BIOCHEMISTRY AND MOLECULAR BIOLOGY EDUCATION
Vol. 40, No. 6, pp. 349–356, 2012

Article

Students' Understanding of External Representations of the Potassium Ion Channel Protein, Part I: Affordances and Limitations of Ribbon Diagrams, Vines, and Hydrophobic/Polar Representations

Received for publication, May 1, 2012, and in revised form, July 23, 2012

Marissa Harle and Marcy H. Towns‡

From the Department of Chemistry, Purdue University, West Lafayette, Indiana 47907

Research on external representations in biochemistry has uncovered student difficulties in comprehending and interpreting external representations. This project focuses on students' understanding of three external representations of the potassium ion channel protein. This is part I of a two-part study, which focuses on the affordances and limitations of representations of the potassium ion channel according to students across the chemistry and biochemistry curriculum. Analysis showed that if the students do not possess the required prior knowledge then they are stymied in their interpretations of the representations. Students were able to easily interpret the familiar ribbon diagram representation; however, they found the vines and hydrophobic/polar representations to be less informative. Suggestions for instruction are to probe student understanding and to help students activate prior knowledge to build a more connected set of concepts pertaining to protein structure.

Keywords: Visual literacy, tertiary education, scholarship of teaching and learning.

Many studies have examined the use of external representations to communicate complex, abstract scientific phenomena in disciplines including physics, chemistry, biochemistry, and biology. Examples of external representations that have been explored include physics diagrams [1], Punnett squares [2], DNA molecules [3], and molecular models [4, 5]. External representations are important in multiple aspects of learning. They can help support conceptual and meaningful learning in complex domains [2, 6], reasoning through problems, and developing relationships within and between concepts [7–10]. Although external representations are important for communicating abstract ideas in science, few studies have been conducted in biochemistry that focus on student understanding of representations of proteins.

Central to the study of protein biochemistry is the intimate relationship between structure and function. De Duve expands on this relationship and highlights the importance of external representations:

> "For complete understanding, explanations correlating form and function must be given in molecular terms. The reason for this is simple: living organisms are chemical machines. Only at the molecular level does structure authentically illuminate function and vice versa" [11, p. 89].

External representations of proteins help students build an understanding of structure-function relationships because they cannot be experienced or observed directly [3]. Different types of external representations such as ribbon diagrams, vines, and hydrophobic/polar are used to depict protein structure and function. More than one type of external representation is often needed to improve understanding of a particular protein concept because "there is rarely, if ever, a single representation that is effective for all tasks" [12].

The American Society for Biochemistry and Molecular Biology (ASBMB) published a recommended curriculum for undergraduate biochemistry and molecular biology students that identifies the importance of teaching protein structure-function concepts [13]. The ASBMB also lists skills that students in biochemistry and molecular biology should develop. Two of these skills are important when learning about protein structure and function: 1) the ability to use computers as information and research tools, and 2) an awareness of what resources are available and knowledge of how to use them.

ASBMB's suggested curriculum emphasizes the ability of students to use and interpret external representations of proteins. Research in other scientific disciplines indicates that it is difficult for students to understand external representations of molecules [4, 14–17]. Such difficulty is likely present for students in biochemistry, but

‡To whom correspondence should be addressed. Tel.: 765-496-1574; Fax: 765-464-0239. E-mail: mtowns@purdue.edu.

This work is supported by the National Science Foundation under Grants No. 073694.

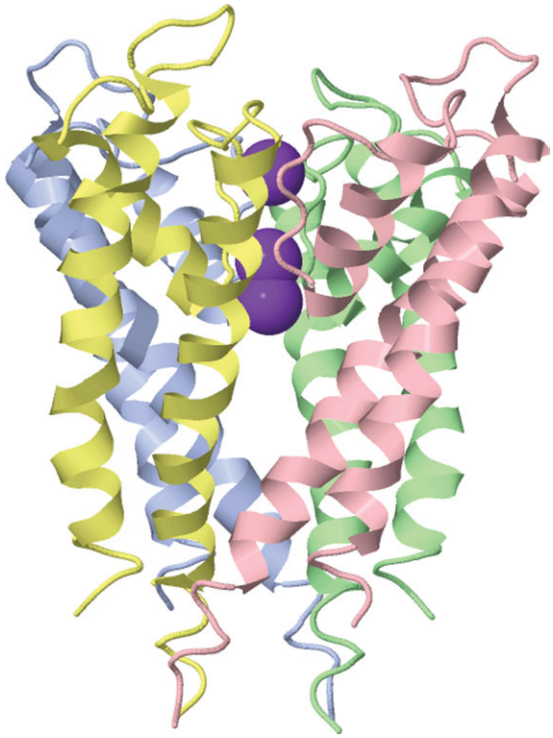

FIG. 1. **The ribbon representation of the potassium ion channel protein (PDB = 1BL8).**

few studies have investigated their understanding of external representations. To understand the influence that external representations have on learning of protein structure-function relationships, it is important to study how such relationships are interpreted by students, thus the guiding research questions were as follows.

