User Guide for the *Standards for Technical Reporting in Environmental and host-Associated Microbiome Studies* (STREAMS)

Are you working with human-associated microbiome samples? Use the STORMS guidelines!

The STREAMS guidelines are a checklist designed to be used by researchers working with environmental, synthetic, and non-human host-associated microbiomes. The guidelines aim to capture the information and metadata required for proper reporting of microbiome studies in journal articles. The checklist can be used by authors, journals, and reviewers to assess what information is being captured and what is not included in the manuscript of interest. Not every item in this checklist will be relevant to all researchers for all of their studies, but it is designed to be informative and helpful for ensuring critical information, especially metadata that is invaluable to data reuse efforts, is reported on in microbiome publications.

There are important considerations for researchers to consider when apply the STREAMS guidelines in their own research:

- The STREAMS guidelines are not all-encompassing and several aspects of microbiome studies may not be covered
- These are meant to be guidelines and not necessarily representative of mandatory content. The Introduction and Discussion sections are designed to be flexible and much of what goes into these sections in manuscripts is not explicitly stated in STREAMS
- The order of the content in STREAMS does not need to be followed in a manuscript
- STREAMS was created with metagenomics, metatranscriptomics, metabolomics, and metaproteomics in mind. Other omics types can be included, but they may not have information specific to their respective methods and results included in the current version of the STREAMS guidelines
- The STREAMS guidelines will be periodically updated to capture new trends in the field and continuously incorporate community feedback. A feedback form is available on the STREAMS website if you have any recommendations for the next version!
- If an author is limited on space in a manuscript, much of this information can be reported in the supplementary information rather than the main text
- Even if requested items in STREAMS are not directly related to your research questions or hypotheses, it can still be important to report comprehensive metadata and contextual information to enable data reuse applications
- Standardization in field, laboratory, and data analysis protocols can lead to higher quality results, more robust conclusions, and an enhanced ability to compare data across studies

and institutions. We encourage the use of community standards e.g., MIxS throughout the research process

- Journal requirements and formats will widely vary, and the STREAMS guidelines may not be applicable across all journals and article formats. Refer to journal-specific guidelines for formatting each manuscript section.
- The FAIR data principles underlie the rationale and execution of the STREAMS guidelines. We encourage you to explore other ways you can ensure your microbiome research and data are FAIR-compliant
- Indigenous data sovereignty and governance, the CARE principles, and reporting ethics are of the utmost importance within the STREAMS guidelines. It is necessary to obtain informed consent from indigenous communities BEFORE sampling or experimental work is started. Please review and research how your work relates to indigenous lands, waters, sites, plants, animals, data, and/or samples, and plan accordingly. Assembling appropriate research teams is often a critical first step
    - https://doi.org/10.1371/journal.pcbi.1009277
    - https://doi.org/10.5334/dsj-2020-043
    - https://doi.org/10.1038/s41564-023-01471-2
- You can join the STREAMS slack to ask questions and connect with other microbiome researchers
- Reach out to our team at streamsmicrobiome@gmail.com with questions, comments, or feedback

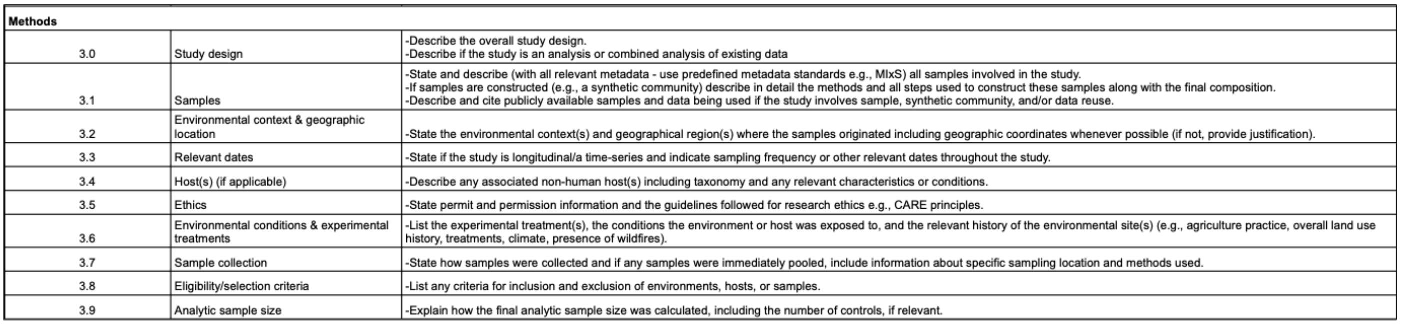
The STREAMS guidelines are accessible through several avenues:

