A corpus-based move analysis of highly-cited biochemistry research articles in high-impact Scopus journals

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ABSTRACT
Rhetorically well-structured manuscripts are crucial for achieving successful publication in high-impact international journals. While a plethora of studies have explored the rhetorical structures of research articles across disciplines, scant attention has been given to the move-step patterns in highly cited biochemistry articles. Addressing this gap, the present study examines the rhetorical organization of 30 biochemistry research articles indexed in Scopus to identify structural conventions that characterize impactful scientific writing. Drawing on a qualitative, corpus-based approach, the analysis applied established models to investigate the rhetorical moves in four key sections: Abstracts, Introductions, Methods, and Results and Discussions. The conventionality of moves and sub-steps was assessed using Kanoksilapatham's criteria. Findings reveal that all four sections exhibit conventional rhetorical structures: the abstracts contain four moves (introduction, purpose, product, conclusion), the introductions three (establishing a territory, a niche, the present work), the methods one (describing the study), and the results and discussions two (presenting key results, explaining/discussing effects). However, only a subset of the associated sub-steps met the threshold for conventionality. These findings offer a new rhetorical organization of high-impact research articles in biochemistry and practical implications for biochemistry researchers aiming to enhance the rhetorical quality of their manuscripts and increase their chances of successful publication in international journals.

Keywords: Biochemistry; genre analysis; move analysis; research articles; Scopus

INTRODUCTION

Publishing research articles in English has become indispensable for scholars aiming to achieve greater visibility and impact. In this context, visibility refers to the accessibility of research outputs to the wider academic community, whereas impact denotes the influence of these outputs within and beyond the discipline (Ebrahim et al., 2014; Shahzad et al., 2017; Theodosiadis, 2017). Both dimensions are frequently measured through citation counts, which in turn affect researcher metrics such as the H-Index (Achugbue & Tella, 2023; Baryah et al., 2020). Accordingly, this study focuses on highly cited research articles published in high-impact journals,

as they exemplify both visibility and impact—qualities that scholars worldwide strive to attain.

High-impact journal articles are predominantly published in English, underscoring their central role in the production and circulation of academic knowledge (Di Bitetti & Ferreras, 2017; Kanoksilapatham, 2012; Suherdi et al., 2020, 2021). Beyond extending scholarly reach, English-language publications, particularly those appearing in high-impact journals, enhance both the professional reputation of researchers and the institutional prestige of their affiliations (Coleman, 2014; Kurniawan, 2023; Kurniawan et al., 2024). Moreover, high-quality publications, especially

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those widely cited, are often regarded as markers of academic excellence and influence, since citation frequency remains a key indicator of a research article's impact (Bornmann & Daniel, 2008; Bornmann & Leydesdorff, 2013; Englander, 2014; Wuchty et al., 2007).

Research articles (RAs), as a specialized genre, follow distinct rhetorical structures and linguistic conventions that facilitate disciplinary communication (Li & Ge, 2009; Maswana et al., 2015). Despite disciplinary variation, the IMRD (Introduction, Method, Results, and Discussion) structure is widely adopted as a conventional organizational template (Nwogu, 1997). However, many novice writers continue to struggle with applying this structure effectively, largely due to limited awareness or understanding of the rhetorical moves required in each section (Kurniawan et al., 2024; Wannaruk & Amnuai, 2016). This highlights the need for a deeper understanding of the rhetorical patterns that shape well-structured scientific articles (Kanoksilapatham, 2005; Nwogu, 1997).

Genre analysis, particularly through move analysis, offers a valuable framework for investigating these rhetorical structures. First introduced by Swales in 1981 and refined in his later work (Swales, 2004), move analysis identifies the communicative functions of rhetorical units (moves) and their subcomponents (steps) in academic texts. Understanding these rhetorical patterns enables both writers and readers to recognize common disciplinary conventions and effectively organize and interpret research findings (Kurniawan & Haerunisa, 2023; Parkinson, 2012; Pratiwi & Kurniawan, 2021; Tikhonova et al., 2017).

A substantial body of research has examined the rhetorical organization of research articles across different disciplines and sections, including studies on abstracts (Darabad, 2016; Kurniawan, 2023; Kurniawan et al., 2019; Lubis et al., 2022; Lubis & Kurniawan, 2020; Pho, 2008; Pratiwi & Kurniawan, 2021; Suherdi et al., 2021; Yudhiantara et al., 2024), introductions (Kanoksilapatham, 2012; Kurniawan & Haerunisa, 2023; Luthfianda et al., 2021; Nabilla et al., 2021; Pashapour et al., 2018; Setiawati et al., 2021), methods (Bruce, 2008; Cotos et al., 2017; Musa et al., 2015), and results and discussions (Lubis & Kurniawan, 2021; Peacock, 2002; Suherdi et al., 2020; Tikhonova et al., 2017). Some studies have applied move analysis across full RA texts in both hard sciences (Kanoksilapatham, 2005; Maswana et al., 2015; Nasirizadeh et al., 2022) and soft sciences (Alamri, 2020; Wannaruk & Amnuai, 2016). Collectively, these investigations suggest a broad consensus: while general rhetorical conventions can be identified within individual sections or across complete articles, such conventions vary across (sub)disciplines, reflecting the distinctive epistemological and communicative practices of each field.