1. How do students understand the features and limitations of three types of protein representations for the potassium ion channel—ribbon diagrams, vines diagrams, and hydrophobic/polar surfaces?
2. How do students use multiple representations to communicate their ideas about the potassium ion channel's structure and function?

This article focuses on reporting the findings from question one and a subsequent article will describe our findings from question two.

METHODS AND EXPERIMENTAL DESIGN

The study used a qualitative approach where the goal was to build a rich description of students' understanding of three types of protein representations [18]. This approach to research originates from the social sciences and uses interviews, observations, and written documents as data sources. It is a valuable approach when focusing on a particular phenomenon of interest such as how students understand external representations of proteins.

Purdue's Institutional Review Board approved the research protocol, which is a necessary requirement for all research involving human subjects. All student names that appear in the findings and discussion section are pseudonyms, but the sex of the respondent was not changed.

Molecule and Representations

To investigate student understanding of the external representations of proteins a suitable molecule must be chosen. After conducting a pilot study using two proteins (carbonic anhydrase and the potassium ion channel), a decision to use the potassium ion channel (PDB = 1BL8) was reached. This protein is composed of four subunits featuring alpha helices and random coil. It is neither overly complex nor simple in terms of its structure.

Three types of external representations of the potassium ion channel protein (ribbon, vines, and hydrophobic/polar) were used to display spatial relationships and organization. Figure 1 is a ribbon diagram of the potassium ion channel protein that explicitly shows the secondary structure of the protein. In a ribbon diagram coiled ribbons represent alpha helices and flat ribbons represent beta sheets. The rope-like structures represent random coil and often join alpha helices or beta sheets together. The molecule was rendered in color thus identifying the individual subunits of the protein.

Figure 2 is the vines representation, which shows a simplified representation of the protein backbone composed of a zig-zag series of cylinders that connect alpha carbon positions in the protein chain, and a wireframe representation of the side chains that shows all of the covalent bonds between the side chain atoms. Atoms that comprise each R-side group have similar color themes to those often used in chemistry. For example, gray represents a carbon atom, red represents an oxygen atom, yellow represents a sulfur atom, and blue represents a nitrogen atom. The vines representation is helpful in examining interactions between specific atoms, ions, or R-side groups within a protein.

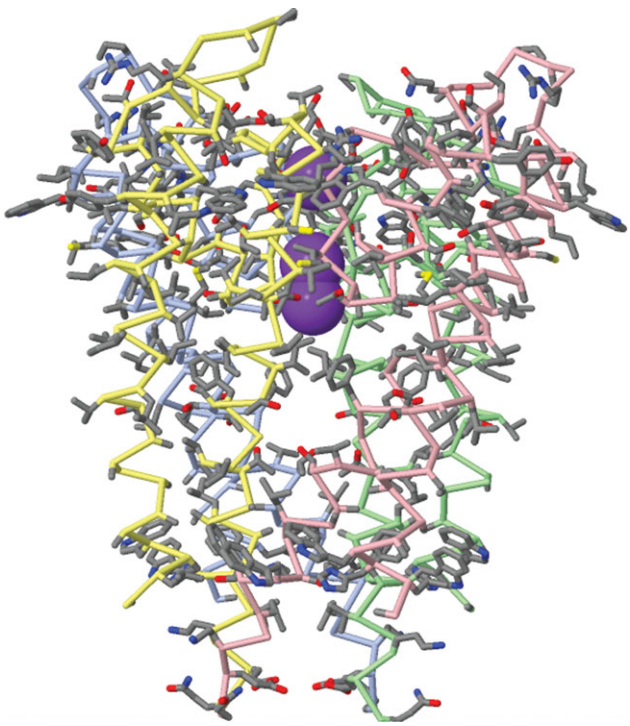

FIG. 2. **The vines representation of the potassium ion channel protein.**

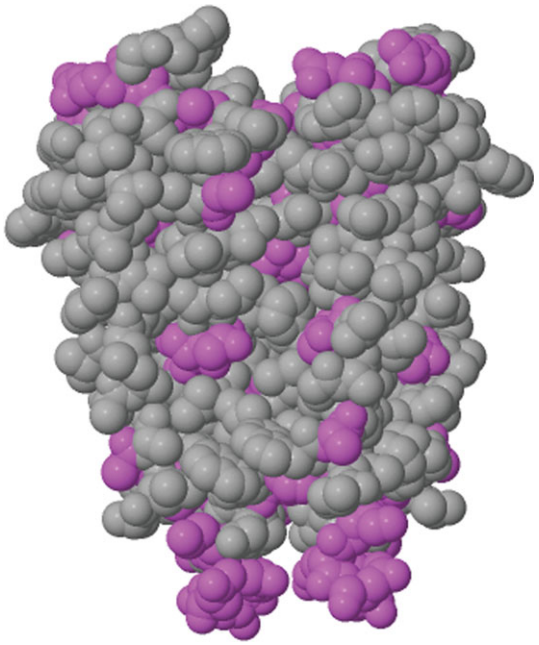

FIG. 3. **The hydrophobic/polar representation of the potassium ion channel protein.**

