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Move Analysis of Chemical Biology Research Article Introductions

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Abstract

Writing research articles is an important and demanding task for members of academia, and the introduction is generally considered the most difficult portion to write (Swales, 1990). Move analysis has proven useful in studying the communicative functions of introductions and other sections of research articles, and is thus beneficial in training novice academic authors. Few studies have included a move analysis on the introduction of research articles in the emerging field of chemical biology. In this study, we conducted a move analysis on 10 research article introductions from a prestigious chemical biology journal to identify their rhetorical structure. The results reveal that all introductions analysed consist of three conventional moves — Move 1: Introducing the research area; Move 2: Pointing out the need(s); and Move 3: Presenting the current research, arranged in two common patterns — Pattern A: (Move 1>Move 2)$_n$>Move 3; and Pattern B: (Move 1>Move 2)$_n$>Move 1>Move 3, where n = a counting number. Insights on the general move patterns as well as variations in submoves frequency from research article introductions from the neighbouring disciplines are helpful to novice

	chemical biologists in writing successful introductions as well as ESP teachers, especially those who teach these scientists writing for publication.

1. Introduction

What make a successful career for scientists in academia? Is good science enough to guarantee a position in a university? Theoretical physicist Peter Higgs does not think so. On his way to Stockholm to receive the Nobel Prize for his work on subatomic particles, Higgs mentioned in an interview with the Guardian, "Today I wouldn't get an academic job. It is as simple as that. I don't think I would be regarded as productive enough" (Aitkenhead, 2013). That may be a surprising statement coming from a Nobel laureate, but if one considers the number of fewer than 10 publications he produced after his revolutionary work in 1964 (Aitkenhead, 2013), in light of the "publish or perish" culture impacting academic communities all over the world (van Dalen & Henkens, 2012), his remark is not as unusual as it first seems. Publication now serves not only as a means for scientists to communicate their findings to the global scientific community and receive constructive comments from their peers, but also an indicator of their accomplishment which can have the final say on their career survival and advancement (Clapham, 2005). "Having published in top-ranked journals" has been identified by a majority of scientists to be a factor contributing to academic success (van Dalen & Henkens, 2012, p. 1289).

Since research article is viewed as one type of genre. It is identified by a recognizable communicative purpose and by the presence of characteristic features with standardized form, function, and presentation that are part of its general conventions. Thus, to produce an effective research article, the writer must adhere to this generic rules and convention. The ability to write research article according to the discourse conventions can help the writer gain recognition in his/her academic disciplines through the publication of the research article (Ahamad & Yosof, 2012). To get published in competitive, high-impact-factor journals, good science is not the only aspect that scientists must account for. According to Brod & Hazelwood-Smith (2014), "even with high-quality

data, you can jeopardize your chances of publication if you don't have a high-quality paper." It has been argued that the art of writing proper academic research articles must be learned by novice researchers whether they are native or non-native speakers of English (Guo, 2014; Hyland, 2016; Pérez-Llantada et al., 2011; Phothongsunan, 2016) to overcome problems ranging from lexicogrammatical to sentence and discourse levels.

This agrees with the interview with four academic scientists at a research university in Thailand, who are at the beginning of their careers as independent scientists and have been published in international journals. Interestingly, though they reported having difficulties with grammar and vocabulary, their greatest concern was about the organization of thoughts in their introductions, which they referred to as the "flow of ideas" or "how to go from one point to another." Swales (1990) affirms that among the different sections of a research article with the standard Introduction-Method-Results-Discussion (IMRD) structure, the introduction has been identified by virtually every author in academia as the most daunting to draft, and his work on genre analysis based on rhetorical moves has helped shed light on the issue.

2. The Move Analysis of Research Article Introductions

According to Paltridge (2012), many of the analyses of the discourse structure of academic texts have been based on Swales's (1981, 1990) work in this area. These studies have examined, for example, the discourse structures of research articles, master's theses, and doctoral dissertations. Swales's (1990) move analysis is a useful tool to elucidate the rhetorical structure of a text. He sees a text as consisting of several "moves," where each move is a unit that performs a certain communicative function to contribute to the text's overall communicative purpose. A move is realized by one or several "steps," which is sometimes called a "submove" (Stoller & Robinson, 2013). As a product of his move analysis on research article introductions, Swales proposed the "Create a Research Space" (CARS) model, which describes the rhetorical structure of the introduction text (Table 1) by drawing upon an ecological metaphor. The CARS model contains three moves. Move 1, establishing a territory, is an attempt to set the stage for the present research. Move 2, establishing

a niche, tries to point out why the present research is needed. Lastly, Move 3, occupying the niche, introduces the present research to fulfil the need previously indicated in Move 2. Swales's CARS model has proved useful in explaining and teaching how to teach the writing of an introduction (Swales & Feak, 1994).

After Swales's (1990) seminal work, several studies have adopted his framework to analyse research article introductions from various disciplines such as biology (Samraj, 2002), biochemistry (Kanoksilapatham, 2005), chemistry (Stoller & Robinson, 2013), EOP and EAP (Atai & Samani, 2012), and physical and social sciences (Behnam & Nikoukhesal, 2017). Samraj (2002) analysed the introductions of 12 research articles from each of the two related subfields in Biology: Wildlife Behaviour and Conservation Biology and found not only structural variations between these two disciplines but also a possibility that literature review can be present in both Move 1 and Move 2. Kanoksilapatham (2005) performed a move analysis on representative 60 full-length biochemistry research articles and proposed in total 15 distinct moves to describe the rhetorical structure of the introduction, methods, results, and discussion sections of those biochemistry research articles. To raise genre awareness in the field of chemistry, Stoller & Robinson (2013) used move analysis to elucidate rhetorical structure of 60 exemplary chemistry research articles from six chemistry subfields of analytical, organic, physical, environmental, food chemistry and toxicology and presented their results in the format of flowchart to make it more accessible for the chemists. Swales also proposed a revised CARS model in 2004 to account for deeper understanding of the rhetorical structures from studies over the years. Although the introductions from these fields follow the main three moves as proposed by Swales (1990), they differ in detail on how those moves are realized due to preferences or the accepted norms in each particular discourse community as shown in Table 1.