Within the hard sciences, biochemistry stands out as one of the most cited fields in recent decades, indicating its robust contribution to contemporary scientific innovation ((Aureliano & Ma, 2025; Van Noorden et al., 2014; van Raan et al., 2003)Noorden et al., 2014; Van Raan, 2003). A key study by Kanoksilapatham (2005) analyzed the rhetorical structures of 60 biochemistry research articles from five top journals. While foundational, this study sampled only 12 articles per journal and did not consider citation frequency as a selection criterion. What is more, this study did not include abstracts as part of the articles to analyze. Consequently, little is known about the rhetorical structures of highly cited biochemistry articles across the complete sections, particularly those indexed in comprehensive databases such as Scopus.

To address this gap, the present study investigates the rhetorical structure of highly cited biochemistry research articles indexed in Scopus. Specifically, it addresses the following research question, i.e., how do move-step patterns manifest across four key sections—Abstract, Introduction, Method, and Results and Discussion in biochemistry articles. By shedding light on the rhetorical strategies employed in impactful biochemistry publications, this study aims to support novice (biochemistry) researchers in crafting structurally effective and internationally publishable manuscripts.

METHOD

As a genre-based study (Hyland, 2009), this research analyzed a total of thirty biochemistry research articles (RAs) indexed in Scopus. The corpus size is deemed adequate for the objectives of the analysis, which concentrated on identifying the communicative intent at the level of phrases, clauses, sentences, and paragraphs across the full sections of the articles. The chosen sample size is consistent with previous genre-based investigations; for example, Nwogu (1997) analyzed thirty RAs in the medical domain, and Alamri (2020) employed an equivalent number in applied linguistics.

The data collection was carried out on citation counts of 29 September 2024 as a reference point. The selection process began by applying filters on Scopus to identify article-type documents published in biochemistry-specific journals, restricted to English-language publications, and sorted by highest citation counts. The focus on highly cited articles was motivated by the assumption that citation counts serve as indicators of research impact; such articles are presumed to exemplify disciplinary standards and thus provide useful benchmarks for novice researchers (Sinatra et al., 2016; Wang et al., 2018). From the resulting list, the fifty most-cited biochemistry RAs were shortlisted without restrictions on the year of publication. A more rigorous selection followed, requiring each

article to follow the conventional IMRD (Introduction, Methods, Results, and Discussion) structure. Ultimately, thirty articles that met these criteria were retained for analysis.

A combination of analytical frameworks was employed to examine each section of the IMRD structure. Hyland's (2000) framework was applied to the abstract section, as it is widely used across disciplines, including in studies by Darabad (2016) and Amnuai (2019). The introduction sections were analyzed using Swales' (2004) Create A Research Space (CARS) model, which has been adopted in both hard sciences (e.g., Kanoksilapatham, 2015; Stoller & Robinson, 2013) and cross-disciplinary studies (e.g., Alamri, 2020; Luthfianda et al., 2021; Setiawati et al., 2021). The methods sections were analyzed using the framework by Cotos et al. (2017), while the results and discussion sections were examined using the model proposed by

Moreno and Swales (2018), which has proven effective in both science/technology and social science fields.

The analytical procedure followed the steps outlined by Nasirizadeh et al. (2022). Each research article was carefully read and its sections segmented. The moves and their constituent steps were then identified in each section using the relevant analytical frameworks and coded accordingly. In the abstract, the units of analysis were typically clauses or sentences, whereas in the other sections, they consisted of sets of sentences within a paragraph. The metadata of each, including citation count, unit of analysis, and move-step categories, was organized in Microsoft Excel (see Table 1). In this study, the quantification focused on the 'salience' of moves, operationalized as the number of articles in which a given move or step appeared (Kurniawan et al., 2019b).

Table 1
Data Coding Sample

Authors	Title	Citation	Section	Unit of analysis	Move	Step
McLean et al., (2010)	GREAT improves functional interpretation of cis-regulatory regions	2817	Introduction	The coupling of chromatin immunoprecipitation with massively parallel sequencing, ChIP-seq, is ushering in a new era of genome-wide functional analysis1–3. Thus far, computational efforts have focused on pinpointing the genomic locations of binding events from the deluge of reads produced by deep sequencing4–8. Functional interpretation is then performed using gene-based tools developed in the wake of the preceding microarray revolution9–11. In a typical analysis, one compares the total fraction of genes annotated for a given ontology term with the fraction of annotated genes picked by proximal binding events to obtain a gene-based P value for enrichment (Fig. 1 and Online Methods).	M1 (Establishing a territory)	S1 (Topic generalizations of increasing specificity)
				This procedure has a fundamental drawback: associating only proximal binding events (for example, under 2–5 kb from the transcription start site) typically discards over half of the observed binding events (Fig. 2a). However, the standard approach to capturing distal events—associating each binding site with the one or two nearest. genes—introduces a strong bias toward genes that are flanked by large intergenic regions12,13. For example, though the Gene Ontology14 (GO) term 'multicellular organismal development' is associated with 14% of human genes, the 'nearest genes' approach associates over 33% of the genome with these genes. This biological bias results in numerous false positive enrichments, particularly for the input set sizes typical of a ChIP-seq experiment (Fig. 2b and Supplementary Fig. 1).	M2 (Establishing a niche)	S1A (Indicating a gap)

