**DNA MODEL CRITERIA**

**Requirements: Points:**

**Anti-parallel backbone 5 \_\_\_\_\_\_\_\_\_\_**

**Deoxyribose & phosphates alternate 4 \_\_\_\_\_\_\_\_\_\_\_**

**Bases bonded to sugar 4 \_\_\_\_\_\_\_\_\_\_\_**

**Bases paired appropriately 5 \_\_\_\_\_\_\_\_\_\_\_**

**Appropriate number of H bonds 5 \_\_\_\_\_\_\_\_\_\_\_**

**Helical shape 5 \_\_\_\_\_\_\_\_\_\_\_**

**Key/all elements identified 5 \_\_\_\_\_\_\_\_\_\_\_**

**Varied sequence (all 4 bases on each side) 3 \_\_\_\_\_\_\_\_\_\_\_**

**10 bps in length (20 nucleotides total) 10 \_\_\_\_\_\_\_\_\_\_\_**

**Neatness/creativity 3 \_\_\_\_\_\_\_\_\_\_\_**

**Name/Title 1 \_\_\_\_\_\_\_\_\_\_\_**

**TOTAL \_\_\_\_\_\_\_\_\_\_\_\_\_/50**

**DNA MODEL CRITERIA**

**Requirements: Points:**

**Anti-parallel backbone 5 \_\_\_\_\_\_\_\_\_\_**

**Deoxyribose & phosphates alternate 4 \_\_\_\_\_\_\_\_\_\_\_**

**Bases bonded to sugar 4 \_\_\_\_\_\_\_\_\_\_\_**

**Bases paired appropriately 5 \_\_\_\_\_\_\_\_\_\_\_**

**Appropriate number of H bonds 5 \_\_\_\_\_\_\_\_\_\_\_**

**Helical shape 5 \_\_\_\_\_\_\_\_\_\_\_**

**Key/all elements identified 5 \_\_\_\_\_\_\_\_\_\_\_**

**Varied sequence (all 4 bases on each side) 3 \_\_\_\_\_\_\_\_\_\_\_**

**10 bps in length (20 nucleotides total) 10 \_\_\_\_\_\_\_\_\_\_\_**

**Neatness/creativity 3 \_\_\_\_\_\_\_\_\_\_\_**

**Name/Title 1 \_\_\_\_\_\_\_\_\_\_\_**

**TOTAL \_\_\_\_\_\_\_\_\_\_\_\_\_/50**

(Brown’s Biology classes) Each criteria up to 4 points 11/30/2015

0 pts not included 2 pts both incomplete & inaccurate

3 pts EITHER incomplete OR inaccurate 4 pts fully complete & fully accurate

Name of evaluator \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Name of person who constructed the model \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Double stranded anti-parallel backbone \_\_\_\_\_\_\_\_

Deoxyribose & phosphates alternate in the backbone \_\_\_\_\_\_\_\_

Nitrogenous bases bonded to deoxyribose \_\_\_\_\_\_\_\_

Accurate complementary base pairing (A to T, C to G) \_\_\_\_\_\_\_\_

Accurate number Hydrogen bonds per base pair \_\_\_\_\_\_\_\_

Helical Shape \_\_\_\_\_\_\_\_

Implies greater strength of covalent bonds in backbone than

Hydrogen Bonds between the nitrogenous bases \_\_\_\_\_\_\_\_

The Key clearly identifies every part of the model \_\_\_\_\_\_\_\_

Varied sequence with all 4 nitrogen bases (A,T,C,G) on each strand \_\_\_\_\_\_\_\_

20 or more deoxyribonucleotide monomers in the double stranded model \_\_\_\_\_\_\_\_

Ease of interpretations (are components & their arrangements clearly

enough identified to prevent guessing about some criteria) \_\_\_\_\_\_\_\_

(2 of the 3 for full credit) Neat, creative, sturdily construction \_\_\_\_\_\_\_\_

Name, title, and key are securely attached to the model \_\_\_\_\_\_\_\_

Name of evaluator \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Name of person who constructed the model \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Double stranded anti-parallel backbone \_\_\_\_\_\_\_\_