Table 1

Rhetorical Structures of Research Article Introductions from Different Fields

Swales (1990)	Samraj (2002)	Swales (2004)	Kanoksilapatham (2005)	Stoller & Robinson (2013)
Move 1: Establishing a territory	**Move 1: Establishing a territory**	**Move 1: Establishing a territory** (citation required) via	**Move 1: Announcing the importance of the field**	**Move 1: Introduce the research area**
Step 1: Claiming centrality (and/or)	Step 1: Claiming centrality - in research (and/or) - in the real world	Topic generalizations of increasing specificity	Step 1: Claiming the centrality of the topic	Submove 1: Identify the research area (citation optional)
Step 2: Making topic generalization(s) (and/or)	Step 2: Presenting background information		Step 2: Making topic generalizations	Submove 2: Establish the importance of the research area (citation obligatory)
Step 3: Reviewing items of previous research			Step 3: Reviewing previous research	Submove 3: Provide essential background information about the research area (citation obligatory)
Move 2: Establishing a niche	**Move 2: Establishing a niche**	**Move 2: Establishing a niche** (citation possible) via	**Move 2: Preparing for the present study**	**Move 2: Identify a gap (or gaps)** (citation obligatory) can be repeated
Step 1A: Counter-claiming (or) Step 1B: Indicating a gap (or) Step 1C: Question-raising (or) Step 1D: Continuing a tradition	Step 1A: Counter-claiming (or) Step 1B: Indicating a gap - in research - in the real world (or) Step 1C: Question-raising (or) Step 1D: Continuing a tradition	Step 1A: Indicating a gap (or) Step 1B: Adding to what is known	Step 1: Indicating a gap Step 2: Raising a question	
	Step 2: Presenting positive justification	Step 2: Presenting positive justification		

		(optional)		
Move 3: Occupying the niche	**Move 3: Occupying the niche**	**Move 3: Presenting the present work** (citation possible)	**Move 3: Introducing the present study**	**Move 3: Fill the gap**
Step 1A: Outlining purposes (or) Step 1B: Announcing present research	Step 1: Presenting goals of present research - giving background information on species or site	Step 1: Announcing present research descriptively and/or purposively (obligatory)	Step 1: Stating purpose(s)	Submove 1: Introduce the current work
		Step 2*: Presenting RQs or hypotheses (optional)		
		Step 3*: Definitional clarifications (optional)		
		Step 4*: Summarizing methods (optional)	Step 2: Describing procedures	
Step 2: Announcing principal findings	Step 2A: principal findings or Step 2B: Predicting results Announcing	Step 5: Announcing principal outcomes (PISF**)	Step 3: Presenting findings	Submove 2: Preview key findings (optional)
		Step 6: Stating the value of the present research (PISF)		
Step 3: Indicating RA structure	Step 3: Indicating RA structure	Step 7: Outlining the structure of the paper (PISF)		

*optional and less fixed in their order of occurrence than the others, **PISF = probable in some fields, but unlikely in others

Move 1 in Swales's (1990) CARS and Kanoksilapatham's (2005) models can be realized by three steps: claiming centrality, making topic generalizations, and reviewing items of previous research. However, Samraj (2002) recognizes only two distinct steps: "centrality claiming" and "making topic generalizations," because she believes neither the presence of citations nor arbitrary perception of generality provide a clear demarcation between making topic generalizations and reviewing items of previous research; hence the two steps should be combined. Stoller & Robinson (2013) also propose similar submoves: identify the research area, establish the importance of the research area, and provide the essential background information of the research area. In contrast,

Swales's (2004) revised model contains a more homogeneous rather than step-wise Move 1 that the entire section simultaneously make centrality claims while providing background information of the study. He points out the possibility of cyclical move recycling, especially between Move 1 and Move 2, as well as possible variations among introductions from different fields.

Move 2 in Swales's (1990) CARS model can be realized by one of these four steps: counter-claiming, indicating a gap, question-raising, or continuing a tradition. Samraj (2002) adopts the same practice and adds another distinct step of presenting positive justification for the research. Swales (2004) combines his first three steps under the description "indicating a gap" because they have similar function, and indicating a gap is most common, and renames "continuing a tradition" to "adding to what is known." He also includes Samraj's (2002) presenting positive justification in his revised CARS model. Kanoksilapatham (2005) agrees that "indicating a gap" is most common in her corpus but also has "raising a question" as an option. Stoller & Robinson (2013) combine everything under "identify the gap(s)."

Move 3 in Swales's (1990) CARS model can be realized by three steps: Step 1 - (1A) outlining purposes or (1B) announcing present research; Step 2 - announcing principal findings; and Step 3 - introducing research article structure. Samraj (2002) has almost the same steps, with the addition of "giving background information on species or site" to Step 1 and "predicting results" as an alternative to Step 2. Swales's (2004) revised CARS model has all the original steps (with Step 1A and 1B combined into a single Step 1) and includes four others: presenting research questions or hypotheses, definitional clarification, summarizing methods, and stating the value of the present research. Kanoksilapatham's (2005) Move 3 has simpler but similar realization involving just three steps: stating purpose(s), describing procedures, and presenting findings. Stoller & Robinson's (2013) model has even simpler submoves: introducing the current work and previewing key findings.