To ensure analytical accuracy, following previous researchers (Kurniawan, 2023; Kurniawan et al., 2024; Kurniawan & Lubis, 2020; Kurniawan & Sabila, 2021; Lubis & Kurniawan, 2021, 2022; Pratiwi & Kurniawan, 2021; Putri & Kurniawan, 2021; Suherdi et al., 2020), inter-rater reliability was assessed with the involvement of two expert

linguists experienced in move analysis. A random sample comprising 25% of the corpus (nine articles) was selected for coding, following Kanoksilapatham (2005). Each rater was provided with a table (e.g., Table 1) containing empty columns for move and step categories, which they independently completed by analyzing the texts and identifying the

relevant categories. The raters' results were then compared with those of the researchers through an inter-coder reliability test (Crookes, 1986) using Cohen's Kappa. The agreement rate reached 90%, which, following Orwin and Vevea's (2009) interpretation, indicates a high level of reliability. Any disagreements were subsequently resolved through follow-up discussions between the researchers and the raters.

To determine the conventionality of each move and step, Kanoksilapatham's (2005) criteria were employed. According to the criteria, a move or a step occurring 60% or more of the corpus was classified as conventional, while one appearing in fewer than 60% was categorized as optional.

FINDINGS AND DISCUSSION

This section presents the results of the analysis conducted on thirty highly cited biochemistry research articles (BRAs) indexed in Scopus. It addresses the central research question: how are move-step patterns realized across the four major sections—Abstract, Introduction, Methods, and Results and Discussion—of biochemistry research articles?

Abstract

The abstract section typically conveys the key findings of the research along with the process by which they were obtained (Kurniawan & Sabila, 2021; Lubis et al., 2022; Pratiwi & Kurniawan, 2021; Stoller & Robinson, 2013). It enables readers to grasp the essence of the research at a glance (Suherdi et al., 2021; Tavakoli Gheinani & Tabatabaei, 2017). Therefore, analyzing the abstracts of highly cited articles offers valuable insights into how successful researchers succinctly present their work (Lubis & Kurniawan, 2021). Table 2 summarizes the distribution of rhetorical moves in the abstracts of the thirty BRAs based on Hyland's (2000) five-move framework. The analysis revealed that Move 1 (Introduction) was the most frequently used and achieved conventional status, appearing in all abstracts. This was followed by Move 4 (Product), Move 2 (Purpose), and Move 5 (Conclusion), all of which also reached conventional status. In contrast, Move 3 (Method) did not meet the threshold for conventional status.

Table 2
The Salience of Moves in the Abstract Section

Move	Total of BRAs (n=30)	%	Status
Move 1: Introduction	30/30	100.0	Conventional
Move 2: Purpose	24/30	80.0	Conventional
Move 3: Method	16/30	53.3	Optional
Move 4: Product	26/30	86.7	Conventional
Move 5: Conclusion	22/30	73.0	Conventional

The infrequent use of Move 3 may be attributed to disciplinary conventions in biochemistry, where methodological details in abstracts are often minimized due to the technical nature of the field. Additionally, journal guidelines may influence this pattern by emphasizing the inclusion of broader findings and conclusions over methodological descriptions.

These results contrast with those of Darabad (2016), who found Move 1 to be the least frequently used in applied chemistry abstracts. However, the present findings align more closely with Amnuai (2019), who identified Moves 2, 4, and 5 as conventional in accounting research abstracts. The realizations of the five moves are shown in Example 1.

Example 1:
There is extensive evidence indicating that new neurons are generated in the dentate gyrus of the adult mammalian hippocampus, a region of the brain that is important for learning and memory (1-5) [Move 1]. However, it is not known whether these new neurons become functional, as the methods used to study adult neurogenesis are limited to fixed tissue [Move 2]. We use here a retroviral vector expressing green fluorescent protein that only labels dividing cells, and that can be visualized in live hippocampal slices [Move 3]. We report that newly generated cells in the adult mouse hippocampus have neuronal morphology and can display passive membrane properties, action potentials and functional synaptic inputs similar to those found in mature dentate granule cells [Move 4]. Our findings demonstrate that newly generated cells mature into functional neurons in the adult mammalian brain [Move 5].

(BRAs No. 4)

The findings of this study revealed that all five moves proposed by Hyland (2000) were present in the abstracts of the biochemistry research articles. However, only four of the five moves appeared consistently enough across the dataset to be considered conventional. As illustrated in Example 1, each move is marked by distinct linguistic features, with key lexical items bolded to highlight their rhetorical function.

In Move 1 (Introduction), authors typically provide general background information related to the research topic. For instance, the use of the verb *"is"* indicates a general, non-specific statement, serving to introduce the research area and offer readers a broad understanding of the context. In Move 2 (Purpose), contrastive markers such as

"However" often signal the identification of a gap in the literature, thereby justifying the study's objectives. In Move 3 (Method), verbs like *"use"* were employed to briefly describe the methodological approach taken. Move 4 (Product) featured reporting verbs such as *"report"*, which were commonly used to present the main findings or outcomes of the study. Lastly, Move 5 (Conclusion) often included expressions like *"Our findings…"*, used by authors to summarize the implications or significance of their results.

These linguistic realizations demonstrate that Hyland's (2000) framework offers a practical and effective guide for structuring abstracts in the field of biochemistry. Novice L2 writers can use this framework to ensure clarity, coherence, and

rhetorical effectiveness in presenting their research concisely.

