

Release Notes

March 2026

Context Management
HAQ Manager

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Context Management

Understand and control AI context by making refinement more interactive and trustworthy, giving users the ability to update sources and prioritize what matters most.

Update AI Blocks directly from the Content View

Select the relevant content, then just click “Edit AI Block”. Weave takes you directly to the template section that generated the content. Use this to make targeted template updates, especially in large files, without having to keep track of what content block came from what template block.

2.6.6 TOXICOLOGY WRITTEN SUMMARY

2.6.6.1 Brief Summary

⊕ ☰ **Table 1: Summary of Toxicology Studies**

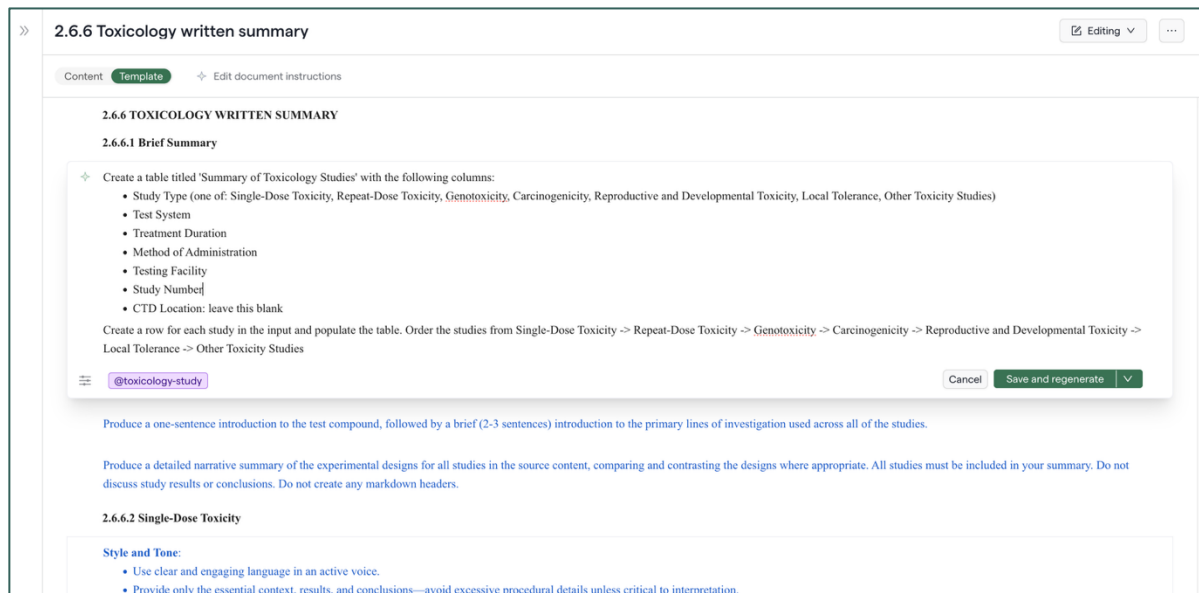
	Test System
city	CrI:CD(SD) rats
city	CrI:CD(SD) rats
	In vitro bacterial reverse mutation assay (Ames test: <i>S. typhimurium</i> TA100, TA1535, TA98, TA1537; <i>E. coli</i> WP2uvrA)
	In vitro chromosomal aberration test (Chinese hamster lung fibroblasts, CHL/IU cells)

Abbreviations: CTD = Common Technical Document

13F-SFA (3,3,4,4,5,5,6,6,7,7,8,8,8-tridecafluorooctyl acrylate; CAS No. 17527-29-6) is a colorless solid. It was evaluated for acute oral toxicity, repeated-dose oral toxicity, bacterial reverse mutation (Ames) testing, and in vitro chromosomal aberration testing.

