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Research · November 2015

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Rhetorical structure of biochemistry research articles

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Abstract

This paper reports on the results of a move analysis [Swales, J. (1990). *Genre analysis*. Cambridge: Cambridge University Press] of 60 biochemistry research articles. First, a corpus was systematically compiled to ensure that it represents core journals in the focused discipline. Then, coding reliability analysis was conducted to demonstrate that, given a set of coding protocols and systematic training and practice, two individuals could agree upon move boundaries. Finally, move analysis of the corpus was conducted. Based on the findings of the analysis, a two-level rhetorical structure (*moves* and *steps*) is proposed for these texts. This structure consists of 15 distinct moves: three moves for the Introduction section, four for the Methods section, four for the Results section, and four for the Discussion section. This study captures a basic yet complete and representative template of rhetorical organization for structuring biochemistry research articles. The template is useful particularly to native and non-native scientists not only allowing them to better understand published research articles but also facilitating the process of writing research articles for publication.

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1. Introduction

English has acquired the status of an international language, especially for science and technology (e.g., Grabe & Kaplan, 1996; Johns & Dudley-Evans, 1991). As a result, research articles in English have become one of the main channels for distributing and advancing scientific knowledge among scholars world-wide. In the context of globalization and increasing international research collaborations, the ability to read and/or write research articles in English is, thus, crucial for academic and professional success in science and technology. To facilitate the reading and/or writing of scientific research articles, both native and non-native speakers of English need to be aware of, among other things, the rhetorical organization conventionally used in their fields of scientific interest.

In this regard, Swales's (1990) ground-breaking work has generated studies providing valuable insights into the rhetorical structure of individual sections (IMRD) of research articles in various disciplines. However, certain criticism of this line of research has been raised. First, move boundaries are semantically determined; lack of explicit rules for decisions on move boundaries reflects the subjectivity of the judgment (Paltridge, 1994). The absence of rules leads to questions of the reliability and empirical validity of the analysis. In addition, the implementations of Swales' move analysis by subsequent researchers are limited in many aspects. For instance, many move-based studies tend to involve a relatively small number of texts (e.g., Peng, 1987; Williams, 1999; Wood, 1982), limiting the generalizability of the results. Moreover, few move-based studies (e.g., Nwogu, 1997; Posteguillo, 1999) have worked with a representative corpus, thus past claims made by these studies have yet to be substantiated. Finally, many studies (e.g., Brett, 1994; Hopkins & Dudley-Evans, 1988; Yang & Allison, 2003; Samraj, 2002; Swales & Najjar, 1987) focused only on a few individual sections of research articles, rendering an incomplete rhetorical description of the texts. In spite of these limitations, Swales' analytical framework and other researchers' work in move analysis have been essential in popularizing the importance of understanding how research articles are constructed.

The main objective of this study is the identification of the complete rhetorical structure of biochemistry research articles through the use of Swales' move analysis. To overcome the shortcomings of previous research using move analysis, the study includes the following procedures. First, a corpus of research articles representing core journals in biochemistry was compiled; to obtain a more complete description of research articles, the four sections of the article were included in the research (Section 2.1). Next, to assess the reliability of the move identification, an expert in biochemistry coded a subset of the corpus to identify the rhetorical moves of the four sections. Then, inter-coder reliability between the author and the expert was analyzed (Section 2.3). Finally, the four sections of the corpus were analyzed for their rhetorical structure (Section 3). The results of this study provide a basic template for the structuring of academic writing in biochemistry and may be valuable to readers who perceive themselves as having difficulty in understanding research articles, as well as to less experienced writers who need assistance when writing for publications to better meet the international scientific community's expectations and demands.

2. Methodology

2.1. Compilation of the corpus

Previous studies on rhetorical organization have shown that disciplinary variations can have discernible influences on rhetorical structure and language use (e.g., Nwogu, 1997; Posteguillo, 1999; Swales, 1990; Thompson, 1993). To control possible disciplinary variation, the choice of discipline for this study is biochemistry. In spite of the focus on one discipline, this study could potentially benefit learners from multiple yet overlapping disciplines, including those in the basic hard sciences (biology and chemistry), the natural sciences (environmental science and ecology), the health/clinical sciences (medicine, veterinary science, and pharmaceutical science), and the several applied sciences (industrial technology, biotechnology, and food science).

To insure that the results obtained from the move analysis would be generalizable to the target discourse, the top five journals in biochemistry were selected. Based on the impact factor¹ reported in *Journal Citation Reports* (1999),² the five journals in biochemistry published in the United States in the year 2000 were *Cell* (C), *Molecular Cell* (MC), *Molecular and Cellular Biology* (MCB), *Journal of Biological Chemistry* (JBC), and *Molecular Biology of the Cell* (MBC). Twelve articles were randomly selected from each journal (e.g., C1–C12, MC1–MC12, etc.), yielding a corpus of 60 biochemistry research articles of approximately 320,000 words.

2.2. Swales' framework and the analysis of the corpus

Move analysis, as articulated by Swales, represents academic research articles in terms of hierarchically organized text made up of distinct sections; each section can be subdivided into moves, and each move can be broken down into steps. According to Swales's (1990) model, the Introduction section includes three basic moves: the beginning move of Move 1: Establishing a territory (establishing the topic), followed by Move 2: Establishing a niche (justifying the present study), and concluded by Move 3: Occupying a niche (describing the present study). Each move can be realized by one or a series of "steps" (Swales, 1990). For example, Move 1 is realized by claiming interest or importance of the topic (Step 1), making topic generalization (Step 2), and reviewing items of previous literature (Step 3). Swales'

¹ The impact factor is the average number of times articles that are published in a specific journal in the two previous years were cited in a particular year. This figure is useful in clarifying the significance of absolute citation frequencies.

² *Journal Citation Reports* is a multidisciplinary database that presents statistical data that systematically provides an objective and quantitative way to determine the relative importance of journals within a broad range of subject categories. The science edition of *Journal Citation Reports* covers about 5,000 leading international science journals. A number of quantitative measures are used for ranking, evaluating, categorizing, and comparing journals. These measures include *total cites*, *impact factor*, *cited half-life*, *immediacy index*, and *total articles*. For more details on definitions of these terms and their calculation, refer to the reference guide accompanying *Journal Citation Reports* (1999: 9).

framework has been successfully extended to other sections of research articles in various academic disciplines (e.g., Nwogu, 1997, on medicine; Peng, 1987, on chemical engineering; Posteguillo, 1999, on computer science; Thompson, 1993, on biochemistry; Wood, 1982, on chemistry).