- The STREAMS website: https://streamsmicrobiome.org/
- Zenodo: https://doi.org/10.5281/zenodo.15014818
- As a DMP Tool template, Template Name: STREAMS Microbiome Guidelines, Funder: STREAMS Microbiome
- Supplementary Table in the STREAMS manuscript

There are also 5 exemplar evaluations of the STREAMS guidelines on published microbiome papers that are available on the STREAMS website and are linked with the STREAMS manuscript. These are meant to provide researchers with examples for each Item and show how these Items are incorporated into microbiome publications.

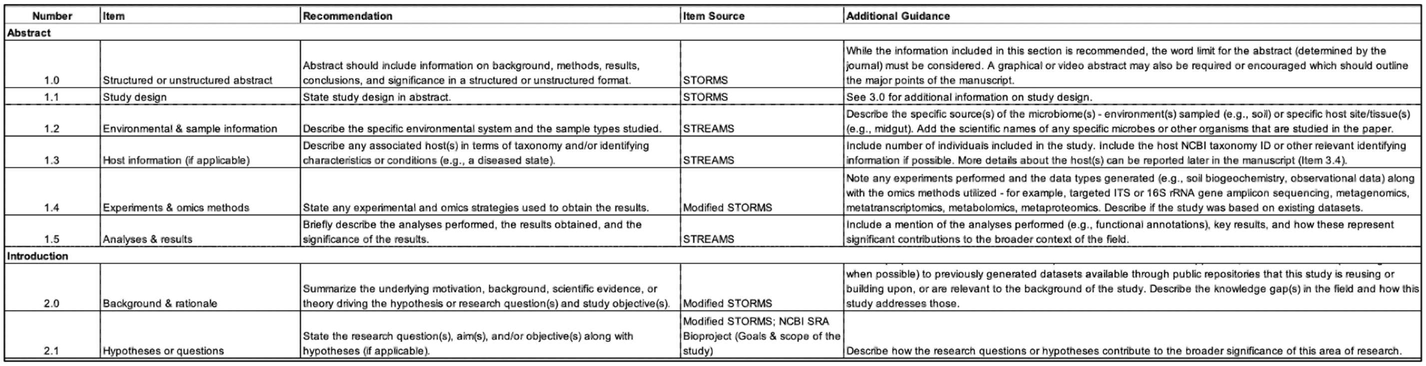
Environment / Host	**Microbiome Study**
Agriculture / Broiler Chickens	Fonseca et al., 2024
Deep-sea corals	Kellogg & Pratte, 2021
Freshwater lake	Berg et al., 2021
Deadwood	Tlaskal et al., 2021
Synthetic community	Novak et al., 2025

A “simplified” version of STREAMS is also available on the STREAMS website to be used as a quick checklist for those who are already familiar with the more comprehensive guidelines, or for those who would prefer a document that is less overwhelming and can then reference the main STREAMS guidelines for context. Below is a small section of the simplified version.



Methods		
3.0	Study design	-Describe the overall study design. -Describe if the study is an analysis or combined analysis of existing data
3.1	Samples	-State and describe (with all relevant metadata - use predefined metadata standards e.g., MIxS) all samples involved in the study. -If samples are constructed (e.g., a synthetic community) describe in detail the methods and all steps used to construct these samples along with the final composition. -Describe and cite publicly available samples and data being used if the study involves sample, synthetic community, and/or data reuse.
3.2	Environmental context & geographic location	-State the environmental context(s) and geographical region(s) where the samples originated including geographic coordinates whenever possible (if not, provide justification).
3.3	Relevant dates	-State if the study is longitudinal/a time-series and indicate sampling frequency or other relevant dates throughout the study.
3.4	Host(s) (if applicable)	-Describe any associated non-human host(s) including taxonomy and any relevant characteristics or conditions.
3.5	Ethics	-State permit and permission information and the guidelines followed for research ethics e.g., CARE principles.
3.6	Environmental conditions & experimental treatments	-List the experimental treatment(s), the conditions the environment or host was exposed to, and the relevant history of the environmental site(s) (e.g., agriculture practice, overall land use history, treatments, climate, presence of wildfires).
3.7	Sample collection	-State how samples were collected and if any samples were immediately pooled, include information about specific sampling location and methods used.
3.8	Eligibility/selection criteria	-List any criteria for inclusion and exclusion of environments, hosts, or samples.
3.9	Analytic sample size	-Explain how the final analytic sample size was calculated, including the number of controls, if relevant.

