A Manuscript Microscope 'Sentence Audit' of:

Identification of biomarkers and candidate regulators for multiple myeloma under the knockout of AURKA

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/10.1101/2021.03.21.436324v1

Manuscript Authors: Hanming Gu, Wei Wang & Gongsheng Yuan

Audit Date: 31/03/21 **Audit Identifier:** XZDDZW6PKR64CZ8 **Code Version:** 3.6

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.

Section No.	Headings	Sentences
Section: 1	Abstract	11
Section: 2	Introduction	16
N/A	--- --- --- --- --- --- ---	0
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The Sentence Audit Of The Research Paper

Title # Identification of biomarkers and candidate regulators for multiple myeloma under the knockout of AURKA

S1 [001] Abstract

S1 [002] Multiple myeloma (MM) is a plasma cell malignancy that is characterized by the overabundance of monoclonal paraprotein.

Multiple myeloma ...
... (MM) ...
... is a plasma cell malignancy ...
... that is characterized ...
... by the overabundance ...
... of monoclonal paraprotein.

S1 [003] Aurora kinase A (AURKA) was upregulated in patients with high-risk MM.

Aurora kinase A ...
... (AURKA) ...
... was upregulated ...
... in patients ...
... with high-risk MM.

S1 [004] AURKA inhibitors were used to inhibit MM cell proliferation by inducing cell apoptosis and injury.

AURKA inhibitors were used ...
... to inhibit MM cell proliferation ...
... by inducing cell apoptosis ...
... and injury.

S1 [005] In our study, we aim to identify biological processes and pathways of MM cells under the knockout of AURKA (AURKA KO) by using a bioinformatics method to elucidate their potential pathogenesis.

In our study, ...
... we aim ...
... to identify biological processes ...
... and pathways ...
... of MM cells ...
... under the knockout ...
... of AURKA ...
... (AURKA KO) ...
... by using a bioinformatics method ...
... to elucidate their potential pathogenesis.

S1 [006] The gene expression profiles of the GSE163589 dataset were originally produced by using the high-throughput BGISEQ-500 (Homo sapiens).

The gene expression profiles ...

... of the GSE163589 dataset were originally produced ...

... by using the high-throughput BGISEQ-500 ...

... (Homo sapiens).

S1 [007] The biological categories and pathways were analyzed by the Kyoto Encyclopedia of Genes and Genomes pathway (KEGG), Gene Ontology (GO), and Reactom enrichment.

The biological categories ...

... and pathways were analyzed ...

... by the Kyoto Encyclopedia ...

... of Genes ...

... and Genomes pathway ...

... (KEGG), ...

... Gene Ontology ...

... (GO), ...

... and Reactom enrichment.

S1 [008] KEGG and GO results indicated the biological pathways related to the immune responses and cancer activities were mostly affected in the development of MM with AURKA KO.

KEGG ...

... and GO results indicated the biological pathways related ...

... to the immune responses ...

... and cancer activities were mostly affected ...

... in the development ...

... of MM ...

... with AURKA KO.

S1 [009] Moreover, we identified several genes including GNG5, UBE2D1, and BUB1B were involved in the regulation of cancer genesis.

Moreover, ...

... we identified several genes including GNG5, ...

... UBE2D1, ...

... and BUB1B were involved ...

... in the regulation ...

... of cancer genesis.

S1 [010] We further predicted novel regulators that had the ability to affect the progression of MM with AURKA KO based on the L1000fwd analysis.

We further predicted novel regulators ...

... that had the ability ...

... to affect the progression ...

... of MM ...

... with AURKA KO based ...

... on the L1000fwd analysis.

S1 [011] Therefore, this study provides further insights into the mechanism of MM under AURKA inhibitor treatments.

Therefore, ...

... this study provides further insights ...

... into the mechanism ...
... of MM ...
... under AURKA inhibitor treatments.

S2 [012] Introduction

S2 [013] Multiple myeloma (MM) is a common malignancy of terminally differentiated plasma cells1.

Multiple myeloma ...
... (MM) ...
... is a common malignancy ...
... of terminally differentiated plasma cells1.

S2 [014] MM cells are originated in the bone marrow, but they also reside in the peripheral blood and other organs2.

MM cells are originated ...
... in the bone marrow, ...
... but they also reside ...
... in the peripheral blood ...
... and other organs2.

S2 [015] MM accounts for about 1.7% of all malignancies in the US.

MM accounts ...
... for about 1.7% ...
... of all malignancies ...
... in the US.

S2 [016] The incidence of MM is higher in Americans but lower in Asian and Hispanic individuals1.

The incidence ...
... of MM is higher ...
... in Americans ...
... but lower ...
... in Asian ...
... and Hispanic individuals1.

S2 [017] MM is characterized by the secretion of monoclonal immunoglobulin proteins that are produced by pathologic plasma cells3.

MM is characterized ...
... by the secretion ...
... of monoclonal immunoglobulin proteins ...
... that are produced ...
... by pathologic plasma cells3.

S2 [018] The clinical manifestations include monoclonal protein, malignant cells, end-organ damage (bone disease with lytic lesions, anaemia, renal insufficiency, and hypercalcarmia)4.

The clinical manifestations include monoclonal protein, ...

... malignant cells, ...

... end-organ damage ...

... (bone disease ...

... with lytic lesions, ...

... anaemia, ...

... renal insufficiency, ...

... and hypercalcarmia)4.

S2 [019] MM cells are affected by the bone marrow microenvironment because of the adhesion of MM cells to extracellular-matrix proteins5.

MM cells are affected ...

... by the bone marrow microenvironment ...

... because of the adhesion ...

... of MM cells ...

... to extracellular-matrix proteins5.

S2 [020] In addition, binding of MM cells to BM accessory cells induces secretion of cytokines, which further promotes tumor cell activation6.

In addition, ...

... binding ...

... of MM cells ...

... to BM accessory cells induces secretion ...

... of cytokines, ...

... which further promotes tumor cell activation6.

S2 [021] Aurora kinases were found to regulate cell-cycle checkpoints and some related molecules such as cyclins and cyclin-dependent kinases7.

Aurora kinases were found ...

... to regulate cell-cycle checkpoints ...

... and some related molecules ...

... such as cyclins ...

... and cyclin-dependent kinases7.

S2 [022] Aurora kinases localize in the centrosome and play important roles in cell division by regulating chromatid segregation in mitotic cells; moreover, loss of chromatid segregation leads to genetic instability and tumorigenesis8.

Aurora kinases localize ...

... in the centrosome ...

... and play important roles ...

... in cell division ...

... by regulating chromatid segregation ...

... in mitotic cells; ...

... moreover, ...

... loss ...

... of chromatid segregation leads ...

... to genetic instability ...

... and tumorigenesis8.

End of Sample Audit

This is a truncated Manuscript Microscope Sample Audit.

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