Following Swales' analytical framework of move analysis, textual boundaries between moves in each section were identified based on content and linguistic criteria. Move 1 (particularly Move 1, Step1: Claiming the centrality of the topic) was selected to elucidate how move boundaries can be determined by, in addition to the content, the linguistic exponents. The realization of this move and step identified from this biochemistry corpus with the linguistic exponents of claiming centrality highlighted is shown in examples (1)–(5).

- (1) *Cell–cell adhesion is **critical** for tissues and organs.* [C9]
- (2) *Protein degradation **plays an important role** in a wide array of cellular events.* [MC8]
- (3) *Iron–sulfur (Fe–S) cluster prosthetic groups **play a key role** in a wide range of enzymatic reactions, as well as serving as regulatory switches.* [MCB6]
- (4) *The angiotensin-converting enzyme (ACE) **has long been** regarded as a central player in the renin–angiotensin system through its action in converting angiotensin I to the vasopressive peptide.* [JBC8]
- (5) *Vesicle transport is **important** in eukaryotic cells for the addition of material to the plasma membrane, for secretion, and for cell polarity.* [MBC4]

Then, the frequencies of individual moves in each section were recorded to determine if a particular move occurred frequently enough to be considered conventional. In this regard, the cut-off frequency of 60% of occurrence was arbitrarily established as a potential measure of move stability for any move posited in this study. Specifically, to be recognized as a conventional move, a move must occur in 60% of the appropriate sections in the corpus. If the frequency of a move falls below 60%, it is considered optional.³ All possible variations that characterize each move and the sequence of moves in each section were identified. Finally, a rhetorical structure for each section was proposed.

2.3. Reliability of move identification

Inter-coder reliability was conducted to demonstrate that a unit of text can be defined in such a way that different individuals can demarcate the boundary of units at a sufficiently high level of agreement. The only move-based study that reported the use of coders to assess coding reliability is Crookes's (1986) study, in which graduate

³ Having a 40% omission cut-off for conventional moves may seem a bit high. However, given the fact that this study aimed to establish which rhetorical moves are more conventional than the others, the rather high cut-off frequency would be beneficial in enhancing the distinction between the two categories of moves.

students in ESL coded research articles in the hard sciences, bio-sciences, and social sciences. Crookes, however, cautioned that these students might not be appropriate as coders, possibly due to their lack of understanding of the topics of scientific research articles. To insure that the coder has expertise in the focused discipline, a Ph.D. candidate in biochemistry served as a coder for this study.

The author conducted a two-hour training session for the coder to become acquainted with the use of the coding system devised by the author and to assure that the coder clearly understood how to code a sample text using the coding scheme. Following this training, the coder was asked to practice coding four randomly selected texts representing the four conventional sections of a research article. After the coding of each section was completed, both the coder and the author went through the text to identify any coding disagreements. Difference in coding led to discussion, negotiation, and clarification of the criteria for coding assignments. Finally, the coder independently coded the four sections of 15 research articles (or 25% of the entire corpus) randomly selected from the five journals.

Given the categorical variables of rhetorical moves, this study used Cohen's κ (Cohen, as cited in Orwin, 1994) to assess the inter-coder reliability of the move coding in each section of each research article. In addition, percentage agreement was also computed to illustrate the level of inter-coder reliability and similarities/differences yielded by the two calculations as shown below:

Results of inter-coder reliability analysis of the four sections

Section	Cohen's κ	Percentage
Introduction	.93	97.58
Methods	.81	96.35
Results	.90	93.16
Discussion	.88	93.02
Average	.88	95.03

Cohen's κ has an upper limit of 1.00 and a lower limit of 0.00 (Brown, 1996). The rules for the interpretation of Cohen's κ are summarized as follows: less than .40 \rightarrow poor, .40–.59 \rightarrow fair, .60–.74 \rightarrow good, and more than .75 \rightarrow excellent (Fleiss, as cited in Orwin (1994)). The figures above indicate that, in spite of some divergences in move coding, high overall inter-coder reliability of identifying rhetorical moves between the author and the coder across the four sections was attained. The findings show that move boundaries were reliably identified by different individuals, suggesting that moves or rhetorical units have psychological reality. The correlations between the researcher's and the coder's coding for each section of research articles were summarized in Appendix A, showing the total number of units coded, the number of units that both the researcher and the coder agreed upon and disagreed upon for each move in each section, the κ value, and the percentage agreement.

3. Results of move analysis

A structure of 15 rhetorical moves – three in the Introduction section, four in the Methods section, four in the Results section, and four in the Discussion section – are presented in [Appendix B](#). These moves were numbered 1–15, reflecting the order in which they most often appeared in the corpus. The model does not claim that these moves only occurred linearly in these positions; in fact, Move 4 and Move 5, Move 8 and Move 9, and Move 10 and Move 11 were typically interwoven. The following sections describe the characteristics of possible variations and the assignment of each move as either conventional or optional.

3.1. The introduction section

The function of Introductions is to contextualize a research study being presented in the relevant literature, claim its novelty, and present main features of the study (Swales, 1990). Based on the cut-off of a 60% occurrence rate, all moves identified in Introductions of biochemistry are conventional.

Move 1: Announcing the importance of the field asserts the importance of the topic of study. Congruent with Swales' framework, Move 1 in this corpus is realized by three variations. **Step 1: Claiming the centrality of the topic** assures that the article developed on the topic is worth investigating and the field is well established. **Step 2: Making topic generalizations** gives overviews about the subject of the study. **Step 3: Reviewing previous research** reports previous research deemed to be relevant to the topic being discussed. The realization of Move 1, Steps 1–3 is illustrated in examples (6)–(11).

Move 1, Step 1: Claiming the centrality of the topic

- (6) *Protein degradation plays an important role in a wide array of cellular events.* [MC8]
- (7) *Iron–sulfur (Fe–S) cluster prosthetic groups play a key role in a wide range of enzymatic reactions, as well as serving as regulatory switches.* [MCB6]

Move 1, Step 2: Making topic generalizations

- (8) *The hammerhead ribozyme (R) is arguably the best-characterized ribozyme.* [MC2]
- (9) *Protein export pathways are less well characterized, although...* [MCB8]

Move 1, Step 3: Reviewing previous research

- (10) *Double-stranded RNA (dsRNA) induces potent cellular responses in diverse biological systems (R).*⁴ [MC11]

⁴ In all of the examples presented in this paper, attributions to previous studies in the corpus were replaced by **R** (Reference).