Although schematic structures for introductions from the neighbouring disciplines of biology, biochemistry, and chemistry have been proposed, few studies have been done on introductions from the emerging field of chemical biology. The field's growing importance is evidenced by the fact that half of the Nobel Prizes in Chemistry during the

first decade of the new millennium "have had a definite biological tinge to them" (Hoffmann, 2012, p. 1734). As mentioned earlier, each discourse community seems to have its own preferences in writing their introductions. Even within the same discipline, introductions from different subdisciplines may vary significantly in occurrence of steps in the move probably due to distinct nature and context of each subdiscipline. Samraj (2002) as mentioned earlier reports variations in steps in two biology subdisciplines, while Kanoksilapatham (2012) describes that among three engineering subdisciplines. We, therefore, propose to perform a move analysis on chemical biology research article introductions. Studies have shown that Swales's CARS model (1990) has not only been adopted for other languages research articles introduction but also in exploring genre analysis of several disciplines (Manzoor et al., 2020). For this study, the researchers have expected that the results will help novice researchers in the field of chemical biology in crafting a crucial section, namely the introduction, of their research articles.

3. Purpose of the Study

With the background and rationale as stated earlier, the researchers would like to understand how chemical biology research article introductions are written. Therefore, we aim to find the moves and submoves of chemical biology research article introductions. The following research question is 'What are the moves and submoves of chemical biology research article introductions?'

4. Methodology

4.1 Article Selection

To perform a move analysis on the introduction of research articles in chemical biology, sample introductions serving as good representatives of high-quality chemical biology research article introductions were needed. Given the small scale of the study (10 introductions) and based on the presupposition that it takes a good introduction to get published in a good journal, this work limited to introductions from a leading journal in chemical biology, Nature Chemical Biology, with a 5-year impact factor

(2017) of 13.990 (About the Journal, 2017). Currently, the journal publishes 12 issues per year, and each issue includes around 10 full-length articles reporting original research. To control variables from authors' mother tongues, all the issues published during 2018 were scanned in order to identify articles authored by native speakers of English.

Due to the diversity of the scientific community, it is virtually impossible to find a paper with all native-speaking authors. With the assumption that the first and corresponding authors contribute most in manuscript preparation, we decided to focus on articles of which first and corresponding authors (1) belong to institutions situated in one of Kachru's (1985) inner circle countries including the USA, the UK, Canada, Australia, and New Zealand, (2) received all tertiary degrees or are currently studying for one from universities in those countries, and (3) whose first and last names are common in English-speaking countries. A paper with first and/or corresponding authors with a name different from point (3) above may be accepted only when there is extra information suggesting that the person grew up in an English-speaking country (e.g., attending high school in an English-speaking country, being a recipient of a fellowship/award that has a nationality requirement, representing an English-speaking country in an international Olympiad). From all the articles that passed the above criteria, 10 final articles, the introductions of which were to be analysed, were randomly selected and are referred to in this paper as CB1-CB10 (See the Appendix). It is noted that this type of introduction will include the background and rationale as well as the literature review of the study.

4.2 Move Analysis

Given that the focus of this study is on the rhetorical structure of chemical biology research article introductions and that rigorous frameworks for describing the introductions from neighbouring disciplines of chemical biology are currently available (Swales, 1990 and 2004; Samraj, 2002; Kanoksilapatham, 2005; Stoller & Robinson, 2013), it was decided to conduct the move analysis in a top-down manner, following the steps proposed by Biber et al. (2007) as presented in Table 2. Linguistic elements were used as clues in the coding process but not analysed in detail as in steps 4 and 5 in Biber et al.'s (2007) procedure, because the

linguistic aspects of the introduction text have already been extensively studied in previous work.

Table 2

Top-Down Corpus-Based Analyses of Discourse Organization (Biber et al., 2007, p. 13)

	Step in the analysis	Realization in this approach
1.	Communicative/Functional Categories	Develop the analytical framework: determine set of possible functional types of discourse units, that is, the major communicative functions that discourse units can serve in corpus
2.	Segmentation	Segment each text into discourse units (applying the analytical framework from Step 1)
3.	Classification	Identify the functional type of each discourse unit in each text of the corpus (applying the analytical framework from Step 1)
4.	Linguistic analysis of each unit	Analyse the lexical/grammatical characteristics of each discourse unit in each text of the corpus
5.	Linguistic description of discourse categories	Describe the typical linguistic characteristics of each functional category, based on analysis of all discourse units of a particular functional type in the corpus
6.	Text structure	Analyse complete texts as sequences of discourse units shifting among the different functional types
7.	Discourse organization tendencies	Describe the general patterns of discourse organization across all texts in the corpus

To develop a move analysis framework for this particular work, five frameworks describing the introductions from related disciplines (Swales, 1990, 2004; Samraj, 2002; Kanoksilpatham, 2005; Stoller & Robinson, 2013, see also Table 1) were consulted. A preliminary framework was constructed by combining all the moves and steps/submoves available in those five frameworks. After a pilot coding was done, the preliminary framework was refined, resulting in the current framework as shown in Table 3. This framework was used to code all 10 selected chemical biology

research article introductions. Despite the appeal of Swales's powerful metaphorical descriptions of the moves, it was decided to follow the examples of Kanoksilpatham (2005) and Stoller & Robinson (2013) of using plain language for move descriptions to make them more readily comprehensible to scientists. It was also decided to employ Stoller & Robinson's (2013) example of using a more intuitive term "submove" rather than "step."

