A Manuscript Microscope 'Sentence Audit' of:

Screening for Potential Interaction Partners with Surface Plasmon Resonance Imaging Coupled to MALDI Mass Spectrometry

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.
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Bonus 1: Improved Productivity: Rapidly refine rough drafts to polished papers.
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Bonus 3: Improved Reputation: Become known for rigorously precise publications.

Manuscript Source: https://www.biorxiv.org/content/10.1101/2020.05.07.082776v3

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Audit Date: 31/03/21 **Audit Identifier:** Y9I1VBROVU26PIL **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	8
Section: 2	1. Introduction	19
N/A	--- --- --- --- --- --- ---	0
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Title # Screening for Potential Interaction Partners with Surface Plasmon Resonance Imaging Coupled to MALDI Mass Spectrometry

S1 [001] ABSTRACT

S1 [002] We coupled SPR imaging (SPRi) with matrix-assisted laser desorption/ionization mass spectrometry (MALDI MS) to identify new potential RNA binders.

We coupled SPR imaging ...
... (SPRi) ...
... with matrix-assisted laser desorption/ionization mass spectrometry ...
... (MALDI MS) ...
... to identify new potential RNA binders.

S1 [003] Here, we improve this powerful method, especially by optimizing the proteolytic digestion (type of reducing agent, its concentration, and incubation time), to work with complex mixtures, specifically a lysate of the rough mitochondrial fraction from yeast.

Here, ...
... we improve this powerful method, ...
... especially ...
... by optimizing the proteolytic digestion ...
... (type ...
... of reducing agent, ...
... its concentration, ...
... and incubation time), ...
... to work ...
... with complex mixtures, ...
... specifically a lysate ...
... of the rough mitochondrial fraction ...
... from yeast.

S1 [004] The advantages of this hyphenated method compared to column-based or separate analyses are (i) rapid and direct visual readout from the SPRi array, (ii) possibility of high-throughput analysis of different interactions in parallel, (iii) high sensitivity, and (iv) no sample loss or contamination due to elution or micro-recovery procedures.

The advantages ...
... of this hyphenated method compared ...
... to column-based ...
... or separate analyses are ...
... (i) ...
... rapid ...
... and direct visual readout ...
... from the SPRi array, ...
... (ii) ...
... possibility ...
... of high-throughput analysis ...

... of different interactions ...
... in parallel, ...
... (iii) ...
... high sensitivity, ...
... and ...
... (iv) ...
... no sample loss ...
... or contamination ...
... due to elution ...
... or micro-recovery procedures.

S1 [005] The model system used is a catalytically active RNA (group IIB intron from Saccharomyces cerevisiae, Sc.ai5γ) and its cofactor Mss116.

The model system used is a catalytically active RNA ...
... (group IIB intron ...
... from Saccharomyces cerevisiae, ...
... Sc.ai5γ) ...
... and its cofactor Mss116.

S1 [006] The protein supports the RNA folding process and thereby the subsequent excision of the intronic RNA from the coding part.

The protein supports the RNA folding process ...
... and thereby the subsequent excision ...
... of the intronic RNA ...
... from the coding part.

S1 [007] Using the novel approach of coupling SPR with MALDI MS, we report the identification of potential RNA-binding proteins from a crude yeast mitochondrial lysate in a non-targeted approach.

Using the novel approach ...
... of coupling SPR ...
... with MALDI MS, ...
... we report the identification ...
... of potential RNA-binding proteins ...
... from a crude yeast mitochondrial lysate ...
... in a non-targeted approach.

S1 [008] Our results show that proteins other than the well-known cofactor Mss116 interact with Sc.ai5γ (Dbp8, Prp8, Mrp13, and Cullin-3), suggesting that the intron folding and splicing are regulated by more than one cofactor in vivo.

Our results show ...
... that proteins other ...
... than the well-known cofactor Mss116 interact ...
... with Sc.ai5γ ...
... (Dbp8, ...
... Prp8, ...
... Mrp13, ...
... and Cullin-3), ...
... suggesting ...
... that the intron folding ...

... and splicing are regulated ...

... by more than one cofactor ...

... in vivo.

S2 [009] 1. Introduction

S2 [010] To identify molecular partners and simultaneously determine the binding affinity, a combination of several analytical methods would usually be required, rendering work laborious and time-consuming.

To identify molecular partners ...

... and simultaneously determine the binding affinity, ...

... a combination ...

... of several analytical methods would usually be required, ...

... rendering work laborious ...

... and time-consuming.

S2 [011] The coupling of surface plasmon resonance imaging (SPRi) with mass spectrometry (MS) that was employed here combines quantitative analysis with unambiguous identification of captured target molecules in a single workflow [1-3].

The coupling ...

... of surface plasmon resonance imaging ...

... (SPRi) ...

... with mass spectrometry ...

... (MS) ...

... that was employed here combines quantitative analysis ...

... with unambiguous identification ...

... of captured target molecules ...

... in a single workflow ...

... [1-3].

S2 [012] SPRi allows to monitor binding affinities and kinetics in real-time and at very low amounts (femtomole range).

SPRi allows ...

... to monitor binding affinities ...

... and kinetics ...

... in real-time ...

... and at very low amounts ...

... (femtomole range).

S2 [013] SPR surfaces are reusable due to regeneration steps between different injections, which allow multiple measurements at different concentrations and, if necessary, various conditions.

SPR surfaces are reusable ...

... due to regeneration steps ...

... between different injections, ...

... which allow multiple measurements ...

... at different concentrations and, ...

... if necessary, ...

... various conditions.

S2 [014] To identify the molecules that were captured on an SPR surface, matrix-assisted laser desorption/ionization mass spectrometry (MALDI MS) and peptide mass fingerprinting were implemented.

To identify the molecules ...

... that were captured ...

... on an SPR surface, ...

... matrix-assisted laser desorption/ionization mass spectrometry ...

... (MALDI MS) ...

... and peptide mass fingerprinting were implemented.

S2 [015] By performing SPR and MALDI MS separately, as usually done [4-6], the throughput and sensitivity would be seriously limited due to the need for target elution, which often leads to sample loss and contaminations.

By performing SPR ...

... and MALDI MS separately, ...

... as usually done ...

... [4-6], ...

... the throughput ...

... and sensitivity would be seriously limited ...

... due to the need ...

... for target elution, ...

... which often leads ...

... to sample loss ...

... and contaminations.

S2 [016] Therefore, performing MALDI MS measurements directly on the SPR chip is beneficial [7,8].

Therefore, ...

... performing MALDI MS measurements directly ...

... on the SPR chip is beneficial ...

... [7,8].

S2 [017] We have previously shown that the identity of interacting proteins not only from pure target solutions but also from cellular lysates can be established [9].

We have previously shown ...

... that the identity ...

... of interacting proteins not ...

... only ...

... from pure target solutions ...

... but also ...

... from cellular lysates can be established ...

... [9].

S2 [018] The only other similar example reported is the study by Musso et al., which demonstrated the detection of α-amylase from human saliva by antibody-arrayed SPRi surfaces [10].

The ...

End of Sample Audit

This is a truncated Manuscript Microscope Sample Audit.

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