- (11) *The movement of lipid and protein components between intracellular organelles requires the regulated interactions of many molecules (R).* [MBC12]

Of all variations of Move 1, Step 3 is invariably present and consistently recognized throughout the biochemistry Introductions, resulting in the “cyclical” or “recursive” occurrence of this move and reflecting the richness of current literature in biochemistry. In contrast, Introductions in computer science do not always have Move 1, Step 3, most likely due to the relatively short history and heavy commercial involvement of computer science (e.g., Cooper, 1985; Hughes, 1989; Posteguillo, 1999). The contrastive findings about the use of Move 1, Step 3 suggest that disciplinary variation is discernible and that scholars can benefit from knowing conventional practices in their own disciplines.

Move 2: Preparing for the present study draws scientists’ attention to weakness in the existing literature and asserts that a particular research question requires an answer. Unlike Move 1, which is always present, Move 2 was recognized in 40 Introductions or 66.66% of the corpus. The data show that Move 2 has two variations: **Step 1: Indicating a gap** and **Step 2: Raising a question**. The realization of Move 2, Steps 1 and 2 is illustrated in examples (12)–(15).

Move 2, Step 1: Indicating a gap

- (12) *The mechanism of processing the nature, 184nt 6S RNA from its precursor has not been characterized.* [C6]
 (13) *Consequently, how related the serotonin N-acetyltransferase catalytic mechanism will be to that of other superfamily members is unclear.* [JBC7]

Move 2, Step 2: Raising a question

- (14) *The key (as yet unresolved) questions in analysis of dsRNA-associated PTGS are (1) Why are both strands required in the trigger RNA? and (2) How can dsRNA exert an effect at concentrations that are substantially lower than those of the endogenous target RNA?* [MC11]
 (15) *Is conformational stability a determinant of rebonuclease cytotoxicity?* [JBC6]

Move 2, Step 1 is pervasive in this corpus, being used in 38 out of 40 Introductions that have Move 2. Move 2, Step 2 is not as frequently used as Move 2, Step 1, as it is found in only six of the 40 Introductions. Similar to Move 1, the cyclical patterning of Move 2 is common, suggesting that the study being presented is complex, accounting for various gaps of previous research.

Move 3: Introducing the present study consists of three steps in this biochemistry corpus. **Step 1: Stating purpose(s)** is characterized by a statement of purpose(s) of the study or by an explicitly stated research question. **Step 2: Describing procedures** focuses on the main features of the study being reported, and **Step 3: Presenting findings** announces the principal findings of the study. The realization of Move 3, Steps 1–3 is illustrated in examples (16)–(21).

Move 3, Step 1: Stating purpose(s)

- (16) *The current investigation was undertaken to accomplish the following: (1) to establish whether P. carinii cell wall assembly occurs through action of a Gsc-1 protein mediating Beta-1 3-glucan synthesis; (2) to clone and characterize the... [JBC12]*
- (17) *The present study was designed to evaluate whether the efficiency and carrier ligand specificity of replicative by pass past Pt-DNA abducts by Poβ could be determined by the mode of translesion synthesis and whether... [JBC4]*

Move 3, Step 2: Describing procedures

- (18) *We therefore investigated AJ formation in primary keratinocytes, which has led us to novel insights. When perfectly contact-inhibited primary cells are stimulated, they form intercellular junctions by an active and dynamic process, driven by actin filament polymerization. This remarkable mechanism involves the calcium-activated production of filopodia, which penetrate and embed into neighboring cells... [C1]*
- (19) *In the study presented herein, we investigated proteins from S. cerevisiae that exhibit strong homology to the bacterial IscA product of the isc gene cluster. Two proteins, designated Isa1p and Isa2p, contain a C-terminal region exhibiting at least 50% similarity to bacterial proteins encoded by orf6 in the nif operon and by iscA in the isc operon, respectively. [MCB6]*

Move 3, Step 3: Presenting findings

- (20) *Our results show that U2snRNP is functionally associated with the E complex and is also required for its assembly. [MC5]*
- (21) *We show that c-Myc proteolysis is mediated by the ubiquitin-proteasome pathway in vivo. We also demonstrate that two regions of the c-Myc protein are important for rapid degradation, a central PEST sequence unnecessary for c-Myc ubiquitination, and an N-terminal region required for efficient ubiquitination. Furthermore, we show that c-Myc is stabilized in a number of Burkitt's lymphoma cell lines... [MCB4]*

In congruence with Swales and Najjar's (1987) study of physics articles, Move 3, Step 3 is frequent in biochemistry Introductions, indicating that announcing the important results of the experiments is not withheld until the Results and Discussion sections. However, as noted by Swales (1990) and shown in the above examples, even though the principal finding is announced, the information concerning the finding is kept to a minimum, consisting of only a brief and specific statement of principal findings. It appears that the scientists would like to withhold details of the findings until the Results section. Move 3 Step 3, which serves as a preview of the entire findings in the Introduction section, is probably used as an attention-catcher device, motivating the readers to read further to understand how the researcher(s) arrived at the finding.

3.2. The methods section

The Methods section generally describes procedures used in the study being reported. Four moves are identified in the biochemistry corpus; two moves are conventional and the other two are optional.

Move 4: Describing materials covers a wide variety of materials used in biochemistry ranging from natural substances, human/animal organs or tissues, to chemicals (e.g., cell lines, antibodies, plasmids, enzymes, nucleotides, microsomes, membranes, serum, proteins, medium, strains, genes, transporons, DNAs). Move 4 can be realized as **Step 1: Listing materials** explicitly itemizing materials or substances used in the study, **Step 2: Detailing the source of the materials** identifying how these items are obtained, such as, by purchase, as a gift, etc., and **Step 3: Providing the background of the materials** including the description, properties, or characteristics of the materials. The realization of Move 4, Steps 1–3 is illustrated in examples (22)–(26).

Move 4, Step 1: Listing materials

(22) *Bacterial strains used in this study and their origin are listed in Table 3.* [C8]

Move 4, Step 2: Detailing the source of the materials

(23) *COS-7 cells were obtained from S.Brandt (Vanderbilt University, Nashville, Tenn).* [MCB4]

(24) *Microsomes derived from samples of human renal cortex were obtained from the Human Cell Culture Center (Laurel, MD), from the International Institute for the Advancement of Medicine (Scranton, PA), and from Dr. Barbara Haehner-Daniels (Indiana University, Indianapolis, IN).* [JBC2]

Move 4, Step 3: Providing the background of the materials

(25) *Antisense riboprobe for RNase protection assay contains the murine mdm2 cDNA fragment spanning from nt+264 to nt +3 (R).* [C10]

(26) *The fun 12 strains J130 and J133 were described previously (R).* [MC10]

The prevalence of this move, particularly Move 4, Step 2, in biochemistry research articles indicates the collaboration and solidarity among scientific institutions involved in scientific experiments. In addition, Move 4, Step 3 shows that due to the common background knowledge of substances in biochemistry, the description of the substances investigated can be captured by a phrasal expression like “*described previously*” in (26).