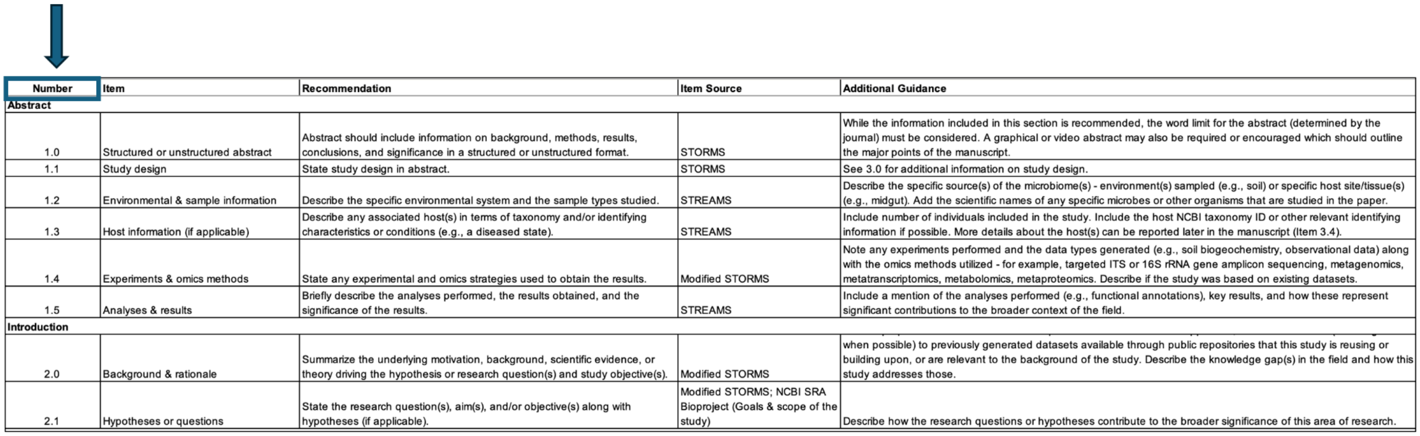
The STREAMS guidelines consist of **67 individual Items** grouped into **18 categories** that span six sections that mirror the organization of a scientific manuscript (Abstract, Introduction, Methods, Results, Discussion, Other Information).



Number	Item	Recommendation	Item Source	Additional Guidance
Abstract				
1.0	Structured or unstructured abstract	Abstract should include information on background, methods, results, conclusions, and significance in a structured or unstructured format.	STORMS	While the information included in this section is recommended, the word limit for the abstract (determined by the journal) must be considered. A graphical or video abstract may also be required or encouraged which should outline the major points of the manuscript.
1.1	Study design	State study design in abstract.	STORMS	See 3.0 for additional information on study design.
1.2	Environmental & sample information	Describe the specific environmental system and the sample types studied.	STREAMS	Describe the specific source(s) of the microbiome(s) - environment(s) sampled (e.g., soil) or specific host site/tissue(s) (e.g., midgut). Add the scientific names of any specific microbes or other organisms that are studied in the paper.
1.3	Host information (if applicable)	Describe any associated host(s) in terms of taxonomy and/or identifying characteristics or conditions (e.g., a diseased state).	STREAMS	Include number of individuals included in the study. Include the host NCBI taxonomy ID or other relevant identifying information if possible. More details about the host(s) can be reported later in the manuscript (Item 3.4).
1.4	Experiments & omics methods	State any experimental and omics strategies used to obtain the results.	Modified STORMS	Note any experiments performed and the data types generated (e.g., soil biogeochemistry, observational data) along with the omics methods utilized - for example, targeted ITS or 16S rRNA gene amplicon sequencing, metagenomics, metatranscriptomics, metabolomics, metaproteomics. Describe if the study was based on existing datasets.
1.5	Analyses & results	Briefly describe the analyses performed, the results obtained, and the significance of the results.	STREAMS	Include a mention of the analyses performed (e.g., functional annotations), key results, and how these represent significant contributions to the broader context of the field.
Introduction				
2.0	Background & rationale	Summarize the underlying motivation, background, scientific evidence, or theory driving the hypothesis or research question(s) and study objective(s).	Modified STORMS	when possible) to previously generated datasets available through public repositories that this study is reusing or building upon, or are relevant to the background of the study. Describe the knowledge gap(s) in the field and how this study addresses those.
2.1	Hypotheses or questions	State the research question(s), aim(s), and/or objective(s) along with hypotheses (if applicable).	Modified STORMS; NCBI SRA Bioproject (Goals & scope of the study)	Describe how the research questions or hypotheses contribute to the broader significance of this area of research.