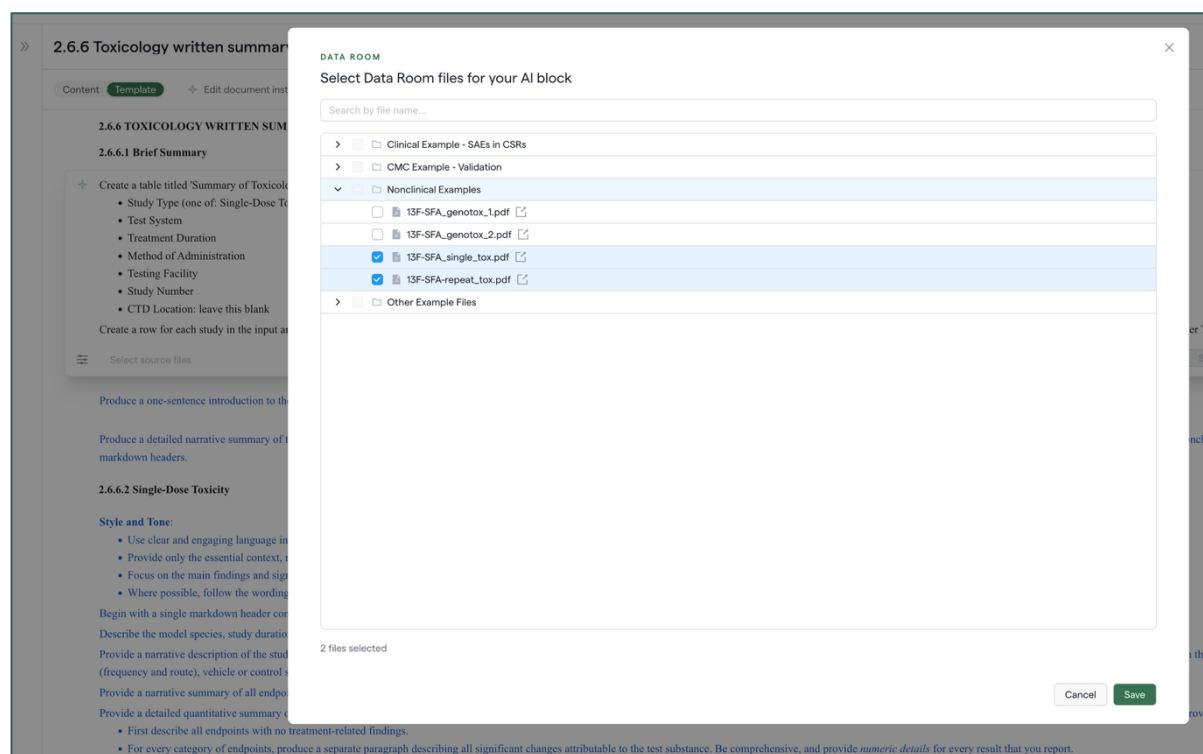
A comprehensive nonclinical assessment of 13F-SFA (3,3,4,4,5,5,6,6,7,7,8,8,8-tridecafluorooctyl acrylate) was conducted. The single-dose toxicity study utilized female Sprague-Dawley CD rats, specifically five nulliparous rats, under Good Laboratory Practice (GLP) standards and followed OECD Guideline 420 (Fixed Dose Method). Clinical observations were recorded during the study period, all animals were euthanized and subjected to gross necropsy, including external and internal examinations.

Once you've updated your template, you can regenerate right from the template. (You can still save and continue editing, if desired.)