Introduction

The *Introduction* section of the research articles typically addresses key components, as displayed in Table 3, such as the background of the study, gaps identified in previous research, and the purpose behind conducting the study (Kanoksilapatham, 2005; Kurniawan et al., 2024; Kurniawan & Haerunisa, 2023). These components aim to provide readers with a clear understanding of the study's relevance and importance. Given these critical functions, the introduction serves as a basis for evaluating the significance and publishability of the research (Luthfianda et al., 2021).

Table 3
The Salience of Moves and Steps in the Introduction Section

Move/Step	N	%	Status
Move 1: Establishing a territory			
Step 1: Topic generalizations of increasing specificity	30/30	100.0	Conventional
Move 2: Establishing a niche			
Step 1A: Indicating a gap	26/30	86.7	Conventional
Step 1B: Adding to what is known	23/30	80.0	Conventional
Step 2: Presenting positive justification	0/30	0.0	Optional
Move 3: Presenting the present work			
Step 1: Announcing present research descriptively and/or purposively	20/30	66.7	Conventional
Step 2: Presenting RQs or hypotheses	2/30	6.7	Optional
Step 3: Definitional clarifications	1/30	3.3	Optional
Step 4: Summarizing methods	8/30	26.7	Optional
Step 5: Announcing principal outcomes	5/30	16.7	Optional
Step 6: Stating the value of the present research	1/30	3.3	Optional
Step 7: Outlining the structure of the paper	2/30	6.7	Optional

Example 2:
Move 1 (Establishing a territory) Step 1 (Topic generalizations of increasing specificity): Self-assembly and biomineralization are used in biology for fabrication of many composite materials. Bone tissue is a particularly complex example of such a composite because it contains multiple levels of hierarchical organization (1). […]

(BRAs No. 10)

Move 2 (Establishing a niche) was found to be conventional in the present study, although only Step 1A (Indicating a gap) and Step 1B (Adding to what is known) were present and considered conventional. In contrast, Step 2 (Presenting positive justification) was completely absent from the data. Step 1A was frequently employed to highlight gaps in prior research or to suggest areas that warrant further exploration. Step 1B, on the other hand, functioned to propose new investigations that contribute to expanding existing knowledge and enhancing the novelty of the research.

The conventional use of Move 2 has also been documented in prior studies across both hard and soft sciences. For instance, it was found to be

conventional in engineering (Kanoksilapatham, 2005) as well as in applied linguistics (Alamri, 2020; Wannaruk & Amnuai, 2016). Similarly, cross-disciplinary studies (Luthfianda et al., 2021; Nabilla et al., 2021) also identified Move 2 as a common rhetorical element in research article introductions. More specifically, the frequent appearance of Step 1A has been supported by the findings of Davis (2020) and Nasirizadeh et al. (2022), further reinforcing its role as a conventional strategy for establishing a niche in academic writing. The realizations of these steps are shown in Examples 3 and 4.

Example 3:
Move 2 (Establishing a niche) Step 1A (Indicating a gap): …Stress, on the other hand, has been related to decreased cell proliferation and memory impairment (13,14). However, the conclusions from all of these studies are based on correlations. It is still unclear whether newly generated cells that express neuronal markers become functional neuron. […]

(BRAs No. 22)

Example 4:
Move 2 (Establishing a niche) Step 1B (Adding to what is known): … Here, we describe a microfluidic

multiplexing technology and show how it can be used to fabricate silicone devices with thousands of valves and hundreds of individually addressable reaction chambers. […]

(BRAs No. 26)

From the two examples discussed above, distinct linguistic markers characterize each step of Move 2 (Establishing a niche). In Step 1A (Indicating a gap), the use of the transition marker *"However"* signals a clear gap in prior research, serving to contrast existing findings with areas that remain unexplored. Conversely, in Step 1B (Adding to what is known), the linguistic expressions employed typically reflect the researchers' intention to build upon or extend existing knowledge, thereby justifying the continuation of scholarly inquiry.

The final move identified as conventional in this section is Move 3 (Presenting the present work), Step 1 (Announcing present research). This step functions to clearly state the objective of the current study and is frequently accompanied by linguistic markers such as *"The main purpose…"* or *"The aim of the study…"*, which explicitly convey the research intent. The conventionality of this move has also been supported by findings in prior studies, including those in applied linguistics (Wannaruk & Amnuai, 2016) and cross-disciplinary research (Kurniawan et al., 2024; Luthfianda et al., 2021; Nabilla et al., 2021).

Example 5:
Move 3 (Presenting the present work) Step 1 (Announcing present research descriptively and/or purposively): … One of our primary objectives in pursuing this approach was to make the technology easily accessible and compatible with standard instrumentation […]

(BRAs No. 21)

Based on the findings, all the rhetorical moves outlined in the framework were conventionally present in our corpus. Although not every step within each move occurred consistently across all texts, the consistent presence of the three main moves highlights their essential role in structuring the introduction sections. This suggests that Swales' (2004) framework serves as a valuable guideline for researchers in composing well-organized and rhetorically effective introductions in biochemistry research articles.