Table 3

Current Move Analysis Framework

Move	Submove	Source
Move 1: Introducing the research area	-	Swales (2004), Stoller & Robinson (2013) (for description)
Move 2: Pointing out the need(s)	Submove 1: Indicating a gap or gaps Submove 2: Presenting positive justification	Swales (1990) Samraj (2002)
Move 3: Presenting the current research	Submove 1: Announcing current research descriptively and/or purposively and/or interrogatively Submove 2: Announcing principal outcome Submove 3: Stating the value of the current research	Swales (2004) Swales (1990) Swales (2004)

4.3 Inter-Coder Reliability

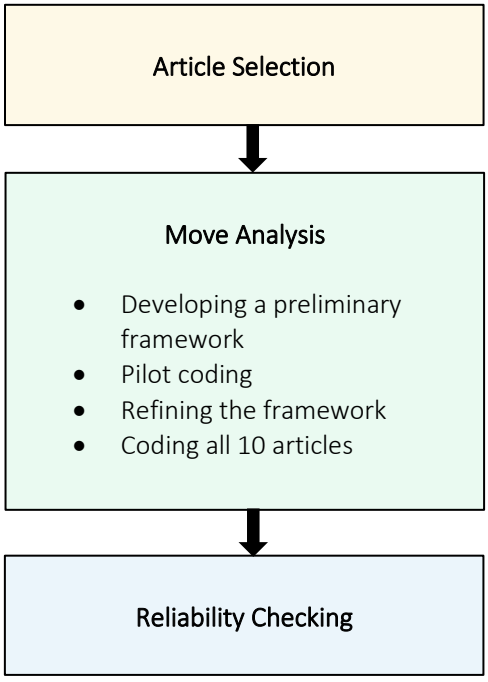
The coding process of a move analysis is done based on the judgment of the coder; hence, it is subjective by nature. To ensure coding process reliability, an inter-coder, who has a Ph.D. in physical science and has published in and served as reviewer for international journals, was asked to code 30 percent of the texts after receiving a training in move analysis. Percentage agreement was then calculated to illustrate inter-coder reliability (Kanoksilapatham, 2005).

$$\text{Percentage agreement} = \frac{\text{Agreed coded units}}{\text{Total coded units}} \times 100 = \frac{70}{75} \times 100 = 93\%$$

It is noted that these 75 coded units are from the three texts coded by both the researcher and the inter-coder, where a coded unit is a sentence in the introduction.

Figure 1

Research Methodology Summary



5. Results and Discussion

5.1 Occurrence of moves and submoves

Moves and submoves in chemical biology research articles identified through move analysis are presented in Table 4. According to Kanoksilapatham (2005), if percentage of occurrence of any move or

submove is equal to or higher than 60, it is regarded as "conventional," and if lower than 60, it is regarded as "optional." Therefore, in chemical biology research article introductions, Move 1: Introducing the research area, Move 2: Pointing out the need(s), and Move 3: Presenting the current research are considered conventional moves, and most submoves are considered conventional, except for Submove 2 (of Move 2): Presenting positive justification, and Submove 1 (of Move 3): Announcing current research descriptively and/or purposively and/or interrogatively, both of which fall in the optional category.

Table 4

Move and Submove Occurrence in Chemical Biology Research Article Introductions

Move/Submove	CB1	CB2	CB3	CB4	CB5	CB6	CB7	CB8	CB9	CB10	%
Move 1: Introducing the research area	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	100
Move 2: Pointing out the need(s)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	100
Submove 1: Indicating a gap or gaps	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	100
Submove 2: Presenting positive justification		✓	✓			✓			✓		40
Move 3: Presenting the current research	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	100
Submove 1: Announcing current research			✓		✓	✓				✓	40
Submove 2: Announcing principal outcomes	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	100
Submove 3: Stating the value of the current research	✓	✓	✓	✓		✓	✓	✓	✓	✓	90

5.2 Explanations and Examples of Moves and Submoves

5.2.1 Move 1

Move 1 marks the beginning of all the introductions in this study. Its purpose is to give information to readers about the research area in which the current research is situated. The realization of Move 1 in the sample introductions agrees best with that in Swales' (2004) revised CARS model: a portion of text can serve more than one functions, both claiming centrality and topic generalizations as in (1) and (2). Though (1) contains a lot of common words for claiming centrality in the real world like "powerful tools," "a myriad of applications," and "several patient deaths," as well as in research like "a growing interest" and "particular interest," one can see that the text does not just try to convince readers of the importance of the research area, but also gives background information about what has been done in the field. On the contrary, (2) may seem to only make generalizations but actually claims centrality implicitly by mentioning the process that has not been clearly understood in the field. Move 1 thus contains no distinct submove but is realized via gradual topic generalizations of increasing specificity leading to the need(s) for the current research. Move 1 can occur in an introduction more than one time, most likely alternating with Move 2. This alternating pattern can recur several times; the further into the introduction, the more specific the content as pointed out by Swales (2004). (See Table 6.)

(1) *[1]CIDs are **powerful tools** for dose and temporal control of protein-protein interactions[1,2,3]. [2]CIDs have been used in **a myriad of applications**, including development of artificial cellular circuits[4], activation of split-enzyme activity[5,6], and control of protein localization. [3]Recently, there has been **a growing interest** in using CIDs to regulate the activity of cell therapies after they have been administered to a patient[7,8]. [4]Of **particular interest** has been the utilization of CIDs as safety switches for chimeric antigen receptor T-cell (CAR T-cell) therapies, as **several patient deaths** have occurred in CAR T-cell clinical trials[9]* [CB2]

(2) *[1]Much of the functional diversity observed in modern enzyme superfamilies originates from*

molecular tinkering with existing enzymes[1]. [2]*New enzymes frequently evolve from enzymes with latent, promiscuous activities*[2] *and often inherit key features of the ancestral enzyme, retaining conserved catalytic groups and stabilizing analogous intermediates or transition states*[3] . [CB5]

5.2.2 Move 2

Move 2: Pointing out the need(s) attempts to explain why a particular work of research is necessary. In this study, Move 2 can be realized through two submoves: Submove 1: Indicating a gap or gaps (to show what is missing) and Submove 2: Presenting positive justification (to provide a good reason why the piece of research should be done). This work follows Stoller & Robinson's (2013) example in combining Swales's (2004) first two steps—"indicating a gap" and "adding to what is known"—into one, because their difference is in quantity rather quality—if there is still room to add to what is known, a gap is also there, even if it is just a smaller one.

a. Submove 1

Here are some examples of Submove 1: Indicating a gap or gaps. Terms with negative connotations like "although," "has not been directly verified," "little," "but," and "neither…nor" are common in this submove to negatively show why the research should be done. Notice that (4) and (5) are from the same introduction; both indicate roughly the same gap, but (5) does it with more specific detail.