The hydrophobic/polar representation in Fig. 3 was the last used in the study. The protein is shown with a space filling representation, with a sphere for each atom. All of the atoms in a particular amino acid are colored magenta or gray depending on whether the amino acid is polar or hydrophobic, respectively. The hydrophobic/polar representation provides information about the hydrophobicity and hydrophilicity of different regions of the protein, providing insights about how the protein folds, and how it interacts with other proteins and membranes.

The representations were displayed one at a time on a computer using FirstGlance in JMol [19, 20] such that the students could manipulate the representation of the potassium ion channel on the screen rotating and flipping the representation smoothly in three-dimensions as they wished to view it from various perspectives. They were also able to zoom in and out on the representation of the molecule if they desired.

Sampling and Participants

For this study, maximum variation sampling methods were used to capture the central themes that cut across participants from a variety of biochemistry courses in the chemistry and biochemistry departments [18]. Recruiting participants from different departments in different colleges meant that there was a great deal of diversity in the sample. The participants had 1) a varying degree of chemistry/biochemistry prior knowledge, 2) different majors, and 3) came from different departments. Having a sample with such heterogeneity may seem like a weakness, but as Patton describes:

> Any common patterns that emerge from great variation are of particular interest and value in capturing the core experiences and central, shared dimensions of a setting or phenomenon [18, pp. 235].

Therefore, when using a small sample of great diversity, the analysis can yield findings that highlight:

> Important shared patterns that cut across cases and derive their significance form having emerged out of heterogeneity [18, pp. 235].

Thus the students in the study ranged from freshman to seniors including two novice students who were not in biochemistry courses. The 21 participating students were from a large Midwestern research university and were enrolled in four different biochemistry courses or one history course, which are described in Table I.

Interview Structure

At the beginning of each interview, participants were given a brief tutorial about FirstGlance in Jmol and were allowed to explore another protein in order to familiarize themselves with the program [19, 20]. Each participant

TABLE I
Course name and abbreviation, the number of participants, and a description of the course

Course name (abbreviation)	Number of participants	Description
Chemistry 333 (CHM 333)	2	"Principles of biochemistry" is a three-credit course offered by the College of Science in the chemistry department. The course is designed for health science majors, and the material covered concentrates on the structure and function of biologically important molecules.
Chemistry 533 (CHM 533)	4	"Introductory Biochemistry" is a three-credit course offered by the College of Science in the chemistry department. The content of this course is a rigorous one-semester introduction to biochemistry geared for students majoring in chemistry.
Biochemistry 100 (BCHM100)	4	"Introduction to Biochemistry" is a two-credit course offered by the College of Agriculture in the biochemistry department. BCHM 100 does not require any college science courses as background or a prerequisite. The content of this course centers around a survey of modern biochemistry using descriptions of contemporary experiments to illustrate the general theories and unifying concepts.
Biochemistry 307 (BCHM 307)	9	"Introduction to Biochemistry" is a three-credit undergraduate-level course offered by the College of Agriculture in the biochemistry department. This course is designed for lift science majors and the material focuses on an introduction to the chemistry, function, and metabolism of compounds found in living organisms.
History 151 (HIST 151)	2	"American history to 1877" is a three-credit undergraduate-level course offered by the College of Liberal Arts.

was asked several warm up questions in order to make them feel comfortable talking with the interviewer, and to turn their attention to proteins. The main portion of the interview included asking participants about the features of the representation of the protein they could interpret in the ribbon, vines, and hydrophobic/polar representations. Next the participants were asked about the limitations of the ribbon, vines, and hydrophobic/polar representations. When asked about the features and limitations of the representation, each participant was shown the representations in the same order and not allowed to switch between them.

Data Analysis

We used an analysis approach known as grounded theory [21], which begins with transcribing all 21 interviews verbatim. Each transcript was coded line-by-line to identify features and limitations of each representation that students described. AtlasTi, a qualitative data analysis software package, was used to sort, store, and retrieve codes during analysis. The codes were sorted into categories, which were then examined for their relationships to each other. The integration and interrelationships of the categories formed the basis of the grounded theory and the assertions, which are discussed in the findings.