Method
The method section typically outlines the steps and procedures undertaken during the research process. It provides readers with a detailed account of how the study was conducted, including the instruments used and the techniques applied for data analysis (see Table 4). Offering such comprehensive descriptions helps to ensure the transparency and replicability of the research, thereby supporting the credibility and originality of the findings (Yang, 2022).

Table 4
The Salience of Moves and Steps in the Method Section

Move/Step	*N*	%	Status
Move 1: Contextualizing Study Methods			
Step 1: Referencing previous work	11/30	36.7	Optional
Step 2: Providing general information	5/30	16.7	Optional
Step 3: Identifying the methodological approach	10/30	33.3	Optional
Step 4: Describing the setting	2/30	6.7	Optional
Step 5: Introducing the subjects/participants	4/30	13.3	Optional
Step 6: Rationalizing pre-experiment decisions	5/30	16.7	Optional
Move 2: Describing the Study			
Step 1: Acquiring the data	5/30	16.7	Optional
Step 2: Describing the data	7/30	23.3	Optional
Step 3: Delineating experimental/study procedures	25/30	83.3	Conventional
Step 4: Describing tools	5/30	16.7	Optional
Step 5: Identifying variables	4/30	13.3	Optional
Step 6: Rationalizing experiment decisions	8/30	26.7	Optional
Step 7: Reporting incremental	3/30	10	Optional
Move 3: Establishing credibility			
Step 1: Preparing the data	0	0	Optional
Step 2: Describing data analysis	10/30	33.3	Optional
Step 3: Rationalizing data processing/analysis	4/30	13.3	Optional

As presented in Table 3, among the three moves and sixteen steps proposed in the framework, only Move 2 (Describing the study) and its Step 3 (Delineating experimental/study procedures) were found to be conventional. This finding aligns with previous research by Cotos et al. (2017), which also highlighted the predominance of Move 2 in biochemistry research articles. Similarly, Kanoksilapatham (2005) reported that the step of describing experimental procedures appeared consistently across the biochemistry articles she examined. The realization of this step is shown in Example 7.

Example 7:
Move 2 (Describing the study) Step 3 (Delineating experimental/study procedures): To determine whether retinal ganglion cells innervating the SCN are capable of phototransduction, we labeled them in the rat retina by retrograde transport of fluorescent microspheres injected into the hypothalamus […]

(BRAs No. 18)

This step typically details the methodological approach used in the study, including experimental design, data collection techniques, and other procedural aspects. Given its frequency and functional significance, Move 2 Step 3 can be considered a core rhetorical element in the method sections of biochemistry research articles.

Result and Discussion

The *Results and Discussion* section presents the research findings and elaborates on how these results were obtained (Suherdi et al., 2020). This section plays a vital role in demonstrating whether the research addresses the questions posed in the *Introduction*. It not only displays the data but also interprets and contextualizes it in relation to existing literature. A key aim of this section is to connect the research results with those from previous studies to evaluate their relevance and contribution to the field (Lubis & Kurniawan, 2021). Moreover, it offers an opportunity to introduce new insights and suggest directions for future research. Therefore, this section serves as the cornerstone of a research article, conveying the main findings and evaluating the original hypothesis (Gao & Pramoolsook, 2022).

Table 5
The Salience of Moves in the Results and Discussion Section

Move/Step	N	%	Status
Move 1: Announcing (Function)			
Step 1: Announcing (sub)sections	6/30	20	Optional
Step 2: Announcing or referring the reader to external sources	2/30	6.7	Optional
Step 3: Announcing moves, steps or propositional meaning	9/30	30	Optional
Move 2: Background Information			
Step 1: Restating key features of the current study	15/30	50	Optional
Step 2: Reporting background information with citations	16/30	53.3	Optional
Step 3: Providing background information without citations	4/30	13.3	Optional
Move 3: Summarizing or restating key result			
Step 1: Presenting results neutrally	28/30	93.3	Conventional
Step 2: Contrasting with other results in the study	13/30	43.3	Optional
Step 3: Highlighting results	14/30	46.7	Optional
Move 4: Connecting on key results or other features			
Step 1: Establishing the meaning of results	9/30	30	Optional
Step 2: Comparing with previous research	8/30	26.7	Optional
Step 3: Explaining results or discussing effects	18/30	60	Conventional
Step 4: Making predictions	3/30	10	Optional
Step 5: Reacting to results or other features	2/30	6.7	Optional
Move 5: Evaluating the current study or other research or practice			
Step 1: Pointing out negative features or limitations of the current study	10/30	33.3	Optional
Step 2: Evaluating the state of knowledge or practice in broad terms	2/30	6.7	Optional
Step 3: Stating the contribution of the current study	12/30	40	Optional
Step 4: Pointing out positive features of the current or proposed study	5/30	16.7	Optional
Step 5: Noting specific gaps in knowledge or deficiencies in other research or practice	4/30	13.3	Optional
Move 6: Drawing Implications			
Step 1: Making recommendations for future research or practice	13/30	43.3	Optional
Step 2: Suggesting the applicability of results or usability of outcomes	8/30	26.7	Optional
Step 3: Hypothesizing for future research	5/30	16.7	Optional
Move 7: Elaborating			
Step 1: Justifying what is stated in a neighboring proposition	1/30	3.3	Optional
Step 2: Exemplifying what has been stated in a previous proposition	0	0	Optional
Step 3: Clarifying what has been stated in a previous proposition	1/30	3.3	Optional

As shown in Table 4, among the seven moves in the framework, only Move 3 (Summarizing or restating key results) and Move 4 (Connecting key results or other features) contained steps that were found to be conventional. Specifically, in Move 3, only Step 1 (Presenting results neutrally) was conventionally used. This indicates that the biochemistry research articles analyzed tended to present findings in a neutral and objective manner,

reflecting the data without interpretative bias. Example 8 illustrates the realization of this step.