(3) [17]***Although*** *it has been assumed that periplasmic proteins aggregate under gastric fluid conditions*[7,8,9,10,11,12]*,* *this supposition* ***has not been directly verified****.* [CB1]

(4) [15]***Little*** *is known about the process of SCWP O-acetylation at the molecular level.* [CB8]

(5) *[18]Both hypothetical PatA proteins are predicted to be members of the family of membrane-bound O-acyltransferases (MBOAT; pfam 03062)[22], **but neither** protein, **nor** any related ortholog, such as AlgI from the alginate O-acetylation pathway[23], have been characterized biochemically.* [CB8]

b. Submove 2

(6) and (7) are examples of Submove 2: Presenting positive justification. Notice the words "for these reasons," "desirable," "great utility," and "reasoned." This submove is one of only two submoves that is in the optional category (with 40 percent occurrence rate).

(6) *[14]**For these reasons**, a general method to design novel CIDs with **desirable** properties for use in regulating human cell therapies would be of **great utility**.* [CB2]

(7) *[21]Nonetheless, we **reasoned** that PduA*-based filamentous structures may present tractable scaffolds for tethering other proteins.* [CB9]

5.2.3 Move 3

Move 3: Presenting the current research is the culmination of the introduction, for it gives the information about the current research. This move has more variations in realization among different models than the first two. The results of a move analysis on the sample introductions reveal that Move 3 in these introductions is realized via three submoves: Submove 1: Announcing the current research descriptively and/or purposively and/or interrogatively (the last manner added to account for a variant found in this study); Submove 2: Announcing principal outcomes; and Submove 3: Stating the value of the current research. These submoves

are not categorically new, but their occurrence rates run counter to expectations.

a. Submove 1

Submove 1, listed as "obligatory" in Swales (2004), occurs in only 40 percent of the introductions in this study, so it is regarded as an "optional" submove. A study can be announced in three manners: "descriptively," as a short description (8); "purposively," by stating the objective(s) (9); and "interrogatively," in the form of an indirect question (10). Although an alternative coding for (10) is presenting research questions or hypotheses (Swales, 2004), its position at the beginning of Move 3 with "here" as a signal word supports the interpretation of announcing the work in a "casual" question-like style rather than presenting a research question after the initial announcement.

(8) [11]***In this work***, *we used ancestral protein reconstruction*[10] *to investigate the biophysical and biochemical mechanisms underlying the evolutionary transition between SBPs and CDTs.* [CB5]

(9) [17]***To address this problem***, *we elected to study the GbnD4 and GbnD5 subunits of the gladiolin PKS, which have KS and DH domains at their C and N termini, respectively.* [CB3]

(10) [22]***Here*** *we asked how a TCR such as DMF5 can productively engage two very different classes of antigens.* [CB6]

b. Submove 2

Though Submove 2: Announcing principal outcomes is labelled "Probable in some fields, but unlikely in others," in Swales (2004) and "optional" in Stoller & Robinson (2013)'s chemistry research article introduction model, it occurs in *all* of the introductions in this study, so it

is considered a "conventional" submove. It can come right at the beginning without any preceding announcement as in (11): notice the word "here," or come after Submove 1 as in (12). Two plausible explanations for this extremely high occurrence are: first, the practice may be influenced by a neighbouring field of biochemistry. As mentioned in Swales (2004), 53 out of 60 introductions in Kanoksilapatham's (2005) biochemistry corpus have this submove. Furthermore, it is perhaps the authors' attempt to emphasize their accomplishments and thus "sell" their work to survive the intensely competitive reviewing process of a top-ranked journal.

(11) *[15]**Here**, we demonstrate a strategy to generate chemical-epitope-selective antibodies that has the potential to turn many known small-molecule-protein complexes into AbCIDs (Fig. 1a). [16]We demonstrate this approach by engineering AbCIDs using the BCL-xL-ABT-737 complex. [17]Furthermore, we show that AbCIDs can be used to regulate cellular processes; including CRISPR activation (CRISPRa)-mediated gene expression and CAR T-cell activity.* [CB2]

(12) *[12]By analyzing the evolutionary trajectory between reconstructed ancestors and extant proteins, we show that the emergence and optimization of catalytic activity involves several distinct processes. [13]The emergence of CDT activity was potentiated by the incorporation of a desolvated general acid into the ancestral binding site, which provided an intrinsically reactive catalytic motif, and reshaping of the ancestral binding site, which facilitated enzyme-substrate complementarity. [14]Catalytic activity was subsequently gained via the introduction of hydrogen bonding networks that positioned the catalytic residue precisely and contributed to transition-state stabilization. [15]Finally, catalytic activity was enhanced by remote substitutions that refined the active site*

structure and reduced sampling of noncatalytic states. [CB5]

c. Submove 3

Submove 3: Stating the value of the current research, despite its absence from four out of five models consulted in this work, occurs in 90 percent of the introductions in this study, so it is regarded as a "conventional" submove. (12) claims the application in "different context" and in treating "cancer," while (13) mentions "compelling insights." The frequent appearance of this submove is probably due to the same reason for the perfect occurrence of Submove 2: The authors must highlight the impact of their work to increase its competitiveness.