After coding the transcripts an inter-rater study was performed to ensure that the coding scheme was reliable. Two raters independently coded two transcripts using the codes and definitions provided by one of the authors (MH). Each rater received directions about the coding process and how to record their responses. When each rater had completed coding the transcripts we met to 1) calculate the percent agreement and 2) discuss any disagreements in the coding. We agreed on 128 out of 178 codes, equaling 72% agreement, which was above the acceptable limit of 70% [22]. Upon discussion of coding disagreements, it became apparent one of the raters (from biochemistry) inferred meaning from participants' statements. At the end of our discussion each rater was confident with the coding instructions and we separately recoded the transcripts. A week later we met, recalculated our percent agreement, and discussed disagreements. After revising codes, we agreed on 158 out of 178 codes, equaling 89% agreement.

External Representations Shown in Biochemistry and Chemistry Courses

The percentage of each type of external representation that was shown in the lecture notes specifically for the unit on amino acids and proteins was calculated in order to guide the interpretation of the findings. Copies of lecture notes were obtained from each chemistry and biochemistry course and frequency counts were tabulated for ribbon, vines, space-filling, ball-and-stick, and hydrophobic/polar representations.

Inter-rater reliability (IRR) calculations were performed to find the percent agreement on the coding scheme. The two raters independently coded all of the representations for the unit on amino acids and proteins in the CHM 533 lecture notes. The percent agreement was 92%, which is above the accepted 70% value [22].

TABLE II
The percentage of ribbon, vines, spacefilling, and ball and stick representations used in each course in the amino acids and proteins unit

Courses	Ribbon (%)	Vines (%)	Spacefilling (%)	Ball and stick (%)
BCHM 100	41	10	16	33
BCHM 307	76	8	4	12
CHM 333	33	2	14	51
CHM 533	55	1	5	38
HIST 151	0	0	0	0

FINDINGS AND DISCUSSION

To interpret the findings it is illustrative to know what kinds of protein representations were used in the courses in which the participants were enrolled. Table II lists the percentage of ribbon, vines, spacefilling, and ball-and-stick representations used in each course. There were no hydrophobic/polar representations used in any course.

Among the types of protein and amino acid representations used in the chemistry and biochemistry courses, the ribbon representation was used most frequently for BCHM 100, BCHM 307, and CHM 533, while the ball-and-stick representation was used most frequently in CHM 333. The vines representation was used least frequently in BCHM 100, CHM 333, and CHM 533. Knowing that participants have little exposure to this type of external representation helped shape the interpretation of the findings.

How do Students Understand the Features of Each Type of Representation?

The aim of the first part of this research question was to examine the features of the protein that participants could interpret from ribbon, vines, and hydrophobic/polar representations. The nature of the interview questions about the features allowed for the use of frequency counts to analyze the data as shown in Table III. The data is grouped by representational type, then by the features the students described.

The discussion of Table III will focus on the eight bolded rows. Given the diversity of the participants, the aim for this discussion will be to describe the features that participants across all courses interpreted and described from the ribbon, vines, and hydrophobic/polar representations. For this study, we considered patterns to be shared across all courses when the frequency count was ≥50%. The total number of participants in the study was 21 ($n = 21$), so ≥11 participants were required to responded to a particular code for the frequency count to be ≥50%. The frequency counts of ≥50% will be discussed in order as they relate to the ribbon, vine, or hydrophobic/polar representation.

The major affordances of the ribbon representation are that it highlights the secondary, tertiary, and quaternary structural elements of a protein. Additionally, the software used in the study (FirstGlance in Jmol [19, 20]) allowed the potassium ions to be shown overlaid on the ribbon representation. Of those major affordances of the ribbon representation, at least 50% of participants were able to

TABLE III
Frequency counts of features described by participants for each representation separated by course

Identified feature by representation	BCHM 307 (9)	BCHM 100 (4)	CHM 333 (2)	CHM 533 (4)	HIST 151 (2)	Total frequency (21)
Ribbon diagram						
Tubular	1 (11%)	1 (25%)	0	2 (50%)	0	4 (19.0%)
Cavity	1 (11%)	0	0	1 (25%)	0	2 (9.52%)
Symmetrical	2 (22%)	2 (50%)	1 (50%)	0	0	5 (23.8%)
Potassium	***9 (100%)***	***3 (75%)***	***2 (100%)***	***4 (100%)***	***2 (100%)***	***20 (95.2%)***
Alpha helices	***9 (100%)***	***4 (100%)***	***2 (100%)***	***4 (100%)***	***1 (50%)***	***20 (95.2%)***
Random coil	1 (11%)	2 (50%)	1 (50%)	2 (50%)	0	6 (28.6%)
Tertiary	***9 (100%)***	***4 (100%)***	***2 (100%)***	***4 (100%)***	***1 (50%)***	***20 (95.2%)***
Quaternary	***6 (66%)***	***2 (50%)***	***2 (100%)***	***3 (75%)***	***0***	***13 (61.9%)***
Vines						
Bonds	1 (11%)	0	0	1 (25%)	0	2 (9.52%)
Backbone	4 (44%)	2 (50%)	0	1 (25%)	1 (50%)	8 (38.1%)
Potassium	0	0	0	0	0	0
R-groups	***5 (55%)***	***4 (100%)***	***2 (100%)***	***1 (25%)***	***0***	***12 (57.1%)***
Alpha helices	1 (11%)	0	1 (50%)	0	0	2 (9.52%)
Tertiary structure	2 (22%)	0	0	0	0	2 (9.52%)
Quaternary structure	4 (44%)	1 (25%)	1 (50%)	0	0	6 (28.6%)
Atoms	***4 (44%)***	***2 (50%)***	***2 (100%)***	***3 (75%)***	***0***	***11 (52.4%)***
Hydrophobic/polar						
Symmetrical	2 (22%)	0	0	2 (50%)	0	4 (19.0%)
Space	0	0	0	1 (25%)	0	1 (4.76%)
Hydrophobic	***9 (100%)***	***4 (100%)***	***2 (100%)***	***4 (100%)***	***2 (100%)***	***21 (100%)***
Polar	***9 (100%)***	***4 (100%)***	***2 (100%)***	***4 (100%)***	***2 (100%)***	***21 (100%)***