> *Example 8:*
> Move 3 (Summarizing or restating key results) Step 1 (Presenting results neutrally): … The results of UniFrac analysis revealed that the five Western diet-associated cecal communities were more similar to each other than to the five lean gut communities (Figure 2). As in the ob/ob model of obesity, the Western diet-associated cecal community had a significantly higher relative abundance of the Firmicutes and a significantly lower relative abundance of the Bacteroidetes (Figure 3A). […]
> (BRAs No. 25)

In this study, Move 3 (Summarizing or restating key results) Step 1 (Presenting results neutrally) reports the research results truthfully and are usually descriptive. In the example given above, it can be seen that the writers reported their findings in the table descriptively and typically may begin by using the phrase "The results..." to indicate that the authors refer to the results of the study. This rhetorical practice is consistent with previous findings in other fields. Ruiying and Allison (2003) reported that the move labeled "Reporting Results" was the most frequently occurring in their study, functioning to objectively report findings with statistical evidence or examples. Likewise, Davis (2020) identified a similar step, "Reporting Findings," which appeared across all medical research articles he analyzed.

In addition to Move 3, Move 4 (Connecting key results or other features), Step 3 (Explaining results or discussing effects) was also found to be conventional. The realization of this step is shown in Example 9.

> *Example 9:*
> Move 4 (Connecting key results or other features) Step 3 (Explaining results or discussing effects): … Direct involvement of NK cell alloreactivity is provided by our transplant models, which demonstrate that infusion of alloreactive NK cells eradicates human leukemia in vivo, prepares mice for MHC-mismatched BMT by killing host lymphohematopoietic cells, and reduces GVHD by eliminating recipient-type APCs. In humans as in mice, NK cells had no effect unless the target was susceptible to alloreactive NK cell killing; for instance, they failed to control ALL, a leukemia histotype that is resistant to alloreactive NK lysis in vitro (18). […]
> (BRAs No. 15)

This step involves explaining the reasons behind the results or discussing their implications. Authors may include citations to support their interpretations or provide a rationale for observed outcomes. According to Moreno and Swales (2018), this step focuses on analyzing relationships between different results and offering interpretations of their significance. Given the conventional nature of these moves and steps in the biochemistry articles analyzed, they may be considered essential components for constructing effective Results and Discussion sections in biochemistry research writing.

To recapitulate, ten moves and seven steps were found to be conventional across the corpus. These findings were then synthesized into a proposed framework for writing research articles in biochemistry, as illustrated in Table 6.

Table 6
The suggested framework for writing research articles in the field of biochemistry

	Move/Step No.*	Move/Step No.**	Move Description
Abstract	Move 1	Move 1	Introduction
	Move 2	Move 2	Purpose
	Move 4	Move 3	Product
	Move 5	*Move 4*	*Conclusion*
Introduction	Move 1	Move 5	Establishing a territory
	Step 1	Step 1	Topic generalizations of increasing a
	Move 2	Move 6	specificity
	Step 1A	Step 1A	Establishing a niche
	Step 1B	Step 1B	Indicating a gap
	Move 3	Move 7	Adding to what is known
	Step 1	*Step 1*	Presenting the present work
			Announcing present research
Method	Move 2	Move 8	Describing the study
	Step 3	*Step 1*	*Delineating experimental/study procedures)*
Results and Discussion	Move 3	Move 9	Summarizing or restating key results
	Step 1	Step 1	Presenting results neutrally
	Move 4	Move 10	Connecting on key results or other features
	Step 3	Step 1	Explaining results or discussing effects

*Note: *Move number according to the original framework; **Move number based on the sequence of appearance*

To the best of our knowledge, this framework represents the first contribution within the genre-analysis literature to systematically outline the conventional rhetorical structures of highly cited biochemistry research articles. The suggested framework is designed to support researchers, particularly novice writers, in structuring their articles more effectively and aligning them with the rhetorical norms of the discipline.

It is instructive to compare our model with that proposed by Kanoksilapatham (2005), as both share a comparable focus and corpus context—biochemistry research articles (see Table 7).

Table 7
Comparison of Conventional Moves in This Study and Kanoksilapatham (2005)

	Our results	**Kanoksilapatham (2005)**
Abstract	Move 1: Introduction Move 2: Purpose Move 3: Product Move 4: Conclusion	unknown
Introduction	Move 5: Establishing a territory Move 6: Establishing a niche Move 7: Presenting the present work	Move 1: Announcing the importance of the field Move 2: Preparing for the present study Move 3: Introducing the present study
Method	Move 8: Describing the study	Move 4: Describing materials Move 5: Describing experimental procedures
Results & Discussion	Move 9: Summarizing or restating key Move 10: Connecting on key results or other features	Move 8: Stating procedures Move 9: Justifying procedures or methodology Move 10: Stating results Move 11: Stating comments on the results Move 12: Contextualizing the study Move 13: Consolidating results Move 14: Stating limitations of the study

The comparison reveals notable differences in the realization of moves, particularly within the Results and Discussion section. Kanoksilapatham's study identified a greater number of moves than those observed in the present corpus. One possible explanation is that the authors in our dataset were more selective, prioritizing moves that most directly contribute to the presentation and interpretation of results. This observation, however, warrants further investigation to determine whether such selectivity reflects disciplinary trends or corpus-specific characteristics. Importantly, this comparison underscores the novelty of our proposed framework, that is, it covers the structure of moves and steps of the complete sections of research articles, and it emphasizes practicality and clarity, making it especially valuable as a guide for novice researchers seeking to align their writing with disciplinary conventions.