Each Item contains:

1. An Item number. The numbering corresponds to groupings of similar Items.



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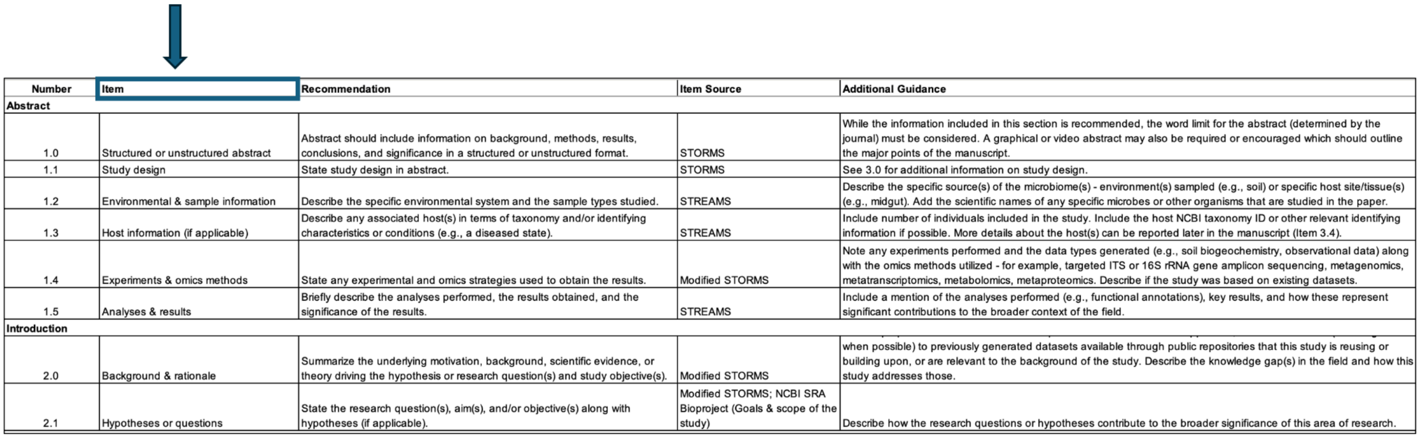
2. An Item Name.



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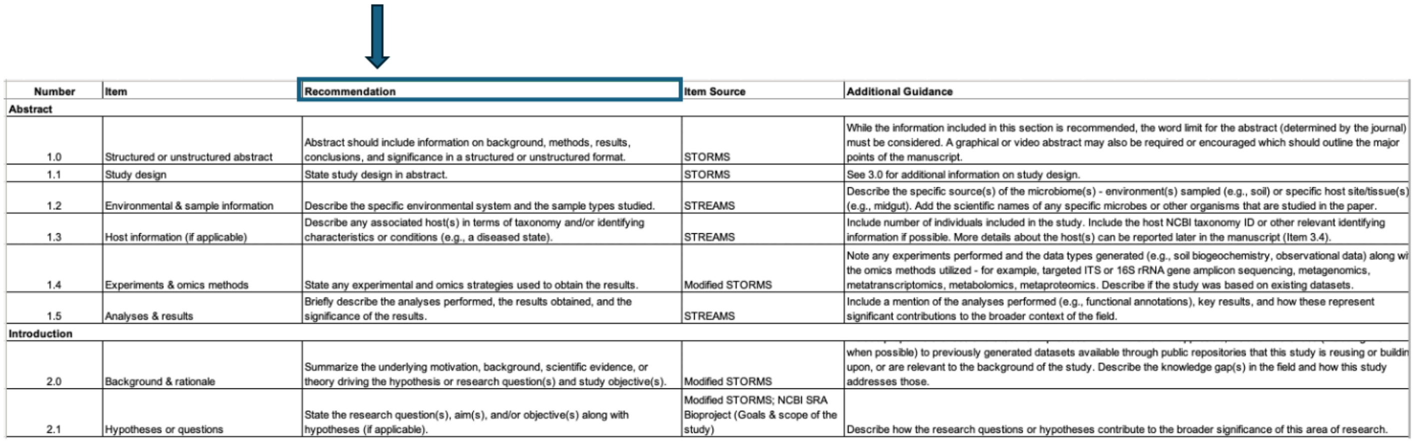
3. A Recommendation for that Item which includes the core information that should be reported on in the manuscript for that specific Item.