The number in parentheses indicates the number of participants from each course that identified a specific feature.

identify the potassium ions and secondary, tertiary, and quaternary structural elements.

Twenty out of twenty-one (95.2%) participants were able to identify alpha helices, a secondary structural element in the protein. These same 20 participants interpreted tertiary structure. The only participant who did not interpret the alpha helices or tertiary structure in the representation was Hank from History 151. Hank stated that the representation looked "curly," but when asked what the curly's represented he was not sure.

Interviewer: Do you have any idea what...what... the curly's represent here?
Hank-HIST 151: No

Thus the ribbons in the diagram held no meaning for him beyond their surface shape. Additionally, Hank did not interpret the protein's tertiary structure.

Schönborn and Anderson noted that one factor related to interpreting an external representation in biochemistry is the retrieval of the appropriate conceptual knowledge related to the representation [1]. With little to no relevant prior biochemistry knowledge, it is unlikely that Hank would be able to reason with and interpret the representation. In other words, representations may have arbitrary, but conventional relations to the things they represent; students cannot elaborate on the representation's content without knowing these conventions [24, 25].

Although most participants discussed the protein's tertiary structure, identifying quaternary structure proved difficult. Thirteen out of twenty-one (61.9%) participants indicated that the protein had a quaternary structure. Even though, participants noticed that each tertiary structure was rendered in a different color, they did not relate the colors to the protein's quaternary structure.

The most important features that can be interpreted from a vines representation are atoms and amino acid side groups (R-side groups). Eleven out of twenty-one (52.4%) participants interpreted atoms in the representation, and 12 out of 21 participants (57.1%) could interpret the R-side groups. The frequency counts for identifying the atoms and R-groups were much lower than those for the ribbon representation. As shown in Table I, the vines representation is shown less frequently in chemistry and biochemistry courses than the ribbon representation. The lower frequency count for identifying the atoms and the R-side groups in the vines representation may originate from a lack of familiarity with this type of representation.

The hydrophobic/polar representation may not provide abundant information about the protein's secondary through quaternary structural elements or provide details about the atoms and R-side groups. However, this type of representation makes clear the locations of polar and hydrophobic regions. Why would this be important? One of the central themes of protein biochemistry is the structure function relationship. By knowing where the polar and hydrophobic regions of the protein are, one may gain insight about the location of the protein in the cell. Within the potassium ion channel protein there are polar regions at the top and bottom that sandwich a hydrophobic region. The location of the hydrophobic/polar regions of the protein maps perfectly onto the hydrophobic/polar regions of the cell membrane. Knowing that the protein is located in the cell membrane highlights its function, which is moving ions from inside to outside the cell. Twenty-one out of twenty-one (100%) participants identified that the hydrophobic/polar representation encoded areas of the protein were hydrophobic and polar. In this representation, a large legend as shown in Fig. 4 made the polarity of the magenta and gray regions clear so it is not surprising that all participants were able to identify the hydrophobic/polar features.

Hydrophobic/Polar: Amino acids are colored either

- Hydrophobic or
- Polar (charged or uncharged)

FIG. 4. **The legend presented with the hydrophobic/polar representation [19].**

How do Students Understand the Limitations of Each Type of Representation?

The second part of the first research question was to examine what students believed were the limitations of each representation. External representations usually emphasize some types of information at the expense of other types of information [12, 24]. Since, there is not one correct representation for a given phenomenon, it is important to evaluate not only the affordances of a representation, but also its limitations.

Four assertions emerged from the analysis of the data. Each assertion is presented with exemplar quotes from the data, which are discussed.