CONCLUSION

The primary objective of this study was to identify the commonly employed rhetorical structures in highly cited biochemistry research articles indexed in Scopus. Additionally, the study aimed to propose a practical and discipline-specific framework that can serve as a writing guide for future authors in the field. By applying a distinct analytical framework for each section of the research article, the study identified the conventional moves and steps that characterize biochemistry research writing.

Given the increasing pressure to publish in high-impact journals and the growing interest in genre-based approaches to academic writing, the findings of this study offer a valuable contribution to our understanding of rhetorical conventions in biochemistry research. More specifically, the framework can be integrated into learning, teaching, or training modules for English for Research Publication Purposes (ERPP), particularly within higher education contexts. This application is consistent with the recommendations of previous studies (Ahmadi, 2022; Amnuai, 2021; Davis, 2020; Dugartsyrenova, 2020; Farnia & Barati, 2017), which emphasize the importance of discipline-specific genre analyses of international research articles as essential components of instructional materials for novice L2 authors. By providing a clear set of conventional rhetorical structures, the framework is expected to significantly assist these authors in producing credible, well-organized, readable, and persuasive research articles that adhere to disciplinary conventions, thereby enhancing their prospects of publication in high-impact international journals and increasing the visibility of their work through citations.

Nonetheless, it is important to acknowledge the limitations of the current study. These include the relatively small size of the corpus, primarily reflecting communicative norms in high-impact journals, and the lack of detailed analysis of linguistic features such as verb tense usage in each section. Future research is encouraged to address these limitations and expand the analysis to include a broader range of articles—for instance, comparing highly cited versus less cited articles or focusing on emerging journals —and linguistic variables, as well as author linguistic backgrounds, which may reveal new or evolving rhetorical strategies and disciplinary practices.

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APPENDIX

Appendix A: List of Corpus Biochemistry Research Articles

Code	Cited by	Research Article
BRAs 1	8763	Uhlén, M., Fagerberg, L., Hallström, B. M., Lindskog, C., Oksvold, P., Mardinoglu, A., Sivertsson, Å., Kampf, C., Sjöstedt, E., Asplund, A., Olsson, I., Edlund, K., Lundberg, E., Navani, S., Szigyarto, C. A. K., Odeberg, J., Djureinovic, D., Takanen, J. O., Hober, S., … Pontén, F. (2015). Tissue-based map of the human proteome. *Science, 347*(6220), 1260419. https://doi.org/10.1126/science.1260419
BRAs 2	5920	Memczak, S., Jens, M., Elefsinioti, A., Torti, F., Krueger, J., Rybak, A., Maier, L., Mackowiak, S. D., Gregersen, L. H., Munschauer, M., Loewer, A., Ziebold, U., Landthaler, M., Kocks, C., le Noble, F., & Rajewsky, N. (2013). Circular RNAs are a large class of animal RNAs with regulatory potency. *Nature, 495*(7441), 333-338. https://doi.org/10.1038/nature11928
BRAs 3	5417	Milo, R., Shen-Orr, S., Itzkovitz, S., Kashtan, N., Chklovskii, D., & Alon, U. (2002). Network motifs: Simple building blocks of complex networks. *Science, 298*(5594), 824-827. https://doi.org/10.1126/science.298.5594.824
BRAs 4	5024	Farmer, H., McCabe, N., Lord, C. *et al.* Targeting the DNA repair defect in *BRCA* mutant cells as a therapeutic strategy. *Nature* 434, 917–921 (2005). https://doi.org/10.1038/nature03445
BRAs 5	4828	Gabriel, S. B., Schaffner, S. F., Nguyen, H., Moore, J. M., Roy, J., Blumenstiel, B., Higgins, J., DeFelice, M., Lochner, A., Faggart, M., Liu-Cordero, S. N., Rotimi, C., Adeyemo, A., Cooper, R., Ward, R., Lander, E. S., Daly, M. J., & Altshuler, D. (2002). The structure of haplotype blocks in the human genome. *Science (New York, N.Y.), 296*(5576), 2225–2229. https://doi.org/10.1126/science.1069424
BRAs 6	4504	Scarselli, F., Gori, M., Tsoi, A. C., Hagenbuchner, M., & Monfardini, G. (2009). The graph neural network model. *IEEE Transactions on Neural Networks, 20*(1), 61-80. https://doi.org/10.1109/TNN.2008.2005605
BRAs 7	4489	Li, W., Moore, M., Vasilieva, N. *et al.* Angiotensin-converting enzyme 2 is a functional receptor for the SARS coronavirus. *Nature* 426, 450–454 (2003). https://doi.org/10.1038/nature02145
BRAs 8	3914	Bryant, H. E., Schultz, N., Thomas, H. D., Parker, K. M., Flower, D., Lopez, E., Kyle, S., Meuth, M., Curtin, N. J., & Helleday, T. (2005). Specific killing of BRCA2-deficient tumours with inhibitors of poly(ADP-ribose) polymerase. *Nature, 434*(7035), 913–917. https://doi.org/10.1038/nature03443
BRAs 9	3733	Dupont, S., Morsut, L., Aragona, M., Enzo, E., Giulitti, S., Cordenonsi, M., Zanconato, F., Le Digabel, J., Forcato, M., Bicciato, S., Elvassore, N., & Piccolo, S. (2011). Role of YAP/TAZ in mechanotransduction. *Nature, 474*(7350), 179–183. https://doi.org/10.1038/nature10137
BRAs 10	3372	Hartgerink, J. D., Beniash, E., & Stupp, S. I. (2001). Self-assembly and mineralization of peptide-amphiphile nanofibers. *Science (New York, N.Y.), 294*(5547), 1684–1688. https://doi.org/10.1126/science.1063187
BRAs 11	2956	Sun, L., Wu, J., Du, F., Chen, X., & Chen, Z. J. (2013). Cyclic GMP-AMP synthase is a cytosolic DNA sensor that activates the type I interferon pathway. *Science (New York, N.Y.), 339*(6121), 786–791. https://doi.org/10.1126/science.1232458
BRAs 12	2875	Dang, L., White, D., Gross, S., et al. (2009). Cancer-associated IDH1 mutations produce 2-hydroxyglutarate. *Nature, 462*, 739-744. https://doi.org/10.1038/nature08617
BRAs 13	2857	Chen, C. Z., Li, L., Lodish, H. F., & Bartel, D. P. (2004). MicroRNAs modulate hematopoietic lineage differentiation. *Science, 303*(5654), 83-86. https://doi.org/10.1126/science.1091903
BRAs 14	2817	McLean, C. Y., Bristor, D., Hiller, M., Clarke, S. L., Schaar, B. T., Lowe, C. B., Wenger, A. M., & Bejerano, G. (2010). GREAT improves functional interpretation of cis-regulatory regions. *Nature Biotechnology, 28*, 495-501. https://doi.org/10.1038/nbt.1666