(13) *[33]This pair of* ***tool compounds can be used*** *to further delineate the functions of TRIM24 and the domain dependence of TRIM24 across* ***different contexts*** *and to define a TRIM24-mediated transcriptional program in* ***cancer****.* [CB4]

(14) *[19]These data provide* ***compelling insights*** *into the mechanism of Cope rearrangement, 6-exo-trig cyclization and electrophilic aromatic substitution for this class of natural product.* [CB10]

5.3 Move-Submove Sequence

These moves and submoves do not necessarily occur in a linear manner but can adopt cyclical patterns (Table 5). Recycling can occur both in the move (e.g., multiple recycling of Move 1 and Move 2 in CB4) and submove levels (e.g., recycling of Submove 1 and Submove 2 of Move 2 in CB2). This shows that even though Move 1, Move 2, and Move 3 are all conventional moves (with 100 percent occurrence rates), there are various patterns of realization of these moves in actual introductions. To extract the structure(s) employed by authors of the sample chemical biology

research article introductions in this study, it is necessary to step back to the move level.

Table 5

Sequence of Move-Submove in Chemical Biology Research Article Introductions

Article	Move-Submove Sequence									
	#1	#2	#3	#4	#5	#6	#7	#8	#9	#10
CB1	1	2-1	3-2							
CB2	1	2-1	2-2	2-1	2-2	3-2	3-3			
CB3	1	2-1	1	2-1	3-1	2-2	3-2	3-3		
CB4	1	2-1	1	2-1	1	2-1	1	2-1	3-2	3-3
CB5	1	2-1	1	3-1	3-2					
CB6	1	2-2	2-1	2-2	1	3-1	3-2	3-3		
CB7	1	2-1	3-2	3-3						
CB8	1	2-1	1	2-1	1	3-2				
CB9	1	2-1	2-2	1	2-2	3-2	3-3			
CB10	1	2-1	1	2-1	3-1	3-3	3-2	3-3		

Note: The first number indicates **move**, while the second number (if applicable) indicates **submove**, e.g., 2-1 means Move 2-Submove 1.

5.4 Move Patterns

From Table 6, there are two major patterns of moves employed by the authors of the introductions in this study. The first one is **Pattern A: $(1>2)_n>3$**, where n = a counting number (1, 2, 3…). The simplest pattern of this (n = 1) is actually the linear move pattern which progresses from Move 1 > Move 2 > Move 3; this pattern accounts for 30 percent of the introductions. When n > 1, Pattern A becomes cyclical with repeated recycling between Move 1 and Move 2, and with increasing specificity of the context as well as the need(s) before progressing to Move 3 to fulfil the need(s) pointed out earlier; 30 percent of the sample introductions fall into this category. Altogether, Pattern A accounts for 60 percent of the introductions. Next, Pattern B: $(1>2)_n>1>3$, n = a counting number, is similar to Pattern A, except that it has an extra Move 1 between (Move 1

> Move 2) and Move 3 to give a more specific context for the current research. Pattern B accounts for 30 percent of the introductions.

Table 6

Patterns of Moves in Chemical Biology Research Article Introductions

Pattern	Move Pattern	Article	Percentage
A	$(1>2)_n>3$		
	n = 1: 1>2>3	CB1, CB2, CB7	30%
	n = 2: 1>2>1>2>3	CB9, CB10	20%
	n = 4: 1>2>1>2>1>2>1>2>3	CB4	10%
			(Subtotal = 60%)
B	$(1>2)_n>1>3$		
	n = 1: 1>2>1>3	CB5, CB6	20%
	n = 2: 1>2>1>2>1>3	CB8	10%
			(Subtotal = 30%)
exc.	1>2>1>2>3>2>3	CB3	10%
	Total		100%

However, there is an exception (exc.) whose pattern is very similar to Pattern A, but with an additional Move 2 in between the two Move 3s. To get a better idea of why the authors chose to write with this sequence, one can refer to the last paragraph of CB3 (15).

(15) *[16]Despite these advances, the mechanism of communication across KS/DH junctions in trans-AT PKSs remains obscure. [17]To address this problem, we elected to study the GbnD4 and GbnD5 subunits of the* ***gladiolin PKS****, which have KS and DH domains at their C and N termini, respectively. [18]****Gladiolin*** *is a macrolide antibiotic with* ***promising activity against drug-resistant strains of Mycobacterium tuberculosis*** *and* ***negligible toxicity toward mammalian cells*** *that we recently discovered as a metabolite of Burkholderia gladioli BCC0238, a clinical isolate from a cystic fibrosis patient[17]. [19]****Here*** *we show that a largely unstructured DD at the C terminus of the GbnD4 KS*

> *domain interacts directly with the GbnD5 DH domain,* ***revealing a new paradigm*** *for subunit communication across KS/DH junctions in PKS assembly lines.* [CB3]

The last paragraph starts with Move 2-Submove 1: Indicating a gap (Sentence 16), followed by Move 3-Submove 1: Announcing current research purposively (Sentence 17). Then there is the unexpected Move 2-Submove 2: Presenting positive justification (Sentence 18), followed by Move 3-Submove 2: Announcing the principal outcomes (the first half of Sentence 19; notice the word, "here") and Move 3-Submove 3: Stating the value of the current research (the second half of Sentence 19; notice the phrase, "revealing a new paradigm"). One alternative coding is that Sentence 18 could actually be Move 3-Submove 3, stating the value. However, this is unlikely because the content of Sentence 18 suggests that the authors are trying to convince the readers that gladiolin is worthy of study in this research because of its "promising activity against drug-resistant strains of Mycobacterium tuberculosis and negligible toxicity toward mammalian cells," which obviously is the function of Move 2-Submove 2. Things become clearer when the concept of Given-New is taken into account. By drawing an informal diagram similar to the one shown in Swales (1990, p. 16), one can see the Given-New relationships in Sentences 16-18. This suggests that the authors are trying to maintain propositional coherence, which "is based on the organization of the propositional content of the discourse" (Lautamatti, 1990, p. 31) by slightly sacrificing the interactional coherence, which is based on "sequences of communicative acts (p. 32)." Therefore, it is not only the communicative functions or common rhetorical structure that dictates the sequence of these moves and submoves, but also the progression of thoughts.

