**Project: Protein Synthesis Storyboard** Name:

Assessed By: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_  
  
**PERFORMANCE-BASED ASSESSMENT:**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Beginning** | **Developing** | **Accomplished** | **Exemplary** |
| **CONTENT**  **(STRUCTURE)** | Many of the components are missing or incorrectly used | The majority of structural components are correctly used, while some components are missing or incorrect | Almost all structural components are correctly used, with some minor errors. | All structural components are correctly used |
| DNA, nucleotide base sequence, enzymes, mRNA, hydrogen bonds, covalent bonds, ribosome, large ribosomal subunit, small ribosomal subunit, codon, start codon (AUG), tRNA, anticodon, tRNA-amino acyl complex, amino acid, methionine, peptide bond, different sites on ribosome, stop codon, release factor (protein) | | | | |
| **CONTENT (PROCESS)** | Many processes are incorrect or not included. | The majority of processes are correct and accurate, with some processes missing or incorrect | Almost all processes are correct and accurate, with some minor errors. | Entire process is correct and accurate |
| Transcription: unzipping, complimentary base pairing, hydrogen bonding between bases, formation of mRNA backbone, covalent bonding, location (nucleus) Translation – Initiation: complimentary base pairing (with hydrogen bonding), assembly of ribosomal subunits, location (cytoplasm/rough ER) Translation – Elongation: complimentary base pairing (with hydrogen bonding), movement of ribosome along mRNA, passing of growing polypeptide chain from outgoing tRNA to incoming tRNA (with peptide bonds), repetition of process, location (cytoplasm/rough ER) Translation – Termination: complimentary base pairing (with hydrogen bonding), release of polypeptide chain, separation of ribosomal subunits, location (cytoplasm/rough ER) | | | | |
| **CLARITY** | Although an attempt is made, it is difficult to understand most of the project.  - Messy - Disorganized | Most sections are well organized with visuals and words, but some sections are not. | Entire project is well organized with clear visuals and clear words. | Entire project is effectively organized.  *-visuals are clear with an effective legend - words are concise and to the point*  *-Project could be used as a teaching tool for all ages.* |
| **APPLICATION** | Visuals are not original and/or have no colour. | Somewhat effective use of colour  no attempt is made to include a theme/analogy | Original, effective use of colour  Theme/analogy attempted, but is not applicable/effective | Original and highly effective use of colour  Theme/analogy effectively complements protein synthesis |

**Project: Protein Synthesis Storyboard** Name:

Assessed By: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_  
  
**PERFORMANCE-BASED ASSESSMENT:**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Beginning** | **Developing** | **Accomplished** | **Exemplary** |
| **CONTENT**  **(STRUCTURE)** | Many of the components are missing or incorrectly used | The majority of structural components are correctly used, while some components are missing or incorrect | Almost all structural components are correctly used, with some minor errors. | All structural components are correctly used |
| DNA, nucleotide base sequence, enzymes, mRNA, hydrogen bonds, covalent bonds, ribosome, large ribosomal subunit, small ribosomal subunit, codon, start codon (AUG), tRNA, anticodon, tRNA-amino acyl complex, amino acid, methionine, peptide bond, different sites on ribosome, stop codon, release factor (protein) | | | | |
| **CONTENT (PROCESS)** | Many processes are incorrect or not included. | The majority of processes are correct and accurate, with some processes missing or incorrect | Almost all processes are correct and accurate, with some minor errors. | Entire process is correct and accurate |
| Transcription: unzipping, complimentary base pairing, hydrogen bonding between bases, formation of mRNA backbone, covalent bonding, location (nucleus) Translation – Initiation: complimentary base pairing (with hydrogen bonding), assembly of ribosomal subunits, location (cytoplasm/rough ER) Translation – Elongation: complimentary base pairing (with hydrogen bonding), movement of ribosome along mRNA, passing of growing polypeptide chain from outgoing tRNA to incoming tRNA (with peptide bonds), repetition of process, location (cytoplasm/rough ER) Translation – Termination: complimentary base pairing (with hydrogen bonding), release of polypeptide chain, separation of ribosomal subunits, location (cytoplasm/rough ER) | | | | |
| **CLARITY** | Although an attempt is made, it is difficult to understand most of the project.  - Messy - Disorganized | Most sections are well organized with visuals and words, but some sections are not. | Entire project is well organized with clear visuals and clear words. | Entire project is effectively organized.  *-visuals are clear with an effective legend - words are concise and to the point*  *-Project could be used as a teaching tool for all ages.* |
| **APPLICATION** | Visuals are not original and/or have no colour. | Somewhat effective use of colour  no attempt is made to include a theme/analogy | Original, effective use of colour  Theme/analogy attempted, but is not applicable/effective | Original and highly effective use of colour  Theme/analogy effectively complements protein synthesis |