**Table 2. Possible extensions, modifications and suggestions, based on grade level or individual student ability.** Extensions or modifications can be used to best suit student and class needs: for example, an introductory biology course can utilize suggestions for “beginner” or “advanced” categories if more supports or greater detail are appropriate.

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| --- | --- | --- | --- |
| Suggested Extension or Modification | Grade/Level(s) most appropriate for: | | |
| Beginner (6-8; 9 / 10 ELL, SPED) | Intermediate (9 / 10, intro biology) | Advanced (TAG; AP and IB) |
| Modify the length of the sequence/polypeptide being produced for individual students or the class as a whole, based upon how much time can be devoted to modeling, and the pace students are progressing at. | ✓ | ✓ | ✓ |
| If students struggle with replication or one component of protein synthesis, use modeling to simulate and practice that particular process, adding additional labels as they are helpful (i.e., label the sense and antisense strand of DNA). This may be especially important if time constraints limit how long can be spent modeling, and priority can be placed on the most challenging components. | ✓ | ✓ | ✓ |
| Use the square-shaped amino acid cutouts offered in Figure 8 to facilitate cutting; cutting out circles can be tedious and time consuming, and requires more dexterity that younger students in particular may not have fully developed yet. | ✓ | ✓ |  |
| Have students write their original DNA strand so letters are visibly grouped into sets of 3, to facilitate more visible and easily read codons later in the activity. It may also be helpful to project a similarly grouped sequence that the students are copying, so there are visual instructions as well as verbal. | ✓ | ✓ |  |
| Ask students to write a *complementary* strand to that displayed on the board, instead of copying the sequence as shown; students will then fill in the opposite side, and can be asked what patterns emerge (i.e., the filled-in strand matches the original) and what it might symbolize (i.e., semiconservative replication) |  | ✓ | ✓ |
| Project a double- or single-stranded molecule of DNA with directionality (5-3” or 3-5”) shown. Ask students which would be the leading and lagging strands, and which direction(s) new bases will be added during replication. This could lead to a more in-depth discussion and/or modeling of the enzymes involved and other key steps that could be factored into the modeling if there is sufficient time (i.e., using another envelope or differently colored pieces of construction paper to simulate the various enzymes involved, depending on the level of detail being covered) |  |  | ✓ |
| When learning about replication prior to modeling, or immediately before simulating replication, it may be useful to show students a visual of base-pairing. This can be done by showing a video recap of base pair rules, such as the animation (<https://www.youtube.com/watch?v=_POdWsii7AI>) and/or by using a mnemonic device like that found at 6:10 in the video: A goes with T like an apple in a tree, and C pairs with G like a car in a garage. Point out the importance of these particular pairings and challenge students to think of their own mnemonic device that will help them remember. Native Spanish speaking students in particular might benefit from the following example: Árbol is like Tree, and Gato is like Cat. | ✓ |  |  |
| Model semi-conservative replication by projecting a double-stranded DNA molecule and asking that students write each strand separately, then fill in the complementary strand for each. Compare and contrast the new strands with one another, and compare with the original strands; ask students what patterns emerge and why. (This could work at all levels, but the time involved may vary by level and should be taken into consideration when planning the length of strand students will use) | ✓ | ✓ | ✓ |
| Ask students to write each new strand in a new color, and label each (on the back of paper strip) so it is visually more clear which was the original strand, which is complementary, and which contains RNA bases. If students are asked to identify DNA versus RNA, answers written on the back can be used to check answers if students are struggling to determine which is which | ✓ |  |  |
| If students are replicating the lagging strand, ask that they write their bases in the same manner as DNA polymerase would (including RNA primase if appropriate); students can write right to left, creating in fragments |  | ✓ | ✓ |
| After replication and transcription are complete, ask students what will happen to the DNA (which was opened up to create the RNA transcript) at this point. A brad could be attached at one end of the sequence so that the model can hinge open during replication or transcription, then be used to simulate the “re-zipping” of DNA at the conclusion of these processes. | ✓ | ✓ | ✓ |
| When creating envelope ribosomes, if students cannot easily size or cut their window accurately or efficiently, a window and slits can be pre-traced on the envelope (about 1” in height and 3 codons wide, according to dimensions of RNA paper strand used). If students struggle to start cutting the window, suggest that they pinch the center of the window area and snip a place to insert scissors to cut the remainder. Make sure students make (or use pre-traced) slits that are level with the window and similar in height. The RNA strand can be used to measure if needed. Before students make any cuts, make it very clear that the window is cut on one side of the envelope only, and the side slits are only a notch in the side—do not cut off a sliver of the entire side! | ✓ | ✓ | ✓ |
| The ribosome can be glued (window side up) into students’ notebooks to return to later for additional practice in class or independently. The window and slit will still be operational once glued in place. All parts can be neatly folded and tucked inside the envelope. If you plan to use the ribosome for notebook storage of parts, ensure students cut the window on the *flap* side of the envelope so it can still open and close. Vertical alignment is easiest (see Figure 7) and allows RNA to be threaded through. | ✓ | ✓ | ✓ |
| Have students draw lines between each codon (using a light pencil mark or a thick marker) to help them keep track of how many letters have passed through the window of the ribosome, and to establish a pattern that helps recognize a codon is three letters long. This can be done together as a class, or can be suggested to specific students. | ✓ |  |  |
| Instruct students to write the anticodon sequence on the amino acid cutouts (either on the front or back). This can be used to retrieve the correct residue based on the codon read, and clarify for students that the codon—not the anticodon—is read to determine the amino acid. If the name of the amino acid and the anticodon are written on opposite sides of the cutout, they can be used as “flashcards” to practice determining an amino acid using an anticodon sequence. |  | ✓ | ✓ |
| Letters can be written above or below the ribosome window to label A, P and E sites so students can be more precise when modeling how tRNA enters, residues are added, and tRNA exits as the polypeptide grows. A video animation demonstrating this process may be useful as an introduction or refresher prior to modeling. |  |  | ✓ |
| Provide students with a chart of amino acid properties (polarity and charge) found online or in your class text and printed in black and white. Ask that students color each property on the chart (polar, nonpolar, acidic, basic) a different color, then color their residues with the corresponding colors. It is recommended amino acids are colored one at a time, as they are needed; it is much easier to color prior to cutting. Once the polypeptide is complete, the colors can then be used to determine how the folding could occur: students can predict based on properties which colors will bond near each other, which face inward or outward. You can ask that students describe how they folded their protein, or ask them to describe any trends they notice (i.e., all of the purple are clustered on the inside…) See Figure 6 for example color coding and folding. |  | ✓ | ✓ |
| After completing the modeling process, show students a video or other computer animation of the steps they modeled, narrating for them as a recap, asking them to describe to a partner, or calling on students to share what each step represents. The aim of this activity is to help ensure that students can connect the analogical, modeled pieces to an approximation of the actual processes look like in a cell (e.g., identifying a ribosome, and recognizing that the small strand passing through it is RNA being read and translated). A great video animation that can be used is found at <https://www.youtube.com/watch?v=D3fOXt4MrOM> or can be simulated online at <http://www.dnai.org/a/index.html>, where students can use the “Putting it together” portion of the “Copying the code” and “reading the code” modules to perform a simulation of translation that closely resembles their own paper models. Either of these animations could potentially serve as a useful and interactive, informal form of assessment as well. | ✓ | ✓ | ✓ |