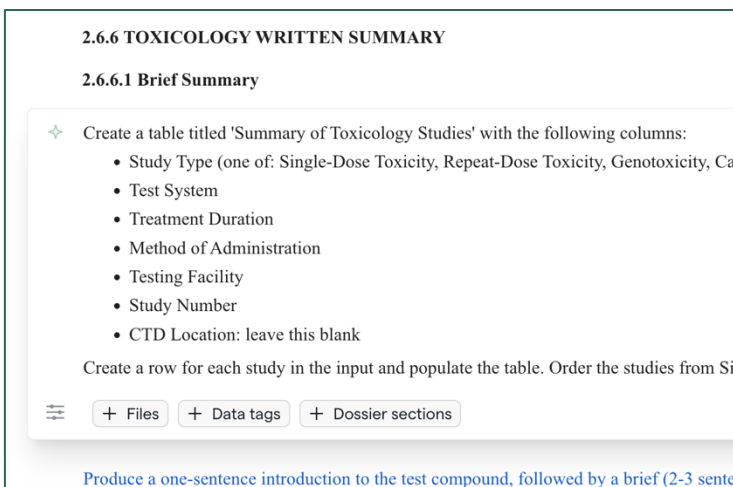


Use a file browser wherever you select files

Whether you're creating a purpose-specific template and want to tag files directly or refining your first draft by editing the source materials, Weave now supports a file browser anywhere you are selecting files. You can still search by name, but you can now use the data room folders to find your content more quickly in the browser.



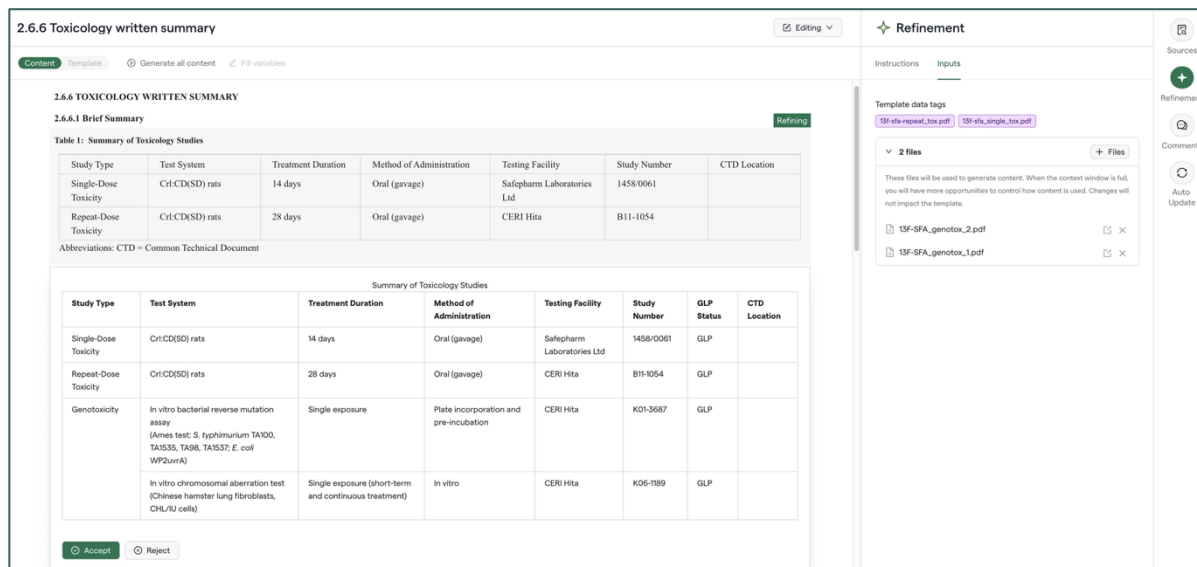
Additionally, the UI for source content selection within the template is improved - the difference between source types is now clearer:



Iteratively build content by controlling context

Get exactly what you want by updating sources. Within refinement, you can now update what sources the AI uses each time you refine your content. You can use this to quickly add content you notice is missing (without regenerating from scratch), or even build out large tables and sections incrementally.

Add an instruction for what to update, then select the files you want to use in the next iteration. The result will incorporate both the existing draft, and the new sources.



Prioritize relevant sections of files

If you're working from a large amount of source information, Weave can now prioritize the content you care about most when refining a section. Add keywords to prioritize the most important source content.

Queries work only on direct word matches. Synonyms or conditional logic should go in refinement instructions. To see exactly what the AI will see, open the file in the data room and review the returned page ranges.