Assertion One: The Absence of Interactions Was a Limitation of the Ribbon Diagram According to Students

Students described a lack of interactions being explicitly shown as a limitation of the ribbon diagrams. The specificity of the nature of the interactions varied between those who talked about general interactions to those who discussed specific types of bonding. The details about the specific types of interactions students were looking for was not always explicit, but students did state that they could not "see" the interactions.

Kate-CHM 533: Um I guess…none that I haven't said already other than it would be nice to see how the interactions are going on

Some students were looking for specific types of bonding and they clearly anticipated seeing them. For example, while viewing the ribbon representation Angie and Ken both spoke about not being able to see the hydrogen bonding.

Angie-BCHM 307: Um…like I don't see any hydrogen bonds

Ken-CHM 533: Um hydrogen bonds don't appear to be shown

Additionally, some students attempted to describe the interaction between the potassium ion and the protein. Bethany and Ashlee believed that the potassium atoms in the channel were bonded to something, but the representation did not show what or how.

Bethany-BCHM 100: Like you know that those are bonded to the potassium, but you don't know exactly how

Ashlee-BCHM 307: I think there's three of them…yeah the three different balls and you don't really see how it actually binds to it

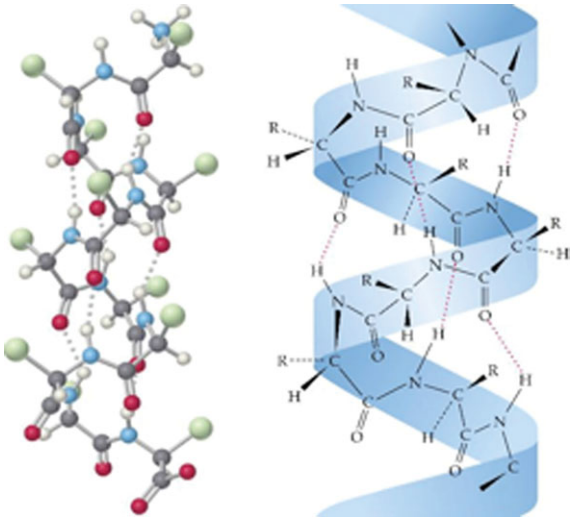

FIG. 5. **An external representation that shows hydrogen bond interactions [**26**].**

Beyond confusion about hydrogen bonding, Bethany and Ashlee expressed confusion about the exact type of interaction that might be occurring between the potassium ion and the protein describing it as a bond.

As the lecture notes from each course were examined, external representations showing hydrogen bonding were shown such as the one in Fig. 5. Notes from every course contained representations that explicitly showed hydrogen bonding interactions between atoms with a dotted line. The percentage of representations showing hydrogen bonding in the amino acid and protein unit of each course was calculated and is shown in Table IV. Note that in Biochemistry 307, nearly one-quarter of the all the representations explicitly show hydrogen bonding.

To help students properly interpret representations in biochemistry it is important to discuss the conventions that are used in addition to the limitations of the conventions.

Assertion Two: Students Were Distracted by the Amount of Detail in the Vines Representation

When students were asked to discuss the limitations of the vines representation, they spoke about the confusing nature of the representation. The vines representation is the most detailed of the three types of representations and the structure of each R-side group on the backbone is shown. Considering that the potassium ion channel protein has 388 R-side groups, it is not surprising that

TABLE IV
The percent of representations that showed hydrogen-bonding interactions in each course

Courses	Percent of representations showing hydrogen bonding interactions
BCHM 100	15
BCHM 307	24
CHM 333	18
CHM 533	8

students found this representation to be visually complex as Bill noted.

Bill-BHCM 100: Um I feel its very con. . .like confusing because there's a lot going on in it

Students such as Allison commented that if the vines representation had been shown before the ribbon representation, they would have had greater difficulty in interpretation.

Allison-BCHM 307: . . .I think um it makes it more confusing. . .if I would have seen this before the other picture this would have um. . .I would have had a lot less idea possibly of what was going on and being able to um

Certainly the lack of familiarity with this type of representation would have made it more challenging to interpret.

Assertion Three: Students Describe the Lack of Secondary Structure or Secondary Structural Elements as a Limitation of the Vines Representation

The major affordance of the vines representation is that it makes explicit each of the R-side groups on the protein backbone. However, students stated that they could not identify or find the secondary structure of the protein. For example, Ben and Angie could not distinguish the secondary structure of this representation.

Ben-BCHM 100: . . .I mean secondary structure now since its. . .you can't really tell
Angie-BHCM 307: Ah secondary structure. . .um no I don't see the secondary structure

Given that the vines representation was viewed after the ribbon representation (which highlighted the protein's secondary structure), students made comparisons between them. The secondary structure in the vines representation was not as obvious as it was in the ribbon representation as Abbie declared.

Abbie-BCHM 307: Um you don't. . .well I guess like the secondary structures aren't as like obvious in this one

The ribbon representation made participants aware of the secondary structure elements in the protein, but if the vines representation had been given first, then determining secondary structure might have been more difficult. Ken specifically was looking for the secondary structure in the vines representation having seen the ribbon diagram first.

