*A Manuscript Microscope 'Sentence Audit' of:*

# Transcriptional census of epithelial -mesenchymal plasticity in cancer

**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/10.1101/2021.03.05.434142v1

**Manuscript Authors:** David P. Cook & Barbara C. Vanderhyden

**Audit Date:** 22/03/21 **Audit Identifier:** ZJU7GR066QVG56B **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 | 7 |
| Section: 2 | INTRODUCTION | 20 |
| N/A | --- --- --- --- --- --- --- | 0 |
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## The Sentence Audit Of The Research Paper

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**Title** # Transcriptional census of epithelial-mesenchymal plasticity in cancer

## S1 [001] ABSTRACT

**S1 [002]** Epithelial-mesenchymal plasticity (EMP) contributes to tumour progression, promoting therapy resistance and immune cell evasion.

Epithelial-mesenchymal plasticity ...
... (EMP) ...
... contributes ...
... to tumour progression, ...
... promoting therapy resistance ...
... and immune cell evasion.

**S1 [003]** Definitive molecular features of this plasticity have largely remained elusive due to the limited scale of most studies.

Definitive molecular features ...
... of this plasticity have largely remained elusive ...
... due to the limited scale ...
... of most studies.

**S1 [004]** Leveraging scRNA-seq data from 160 tumours spanning 8 different cancer types, we identify expression patterns associated with intratumoural EMP.

Leveraging scRNA-seq data ...
... from 160 tumours spanning 8 different cancer types, ...
... we identify expression patterns associated ...
... with intratumoural EMP.

**S1 [005]** Integrative analysis of these programs confirmed a high degree of diversity among tumours.

Integrative analysis ...
... of these programs confirmed a high degree ...
... of diversity ...
... among tumours.

**S1 [006]** These diverse programs are associated with combinations of various common regulatory mechanisms initiated from cues within the tumour microenvironment.

These diverse programs are associated ...
... with combinations ...
... of various common regulatory mechanisms initiated ...
... from cues ...
... within the tumour microenvironment.

**S1 [007]** We highlight that inferring regulatory features can inform effective therapeutics to restrict EMP.

We highlight ...
... that inferring regulatory features can inform effective therapeutics ...
... to restrict EMP.

## S2 [008] INTRODUCTION

**S2 [009]** Epithelial-mesenchymal plasticity (EMP) refers to the ability of cells to interconvert between epithelial and mesenchymal phenotypes, dynamically adopting mixed features of these states in response to signals in the cells' microenvironment (Yang et al., 2020).

Epithelial-mesenchymal plasticity ...
... (EMP) ...
... refers ...
... to the ability ...
... of cells ...
... to interconvert ...
... between epithelial ...
... and mesenchymal phenotypes, ...
... dynamically adopting mixed features ...
... of these states ...
... in response ...
... to signals ...
... in the cells' microenvironment ...
... (Yang et al., 2020).

**S2 [010]** Throughout a tissue, cells with phenotypes spanning an epithelial/ mesenchymal (E/M) continuum can be observed, emerging in response to specific features of their local environment.

Throughout a tissue, ...
... cells ...
... with phenotypes spanning an epithelial/ mesenchymal ...
... (E/M) ...
... continuum can be observed, ...
... emerging ...
... in response ...
... to specific features ...
... of their local environment.

**S2 [011]** At the leading edge of tumours, for example, epithelial architecture becomes progressively disorganized and the cancer cells express higher levels of mesenchymal-associated genes (Gabbert et al., 1985; Puram et al., 2017).

At the leading edge ...
... of tumours, ...
... for example, ...
... epithelial architecture becomes progressively disorganized ...
... and the cancer cells express higher levels ...

... of mesenchymal-associated genes ...
... (Gabbert et al., 1985; ...
... Puram et al., 2017).

**S2 [012]** In cancer, this plasticity has been broadly associated with promoting metastasis, chemoresistance, and immunosuppression (Dongre and Weinberg, 2019).

In cancer, ...
... this plasticity has been broadly associated ...
... with promoting metastasis, ...
... chemoresistance, ...
... and immunosuppression ...
... (Dongre ...
... and Weinberg, 2019).

**S2 [013]** Given its supposed impact on tumour progression and treatment, understanding the molecular mechanisms that drive EMP and developing therapeutic strategies to modulate it have been a priority for years (Bhatia et al., 2020; Horn et al., 2020; Ramesh et al., 2020; Yang et al., 2020).

Given its supposed impact ...
... on tumour progression ...
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... that drive EMP ...
... and developing therapeutic strategies ...
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... for years ...
... (Bhatia et al., 2020; ...
... Horn et al., 2020; ...
... Ramesh et al., 2020; ...
... Yang et al., 2020).

**S2 [014]** Identifying molecular determinants of EMP has largely focused on studying dynamics associated with the epithelial-mesenchymal transition (EMT) induced in experimental settings, through the addition of exogenous cytokines (eg. TGFB1) or genetic manipulation.

Identifying molecular determinants ...
... of EMP has largely focused ...
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... with the epithelial-mesenchymal transition ...
... (EMT) ...
... induced ...
... in experimental settings, ...
... through the addition ...
... of exogenous cytokines ...
... (eg. TGFB1) ...
... or genetic manipulation.

**S2 [015]** Over the last two decades, however, it has become increasingly clear that molecular features of the EMT are highly context specific (Cook and Vanderhyden, 2020; Peixoto et al., 2019; Stemmler et al., 2019; Taube et al., 2010; Williams et al., 2019; Yang et al., 2020).

Over the last two decades, ...

... however, ...
... it has become increasingly clear ...
... that molecular features ...
... of the EMT are highly context specific ...
... (Cook ...
... and Vanderhyden, 2020; ...
... Peixoto et al., 2019; ...
... Stemmler et al., 2019; ...
... Taube et al., 2010; ...
... Williams et al., 2019; ...
... Yang et al., 2020).

**S2 [016]** The reliability of even the most canonical EMP genes (eg. SNAI1, SNAI2, CDH1, CDH2, VIM) has become unclear and the reliance on specific genes as molecular markers of EMP has led to controversy about its implication in metastasis (Aiello et al., 2017; Fischer et al., 2015, 2017; Ye et al., 2017; Zheng et al., 2015).

The reliability ...
... of even the most canonical EMP genes ...
... (eg. SNAI1, ...
... SNAI2, ...
... CDH1, ...
... CDH2, ...
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... and the reliance ...
... on specific genes ...
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... of EMP has led ...
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... about its implication ...
... in metastasis ...
... (Aiello et al., 2017; ...
... Fischer et al., 2015, 2017; ...
... Ye et al., 2017; ...
... Zheng et al., 2015).

**S2 [017]** As a result, recent guidelines from “the EMT International Association” suggest that the primary criteria for defining EMP should focus on changes to cellular properties (eg. loss of cell-cell junctions, enhanced migratory capacity) (Yang et al., 2020).

As a result, ...
... recent guidelines ...
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... enhanced migratory capacity) ...
... (Yang et al., 2020).

**End of Sample Audit**

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This is a truncated Manuscript Microscope Sample Audit.

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