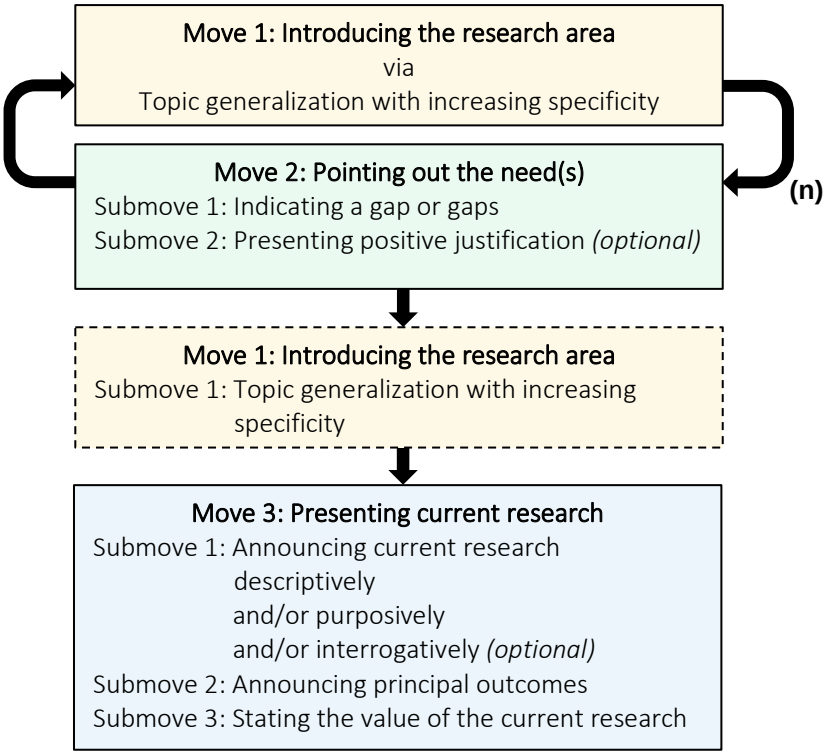
6. Conclusion and Pedagogical Implications

In this study, a move analysis based on a framework adapted from Swales (1990, 2004), Samraj (2002), Kanoksilapatham (2005), Stoller & Robinson (2013) has been conducted on 10 selected chemical biology research article introductions from a leading journal in the field, Nature Chemical Biology. The resulting rhetorical structure consists of three

conventional moves, each realized by submove(s) listed in the same box (Figure 2). All moves and submoves shown are conventional (occurrence rate ≧ 60%), except where indicated otherwise. Two common move patterns have been discovered: **Pattern A: $(1>2)_n>3$** and **Pattern B: $(1>2)_n>1>3$**, where n = a counting number. However, these patterns are not entirely rigid but can be varied due to other factors such as propositional coherence or thought progression.

Figure 2

Rhetorical Structure of Chemical Biology Research Article Introductions



Data from this study suggest that though chemical biology as a field is related to chemistry and biochemistry and shares a lot of common conventions in writing introductions (such as moves and move patterns in general), members of this discourse community seem to have their own preferences in writing introductions, especially in move realization. This

observation is beneficial for ESP teachers who teach writing for publication, in that they can share the information gained from this study with novice chemical biologists, if there are any in their classes, on how to write in a manner that is acceptable to their discourse community. They can also use results from this study with students from other fields to raise awareness of possible variations in expectations in writing across neighbouring disciplines.

7. Limitations

There are some limitations in this study that need to take into consideration. Firstly, since the introductions which were analysed are from only one top journal, Nature Chemical Biology, the sample size of 10 articles may be small. Thus, with these 10 articles, the findings from this study may not be statistically generalizable. Nevertheless, the results suggest plausible general move patterns of the chemical biology research article introductions. Therefore, future studies on this area may include a larger number of introductions from other respected chemical biology journals, e.g., ACS Chemical Biology and Cell Chemical Biology.

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Appendix

A List of Selected Articles

Article	Title	First Author(s)	Corresponding Author(s)
CB1	**In vivo chloride concentrations surge to proteotoxic levels during acid stress** https://www.nature.com/articles/s41589-018-0143-z (retrieved 11/15/2018)	**Frederick Stull** PhD, University of Michigan BS, University of South Florida https://www.linkedin.com/in/frederick-stull-a50540a6/ https://sites.lsa.umich.edu/bardwell-lab/lab-members-2/ (retrieved 11/15/2018)	**James C. A. Bardwell** B.Sc., University of Saskatchewan Ph.D., University of Wisconsin, Madison bardwell_jc_0626_suppl.pdf (retrieved 11/15/2018)
CB2	**Human antibody-based chemically induced dimerizers for cell therapeutic applications** https://www.nature.com/articles/nchembio.2529 (retrieved 11/14/2018)	**Zachary B Hill** University of Alaska Fairbanks University of Washington, Seattle University of California, San Francisco https://academictree.org/chemistry/publications.php?pid=152666 (retrieved 11/15/2018)	**James A Wells** PhD, Biochemistry, Washington State University, 1979 BA, Biochemistry, University of California, Berkeley, 1973 https://pharmacy.ucsf.edu/jim-wells (retrieved 11/15/2018)
CB3	**Mechanism of intersubunit ketosynthase–dehydratase interaction in polyketide synthases** https://www.nature.com/articles/nchembio.2549 (retrieved 11/16/18)	**Matthew Jenner** BSc, PhD, University of Nottingham https://www.linkedin.com/in/matthew-jenner-493ba572/ (retrieved 11/16/18)	**Gregory L Challis** BSc in Chemistry, Imperial College London DPhil in Organic Chemistry, the University of Oxford https://warwick.ac.uk/fac/sci/chemistry/research/challis/challisgroup/challis/ (retrieved 11/15/18)