Deoxyribose & phosphates alternate in the backbone \_\_\_\_\_\_\_\_

Nitrogenous bases bonded to deoxyribose \_\_\_\_\_\_\_\_

Accurate complementary base pairing (A to T, C to G) \_\_\_\_\_\_\_\_

Accurate number Hydrogen bonds per base pair \_\_\_\_\_\_\_\_

Helical Shape \_\_\_\_\_\_\_\_

Implies greater strength of covalent bonds in backbone than

Hydrogen Bonds between the nitrogenous bases \_\_\_\_\_\_\_\_

The Key clearly identifies every part of the model \_\_\_\_\_\_\_\_

Varied sequence with all 4 nitrogen bases (A,T,C,G) on each strand \_\_\_\_\_\_\_\_

20 or more deoxyribonucleotide monomers in the double stranded model \_\_\_\_\_\_\_\_

Ease of interpretations (are components & their arrangements clearly

enough identified to prevent guessing about some criteria) \_\_\_\_\_\_\_\_

(2 of the 3 for full credit) Neat, creative, sturdily construction \_\_\_\_\_\_\_\_

Name, title, and key are securely attached to the model \_\_\_\_\_\_\_\_

(Brown’s Biology classes) Each criteria up to 4 points 11/30/2015

0 pts not included 2 pts both incomplete & inaccurate

3 pts EITHER incomplete OR inaccurate 4 pts fully complete & fully accurate

Name of evaluator \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Name of person who constructed the model \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Double stranded anti-parallel backbone \_\_\_\_\_\_\_\_

Deoxyribose & phosphates alternate in the backbone \_\_\_\_\_\_\_\_

Nitrogenous bases bonded to deoxyribose \_\_\_\_\_\_\_\_

Accurate complementary base pairing (A to T, C to G) \_\_\_\_\_\_\_\_

Accurate number Hydrogen bonds per base pair \_\_\_\_\_\_\_\_

Helical Shape \_\_\_\_\_\_\_\_

Implies greater strength of covalent bonds in backbone than

Hydrogen Bonds between the nitrogenous bases \_\_\_\_\_\_\_\_

The Key clearly identifies every part of the model \_\_\_\_\_\_\_\_

Varied sequence with all 4 nitrogen bases (A,T,C,G) on each strand \_\_\_\_\_\_\_\_

20 or more deoxyribonucleotide monomers in the double stranded model \_\_\_\_\_\_\_\_

Ease of interpretations (are components & their arrangements clearly

enough identified to prevent guessing about some criteria) \_\_\_\_\_\_\_\_

(2 of the 3 for full credit) Neat, creative, sturdily construction \_\_\_\_\_\_\_\_

Name, title, and key are securely attached to the model \_\_\_\_\_\_\_\_

Name of evaluator \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Name of person who constructed the model \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Double stranded anti-parallel backbone \_\_\_\_\_\_\_\_

Deoxyribose & phosphates alternate in the backbone \_\_\_\_\_\_\_\_

Nitrogenous bases bonded to deoxyribose \_\_\_\_\_\_\_\_

Accurate complementary base pairing (A to T, C to G) \_\_\_\_\_\_\_\_

Accurate number Hydrogen bonds per base pair \_\_\_\_\_\_\_\_

Helical Shape \_\_\_\_\_\_\_\_

Implies greater strength of covalent bonds in backbone than

Hydrogen Bonds between the nitrogenous bases \_\_\_\_\_\_\_\_

The Key clearly identifies every part of the model \_\_\_\_\_\_\_\_

Varied sequence with all 4 nitrogen bases (A,T,C,G) on each strand \_\_\_\_\_\_\_\_

20 or more deoxyribonucleotide monomers in the double stranded model \_\_\_\_\_\_\_\_

Ease of interpretations (are components & their arrangements clearly

enough identified to prevent guessing about some criteria) \_\_\_\_\_\_\_\_

(2 of the 3 for full credit) Neat, creative, sturdily construction \_\_\_\_\_\_\_\_

Name, title, and key are securely attached to the model \_\_\_\_\_\_\_\_