Move 5: Describing experimental procedures indicates that biochemistry as a discipline is well established and its procedures, methods, and techniques are usually protocolized. This move has three variations or steps. **Step 1: Documenting established procedures** recounts an experimental process that is already established by previous researchers. As a result of the standardization of experimental procedure, simple reference to the specific name of the method or procedure used to conduct research is adequate. Occasionally, certain procedures are unique or unorthodox for a particular study. In such cases, **Step 2: Detailing procedures** is used to provide detailed description of the procedures to enable future research replication. Move 5 can also be realized by **Step 3: Providing the background of the procedures**, providing justification for the choice of technique or procedure, and comments or observations made during the experiment (Step 3). The realization of Move 4, Steps 1–3 is illustrated in examples (27)–(31).

Move 5, Step 1: Documenting established procedures

- (27) *The syd² mutant was identified by screening in 3rd chromosome EMS lethal lines (bq; st (3)EMS/TM6B, TB) obtained from Charles Zuker (UCSD) as described previously (R).* [C11]
- (28) *Detection employed the ECL kit (American Pharmacia Biotech) according to the manufacturer's specification.* [MCB6]

Move 5, Step 2: Detailing procedures

- (29) *Proteins in both fractions were precipitated by the addition of 4 volumes of cold acetone, collected by centrifugation, and resuspended in electrophoresis sample buffer.* [MBC7]

Move 5, Step 3: Providing the background of the procedures

- (30) *Complete details of all constructions will be provided upon request.* [JBC10]
- (31) *They were referred to as Cre-Mate mice, since the nature of the gene targeted for conditional ablation in the epidermis was irrelevant for that study.* [C1]

Move 4 and Move 5 of the Methods section are highly interwoven and recursive, as shown in the following example of (32):

DNA Construction

- (32) **(S1)** *The following murine expressed sequence tag (EST) clones were obtained from the American Type Culture Collection (Manassas, VA): GenBank Accession Nos. AA000682, W09622, AA119182, AA017916, and W09622. (S2) The plasmid DNA was isolated and sequenced. (S3) These EST clones and the full length cDNA of SH3P7/mAbp1 in pExkix were used to generate the different constructs used in this study. (S4) The serine 235 colon for which we found a polymorphism was included in all generated plasmids containing this region. (S5) To construct glutathione S-transferase (GST)-mAbp1 fusion plasmids for expression in bacteria, DNA sequences encoding either the full-length protein (aa-433) or truncations were amplified by PCR using primers that generate BamHI and HindIII sites at the 5' and 3' ends, respectively. .* [MBC1]

In the above example, the source of the substances investigated is identified (Move 4, Step 2) in S1. After providing information concerning material preparation (Move 5, Step 1) in S2, the section moves on to mention materials that are readily available (Move 4, Step 1) in S3. Then, the section describes procedures in detail (Move 5, Step 2) in S4 and S5. The example depicting the interplay between Moves 4 and 5 raises the possibility that the order of these two moves might not be fixed in biochemistry research articles.

Move 6: Detailing equipment provides detailed information regarding the setting of the apparatus used for a particular task in an experiment, the information crucial for future research replication. Commonly used apparatuses in biochemistry include microscopes, cameras, spectrophotometers, etc. Only six of 60 research articles or 10% of the corpus contained this move, as in examples (33) and (34).

- (33) *Ultraviolet and visible absorbance measurements were made with a Cary 3 double beam spectrophotometer equipped with a Cary temperature controller from Varian (Sugar Land, Texas).* [JBC6]

- (34) *Images were recorded through a Hamamatsu C-2400 New vicon camera using a 10 x objective and brightfield optics. Video images were digitized at a rate of 6 frames/min as described above. [MBC8]*

Move 7: Describing statistical procedures is used in only eight of 60 research articles or 13.33% of the corpus. The realization of Move 7 is illustrated in examples (35) and (36).

- (35) *The t-test was used to statistically compare the individual ratios from two given strains. [MC1]*
- (36) *The data were fitted to the Michaelis–Menten Equation 1 by using a non-linear least squares approach and the kinetic constants \pm SE. [JBC7]*

The four rhetorical moves identified in the Methods section vary widely in terms of their occurrence. The two central moves are **Move 4: Describing materials** and **Move 5: Describing experimental procedures**. In sharp contrast, **Move 6: Detailing equipment** and **Move 7: Describing statistical procedures** were rarely found and are thus considered optional. However, Moves 6 and 7, if present, tend to be interwoven with the pervasive Move 5 and are likely to end the Methods section. The low occurrence of Moves 6 and 7 interestingly raises further questions as to whether these two moves indicate an emerging trend in biochemistry or accommodate the uniqueness of the study being reported.

3.3. The results section

The Results section is generally perceived to describe the findings in an ostensibly objective manner. However, as will be shown later, the Results sections of biochemistry research articles investigated in this study do not seem to conform to such typical nomenclature. The four moves comprising the Results section of this corpus are conventional.

Move 8: Stating procedures explains *why* and *how* the data of the study have been produced. This move occurs frequently in 95% of the corpus and can be realized by various steps. **Step 1: Describing aims and purposes** states aim(s) or purpose(s) of the study. **Step 2: Stating research questions** explicitly states research questions. **Step 3: Making hypotheses** presents hypothetical statements. **Step 4: Listing procedures or methodological techniques** details the procedures or methodological techniques employed in the data production. The co-occurrence of these steps of Move 8 is quite common as illustrated in examples (37) and (38).

Move 8, Step 1: Describing aims and purposes and Step 4: Listing procedures or methodological techniques

- (37) *To determine whether these GTPases participate in the phagocytosis of *P. aeruginosa*, we expressed guanine nucleotide binding-deficient alleles of *Rac1* or *Cdc42*, or a GAP for both proteins, in RAW LR²FMLPR.2 cells, and performed association and phagocytosis assays. [JBC1]*

Move 8, Step 3: Making hypotheses, Step 1: Describing aims and purposes, and Step 4: Listing procedures or methodological techniques

- (38) *Mondo A and Mlx heterodimerize are predicted, based on primary amino acid sequences, to bind CACGTG E-box sequences. To determine whether p19 cells contained E-box binding activity associated with MondoA-Mlx heterodimers, P19 cytoplasmic extracts were incubated with double-stranded CACGTG oligonucleotides immobilized on beads and following extensive washing, retention of MondoA Mlx heterodimers on the DNA beads was determined by Western blotting.* [MCB12]

In (37), Move 8 is expressed as a statement of aim (Step 1), followed by procedures used in the study (Step 4). As found in (38), Move 8 includes Step 3 of a hypothetical statement (*Mondo A and Mlx heterodimerize are predicted*), Step 1 of a research aim (*To determine...*), and Step 4 of a procedure (*P19 cytoplasmic extracts were incubated...*).