Article	Title	First Author(s)	Corresponding Author(s)
CB4	**Functional TRIM24 degrader via conjugation of ineffectual bromodomain and VHL ligands** https://www.nature.com/articles/s41589-018-0010-y (retrieved 11/15/18)	**Lara N. Gechijian** BA, Wellesley College PhD, Harvard University https://www.linkedin.com/in/lara-nicole-gechijian/ (retrieved 11/16/18) **Dennis L. Buckley** BS, SUNY Geneseo PhD, Yale University https://www.linkedin.com/in/dennis-buckley-34b6ba11/ (retrieved 11/15/18)	**James E. Bradner** BA, Harvard University MD, The University of Chicago Master's Degree, Harvard Medical School https://www.bloomberg.com/research/stocks/private/person.asp?personId=59181636&privcapId=382553 (retrieved 11/16/18) **Nathanael S. Gray** PhD, University of California Berkeley BS, University of California Berkeley https://www.bloomberg.com/research/stocks/private/person.asp?personId=48817410&privcapId=236291486 (retrieved 11/15/18)
CB5	**Evolution of cyclohexadienyl dehydratase from an ancestral solute-binding protein** https://www.nature.com/articles/s41589-018-0043-2 (retrieved 11/15/18)	**Ben E. Clifton** PhD, ANU Bachelor of Philosophy — a research intensive program — at the ANU http://chemistry.anu.edu.au/news-events/meet-our-alumni-ben-clifton (retrieved 11/15/18)	**Colin J. Jackson** PhD, ANU BSc, Otago http://chemistry.anu.edu.au/people/colin-jackson (retrieved 11/15/18)
CB6	**T cell receptor cross-reactivity expanded by dramatic peptide–MHC adaptability** https://www.nature.com/articles/s41589-018-0130-4 (retrieved 11/15/2018)	**Timothy P. Riley** graduate student, University of Notre Dame B.S., Purdue University West Lafayette http://bmblab.org/team/trilley/ (retrieved 11/15/2018)	**Brian M. Baker** Ph.D. in Biochemistry, University of Iowa B.S. in Biochemistry, New Mexico State University https://chemistry.nd.edu/people/brian-m-baker/ (retrieved 11/15/2018)
CB7	**Enzyme promiscuity drives branched-chain fatty acid synthesis in adipose tissues** https://www.nature.com/articles/s41589-018-0132-2 (retrieved 11/16/18)	**Martina Wallace** BSc, PhD, University College Dublin https://www.linkedin.com/in/martina-wallace-53536529/ (retrieved 11/16/18)	**Christian M. Metallo** BS, University of Pennsylvania PhD, UW-Madison http://www.metallo.ucsd.edu/people.html (retrieved 11/16/18)
CB8	**PatB1 is an *O*-acetyltransferase that decorates secondary cell wall polysaccharides**	**David Sychantha** BSc in Microbiology, MSc and PhD, University of Guelph	**Anthony J Clarke** BSc, University of Waterloo PhD in Biochemistry, University of Waterloo

Article	Title	First Author(s)	Corresponding Author(s)
	https://www.nature.com/articles/nchembio.2509 (retrieved 11/16/18)	http://www.thewrightlab.com/david-sychantha/ (retrieved 11/16/18)	https://www.uoguelph.ca/mcb/people/dr-anthony-clarke (retrieved 11/16/18)
CB9	**Engineered synthetic scaffolds for organizing proteins within the bacterial cytoplasm** https://www.nature.com/articles/nchembio.2535 (retrieved 11/16/18)	**Matthew J Lee** BSc, MSc, PhD University of Kent https://www.linkedin.com/in/matthew-lee-26625a112/?originalSubdomain=uk (retrieved 11/16/18)	**Derek N Woolfson** PhD, University of Cambridge Undergrad, Chemistry, University of Oxford http://www.bris.ac.uk/chemistry/people/dek-n-woolfson/ (retrieved 11/16/18) **Martin J Warren** Undergrad, PhD, Southampton University https://www.kent.ac.uk/bio/profiles/staff/warren.html (retrieved 11/16/18)
CB10	**Structural basis of the Cope rearrangement and cyclization in hapalindole biogenesis** https://www.nature.com/articles/s41589-018-0003-x (retrieved 11/15/18)	**Sean A. Newmister** BS, Ohio State University PhD, UW-Madison https://www.linkedin.com/in/sean-newmister-9722a264/ (retrieved 11/15/18)	**Robert M. Williams** BA, Syracuse University PhD, MIT https://rmwilliamsgroup.wordpress.com/robert-williams/ (retrieved 11/15/18) **K. N. Houk** A.B. 1964, Ph.D. 1968, Harvard University http://www.chem.ucla.edu/dept/Faculty/houk.html/houk.htm (retrieved 11/15/18) **David H. Sherman** BA UC Santa Cruz PhD Columbia University https://www.linkedin.com/in/david-h-sherman-204a9614/ (retrieved 11/15/18)