A Manuscript Microscope 'Sentence Audit' of:

TCRβ rearrangements without D-segment are common, abundant and public

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/10.1101/2021.03.05.434088v1

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Audit Date: 22/03/21 **Audit Identifier:** N8MG0B5XJ6JQR4J **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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The Sentence Audit Of The Research Paper

Title # TCRβ rearrangements without D-segment are common, abundant and public

S1 [001] Abstract

S1 [002] T cells play an important role in adaptive immunity.

T cells play an important role ...
... in adaptive immunity.

S1 [003] An enormous clonal diversity of T-cells with a different specificity, encoded by the T-cell receptor (TCR), protect the body against infection.

An enormous clonal diversity ...
... of T-cells ...
... with a different specificity, ...
... encoded ...
... by the T-cell receptor ...
... (TCR), ...
... protect the body ...
... against infection.

S1 [004] Most TCRβ chains are generated from a V-, D-, and J-segment during recombination in the thymus.

Most TCRβ chains are generated ...
... from a V-, ...
... D-, ...
... and J-segment ...
... during recombination ...
... in the thymus.

S1 [005] Although complete absence of the D-segment is not easily detectable from sequencing data, we find convincing evidence for a substantial proportion of TCRβ rearrangements lacking a D-segment.

Although complete absence ...
... of the D-segment is not easily detectable ...
... from sequencing data, ...
... we find convincing evidence ...
... for a substantial proportion ...
... of TCRβ rearrangements lacking a D-segment.

S1 [006] Additionally, sequences without a D-segment are more likely to be abundant within individuals and/or shared between individuals.

Additionally, ...
... sequences ...
... without a D-segment are more likely ...

... to be abundant ...
... within individuals ...
... and/or shared ...
... between individuals.

S1 [007] We find that such sequences are preferentially generated during fetal development and persist within the elderly.

We find ...
... that such sequences are preferentially generated ...
... during fetal development ...
... and persist ...
... within the elderly.

S1 [008] Summarizing, TCRβ rearrangements without a D-segment are not uncommon, and tend to allow for TCRβ chains with a high abundance in the naive repertoire.

Summarizing, ...
... TCRβ rearrangements ...
... without a D-segment are not uncommon, ...
... and tend ...
... to allow ...
... for TCRβ chains ...
... with a high abundance ...
... in the naive repertoire.

S2 [009] ## 1 Introduction

S2 [010] The adaptive immune system relies on large and diverse repertoires of B- and T-lymphocytes.

The adaptive immune system relies ...
... on large ...
... and diverse repertoires ...
... of B- ...
... and T-lymphocytes.

S2 [011] When encountering antigen, specific lymphocytes start proliferating to clear the pathogen.

When encountering antigen, ...
... specific lymphocytes start proliferating ...
... to clear the pathogen.

S2 [012] Many of the cells die after clearance, but others are maintained and form a memory that can be recalled after repeated antigen exposure.

Many ...
... of the cells die ...
... after clearance, ...
... but others are maintained ...

... and form a memory ...
... that can be recalled ...
... after repeated antigen exposure.

S2 [013] The specificity of αβ T-cells is determined by the α and β chain of the T-cell receptor (TCR).

The specificity ...
... of αβ T-cells is determined ...
... by the α ...
... and β chain ...
... of the T-cell receptor ...
... (TCR).

S2 [014] These are generated by recombination of variable (V), diversity (D) and joining (J) regions for the TCRβ and V and J for the TCRα chain.

These are generated ...
... by recombination ...
... of variable ...
... (V), ...
... diversity ...
... (D) ...
... and joining ...
... (J) ...
... regions ...
... for the TCRβ ...
... and V ...
... and J ...
... for the TCRα chain.

S2 [015] During V(D)J-recombination in the thymus, one variant of each of these segments is recombined in a semi-random manner, with deletions and non-templated insertions occurring at the junction(s).

During V(D)J-recombination ...
... in the thymus, ...
... one variant ...
... of each ...
... of these segments is recombined ...
... in a semi-random manner, ...
... with deletions ...
... and non-templated insertions occurring ...
... at the junction(s).

S2 [016] The combination of the generated β and α chains of the TCR yield an enormous potential diversity (> 1020 [25, 12]), of which only a small subset is realized in the actual TCR repertoire with a diversity estimated to be around 108 [15].

The combination ...
... of the generated β ...
... and α chains ...
... of the TCR yield an enormous potential diversity ...
... (> 1020 ...
... [25, 12]...

...), ...
... of which ...
... only a small subset is realized ...
... in the actual TCR repertoire ...
... with a diversity estimated ...
... to be ...
... around 108 ...
... [15].

S2 [017] The recombination process is guided by recombination signal sequences (RSSs) flanking the V, D and J segments.

The recombination process is guided ...
... by recombination signal sequences ...
... (RSSs) ...
... flanking the V, ...
... D ...
... and J segments.

S2 [018] The RSSs contain spacers of 12 or 23 basepairs (bp), and two gene segments can only be recombined when they have different spacer lengths, a principle that is known as the 12/23 rule.

The RSSs contain spacers ...
... of 12 ...
... or 23 basepairs ...
... (bp), ...
... and two gene segments can ...
... only be recombined ...
... when they have different spacer lengths, ...
... a principle ...
... that is known ...
... as the 12/23 rule.

S2 [019] In the TCRB locus, the 3’ ends of V and D segments have 23-bp spacer RSSs, while the 5’ end of D and J segments have 12-bp spacer RSSs.

In the TCRB locus, ...
... the 3’ ends ...
... of V ...
... and D segments have 23-bp spacer RSSs, ...
... while the 5’ end ...
... of D ...
... and J segments have 12-bp spacer RSSs.

S2 [020] Following the 12/23 rule, it is therefore possible to have direct V-to-J rearrangements, not including a D-segment.

Following the 12/23 rule, ...
... it is therefore possible ...
... to have direct V-to-J rearrangements, ...
... not including a D-segment.

End of Sample Audit

This is a truncated Manuscript Microscope Sample Audit.

To get the full audit of this text (or any other research paper),
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