribosomal or ribosomal.

Pathways ...
... and mechanisms ...
... to minimize errors are classified ...
... as pre-ribosomal ...
... or ribosomal.

S1 [004] Pre-ribosomal pathways are primarily concerned with appropriate pairing of tRNAs with their cognate amino acid, whereas to date, ribosomal proof-reading has been thought to only be concerned with minimizing decoding errors, since it has been assumed that the ribosomal decoding centre is blind to mischarged tRNAs.

Pre-ribosomal pathways are primarily concerned ...
... with appropriate pairing ...
... of tRNAs ...
... with their cognate amino acid, ...
... whereas ...
... to date, ...
... ribosomal proof-reading has been thought ...
... to ...
... only be concerned ...
... with minimizing decoding errors, ...
... since it has been assumed ...
... that the ribosomal decoding centre is blind ...
... to mischarged tRNAs.

S1 [005] Here, we identified that in mycobacteria, deletion of the 16S ribosomal RNA methyltransferase gidB led to increased discrimination of mischarged tRNAs.

Here, ...
... we identified ...
... that in mycobacteria, ...
... deletion ...
... of the 16S ribosomal RNA methyltransferase gidB led ...
... to increased discrimination ...

... of mischarged tRNAs.

S1 [006] GidB deletion was necessary but not sufficient for reducing mistranslation due to misacylation.

GidB deletion was necessary ...
... but not sufficient ...
... for reducing mistranslation ...
... due to misacylation.

S1 [007] Discrimination only occurred in mycobacteria enriched from environments or genetic backgrounds with high rates of mistranslation.

Discrimination ...
... only occurred ...
... in mycobacteria enriched ...
... from environments ...
... or genetic backgrounds ...
... with high rates ...
... of mistranslation.

S1 [008] Our data suggest that mycobacterial ribosomes are capable of discriminating mischarged tRNAs and that 16S rRNA methylation by GidB may act as a capacitor for moderating translational error.

Our data suggest ...
... that mycobacterial ribosomes are capable ...
... of discriminating mischarged tRNAs ...
... and that 16S rRNA methylation ...
... by GidB ...
... may act ...
... as a capacitor ...
... for moderating translational error.

S2 [009] Introduction

S2 [010] All cells in all clades of life have evolved multiple, redundant pathways to reduce translational error [1, 2].

All cells ...
... in all clades ...
... of life have evolved multiple, ...
... redundant pathways ...
... to reduce translational error ...
... [1, 2]...
... .

S2 [011] Yet errors in protein synthesis are remarkably common and are orders of magnitude more frequent than errors in DNA or RNA synthesis [3–7].

Yet errors ...
... in protein synthesis are remarkably common ...
... and are orders ...
... of magnitude more frequent ...
... than errors ...
... in DNA ...
... or RNA synthesis ...
... [3–7].

S2 [012] There is no one 'optimal' rate of error.

There is no one 'optimal' rate ...
... of error.

S2 [013] Tolerable error rates are both species and even organelle specific [1, 8], and the major source of errors vary by mechanism and species [1].

Tolerable error rates are both species ...
... and even organelle specific ...
... [1, 8]...
... , ...
... and the major source ...
... of errors vary ...
... by mechanism ...
... and species ...
... [1].

S2 [014] Furthermore, translational errors, mistranslation, may result in adaptive phenotypes, particularly in the context of environmental stressors [1, 5, 6, 9–20].

Furthermore, ...
... translational errors, ...
... mistranslation, ...
... may result ...
... in adaptive phenotypes, ...
... particularly ...
... in the context ...
... of environmental stressors ...
... [1, ...
... 5, ...
... 6, ...
... 9–20].

S2 [015] However, excess mistranslation can also cause protein aggregation [21, 22], organ degeneration [23, 24] and is the mechanism for the bactericidal activity of aminoglycosides [25], suggesting that an optimal balance for translational error does exist, but one that is tunable and context specific [1, 3, 5, 26].

However, ...
... excess mistranslation can also cause protein aggregation ...
... [21, 22]...
... , ...
... organ degeneration ...
... [23, 24]...

... ..
 ... and is the mechanism ...
 ... for the bactericidal activity ...
 ... of aminoglycosides ...
 ... [25], ...
 ... suggesting ...
 ... that an optimal balance ...
 ... for translational error does exist, ...
 ... but one ...
 ... that is tunable ...
 ... and context specific ...
 ... [1, ...
 ... 3, ...
 ... 5, 26]...

S2 [016] In addition, molecular mechanisms of translational error whether physiological or undesirable vary considerably, as do the proof-reading pathways that have evolved to reduce them.

In addition, ...
 ... molecular mechanisms ...
 ... of translational error ...
 ... whether physiological ...
 ... or undesirable vary considerably, ...
 ... as do the proof-reading pathways ...
 ... that have evolved ...
 ... to reduce them.

S2 [017] Generally, sources of error and proof-reading can be divided into pre-ribosomal and ribosomal mechanisms [1].

Generally, ...
 ... sources ...
 ... of error ...
 ... and proof-reading can be divided ...
 ... into pre-ribosomal ...
 ... and ribosomal mechanisms ...
 ... [1].

S2 [018] Pre-ribosomal proof-reading mechanisms include pre- and post-transfer editing functions of aminoacyl tRNA synthetases [27].

Pre-ribosomal proof-reading mechanisms include pre- ...
 ... and post-transfer editing functions ...
 ... of aminoacyl tRNA synthetases ...
 ... [27].

S2 [019] Following aminoacyl-tRNA synthesis, trans-acting editing mechanisms can reject mischarged tRNAs [28, 29], and the aminoacyl-tRNA chaperone, EF-Tu optimally binds cognate aminoacyl-tRNAs compared with mischarged tRNAs [30].

Following aminoacyl-tRNA synthesis, ...
 ... trans-acting editing mechanisms can reject mischarged tRNAs ...

End of Sample Audit

This is a truncated Manuscript Microscope Sample Audit.

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