Given the existence of the preceding Methods section, Move 8 does not provide novel information about the study being reported. This move, however, highlights some crucial information of the preceding Methods section and prepares the readers for the findings or Move 10 (Statement of results) in the Results section, to be discussed.

Move 9: Justifying procedures or methodology provides the rationale for the scientists' decision to use particular experimental methods, procedures, or techniques. This move can be expressed by **Step 1: Citing established knowledge of the procedure** and **Step 2: Referring to previous research**. Both steps either cite the established findings or refer to the findings of the previous research that have an impact on the choice of procedures. The realization of Move 9, Steps 1 and 2 is italicized in examples (39) and (40).

Move 9, Step 1: Citing established knowledge of the procedure

- (39) (We chose the more precisely defined LSTer region over the RSTer region for analysis.) *LSTer region contains two approximately equivalent arrest sites, LSTer 2, separated by about 27 kbp (R).*...[MC12]

Move 9, Step 2: Referring to previous research

- (40) ...*However, both identified murine GBPs had C20-type Cax motifs, and the mGBP1 protein appeared to be successfully C20 modified (R).* (Therefore, mGBP1 was examined to determine if it would also be C20 modified or might instead be farnesylated.) [MBC7]

Move 9 is rather unique in biochemistry research articles because it was not reported in move studies in other disciplines (e.g., computer science: Posteguillo, 1999; social science: Brett, 1994; or medical science: Williams, 1999). This move was first recognized in biochemistry research articles⁵ by Thompson (1993) who

⁵ Thompson (1993) analyzed 16 biochemistry research articles authored by a Nobel Prize Winner. Therefore, the prevalent use of Methodological Justification Move found in Thompson's corpus might reflect the author's idiosyncrasy rather than biochemists in general.

identified it in 93.75% or in 15 out of 16 research articles analyzed. In the present investigation, Move 9 occurs in 71% of the articles, verifying the trend of this procedural justification move in biochemistry. As Thompson claimed, the use of Move 9 implies that scientists do not feel research results can persuasively speak for themselves. To gain acceptance from the larger scientific community, the results have to be carefully situated, assuring the reader that the results have been obtained from a sound and justified methodology. The presence of the move also indicates that a procedural choice is not assumed, and scientists must justify a preference for one particular technique rather than other options.

Move 10: Stating results highlights the results obtained from the study. Move 10 can be realized by two steps: **Step 1: Substantiating results** and **Step 2: Invalidating results**. Step 1 indicates the validity of the finding; the scientists are making an appeal to the scientific community that their results should be a part of the consensual knowledge of the field. Step 2 highlights a difference between the result of the current study and that of previous studies, suggesting to the scientific community that the scientists are contributing something novel that might be worth further investigation. The realization of Move 10, Steps 1 and 2 is illustrated in examples (41)–(44).

Move 10, Step 1: Substantiating results

- (41) *We were not able to target the endogenous E. coli 6S RNA with antisense oligonucleotides. Secondary structure predictions and the observation that 6S RNA in extracts is relatively resistant to nuclease digestion suggest that the E. coli 6S RNA is highly structured and does not contain single-strained regions accessible for binding and exogenous oligonucleotide.* [C6]
- (42) *Full length VASP-GFP localized to adhesion zippers and cell–cell borders with no obvious deleterious effects (Figs. 6A–D). This was true in the majority (>90%) of transfected cells, even those that fluoresced highly with GFP (examples shown).* [C1]

Move 10, Step 2: Invalidating results

- (43) *However, there is a 6S-like RNA in the genomic sequence of Haemophilus influenzae that has an insertion of 13 nt at the end of the predicted stem of the E. coli 6SRNA.* [C6]
- (44) *In contrast, TD-GFP interfered with formation of adhesion zippers and epithelial sheets (Figs. 6E–H).* [C1]

It is also common to find these two steps of Move 10 co-occur in the corpus as shown examples (45) and (46).

Move 10, Step 1: Substantiating results and Step 2: Invalidating results

- (45) *The C65A/C72A/G88R and C40A/G88R/C95A variants are approximately 90 and 60% folded at 37 C, respectively (data not shown). Compared with G88R Rnase A, the T_m values for the C65A/C72A/G88R and C40A/G88R/C95A variants are decreased by 18.1 and 13.6 C, respectively. In contrast to these variants, wild type Rnase A and the G88R, A4C/G88R/V118C, and A4C/C65A/C72A/G88R/V118C variants are folded at 37 C.* [JBC6]

- (46) *Cultures shifted to glucose are blocked in [³H] inositol incorporation into protein, whereas the control culture in galactose remains capable of incorporating this precursor (Fig. 3).* [MBC5]

As shown in the above examples, this move is typically accompanied by a pointer (e.g., *Fig. 1, data not shown, examples shown*, etc.). **Move 10: Stating results** is the most central move of the Results section, occurring in 100% of the corpus. Like certain moves in the Introduction and Methods sections, Move 10 is cyclical, demonstrating the complexity of a single study that entails a number of results. Each result is, in turn, objectively presented.

Move 11: Stating comments on the results presents the scientists' subjective comments, which are not absolutely established by the data; it occurs in 91% of the articles. Move 11 is realized variously as **Step 1: Explaining the results**, **Step 2: Making generalizations or interpretations of the results**, **Step 3: Evaluating the current findings with those from previous studies or with regard to the hypotheses**, **Step 4: Stating limitations**, and **Step 5: Summarizing**. Like Move 10, Move 11 is frequently found in the corpus. Moreover, the co-occurrence of Move 10 and Move 11 is very common, as shown in examples (47)–(49).