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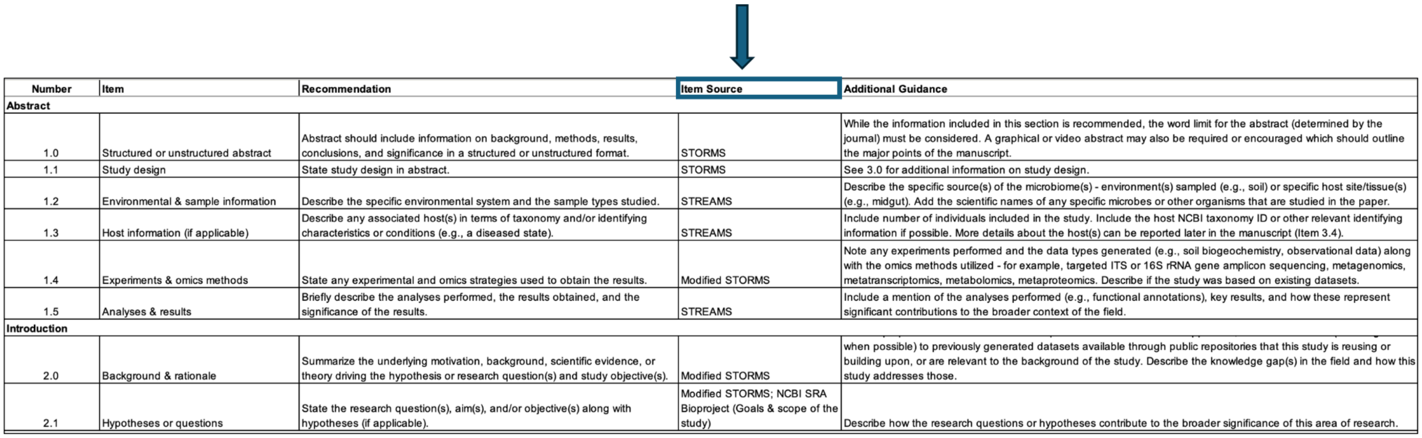
4. The Item Source which references where that particular Item was derived from.

Many of the Item Sources say "STORMS" or "Modified STORMS" for the Items that were taken directly from the STORMS guidelines or were slightly modified to better fit environmental microbiome studies. Those that have STREAMS as the Item Source mean that those are new Items and Recommendations specifically for STREAMS. The STROBE and STREGA guidelines as well as ENVO, the OBO Foundry, the Chemical Analysis Working Group of the Metabolomics Standards Initiative are also referenced in this column as direct sources or the inspiration for certain Items.

This column also includes references to specific MIxS terms and other MIxS guidance that can help you to collect, record, and properly report these metadata items. You can also browse through additional MIxS terms and find a full set of metadata guidelines for your sample through MIxS.

Within the Item Source, there are also references to NCBI BioSample and SRA guidance. When submitting sample and sequence information to NCBI, there are certain fields and terms that have to be included or are recommended to be included. The references to BioSample and SRA fields here are meant to assist with interoperability between NCBI submissions and STREAMS. More information about the referenced NCBI BioSample attributes as well as additional terms can be viewed online or downloaded in xml format. The SRA submission spreadsheets and online guidance can also help with navigating the formatting and file upload process.