BRAs 15   2815   Ruggeri, L., Capanni, M., Urbani, E., Perruccio, K., Shlomchik, W. D., Tosti, A., Posati, S., Rogaia, D., Frassoni, F., Aversa, F., Martelli, M. F., & Velardi, A. (2002). Effectiveness of donor natural killer cell alloreactivity in mismatched hematopoietic transplants. *Science (New York, N.Y.)*, *295*(5562), 2097–2100. https://doi.org/10.1126/science.1068440

BRAs 16   2791   Gorre, M. E., Mohammed, M., Ellwood, K., Hsu, N., Paquette, R., Rao, P. N., & Sawyers, C. L. (2001). Clinical resistance to STI-571 cancer therapy caused by BCR-ABL gene mutation or amplification. *Science (New York, N.Y.)*, *293*(5531), 876–880. https://doi.org/10.1126/science.1062538

BRAs 17   2766   Bodine, S. C., Latres, E., Baumhueter, S., Lai, V. K., Nunez, L., Clarke, B. A., Poueymirou, W. T., Panaro, F. J., Na, E., Dharmarajan, K., Pan, Z. Q., Valenzuela, D. M., DeChiara, T. M., Stitt, T. N., Yancopoulos, G. D., & Glass, D. J. (2001). Identification of ubiquitin ligases required for skeletal muscle atrophy. *Science (New York, N.Y.)*, *294*(5547), 1704–1708. https://doi.org/10.1126/science.1065874

BRAs 18   2705   Berson, D. M., Dunn, F. A., & Takao, M. (2002). Phototransduction by retinal ganglion cells that set the circadian clock. *Science (New York, N.Y.)*, *295*(5557), 1070–1073. https://doi.org/10.1126/science.1067262

BRAs 19   2683   Gillooly, J. F., Brown, J. H., West, G. B., Savage, V. M., & Charnov, E. L. (2001). Effects of size and temperature on metabolic rate. *Science (New York, N.Y.), 293(*5538), 2248–2251. https://doi.org/10.1126/science.1061967

BRAs 20   2554   Olive, K. P., Jacobetz, M. A., Davidson, C. J., Gopinathan, A., McIntyre, D., Honess, D., Madhu, B., Goldgraben, M. A., Caldwell, M. E., Allard, D., Frese, K. K., Denicola, G., Feig, C., Combs, C., Winter, S. P., Ireland-Zecchini, H., Reichelt, S., Howat, W. J., Chang, A., Dhara, M., … Tuveson, D. A. (2009). Inhibition of Hedgehog signaling enhances delivery of chemotherapy in a mouse model of pancreatic cancer. *Science (New York, N.Y.)*, *324*(5933), 1457–1461. https://doi.org/10.1126/science.117136

BRAs 21   2537   MacBeath, G., & Schreiber, S. L. (2000). Printing proteins as microarrays for high-throughput function determination. *Science (New York, N.Y.)*, *289*(5485), 1760–1763. https://doi.org/10.1126/science.289.5485.1760

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