Move 10 and Move 11, Step 2: Making generalizations or interpretations of the results

- (47) Move 10. *an inhibitor of lysosomal cysteine proteases (R), had a significant effect on c-Myc degradation (Fig. 1B).*
Move 11, Step 2 *These results suggest that proteolysis of c-Myc is proteasome dependent.* [MCB4]

Move 10 and Move 11, Step 5: Summarizing

- (48) Move 10. *exhibited more frequent lateral pseudopod activity and more frequent changes in direction (see arrows, Fig. 7B).*
Move 11, Step 5 *Together, these results demonstrate that reg A⁻ cells are capable of assessing the direction of a spatial gradient of cAMP and moving in a directed manner, but. . .* [MBC8]

Move 10 and Move 11, Step 1: Explaining the results

- (49) Move 10 *Our results determine localization of these mutants in vivo using GFP-tagged Ste18p.*
Move 11, Step 1 *We presume that the localization of GFP-tagged Ste18p is representative of native Ste18p because the wild-type fusion protein rescues mating in a ste18 strain.* [MBC3]

The above examples show that the Results section in biochemistry research articles not only reports data but also comments on them, a deviation from the style prescribed in a manual for writing for publications. For instance, as stipulated by [Publication Manual of the American Psychological Association \(1996\)](#), the Results section should focus exclusively on the results of the study, leaving all subjective evaluation and comments to the Discussion section. Clearly, such a rigid boundary

does not seem to exist in this biochemistry corpus. The integration of comments in the Results section thus suggests that scientific findings are of relatively limited value unless they are situated in a wider context.

The sequence of these four Results moves is not rigidly fixed, which allows for a number of possible variations. For instance, **Move 9: Justification procedures or methodology** precedes **Move 8: Stating procedures** in some articles. The moves in the Results section also show cyclical patterning, particularly with Move 8 and Move 9, and Move 10 and Move 11. Move 10 is the core of a cycle and is repeated until the discussion of the data is exhausted.

3.4. The discussion section

The Discussion section contextualizes the reported study and relates it to previous work in the field, reflecting a sense of membership in the larger scientific community. Four moves are identified in the Discussion section. The first three moves are conventional, whereas the last one is optional.

Move 12: Contextualizing the study occurs in 90% of the corpus, providing a detailed description of the study. Move 12 is realized by two steps. **Step 1: Describing established knowledge** situates the study being reported in the interest of the discourse community. **Step 2: Presenting generalizations, claims, deductions, or research gaps** allows the scientists to go beyond the results and place their work under the scrutiny of the discourse community. The realization of Move 12, Steps 1 and 2 is illustrated in examples (50) and (51).

Move 12, Step 1: Describing established knowledge

- (50) *Type III secretion systems translocate proteins out of cells and often require chaperones specific for each of the secreted substrates. Chaperones were thought to prevent internal degradation of the secretion substrate and to deliver that protein to the secretion apparatus. [C7]*

Move 12, Step 2: Presenting generalizations, claims, deductions, or research gaps

- (51) *(S1) A detailed understanding of the catalytic mechanisms and substrate selectivity of HAT enzymes is an important component of defining the molecular basis of their biological functions. (S2) Furthermore, such understanding is likely to enhance the design of potent and selective HAT inhibitors. (S3) Prior to this investigation, a preliminary mechanistic analysis on the HAT enzyme GCN-5 was reported. (S4) In this study, mixed histone substrates were used as the acetyl-CoA acceptor (R). (S5) Whereas this study revealed an intersecting line pattern for GCN-5 suggestive of a ternary complex mechanism, more detailed studies investigating order of substrate binding were not described. (S6) The complexity of the mixed histone substrate may have made detailed mechanistic studies difficult. [JBC7]*

The example from (51) is a representative example of an extensive Move 12. It begins with generalizations (Step 2) covering the first two sentences of the section (S1-S2). Then, a previous study (Step 1) is reported to support any generalizations

made at the beginning of the section (S3–S4). A research gap that refers to the absence of detailed studies (Step 2) is identified (S5), followed by an account that explains the reason for the difficulty of conducting mechanistic studies (S6). This example displays how two strategies of Move 12 are integrated by claiming the centrality of the topic, being reinforced by citing a previous investigation and by pinpointing a limitation of the investigation.

Move 13: Consolidating results conventionally highlights the strengths of the study and defends their research successes. This move is realized as one step or a combination of steps: **Step 1: Restating methodology**, **Step 2: Stating selected findings**, **Step 3: Referring to previous literature**, **Step 4: Explaining differences in findings**, **Step 5: Making overt claims or generalizations**, and **Step 6: Exemplifying**. The realization of Move 13, Steps 1–3 is illustrated in examples (52)–(57).

Move 13, Step 1: Restating methodology

- (52) *To identify the mechanism by which kinesin-I binds axonal cargo, we screened for novel axonal transport mutants in Drosophila.* [C11]

Move 13, Step 2: Stating selected findings

- (53) *We show that the essential Gpi11 and Gpi13 proteins are involved in late stages in the formation of the yeast GPIs, and we identify and characterize three new candidates GPI precursors.* [MBC5]

Move 13, Step 3: Referring to previous literature

- (54) *Here we report the characterization of purified functional spliceosomal complex E. In contrast to the current model of spliceosome assembly, which proposes that U2 snRNP first binds in the A complex, our data indicate that U2 snRNP first associates with pre-mRNA during E complex formation.* [MC5] *The experiments presented here confirm the previously reported data (R), showing that polβ can catalyze extensive bypass of platinum-DNA adducts in a single-stranded region of DNA.* [JBC4]

Move 13, Step 4: Explaining differences in findings

- (55) *...they were not easily distinguished in centroid tracks of regA[−] cells (Fig. 4D–F), primarily because the peak velocities of regA[−] cells were in many cases depressed and the tracks were not as persistent and directional during period of increased velocity.* [MBC8]

Move 13, Step 5: Making overt claims or generalizations

- (56) *...Simply changing the CaaX motif of mGBP1 to a form recognized by Ftase significantly improved mGBP1 modification. This result also indicates that the CaaX motif of mGBP1 is not likely to be buried within the structure of the protein, because such masking would presumably impede interaction with either Ftase or GGTase I.* [MBC7]

Move 13, Step 6: Exemplifying

- (57) *This is not meant to imply that protein substrate recognition by PCAF would not be influenced by the non-catalytic domains of PCAF. For example, a 25-amino acid peptide derived from the known acetylation site of p53 is a very weak PCAF (full-length)...* [JBC7]

The above extracts display how various steps Move 13 are contributing to a common function of consolidating the results presented. For instance, Step 1 assures the readers that the study has a specific purpose and that the study is carefully designed to serve that purpose. Step 3 contextualizes the findings within relevant research conventions by comparing or contrasting the current findings with those generated by another study.

Move 14: Stating limitations of the present study makes explicit the scientists' views of the limitations of the study about the findings (Step 1), the methodology (Step 2), or the claims made (Step 3). The realization of Move 14, Steps 1–3 is illustrated in examples (58)–(66).