Ken-CHM 533: I mean now that I know that I'm looking for it [secondary structure] yeah, but if you had given me this first probably not

While some students only spoke of general secondary structure, others discussed the lack of alpha helices as a limitation. The predominant type of secondary structure present in the potassium ion channel protein is the alpha helices. Bethany, Al, and Kate professed that they could not "see" the alpha helices in the vines representation.

Bethany-BCHM 100: Mmm. . .you can't really see the alpha helices
Al-BHCM 307: You can't tell which one's alpha helix or I can't tell at least what's an alpha helix or which one's an alpha helix
Kate-CHM 533: Um you really can not see the alpha helices

The students had viewed the ribbon representation immediately beforehand, which showed each alpha helix in the protein. Thus, the surface features of the protein, the alpha helices, were fresh in their minds and they were primed to search for them.

Assertion Four: Students Describe not Being Able to See the Channel as a Limitation of the Hydrophobic/Polar Representation

The hydrophobic/polar representation displays the hydrophobic/polar regions of the protein. However, the space-filling nature of the representation makes it difficult to discern that the protein has a channel, especially when compared to the ribbon and vines representations, which have a clear view of the channel because of the rendering of the representation. The students anticipated seeing the channel in this representation as Kate noted.

Kate-CHM 533: No I cannot see down the middle of it. . .I have no idea what's going on in the middle

Students such as Christine, Amy, and Kyle described not being able to see the potassium ions as a limitation of the hydrophobic/polar representation.

Christine-CHM 333: . . .and um you can't see those ah potassiums ions any more
Amy-BCHM 307: Well you can't see the potassium any more but
Kyle-CHM 533: I can't see the. . .if there are ions inside

Again, the students were primed by previous representations to see the potassium ions.

CONCLUSIONS AND TEACHING IMPLICATIONS

Students use their prior knowledge and experiences to actively create their understanding of new information. For example, the majority of students used their prior knowledge about protein structure to interpret the ribbon representation of the potassium ion channel protein and identify its secondary, tertiary, and quaternary structure. On the basis of our analysis of course lecture notes the ribbon diagram was a frequently used representation in all chemistry and biochemistry courses in the study. Thus, the students were able to use their prior knowledge to make sense of a protein representation that was new to them.

However, when presented with a less familiar representational type, students tried to use their prior knowledge (what little they had) and the cues from the ribbon

diagram to interpret these representations. As Von Glasersfeld wrote,

> A representation does not represent by itself—it needs interpreting, to be interpreted, it needs an interpreter [27, p. 215].

Analysis of the data in our study demonstrated that if the students do not possess the required prior knowledge then they are stymied in their interpretations of the representations. Further they retrieve their prior knowledge and attempt to use it even if the representations do not contain that information. We hypothesize this is what happened when the students looked for "interactions" or "hydrogen-bonds" as noted in the findings. These conventions orient the students to certain concepts just as hydrophobicity and hydrophilicity would help students understand the orientation of the potassium ion channel in a cell membrane.

When faculty use representations of proteins in the classroom it is paramount that they make clear to the students how to interpret the representation as Schönborn and Anderson have noted previously in this journal [8, 9, 23]. The information that is or is not encoded in a representation may be clear to faculty, but it is not clear for the students. Further, relating across multiple representations is not simple matter as Shaaron Ainsworth's research has made clear [12]. In cases where multiple representations are used to complement, constrain, or construct student understanding it is again of utmost importance for faculty to clearly articulate how the representations are related to one another.

Faculty can also help deepen and connect student learning meaningfully when students use their prior knowledge to interpret representations. In this study, students used terms relating to protein structure, amino acids, hydrophobicity, and hydrophilicity. Additionally, they used the words "interactions" and "hydrogen-bonding." For faculty there are ways in which all those words and concepts connect together meaningfully to describe representations of proteins. But to students those words, those concepts, may not be connected. For example, the student who talked about looking for interactions may not have meant hydrogen bonds at all. The students who talked about looking for hydrogen bonds may not describe them as interactions. Yet to faculty the terms hydrogen bonds and interactions embody specific and related concepts. Further, they know how those concepts relate to amino acids, protein structure, hydrophobicity, and hydrophilicity, which are key concepts in understanding protein structure and function. Faculty must repeatedly probe and extend students' prior knowledge to help them deepen the connections between concepts and to construct new understandings in the most meaningful way possible.

Acknowledgments— The authors thank Dr. David Goodsell for comments and suggestions during revision of the manuscript. Any opinions, findings, and conclusions or recommendations expressed in this material are those of the authors and do not necessarily reflect the views of the National Science Foundation.

REFERENCES

[1] M. T. H. Chi, P. J. Feltovich, R. Glaser (1981) Categorization and representation in physics problems by experts and novices, *Cognit. Sci.* **5**, 121–152.