The screenshot displays the 'Refinement' interface. At the top, there are tabs for 'Instructions' and 'Inputs'. Under 'Inputs', there are three purple tags with the text 'clinical-example-saes-in-csrs/b...' and 'clinical-example-saes-in-csrs/g...'. Below this is a section for '3 files' with a '+ Files' button. A blue warning icon indicates 'The context window is full'. A text box contains the keyword 'serious adverse event sae' and a 'Refresh page ranges' button. The bottom section lists three files with their respective page ranges and 'Show more' links.

File Name	Included Pages
clinical-example-saes-in-csrs/gsk-49653-284-clinic...	45% of document • Included pages: 15, 45-148, 151-192, 413-432, 454-485, 491-545, 720-739, 840-924, 934-983, ...
clinical-example-saes-in-csrs/gsk-100344-clinical-...	26% of document • Included pages: 2-134, 282-301, 309-328, 383-414, 430-523, 578-654, 678-702, 727-760, 79...
clinical-example-saes-in-csrs/brl49653-137-clinical-...	7% of document • Included pages: 2-114, 565-584, 771-790, 813-832, 989-1008, 1167-1186, 1220-1239, 1343-13...

























HAQ Manager

Improved response source file identification

More relevant response source files will be returned than before, based on keyword search and question decomposition. The new relevance indicator shows High or Medium or Low for each file, ranked relatively in the context of a question. Relevance statements for each response source file will also be more detailed and specific than previous.

Response source files ✨

These files will be used as input to the generated response.

>	 justification-of-specification.pdf	High		
>	 justification-of-specification.pdf	High		
>	 validation-analyt-procedures-assay-relate...	High		
>	 analytical-procedure-assay-related-subst...	Medium		
>	 stability-summary.pdf	Medium		
>	 drug-substance-characterisation.pdf	Low		
>	 validation-analyt-procedures.pdf	Low		
∨	 drug-product-stability.pdf			

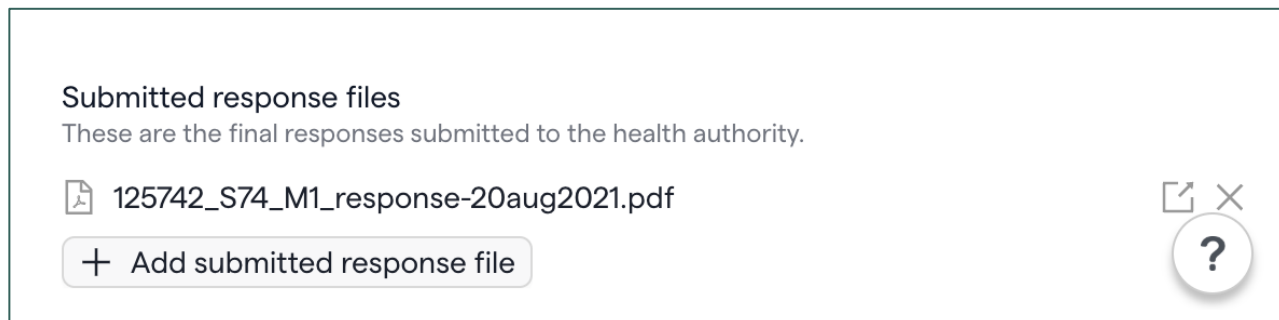
Manually added

+ Add response source file

Adding a response source file will now utilize the same Data Room file selection modal as templates.

Associate final submitted response file to original question file

Close the loop using the new “Submitted response files” section for each question file. Add one or more files to track the final response file submitted back to the health agency.



New and improved functionality

New:

- Source selection in refinement
- Keyword-based prioritization for complex source content
- Ability to associate submitted response files in the Data Room to a question file
- HAQ Manager full table loading state
- HAQ Manager column filtering bug fix
- HAQ Manager table default sort by Added Date column descending

Improved:

- Template tag UI
- Regeneration workflow
- Response source file identification and relevance indicator
- More similar questions identified with a lower threshold