Move 14, Step 1: Limitations about the findings

- (58) *As yet, we have not detected 6S RNA-dependent differences in the recovery of growth after stationary phase (R). [C6]*
- (59) *...we, are unable to provide any new insight into the catalytic role (if any) of the conserved nucleotides augmenting Stem II, as any such changes are small in magnitude compared to that observed for the cleavage site nucleotide (C-17). [MC2]*
- (60) *Many questions still remain as to how the C-Vps complex mediates the regulation of SNARE complex assembly. [MC9]*

Move 14, Step 2: Limitations about the methodology

- (61) *Additionally, some interactions may be too transient for detection by FRET. [MC1]*
- (62) *However, as formal CNS testing was not performed, in part due to growth retardation and rapid onset of lymphomas, we have not excluded more subtle structural and functional CNS defects in viable Lig4deficient animals. [MC6]*

Move 14, Step 3: Limitations about the claims made

- (63) *Our crystallographic results also do not rule out a proposed mechanism in which the phosphates together coordinate a single metal ion (R). [MC2]*
- (64) *...and the data presented in this manuscript do not exclude either additional roles for 14-3-3 in BAD inactivation, or the existence of additional constraints on 14-3-3/BAD to BCL-X. [MC7]*
- (65) *Our data do not enable us to rule out a requirement for additional, non-PMA-activated pathways in the activation of CD45 alternative splicing in primary T cells. [MBC1]*
- (66) *Our data do not address the possibility that intermediate filaments and lysosomes are transported by conventional kinesin because Drosophila lack intermediate filament proteins and because lysosomes in the Drosophila tissues that we analyzed have not been characterized. [MBC4]*

Move 14 is present in 48 Discussions or 80% of the entire corpus and is deemed conventional in this biochemistry corpus. The prevalence of this move in the corpus indicates the scientists' carefulness and honesty in acknowledging the limitations of the various aspects of the study.

Move 15: Suggesting further research allows the scientists to advocate the need to offer recommendations for the course of future research by pinpointing particular research questions to be addressed or improvements in their research methodology. The realization of Move 15 is illustrated in examples (67)–(69).

- (67) *In the future, it will be challenging to assess what contribution DNA unwinding makes to the distribution of replication start sites in vivo.* [MC4]
- (68) *...further studies on the functional impact of the interaction of p38^{JAB1} with the LHR precursor may also help improve our understanding of the pathophysiology of these disorders.* [JBC5]
- (69) *Clearly, further characterization of methylation-mediated repression will require that mCpG density be taken into account.* [MCB2]

Move 15 is used in 31 Discussions (53.33% of the corpus) and thus deemed as an optional move. A possible reason for this low occurrence offered by Berkenkotter and Huckin (1995) is due to the fierce competition for the grants in the sciences. That is, the scientists do not want to reveal what directions future research could take because they themselves may want to conduct that research. They would rather save the idea for their own grant proposals. The Discussion section, consistent with previous researchers (e.g., Belanger, 1982; McKinlay, 1983; Peng, 1987), displays a cyclical organization. The cycles usually involve Moves 12 and 13, particularly when several results are presented serially. The next cycle then begins with another statement of result, and the pattern repeats itself.

4. Discussion and conclusion

The purpose of the present study was to capture the rhetorical structure commonly followed in biochemistry research articles. As shown by this study, Swales' move analysis, originally conducted on Introductions of research articles, has been successfully extended to other sections of these professional texts. In this corpus of biochemistry texts, the Introduction section generally conforms to Swales' rhetorical model in terms of the presence of the moves and to their sequence. The primary departure from Swales' model lies in the patterns of cyclical configuration between Moves 1, 2 and 3. That is, each move can recur in Introductions a number of times depending on the complexity of the study being presented. Meanwhile, the cyclicity of moves found in the Introduction section of this corpus is congruent with Posteguillo's finding in his computer research article corpus (1999, pp. 152–153).

A second deviation from Swales' model is found in Move 2: Preparing for the present study. That is, some of the articles in the corpus did not include Move 2 in their Introductions. It is possible that, if the study continues established research, Move 2 might not be used because the scientists assume that the readers understand that the work presented is conducted in the same manner as previous studies. Meanwhile, the frequent use of Move 2, Step 1: Indicating a gap in this corpus indicates the scientists' preference to move the field forward by filling gaps in previous research.

Move 2 has been of interest to many contrastive rhetoric scholars, such as Taylor and Chen (1991) and Ahmad (1997). They found that this move was used cautiously. For instance, Chinese scholars would hesitate to use Move 2 in their Introductions, perceiving this move as a fault-finding strategy and potentially face-threatening to readers (Taylor & Chen, 1991). Similarly, Ahmad (1997) found that Malaysian scholars typically avoid using this move. If this move is employed, it is not to indicate the gap but to replicate studies previously conducted in other countries, using local materials available in Malaysia to satisfy local needs. This move thus shows that besides disciplinary variation, cultural variation plays a vital role within the genre of research articles determining the rhetorical structure of Introductions. This also raises a question about whether disciplinary expectations may be changing in international journals, or if writers are modifying their preferred rhetorical styles to match publishing contexts. It would be intriguing and insightful to examine how non-English speaking scholars approach the process of writing research articles in their native languages and how they modify their strategies when writing them in English.

Move 3 in biochemistry research articles displays another distinct departure from what Swales' model prescribed. That is, no explicit outline of the structure of the research article was found in this biochemistry corpus. Disciplinary variation is discernible and, therefore, modifications to Swales' model of Introductions are vital to make the model proposed appropriate for the specific discourse of biochemistry.

The Methods section, as opposed to other sections, receives relatively scant attention and thus there has been no clear model for the section (e.g., Nwogu in medicine, 1997; Weissberg & Buker, 1990; Wood in chemistry, 1982). Wood's and Nwogu's studies focus on a relatively small number of texts ($N = 10$ and 15 , respectively). Weissberg and Buker's (1990) analysis ($N =$ unspecified) focuses on twelve different disciplines including hard sciences, applied sciences, social sciences, business, and humanities. Given the extreme diversity of aims and methods across these disciplines, Weissberg and Buker's model⁶ remains to be substantiated by an analysis focusing on each discipline. Nevertheless, the analysis of this study revealed unique characteristics of the biochemistry Methods section. In this discipline, many experimental procedures are well established and familiar to scientists in the field. However, these established procedures are employed with some adjustments to accommodate the particular features and purposes of a specific study.

The Results section of biochemistry articles confirms Swales' assertion (1990, p. 170) that disciplinary variations occur not only in the Introductions section, but also in the Results section. The Results section of biochemistry articles are distinguished from those of other disciplines by including Move 9 (Justifying procedures or methodology) and Move 11 (Stating comments on the results). The trend of incorporating

⁶ Weissberg and Buker's (1990) model for the Methods section consists of nine information elements, in Weissberg and Buker's terms, or nine rhetorical moves. These moves are: overview of the experiment, population/sample, location, restrictions/limiting conditions, sampling technique, procedures, materials, variables, and statistical treatment.

the Methodological Justification Move, as discovered by Thompson (1993), is confirmed by this study. This is probably due to the availability of many established experimental procedures in the field; therefore, justification for a particular procedure has to be made explicit and validated. The use of Move 11 (Stating comments on the results) in the Results section to express the scientists' comments on the results indicates a deviation from general guidelines for writing for publications. Additionally, the cyclical pattern of Results and Comments Moves is predominant in biochemistry research articles.