[2] A. M. L. Cavallo (1996) Meaningful learning, reasoning ability, and students' understanding and problem solving of topics in genetics, *J. Res. Sci. Teach.* **33**, 625–656.

[3] M. D. Patrick, G. Carter, E. N. Wiebe (2005) Visual representations of DNA replication: middle grades students' perceptions and interpretations, *J. Sci. Educ. Technol.* **14**, 353–365.

[4] V. Ferk, M. Vrtacnik, A. Blejec, A. Gril (2003) Students' understanding of molecular structure representations, *Int. J. Sci. Educ.* **25**, 1227–1245.

[5] M. H. Towns, J. R. Raker, N. Becker, M. Harle, J. Sutcliffe (2012) The biochemistry tetrdadron and development of the taxomony of biochemistry external representations (TOBER), *Chem. Educ. Res. Pract.*, **13**, 296–306.

[6] P. C. H. Cheng (1999) Unlocking conceptual learning in mathematics and science with effective representational systems, *Comput. Educ.* **33**, 109–130.

[7] M. P. Peterson, in A. M. Ceachren, D. F. Taylor, Eds. (1994) Visualization in Modern Cartography, Pergamon, Oxford, pp. 27–43.

[8] T. R. Anderson, K. J. Schönborn (2008) Bridging the educational research-teaching practice gap: conceptual understanding, Part 1: The multifaceted nature of expert knowledge, *Biochem. Mol. Biol. Educ.* **36**, 309–315.

[9] K. J. Schönborn, T. R. Anderson (2010) Bridging the educational research-teaching practice gap: foundations for assessing and developing biochemistry students' visual literacy, *Biochem. Mol. Biol. Educ.* **38**, 347–354.

[10] K. J. Schönborn, T. R. Anderson (2009) A model of factors determining students' ability to interpret external representations in biochemistry. *Int. J. Sci. Educ.* **31**, 193–232.

[11] C. De Duve, in B. S. C. Study, Ed. (1993) Developing Biological Literacy: a Guide to Developing Secondary and Post-Secondary Biology Curricula, Kendall/Hunt, Dubuque, IA, pp. 88–91.

[12] S. E. Ainsworth (1999) The functions of multiple representations, *Comput. Educ.* **33**, 131–152.

[13] American Society of Biochemistry and Molecular Biology (ASBMB). Retrieved January12, 2012, from http://www.asbmb.org/CareersAndEducation.

[14] K. C. Anderson, G. Leinhardt (2002) Maps as representations: expert novice comparison of projection understanding, *Cognition. Instruct.* **20**, 283–321.

[15] M. M. Cooper, N. Grove, S. M. Underwood, M. Klymkowsky (2010) Lost in Lewis structures: an investigation of student difficulties in developing representational competence, *J. Chem. Educ.* **87**, 869–874.

[16] R. M. Kelly, L. T. Jones (2007) Exploring how different features of animations of sodium chloride dissolution affect students' explanations, *J. Sci. Educ. Technol.* **16**, 413–429.

[17] R. M. Kelly, L. L. Jones (2008) Investigating students' ability to transfer ideas learned from molecular animations of the dissolution process, *J.Chem. Educ.* **85**, 303–309.

[18] M. Q. Patton (2002) Qualitative Research and Evaluation Methods, 3rd ed., Thousand Oaks, Sage.

[19] FirstGlance in Jmol, http://bioinformatics.org/firstglance/fgij/ (Accessed June 10, 2012).

[20] Jmol: an open-source Java viewer for chemical structures in 3D. http://www.jmol.org/ (Accessed June 10, 2012).

[21] A. Strauss, J. Corbin (1998) Basics of Qualitative Research: Techniques and Procedures for Developing Grounded Theory, 2nd ed., Thousand Oaks, Sage.

[22] W. R. Borg, M. D. Gall (1989) Educational Research: An introduction, 5th ed., Longman, New York, NY.

[23] K. J. Schönborn, T. R. Anderson (2006) The importance of visual literacy in the education of biochemists, *Biochem. Mol. Biol. Educ.* **34**, 94–102.

[24] W. M. Roth, G. M. Bowen (2001) Professionals read graphs: a semiotic analysis. *J. Res. Math. Educ.* **32**, 159–194.

[25] M. Petre, T. R. G. Green (1993) Learning to read graphics: some evidence that "seeing" an information display is an acquired skill, *J. Visual Lang. Comput.* **4**, 55–70.

[26] What does Keratin help with? http://www.innovateus.net/innopedia/what-does-keratin-help (accessed June 10, 2012).

[27] E. Von Glasersfeld, in C. Janvier, Ed. (1987) Problems of Representation in the Teaching and Learning of Mathematics, Erlbaum, Hillsdale, NJ, pp. 215–226.