

Results Comparison Table

Llm Result Id	Peer Result Id	Llm Status	Peer Status	Agreement Status	Notes	N Llm	N Peer	N Itx	Llm Reasoning	Peer Reasoning
R7	R7	UNCERTAIN	UNCERTAIN	agree	Both assess forward-looking adaptability/ontology/community claims as UNCERTAIN (shared: C72, C73, C75, C76, C82, C85). LLM also includes C68, C69, C70, C87.	10	6	6	Proposed benefits for reprocessing, artifact/batch-effect analyses, and transparency (C68–C71, C87), broader platform adaptability and extensions (C72–C76), and ontology/incentivization claims (C82, C85) are forward-looking. They are plausible but not supported by empirical case studies, quantitative evaluations, or user adoption evidence in the manuscript.	These forward-looking claims about universal applicability, platform adaptability, ontology development, and community deposition are not validated by data in the reviews. Reviewer 2 specifically requests details on versioning and backwards compatibility (especially for archival contexts), indicating that long-term adaptability and adoption remain to be demonstrated.
R5	R5	SUPPORTED	SUPPORTED	agree	Both support availability via DOI/web resource (C6).	2	1	1	The resource availability via DOI (C6) and the report of 49 assay specifications in the initial release (C74) are concrete, verifiable statements of release content. No additional validation is required beyond the stated availability.	Availability is consistent with reviewer comments noting a linked web page of current specifications. No reviewer disputes the stated availability via the provided resources; instead, they recommend broader release channels (PyPI/Bioconda), reinforcing the notion that the software/spec are accessible.
R5	R6	SUPPORTED	UNCERTAIN	disagree	Count of specifications (C74): LLM supports 49 in initial release; reviewers note a web listing of 38 and seek clarification.	2	1	1	The resource availability via DOI (C6) and the report of 49 assay specifications in the initial release (C74) are concrete, verifiable statements of release content. No additional validation is required beyond the stated availability.	Reviewer 1 notes the web page lists “currently 38” specifications, whereas the manuscript claims 49 in the initial release. This discrepancy suggests a timing or counting mismatch and warrants clarification before the exact number can be considered supported.
R1	R3	SUPPORTED	SUPPORTED	agree	Both support CLI subcommands/integration details for processing tools (shared: C52–C61). Sets are broader on each side but align on overlap.	28	14	10	The manuscript specifies a YAML-based, machine-readable format with Regions/meta-Regions and ordered composition (C30–C33, C43, C47–C48) and enumerates concrete region properties (C35–C42). It also details an operational CLI with explicit subcommands and behaviors (C49–C61). Together these descriptive claims coherently support that the specification and tool exist and perform as stated.	Reviewers acknowledge a command-line utility that extracts information from specifications to parameterize read-processing tools, aligning with the described subcommands and integrations. Reviewer 1 even suggests additional CLI features (e.g., fetching specs by identifier), indicating confidence in and reliance on the existing functionality rather than disputing it.

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R3	R2	UNCERTAIN	SUPPORTED	disagree	Standardization/utility and immediate usefulness (C4, C71, C84): LLM is cautious due to lack of empirical evidence; reviewers are supportive.	4	9	3	While seqspec plausibly facilitates standardization and uniform processing (C4, C71) and is asserted to be immediately useful (C84), no benchmarking, adoption metrics, or cross-assay reproducibility analyses are presented. The generalization to other assay types via modularity (C65) is reasonable but not empirically demonstrated.	Reviewers accept the introduction of seqspec and its CLI and emphasize its value and timeliness. Reviewer 1 describes it as the first attempt to harmonize such metadata across protocols and praises the work; Reviewer 2 calls it important and timely, implying acceptance that the tool enables standardized, uniform processing and innovates beyond current practice.
R2	R3	SUPPORTED	SUPPORTED	agree	Both support that seqspec index/integrations generate parameters for tools (shared: C62–C64).	4	14	3	The authors state that seqspec index generates technology strings and demonstrate implementations for kallisto bustools, alevin-fry, and STARsolo (C62–C64). They further assert seqspec can define options for preprocessing tools (C83); these are capability/implementation claims consistent with the described tool behavior.	Reviewers acknowledge a command-line utility that extracts information from specifications to parameterize read-processing tools, aligning with the described subcommands and integrations. Reviewer 1 even suggests additional CLI features (e.g., fetching specs by identifier), indicating confidence in and reliance on the existing functionality rather than disputing it.
R2	R2	SUPPORTED	SUPPORTED	agree	Both support that seqspec can define options for preprocessing tools (C83).	4	9	1	The authors state that seqspec index generates technology strings and demonstrate implementations for kallisto bustools, alevin-fry, and STARsolo (C62–C64). They further assert seqspec can define options for preprocessing tools (C83); these are capability/implementation claims consistent with the described tool behavior.	Reviewers accept the introduction of seqspec and its CLI and emphasize its value and timeliness. Reviewer 1 describes it as the first attempt to harmonize such metadata across protocols and praises the work; Reviewer 2 calls it important and timely, implying acceptance that the tool enables standardized, uniform processing and innovates beyond current practice.
R4	R1	SUPPORTED	SUPPORTED	agree	Both support that lacking a formal spec limits utility/expandability (C29). LLM also discusses context (C26, C28).	3	12	1	The existence of the prior database (C26) and its HTML, non-machine-readable nature (C28) are factual statements. The inference that lacking a formal specification constrains utility/expandability (C29) is logically consistent with those facts and widely accepted in data standards practice.	Both reviewers affirm the problem framing and need for standardization across diverse protocols. Reviewer 1 calls the approach “of high value” for harmonizing protocol-specific regions and notes the manuscript illustrates the diversity of read structures and the need for harmonization; Reviewer 2 deems the project timely given the growth of new protocols. No reviewer contests the claims about current custom tooling, divergent parameters, or format limitations hindering reuse.