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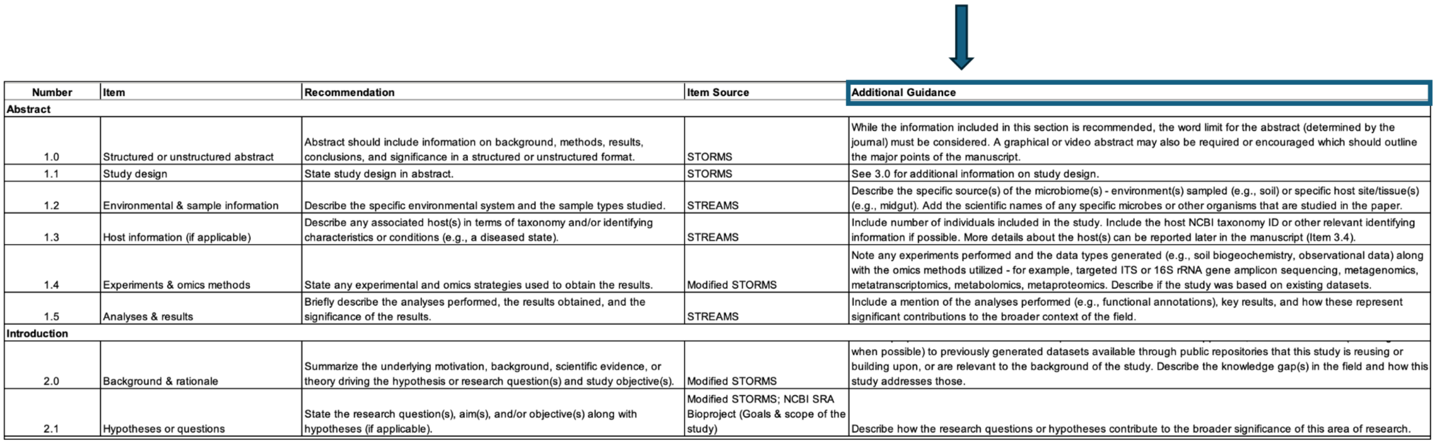
5. Additional Guidance for the Item which includes more detailed descriptions, links, and other helpful information.



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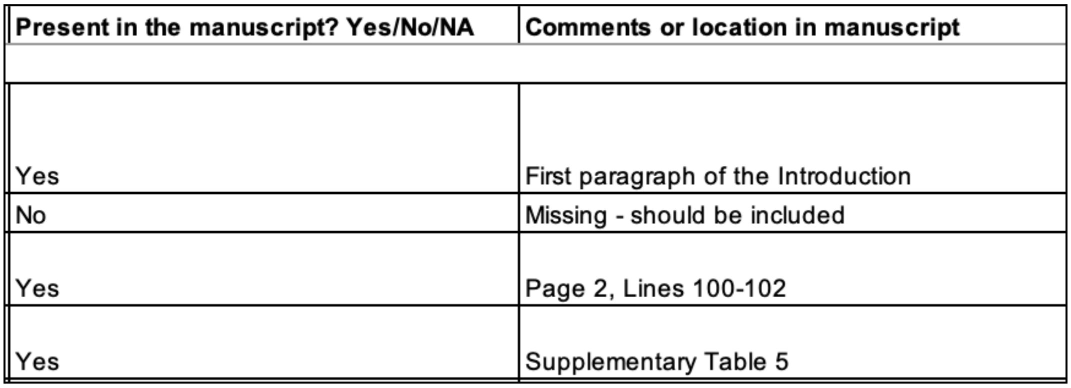
6. A column for noting if something is “Present in the manuscript?” which can be answered with Yes, No, or N/A.



Present in the manuscript? Yes/No/NA	Comments or location in manuscript
Yes	First paragraph of the Introduction
No	Missing - should be included
Yes	Page 2, Lines 100-102
Yes	Supplementary Table 5

7. A column for Comments or the location in the manuscript where that Item can be found.

These last two columns are designed to help researchers identify what might be missing in their own manuscripts prior to submission, and to help peer reviewers with noting what may be missing in the paper. The comments and location can be filled out in a manner that is most helpful to you (e.g., Line numbers, page numbers, specific paragraphs, copied & pasted in, etc.)