The final section, Discussion, is varied due to the diverse strategies that the scientists choose to integrate. A unique feature of biochemistry research articles is that both Move 12 (Contextualizing the study) and Move 13 (Consolidating results) are conventional in this biochemistry corpus. These features are emphasized because of scientists' sensitivity to carefully situating their work in the interest of their discourse community; this allows the scientists' studies to be scrutinized with respect to their contributions to their field.

Given the representation of the corpus, it would be appropriate to expect the findings of this study to be generalized to the writing used in sections of research articles in biochemistry. However, the proposed model capturing observable moves is only a means of marshalling ideas into an appropriately ordered text. This present study does not claim that the list of series of moves presented is exhaustive. Furthermore, the structure postulated exhibits rhetorical moves that incorporate various degrees of flexibility in their positions. Some rhetorical moves have more stable positions in the overall organization of biochemistry research articles, while others are less stable.

The study expands the application of move analysis to biochemistry research articles in their entirety, thus adding to the ever-evolving knowledge of how writing in disciplines can be understood as having predictable and expected structures. The knowledge gained from this study contributes to an understanding of the discourse in research articles and reinforces how well move analysis gives an in-depth perspective on the formation of a distinctive section of a research article. The rhetorical organization delineated in this study contributes to demystifying academic writing, thus facilitating the entry of newcomers' to the highly selective academic discourse community of biochemistry researchers.

In addition to the theoretical contributions to discourse analysis, this study offers practical implications to those interested in pedagogy—for native and non-native speakers, as well as novice and seasoned scientists, in reading and writing instruction. The rhetorical structure captured by move analysis can be presented in the classroom to raise learners' consciousness of discipline specific reading skills. The awareness of the conventions of research articles can empower learners to become proficient academic readers. The template proposed by the study builds up a schema for research article readers as to what to expect while reading, in what sequence, and what purposes the authors have while writing an article. Similarly, the template also provides a foundation for less experienced authors to write in such a manner that conforms to the conventions or expectations of the discourse community.

Acknowledgements

The study was supported by Doctoral Dissertation Improvement Grant #BCS 0213948 from the National Science Foundation (NSF) and TOEFL Small Grants for Doctoral Research from the Education Testing Service (ETS), USA. This paper is based on part of my doctoral dissertation completed at Georgetown University. I am grateful to Dr. Jeffrey Connor-Linton and Dr. Andrea Tyler, for their guidance through the entire process of my doctoral work. My heartfelt gratitude goes to John Swales, one of the readers on my dissertation committee. My special thanks go to Lisa Russell-Pinson for her constructive feedback on the previous draft of this article. Finally, I appreciate the feedback from the two anonymous reviewers.

Appendix A

Summary table of inter-coder analysis of the four sections

Section	Coded Unit	Agreement	Disagreement	κ	Percent
<i>Introduction</i>					
Move 1	348	347	1		
Move 2	26	19	7		
Move 3	40	38	2		
Subtotal	414	404	10	.93	97.58
<i>Methods</i>					
Move 4	46	33	13		
Move 5	736	729	7		
Move 6	5	5	0		
Move 7	8	8	0		
Subtotal	795	775	20	.81	96.35
<i>Results</i>					
Move 8	323	304	19		
Move 9	176	165	11		
Move 10	647	601	46		
Move 11	273	252	21		
Subtotal	1419	1322	97	.90	93.16
<i>Discussion</i>					
Move 12	388	344	44		
Move 13	450	436	14		
Move 14	9	8	1		
Move 15	13	12	1		
Subtotal	860	800	60	.88	93.02
Total	3488	3301	187	.88	95.03

Appendix B

Move structure for biochemistry research articles

Move/step	Frequency of occurrence (%)
<i>Introduction</i>	
Move 1: Announcing the importance of the field	100.00
By Step 1: Claiming the centrality of the topic	
By Step 2: Making topic generalizations	
By Step 3: Reviewing previous research	
Move 2: Preparing for the present study	66.66
By Step 1: Indicating a gap	
By Step 2: Raising a question	
Move 3: Introducing the present study	100.00
By Step 1: Stating purpose(s)	
By Step 2: Describing procedures	
By Step 3: Presenting findings	
<i>Methods</i>	
Move 4: Describing materials	100.00
By Step 1: Listing materials	
By Step 2: Detailing the source of the materials	
By Step 3: Providing the background of the materials	
Move 5: Describing experimental procedures	100.00
By Step 1: Documenting established procedures	
By Step 2: Detailing procedures	
By Step 3: Providing the background of the procedures	
Move 6: Detailing equipment (optional)	10.00
Move 7: Describing statistical procedures (optional)	13.32
<i>Results</i>	
Move 8: Stating procedures	95.07
By Step 1: Describing aims and purposes	
By Step 2: Stating research questions	
By Step 3: Making hypotheses	
By Step 4: Listing procedures or methodological techniques	
Move 9: Justifying procedures or methodology	71.59
By Step 1: Citing established knowledge of the procedure	
By Step 2: Referring to previous research	

Appendix B (*continued*)

Move/step	Frequency of occurrence (%)
Move 10: Stating results	100.00
By Step 1: Substantiating results	
By Step 2: Invalidating results	
Move 11: Stating comments on the results	91.01
By Step 1: Explaining the results	
By Step 2: Making generalizations or interpretations of the results	
By Step 3: Evaluating the current findings	
By Step 4: Stating limitations	
By Step 5: Summarizing	
<i>Discussion</i>	
Move 12: Contextualizing the study	89.94
By Step 1: Describing established knowledge	
By Step 2: Presenting generalizations, claims, deductions, or research gaps	
Move 13: Consolidating results	100.00
By Step 1: Restating methodology (purposes, research questions, hypotheses restated, and procedures)	
By Step 2: Stating selected findings	
By Step 3: Referring to previous literature	
By Step 4: Explaining differences in findings	
By Step 5: Making overt claims or generalizations	
By Step 6: Exemplifying	
Move 14: Stating limitations of the study	80.00
By Step 1: Limitations about the findings	
By Step 2: Limitations about the methodology	
By Step 3: Limitations about the claims made	
Move 15: Suggesting further research (optional)	53.33

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