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R3	R3	UNCERTAIN	SUPPORTED	disagree	Generalization/modularity across assays (C65): LLM deems unproven; reviewers accept it within the described functionality.	4	14	1	While seqspec plausibly facilitates standardization and uniform processing (C4, C71) and is asserted to be immediately useful (C84), no benchmarking, adoption metrics, or cross-assay reproducibility analyses are presented. The generalization to other assay types via modularity (C65) is reasonable but not empirically demonstrated.	Reviewers acknowledge a command-line utility that extracts information from specifications to parameterize read-processing tools, aligning with the described subcommands and integrations. Reviewer 1 even suggests additional CLI features (e.g., fetching specs by identifier), indicating confidence in and reliance on the existing functionality rather than disputing it.
R1	R2	SUPPORTED	SUPPORTED	agree	Both support CLI introduction/usage details (C49, C50).	28	9	2	The manuscript specifies a YAML-based, machine-readable format with Regions/meta-Regions and ordered composition (C30–C33, C43, C47–C48) and enumerates concrete region properties (C35–C42). It also details an operational CLI with explicit subcommands and behaviors (C49–C61). Together these descriptive claims coherently support that the specification and tool exist and perform as stated.	Reviewers accept the introduction of seqspec and its CLI and emphasize its value and timeliness. Reviewer 1 describes it as the first attempt to harmonize such metadata across protocols and praises the work; Reviewer 2 calls it important and timely, implying acceptance that the tool enables standardized, uniform processing and innovates beyond current practice.
R7	R2	UNCERTAIN	SUPPORTED	disagree	Platform adaptability claim (C70): LLM is UNCERTAIN; reviewers are supportive.	10	9	1	Proposed benefits for reprocessing, artifact/batch-effect analyses, and transparency (C68–C71, C87), broader platform adaptability and extensions (C72–C76), and ontology/incentivization claims (C82, C85) are forward-looking. They are plausible but not supported by empirical case studies, quantitative evaluations, or user adoption evidence in the manuscript.	Reviewers accept the introduction of seqspec and its CLI and emphasize its value and timeliness. Reviewer 1 describes it as the first attempt to harmonize such metadata across protocols and praises the work; Reviewer 2 calls it important and timely, implying acceptance that the tool enables standardized, uniform processing and innovates beyond current practice.
R1	R4	SUPPORTED	UNCERTAIN	disagree	Schema checking/readability (C51): LLM supports; reviewers question robustness of YAML validation, marking UNCERTAIN.	28	3	1	The manuscript specifies a YAML-based, machine-readable format with Regions/meta-Regions and ordered composition (C30–C33, C43, C47–C48) and enumerates concrete region properties (C35–C42). It also details an operational CLI with explicit subcommands and behaviors (C49–C61). Together these descriptive claims coherently support that the specification and tool exist and perform as stated.	Reviewer 2 raises concrete concerns about YAML pitfalls (booleans, numbers, whitespace) and asks how correctness of manually written files is ensured and whether seqspec check handles this. While the manuscript claims readability and schema checking, the reviewer's questions indicate uncertainty about the sufficiency and robustness of validation for YAML-specific issues.

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R6		SUPPORTED		partial	Visualization/comparison observations (C77–C81) appear only in LLM results; no corresponding peer evaluation found.	5		0	The paper claims that comparing/visualizing seqspecs reveals similarities/differences (C77) and provides specific observations: SPLIT-seq vs SHARE-seq similarity via split-pool barcoding (C78–C79) and sci-CAR barcoding in indices (C80–C81). These are descriptive, citation-backed observations consistent with known assay designs, supporting the result.	